A Defence of Biodiversity as the Goal of Conservation Biology

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Dedication

For my son Caelin,
Who was born when this project began
But was arguing with me by the time it was completed.
May you have as much grass to run on as I did.
Abstract

Biodiversity has been the goal of conservation for thirty years but recent work by biodiversity eliminativists has raised serious challenges to its suitability as the primary goal of conservation. This project groups those challenges into three major arguments: the conceptual case for biodiversity’s elimination, the empirical case for biodiversity’s elimination, and the value compass case for biodiversity’s elimination. Aside from discussing biodiversity as a property, this thesis will also discuss biodiversity as a concept (as in biodiversity), and refer to the word biodiversity (as in ‘biodiversity’). In the conceptual case for biodiversity’s elimination, eliminativists argue that biodiversity misdirects the efforts of conservation and is not a scientifically coherent concept. In the empirical case, eliminativists argue that biodiversity is not operationalisable. In the value compass case, eliminativists argue that biodiversity does not reliably track biological value. I will argue that all three cases for biodiversity’s elimination are unsuccessful. Biodiversity is a complex concept with multiple dimensions of biological diversities but understanding it as a homeostatic property cluster avoids the conceptual case for its elimination. The empirical case is unsuccessful because the surrogacy strategy for measuring biodiversity can be defended against its limitations and the expanding multiplicity of biodiversity measures is overblown. The value compass case is correct about the inability of biodiversity to track pluralistic biological value, but for the wrong reasons. Biodiversity is not a reliable compass for pluralistic biological value because there are no reliable compasses for pluralistic biological value. However, biological value is distinct from conservation normativity—understood as what conservationists ought to do—and biodiversity is an excellent guide to conservation normativity. This makes biodiversity an excellent conceptual and empirical fit for its role as a guide to conservation normativity.
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Introduction

I Opening Remarks

Biodiversity is an important goal of conservation.\(^1\) It has been an environmental priority for over three decades but recently several authors have argued that it should be eliminated as the goal of conservation. Carlos Santana, Paul Angermeier, and James Karr build on the critical discussion of biodiversity to argue that it is the wrong goal for conservation. Conservation goals should be scientifically rigorous. As a concept ‘biodiversity’ should have a clear meaning and as a property biodiversity should be adequately measurable and able to reliably track the goals of conservation. Biodiversity eliminativists argue that biodiversity does not meet these requirements.

Recent work in the philosophy of biology has attempted to clarify and defend the use of the biodiversity concept in conservation science. I argue against these views, and give reasons to think that the biodiversity concept is a poor fit for the role we want it to play in conservation biology on both empirical and conceptual grounds. (Santana 2014, 761)

Our review of current conceptions of integrity and diversity indicates that resource policy would be most effective if based on the more comprehensive goal of protecting biological integrity. Specific policy shifts related to that goal include a reliance on preventive rather than reactive management and a focus on landscapes rather than populations. We draw heavily from our experience with aquatic systems, but our conclusions apply equally to terrestrial systems. (Angermeier and Karr 1994, 690)

Criticisms is essential to the empirical reputation of science. The evidence we collect gives weight to our theories, but criticism decides if a theory should be entertained or rejected. Rejection is rarely immediate because most theories can be adapted in the face of small criticisms. One of the reasons for the success of science is that it treats all its theories as corrigible in the light of future experience. When there is a counterexample to an existing theory critical debate decides if the theory should adapt to the new evidence or be eliminated in favour of a new theory. Science has the empirical reputation that it does because it respects and invites criticism. Theories which survive that criticism are made stronger.

This project will discuss biodiversity as a concept, a word, and a property. In this thesis italics will indicate a concept, single quotes will mention a word and standard type face will indicate the property. So, Carlos Santana wants to eliminate biodiversity from its role in conservation because he argues that ‘biodiversity’ has no clear meaning and he doubts that biodiversity exists. Biodiversity eliminativists have collectively presented serious criticisms of biodiversity as a goal for conservation. The critical debate will decide

\(^1\) Throughout this thesis I will use ‘goal of conservation’ as shorthand for the complex relation between conservation and its possible targets. Biodiversity is the goal of conservation in the sense that conservationists wish to preserve as much biodiversity as possible. However, it is also the goal of conservation in the senses that: it is the current theoretical focus of conservation efforts, that it is an empirical measure of the success of conservation, and that it is a means to the end of maximising biological value. It is these roles in conservation, for which I defend biodiversity.
if biodiversity should be adapted to its counterexamples or eliminated in favour of a different goal for conservation.

II Eliminativism about Biodiversity

Biodiversity eliminativism is a criticism of the continued adaptations of biodiversity to its counterexamples. ‘Biodiversity’ is a short hand for biological diversity and was coined as a term for the accelerating rate of species extinction during the modern period (Takacs 1996, 37). But it is better for a group of species to be thriving than critically endangered so biodiversity should also take abundance into account. An additional species of moth adds fewer novel features to a group of moths than an ancient species of lizard, so biodiversity should also consider the evolutionary relationships species bear to one another. These adaptations still overlook the important functional roles of species and interactions between them so biodiversity should also include functional diversity. As a concept biodiversity has adapted many times to include important biological elements but that process of continued adaptation has had implications for its conceptualisation, operationalisability, and its relationship with biological value.

Where biodiversity’s defenders believe these adaptations to be important improvements to the goal of conservation, biodiversity eliminativists believe that the concept has stretched to breaking point. As a concept they argue that ‘biodiversity’ misleads conservation efforts and has no clear meaning. As an empirical target for conservation Santana argues that biodiversity is not operationalisable. As a compass to biological value they argue that it prioritises the wrong elements for conservation and cannot explain why conservation preserves the elements which it does. Taken collectively, their criticisms of biodiversity raise serious concerns about the suitability of biodiversity as the goal of conservation. They argue that it ought to be eliminated as the goal of conservation.

III Why a Defence of Biodiversity Is Important

A defence of biodiversity is required for three reasons: to answer the criticisms of biodiversity eliminativists, to establish an argument for the success of biodiversity as a goal of conservation, and to maintain the effectiveness of environmental policy. Firstly, a defence of biodiversity is required in response to the arguments for its elimination. Biodiversity eliminativists have raised serious criticisms. They deserve a serious response. Secondly, there are currently few standard defences for biodiversity in the literature. With the exception of the recent publication by Burch-Brown and Archer (2017), the suitability of biodiversity as the goal conservation is often presumed rather than justified. There is interesting work on what biodiversity is, on the ability of surrogates to track biodiversity, and the relationship between biodiversity and biological value, but there are few standard defences of biodiversity.

Thirdly, eliminating biodiversity will have a serious impact on environmental policy world-wide. Aside from the many legal changes which would be required, the target of conservation has gone through a number of changes. Once it was the balance of nature,
then it was wilderness, then it was species number, and now it is biodiversity (Takacs 1996, 11). Because conservation asks people to sacrifice resources, it risks becoming unpopular with the people whose help it needs. Prematurely eliminating biodiversity will exacerbate that risk because biodiversity has only been our goal for three decades. Eliminating biodiversity calls into question the sacrifices which people have made to conserve biodiversity. It would also happen at a time when conservation needs support the most. The solutions to climate change, pollution, and the depletion of our natural resources are tenable but they are utterly reliant on the cooperation of human beings. These are three good reasons why academic literature will benefit from a defence of and the conservation of biodiversity against biodiversity eliminativism.

IV What I Will Argue in This Project
The aim of this project is to answer the criticisms of biodiversity eliminativists whilst providing a standard defence for biodiversity as the goal of conservation which is available to both biodiversity realists and instrumentalists. This project will discuss biodiversity as a concept, a word, and a property. Italics indicate a concept such as biodiversity. Single quotes mention a word such as ‘biodiversity’. Standard typeface indicates a property such as biodiversity. This thesis will answer the criticisms of biodiversity eliminativists by grouping them into three categories; the conceptual case for elimination, the empirical case for elimination, and the ‘value compass’ case for elimination.

In chapter one I will discuss conceptual issues with biodiversity and outline the case for its elimination. I outline the different meanings of ‘biodiversity’ before using the diversity of meanings to motivate the conceptual case for eliminativism. I outline Angermeier and Karr’s argument that a lack of meaning hampers both conservation efforts and Santana’s meaning-dilemma argument. I justify both horns of Santana’s meaning-dilemma that specific meanings of ‘biodiversity’ have counterexamples but general meanings are uninformative. In chapter two I will respond to the conceptual case for biodiversity’s elimination. I discuss the recent response to Santana by Burch-Brown and Archer before developing an overlooked possibility that biodiversity can be understood as a homeostatic property cluster. I outline a conception of biodiversity as a homeostatic property cluster and argue that its ability to address the species problem sets an important precedent for the biodiversity problem. In chapter three I will argue that the conceptual case for elimination is unsuccessful if biodiversity is a homeostatic property cluster. An HPC conception of biodiversity reduces misdirection in conservation efforts and avoids Santana’s meaning-dilemma because it is both a general and informative meaning for ‘biodiversity’. I also discuss other reasons to retain biodiversity even if it is uninformative.

In chapter four I will outline the surrogacy strategy for measuring biodiversity and the empirical case for its elimination. I group Santana’s empirical reasons for eliminating biodiversity into the empirical poor fit argument and argue that it has been unintentionally motivated by biodiversity conservationists who emphasise the growing multiplicity of biodiversity measures. I then categorise Santana’s objections as limitations generated by either incommensurability or the use of multiple surrogates. I reply to both limitations before I argue that the empirical case is misrepresenting the state of biodiversity measures.
I argue that the apparent limitations of the surrogacy strategy are advantages and that familiarity with the methodological detail of its surrogates makes it clearer that biodiversity is operationalisable.

In chapter five I will continue my empirical defence of biodiversity by outlining the methodological detail of three measurement surrogates: species richness, species diversity, and phylogenetic diversity. I use the methodological detail to argue that all three surrogates are operationalisable and that the apparent expanding multiplicity of biodiversity measures is overblown. In chapter six I will conclude my empirical defence of biodiversity by outlining the methodological detail of two measurement surrogates: theoretical morphology and functional diversity. I argue that the methodological detail indicates that neither surrogate is operationalisable. I use the arguments from chapter four and the methodological detail from chapters five and six to argue that the empirical case for biodiversity’s elimination is unsuccessful because biodiversity is operationalisable.

In chapter seven I will outline the value compass case for biodiversity’s elimination. The value compass case treats the goal of conservation as a compass which ought to point towards biological value. Santana, Angermeier, and Karr argue that as a compass for conservation, biodiversity is not a reliable guide to biological value. The focus of chapter seven is identifying the type of value which eliminativists appeal to in their examples. I consider whether the value compass case for elimination is appealing to instrumental value, intrinsic value, or a different kind of non-anthropocentric value. I argue that the value compass case actually appeals to pluralistic biological value and that eliminativists’ examples equivocate on the meaning of ‘value’. In chapter eight I will adapt the value compass case to use pluralistic biological value as the goal which biodiversity is intended to track. I then argue that it is unsuccessful for three reasons. There are problems with using pluralistic biological value as the minimum standard for a conservation goal. Furthermore, there are still good reasons to retain biodiversity even if is not a reliable value compass and the value compass case conflates biological value with normativity. Having successfully defended biodiversity against the conceptual, empirical, and value compass case for its elimination, I conclude that it should be retained as the goal of conservation.
1 Conceptual Issues with *Biodiversity* and the Case for Its Elimination

1.1 Introduction

The nature of *biodiversity* is controversial because we need the concept to be operationalisable for conservation but also to encompass all the important elements of the environment that conservationists want to protect. ‘Biodiversity’ itself is a young term with an age of more than 30 years and whilst it was initially coined in response to the rapid extinction rate of species, its meaning grew to encompass multiple other valuable dimensions of the environment. In section 1.4 I will discuss the many specific dimensions of biodiversity such as phylogeny, genetics, functionality, and a holistic view of ecosystems. The combination of specific biological dimensions and generalisations has created a lack of consensus in biology about what biodiversity actually is. That is problematic because the goal of conservation is to preserve biodiversity and it is difficult to preserve something when you cannot identify what it is. The problem is severe enough that some authors have argued we should replace or eliminate *biodiversity*. Angermeier and Karr both argue that the conceptual issues mislead conservation efforts so biological integrity is a more suitable goal (Angermeier 2000, 375; Karr 1993, 298). Santana believes that we should eliminate the concept entirely and presents a sophisticated meaning-dilemma argument (Santana 2017, 86). Specific meanings of ‘biodiversity’ have multiple counterexamples and general meanings are uninformative so we should eliminate the concept from academic discourse.

In this chapter I will discuss conceptual issues with *biodiversity* and outline the case for its elimination. I start with a discussion of the multiple ways in which ‘biodiversity’ is used. The term was coined in 1986 so I begin with its analytic use as shorthand for ‘biological diversity’, in response to the species crisis. Next I present an account of the sociological project of David Takacs who surveyed academics for a one-sentence definition of ‘biodiversity’ (Takacs 1996, 46–50). I group these multiple meanings into general and specific categories before discussing the contesting uses of ‘biodiversity’ in modern academia. I then outline Sarkar’s deflationary meaning of ‘biodiversity’ as the relation used to prioritise conservation efforts. Next I use this evidence of multiple meanings to motivate the argument for eliminating *biodiversity*. I discuss Angermeier and Karr’s concerns that the conceptual confusion misleads conservation goals, and I outline Santana’s meaning-dilemma argument for eliminating *biodiversity*. I motivate his argument by discussing the two horns of his dilemma: specific meanings have multiple counterexamples but general meanings of ‘biodiversity’ are uninformative. I conclude that the eliminativist case is compelling and that my strategy in chapters two and three will be to deny the second horn of the dilemma. In those chapters I will argue that conceptions of biodiversity can be both general and informative.
1.2 The Multiple Uses of ‘Biodiversity’

In this section I will discuss the multiple uses of ‘biodiversity’ in academia to highlight the conceptual debate over its nature. I begin with a brief account of the term’s inception before its rise to popularity. Then I outline the work of David Takacs, whose book *The Idea of Biodiversity: Philosophies of Paradise* provides a comprehensive sociological account of the uses and meanings of ‘Biodiversity’ (Takacs 1996). I use Takacs’ sociological account to draw a distinction between specific and general meanings of ‘biodiversity’. Specific meanings narrowly conceive of biodiversity along a single dimension such as species richness or phylogeny whereas general meanings conceive of biodiversity along multiple dimensions. Next I apply this distinction to modern uses of ‘biodiversity’ discussing Sarkar’s deflationary meaning of ‘biodiversity’. Sarkar’s meaning is distinct in that it reduces biodiversity to the ranking procedure for places and because he uses the conceptual debate to justify his deflationary account. Sarkar is not a biodiversity eliminativist but his strategy is the template for biodiversity eliminativism. Santana argues that the conceptual controversy leads to deflationary accounts which justify eliminating biodiversity all together (Santana 2014, 765).

1.2.1 Meanings in the 80s and 90s

Although the origins of ‘biodiversity’ are a point of contention among some, Takacs and Sarkar credit the term’s creation to Walter G. Rosen, who coined the term as shorthand for ‘biological diversity’ (Takacs 1996, 37; Sarkar and Margules 2002, 131). Rosen noticed that a concern which frequently came up at conferences at the National Academy of Science was the frequency of extinctions and what this meant for biological diversity. Rosen suggested having a forum on “Biodiv . . . Biological Diversity”, and so the national forum on Biodiversity and the term itself were created (Takacs 1996, 36).

‘Biodiversity’ captured many intuitions about the target of conservation efforts. During 1988 ‘biodiversity’ never appeared as a key word in biological abstracts but ‘biological diversity’ appeared once. By 1993 those numbers had substantially increased and ‘biodiversity’ appeared 72 times in biological abstracts compared to 19 times for ‘biological diversity’ (Takacs 1996, 39). Some of this increase may be due to the inflation in the number of publications as total numbers of academics increased but the evidence shows that academia quickly adopted the term. A Google Ngram viewer can track use frequency for individual terms and produce a graph of term use frequency (indicated along the Y axis) over time. This is a comparative Google Ngram for ‘Biological Diversity’ and ‘biodiversity’.
While ‘biological diversity’ appeared in the sixties it did not take off until after the popularity of ‘biodiversity’ surged in the late 1980s following the National Forum of Biodiversity, which was held from 21st to the 24th of September in 1986 (Takacs 1996, 38). By 2000 ‘biodiversity’ has clearly emerged as the preferred term. The popularity of ‘biodiversity’ is most likely due to its flexible meaning. The useful thing about ‘biodiversity’ is that it can refer to both a very specific aspect of biological life such as the number of species in a local ecosystem or it can refer to the entire ecosystem itself (Takacs 1996, 52). This flexibility means that ‘biodiversity’ captures a multiplicity of intuitions about conservation but could also lead one to be sceptical about its meaning.

David Takacs discuss the conceptual development of the meaning of ‘biodiversity’, going into the term’s invention, history, and many uses with some detail. In his research Takacs asked several notable academics for a brief definition of ‘biodiversity’ (Takacs 1996, 46). Below are some of the responses which he received.

The standard definition is species diversity, and then diversity of communities or habitats that the species combine into, and then, on the other side of the scale, the genetic diversity that the species are comprised of. — Peter Brussard

I don’t have a definition of ‘biodiversity’. I’ve tried very hard to stay away from formal definitions. When I deal with it in the journal [conservation biology] . . . it obviously means to some people species diversity; other people expand that to include populations. To other people it means really genetic diversity, heterozygosity, allelic diversity, often within populations. To many people, it means variety of ecosystems or ecosystem types, landscape types. Obviously its all of those things. — David Ehrenfeld

To me, biodiversity is the living resources of the planet. — Paul Ehrlich

Biodiversity is the total number of genetic lineages on earth. I just made that up; if I think about it, chances are I’ll change my definition rapidly. — Thomas Eisner
. . . It is the sum of earth species including all their interactions and variations within their biotic and abiotic environment in both space and time. — Terry Erwin

I think of it as fundamentally a measure of difference. And the most important aspect of the definition for me is that it exists at many different levels of biological organization, even though we tend as mental habit to focus most on species diversity. . . So I guess I would describe it as the dimension of difference at multiple levels of organization. — Donald Falk

Biodiversity is the complete array of organisms, biologically mediated processes, and organically derived structure out there on the globe. — Jerry Franklin

I guess . . . ‘biodiversity’ to me means importance: which areas do we have to concentrate on, or which groups are more important in terms of preserving than others. — Vickie Funk

Well it’s just the diversity of living things on the face of the earth. — Hugh Iltis

The whole package of genes, populations, species, and the cluster of interactions that they manifest. — Daniel Janzen

The variations or the variability or the variety of living organisms . . . which includes intraspecific variation. . . You’re looking at the community level, you’re looking at ecosystem level, at landscape level, and so on. — K.C. Kim

The term is really supposed to mean diversity at all levels of organization. But the way its most often used is basically relating to species diversity. — Thomas Lovejoy

Biodiversity encompasses the number, the variability, and the variety of life on Earth . . . at three levels of biological organization: genetic, species, and ecosystem. — Jane Lubchenco

The total biotic diversity as indicated by the number of species and genetic diversity they encompass. — S. J. Mcnaughton

Well, ‘biodiversity’, to me is shorthand for all the richness of life. — Reed Noss

‘Biodiversity’ is a very comprehensive term which reflects the diversity of living organisms at all levels, from . . . populational—genetic and geographical—diversity to species, to lineages, and higher taxonomic categories, to ecological systems. — Gordon Orians

The term ‘biodiversity’ really focuses on the mix of species or diversity. — David Pimentel

The sum total of plants, animals, fungi, and microorganisms in the world including their genetic diversity and the way in which they fit together into communities and ecosystems. — Peter Raven

What we’re looking at in biodiversity is the history of biology, the history of life in all its forms over the entire time it’s existed on our planet. . . And one of the things I think it should not be seen as . . . is just an accounting of the number of species — G. Carelton Ray

I’d rather not [try to define biodiversity] . . . biodiversity is something that occurs at a community level, at a species level, you know that it’s genetic as well as—whatever. — Walter Rosen
The short way [to define biodiversity] is the best. And it’s life in all of its dimensions and richness and manifestations, not only at the level of individuals and species, but at the level of aggregation, communities, or what have you. — Michael Soule

Biodiversity is the variety of life across all levels of organization from genic diversity within populations, to species, which have to be regarded as the pivotal unit of classification, to ecosystems. — E. O. Wilson

I take a very holistic view of biodiversity. It’s made up of individuals that make up populations that make up species. — David Woodruff (Takacs 1996, 46–50)

These definitions indicate two things. Firstly, while academics differ in their concepts of biodiversity, the responses can be grouped into two distinct categories. Franklin, Soule, Noss, Wilson and Woodruff etc are using ‘biodiversity’ in a very general sense. They take ‘biodiversity’ to mean the variety of life, the richness of life, or the complete array of organisms which make it up. This broadly captures what biodiversity is but seems too general to be operationisable. Contrast this with some of the more specific accounts provided by Brussard, Eisner, Janzen, and Raven. Biodiversity is species diversity, the number of genetic lineages, the package of genes, populations, and species, or the sum total of plants, animals, fungi and microorganisms. These distinct categories indicate that while there is disagreement about the meaning of ‘biodiversity’ there is enough overlap to ensure that the problem of what ‘biodiversity’ means is not intractable. These two categories form the basis of my distinction between general and specific meanings. Specific meanings of biodiversity identify it with a single dimension whereas general meanings identify it with multiple dimensions. However, during this chapter it will benefit the project to bear in mind the response of David Ehrenfeld who doesn’t have a definition of ‘biodiversity’ because “Obviously it’s all of those things.” (Ehrenfeld in Takacs 1996, 46).

Secondly, these responses suggest that some kind of species count is central to the meaning of ‘biodiversity’. A count of species is frequently mentioned as part of biodiversity in this survey of well-known conservationists and biologists.2 These one-sentence definitions indicate two important areas of agreement: biodiversity has something to do with species counting but it is also a mistake to reduce biodiversity down to nothing other than a species count. Thus my distinction groups meanings of ‘biodiversity’ in the following way.

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2 More precisely: Peter Brussard, David Ehrenfeld, Terry Erwin, Donald Falk, Daniel Janzen, Thomas Lovejoy, Jane Lubchenco, S. J. Mcnoughton, Gordon Orians, David Pimentel, Peter Raven, Walter Rosen, Michael Soule, E. O. Wilson, and David Woodruff. G. Carelton Ray is omitted from this list because he insisted that biodiversity should absolutely not be a mere accounting of species.
Some Meanings of ‘Biodiversity’

<table>
<thead>
<tr>
<th>In the General Sense</th>
<th>In the Specific Sense</th>
</tr>
</thead>
<tbody>
<tr>
<td>variation of biological life</td>
<td>number of species</td>
</tr>
<tr>
<td>value of the natural world</td>
<td>population levels</td>
</tr>
<tr>
<td>the local ecosystem</td>
<td>number of unique genes</td>
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<tr>
<td>evolutionary history of biological life</td>
<td>total interactions between organisms</td>
</tr>
<tr>
<td>... et al</td>
<td>... et al</td>
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Table 1.1: Some of the Different Meanings of ‘Biodiversity’

Table 1.1 separates the general meanings of ‘biodiversity’ such as the total variation of biological life from its specific meanings such as the number of unique species or genes in a local ecosystem. There are some meanings which are resistant to categorisation in this framework. Dimensions of biodiversity such as the interactions between organisms and the evolutionary history of biological life seems prima facie like a general concept, but work on phylogenetics and the tree of life suggest that this could also be taken as a specific meaning of ‘biodiversity’ (Faith 1994). This table does not contain all meanings of ‘biodiversity’. There are other accounts of what biodiversity is, such as morphology and phylogenetic diversity (PD) which I will discuss in later chapters. The meanings listed above are simply examples intended to show that the meanings of ‘biodiversity’ broadly sit into two categories.

I say ‘broadly’ because the distinction between general and specific meanings is vague rather than a sharp one. Specific meanings have a tendency to focus on one or two dimensions of biodiversity whereas general meanings incorporate as many dimensions of biological interest as possible. This leaves room for meanings of ‘biodiversity’ which occupy a middle ground in that they capture multiple dimensions of biodiversity but exclude others. The categories of ‘general’ and ‘specific’ meanings of biodiversity are intended to provide a framework for sorting and analysing the many different ways that ‘biodiversity’ may be understood. In the next section I will discuss meanings of ‘biodiversity’ which appear to occupy a middle ground between general and specific. I will argue that whilst there are meanings of ‘biodiversity’ which occupy vague ground on this distinction, there are good reasons to think that they tend to lean towards general or specific meanings. I return to this issue in section 1.3.2 in which I motivate Santana’s meaning-dilemma argument that relies on this distinction.

A final point of interest with this framework is that while the general senses seem to do a better job of capturing all the aspects of biodiversity, the specific meanings are much easier to quantify and measure. This is the first major indication of separation between what biodiversity is and what is measured. This problem will be discussed in the chapters on measurement. In the next section I will apply this distinction to modern uses of ‘biodiversity’. Takacs’ work was completed over 20 years ago which amounts to nearly half the age of ‘biodiversity’ itself, given that it was coined in 1986 (Takacs 1996, 36). In
the next subsection I will extend Takaes’ method to examples from academic papers and discuss whether my distinction can accommodate the more recent uses of ‘biodiversity’.

1.2.2 General and Specific Meanings in Academia
In this section I will apply my distinction between general and specific meanings of ‘biodiversity’ to modern uses in academia. I will present textual evidence from a paper and then discuss its implications for my distinction. I begin with two biodiversity eliminativists Angermeier and Karr who have jointly agreed on the following conception of biodiversity.

One of the first formal definitions of biological diversity termed it “the variety and variability among living organisms and the ecological complexes in which they occur” (OTA 1987, p. 3). In addition, because "items are organized at many [biological] levels," biodiversity “encompasses different ecosystems, species, genes, and their relative abundance”. (Angermeier and Karr 1994, 690–91)

This quote from Angermeier and Karr is a good example of how authors attempt to incorporate both general and specific meanings of ‘biodiversity’ into their discussions. The total variability and interactions of living organisms is a general conception but the authors also mention more specific variation at lower structural levels in an ecosystem. The authors state that biodiversity encompasses species and genes etc because items are organized at many biological levels. Following this line of thought, a general meaning of ‘biodiversity’ encompasses the more specific ones. The planet’s natural resources include species diversity.

‘Biodiversity’ is often defined as “the variety of all forms of life, from genes to species, through to the broad scale of ecosystems” (Faith 2008). In this quote Faith outlines biodiversity as the “variety of all forms of life”. This particular quote is from the introductory section of the Stanford Encyclopaedia of Philosophy’s article on biodiversity. Hence, it is a thoroughly general conception of biodiversity which means the variety of all forms of life. Faith’s personal view of biodiversity is more specific.

One link is apparent from recent work on phylogenetic diversity that incorporates probabilistic estimates of vulnerability into PD [Phylogenetic Diversity] calculations (Witting & Loeschke 1995). Phylogenetic and vulnerability criteria then do not conflict but together determine overall "expected" feature diversity (Weitzman 1992; Faith & Walker 1995a). (Faith 1996, 1286)

In this paper, Faith approximates biodiversity by performing a phylogenetically informed species count. It is a specific conception of biodiversity because it narrowly conceives of it along a single dimension: phylogenetic diversity. Contrast this with the general conception put forward by Maclaurin and Sterelny.

We have argued for a multidimensional view of biodiversity, though without (of course!) identifying all the dimensions, or specifying their relations one to another. We have done so mostly by tracking the fate of species richness as a core concept of biodiversity (Maclaurin and Sterelny 2008, 174)
Maclaurin and Sterelny hesitate to give a precise account of biodiversity. Instead they identify a strong core of species richness in biodiversity but acknowledge that such a core is not enough in and of itself because biodiversity also requires dimensions of disparity, a phylogenetic bias, and consideration of functions and ecosystems (Maclaurin and Sterelny 2008, 174).

This example is important because the authors are appealing to both general and specific conceptions of biodiversity. Whilst the authors argue for a multidimensional view of biodiversity they also argue that it has a core concept of species richness. Authors find a middle ground between general and specific meanings of ‘biodiversity’ by either identifying the general meaning with a specific dimension or by arguing that a specific dimension approximates more general features of biodiversity. The strategy of identifying a main dimension of biodiversity and employing a specific dimension to represent values from other dimensions is a reoccurring theme in the literature. Maclaurin and Sterelny understand biodiversity as species richness supplemented with phylogenetic diversity whilst others such as Grenyer use a single dimension as a proxy for biodiversity.

Phylogenetic diversity (PD) is a biodiversity index that measures the length of evolutionary pathways that connect a given set of taxa. PD therefore identifies sets of taxa that maximize the accumulation of ‘feature diversity’. (Grenyer et al. 2007, 757)

In this multi-authored paper the writers explain their phylogenetically informed species richness account of biodiversity. Broadly construed, phylogenetics is the practice of analysing biological organisms in terms of their evolutionary history (Maclaurin and Sterelny 2008, 139). By aiming to maximise phylogenetic diversity we aim to preserve as much of the tree of life as possible. In this example the authors use phylogenetic diversity as the main dimension of biodiversity to also represent other dimensions such as feature diversity.

In the present paper we describe how to estimate the expected loss of biodiversity. This is done by combining a phylogenetic evaluation with the degree of vulnerability to a species (its probability to become extinct). (Witting and Loeschcke 1995, 205)

In this quote it first appears that Loeschcke and Witting are another example of authors who mean some notion of phylogenetic diversity when they use ‘biodiversity’, but a closer reading of their work indicates a more specific understanding.

Hence, the probability of losing the unique information that is common to two species is the product of the extinction probabilities of the two species (assuming independent extinction events). Figure 1(b) shows how to calculate the number of unique genes that is expected to be lost from the species shown in Fig. 1 (a). (Witting and Loeschcke 1995, 205 emphasis added)

The authors are arguing that biodiversity conservation can be optimised by minimising the unique genetic information which is lost, so they understand biodiversity specifically as genetic diversity. It is also another example of authors using a single dimension of biodiversity to represent other dimensions of biodiversity such as evolutionary history.
These authors are also approximating a general conception of biodiversity with a specific one.

Applying the distinction between general and specific meanings of ‘biodiversity’ to modern uses shows that there is still considerable debate over the meaning of the term. In the Stanford encyclopaedia of philosophy (hereafter, S.E.P.) Faith (2008) covers a number of different conceptions. Maclaurin and Sterelny endorse a general conception of biodiversity, whereas authors such as Loeschcke and Witting present biodiversity in a specific sense. They use a formula which calculates biodiversity loss in terms of the probability of losing unique genetic material to extinction. This is a serious conceptual issue because it suggests that while there are many different ways to understand ‘biodiversity’ there is still little consensus about what it is. Biodiversity requires a handful of operationalisable dimensions for the purposes of conservation but we also expect the term to accommodate our many intuitions about biological value. My distinction between general and specific meanings highlights this tension. Those with a general account such as Maclaurin and Sterelny attach it to a smaller number of manageable dimensions (Maclaurin and Sterelny 2008, 174). Those with a specific account such as advocates for phylogenetic diversity argue that it can represent the many general features of biological value (Faith 2002, 249). It is this lack of conceptual consensus which motivates Sarkar to reject biodiversity as a number of biological dimensions and deflate the concept to a ranking procedure for prioritising conservation efforts (Sarkar and Margules 2002, 132).

1.2.3 Sarkar’s Deflationary Meaning as a Proto-form of Eliminativism

In Biodiversity and Environmental Philosophy Sarkar puts forward a deflationary meaning of ‘biodiversity’ which understands the term as a conservation tool relative to whatever the target of conservation happens to be.

Instead of adopting any of the possibilities emerging from the hierarchies mentioned earlier, the position taken here will be that ‘biodiversity’ should be (implicitly) operationally defined as what is being optimized by the place prioritization procedures that prioritize all places on the basis of their biodiversity content using true surrogates. Thus biodiversity is the relation used to prioritize places.” (Sarkar 2005, 182)

In his use of ‘relation used to prioritise places’ Sarkar is employing the conservation strategy itself as the target of conservation. This position is reinforced by his statements in other publications. “Put bluntly, the position that this paper will argue for is that biodiversity is to be (implicitly) defined as what is being conserved by the practice of conservation biology.” (Sarkar and Margules 2002, 132). His justification for this deflationary position is later adopted by Santana to motivate eliminativism. Sarkar considers the typical specific meanings of ‘biodiversity’ and rejects them for failing to capture important examples of biodiversity.

The standard move at this stage is to suggest that three entities capture what is important about biodiversity: genes (alleles), species, and ecosystems. . . Nevertheless, even this catholic proposal falls afoul of the diversity of biological phenomena and does so in a rather spectacular manner. (Sarkar 2005, 180)
Sarkar then offers several compelling examples of biological phenomena which are not preserved by protecting, genes, species, or ecosystems. The monarch butterfly, *Danaus plexippus*, has a multi-generational migration pattern. These butterflies populate high altitude fir forests in the millions. Beginning in late August they migrate to Mexico and begin a very long migration towards Canada. Since the distance is great and the life span of a monarch is only 8 months, it takes several generations (and suitable ecosystems along the way) to reach their goal. Then they begin to migrate back towards Mexico (Sarkar 2005, 180–81). He also points out that a particular species of bamboo, *Thrysostachys oliveri*, manages to flower simultaneously despite the seeds being sent to locations roughly 1,500 km apart. Sarkar goes on to point out that “This is the phenomenon that would disappear if these habitats were to disappear, even if the species persisted somewhere else (for instance, as isolated stands in botanical gardens). Protecting the holy trinity of genes, species, and ecosystems will typically not save such phenomena.” (Sarkar 2005, 182).

He also rejects general meanings of ‘biodiversity’ on the grounds that they are no more informative than the expression ‘all of biology’.

Conserving biodiversity, and construing the term intuitively to refer to all biological diversity that there is, at every level of both hierarchies, amounts to saying that ‘biodiversity’ refers to all biological entities. ‘Biodiversity’ in fact becomes all of biology (Sarkar 2005, 180) . . . the position taken here will be that biodiversity should be (implicitly) operationally defined as what is being optimized by the place prioritization procedures that prioritize all places on the basis of their biodiversity content using true surrogates. Thus biodiversity is the relation used to prioritize places (Sarkar 2005, 182)

Once Sarkar has rejected both specific and general conceptions of biodiversity he then advances his deflationary understanding of the term. ‘Biodiversity’ is just a name for the target of conservation: it may be employed to outrank a less important target of conservation but there is no deeper meaning to it. Conservationists who are attempting to preserve biodiversity are just attempting to preserve the target of conservation.

One problem with Sarkar’s deflationary position is that it requires denying that biodiversity is an agent independent property of the natural world. Biodiversity is a complex property but it is also widely viewed as a resource which is rapidly diminishing (Faith 2008, section 1). If Sarkar’s meaning of ‘biodiversity’ is correct then all these views of biodiversity are simply false. Since there is no biodiversity resource it cannot be diminishing and large chunks of conservation, biology, and ecology are mistakenly arguing for funds to protect something that doesn’t exist. Under Sarkar’s deflationary interpretation, to say that ‘biodiversity is a diminishing resource which requires protection’ is simply to express that ‘the targets of conservation are a diminishing resource which require protection’. This is a factual claim but it is also a poor justification for why this diminishing resource should evoke any sort of concern beyond human preference for the preservation of that resource.

A second caveat is that Sarkar’s examples needn’t be taken as proof of the inability of biodiversity to approximate biological value. They could also just identify a specific dimension of biodiversity, such as functionality, that is poorly approximated by the
dimensions of genes, species, and ecosystems. Indeed the most recent version of the S.E.P. article on biodiversity stresses the role of function and interactions as an important part of biodiversity (Faith 2008, section 3.1). The important lesson is that counterexamples can demonstrate the complexity of a property as much as they can deflate it. Sarkar offers strong counterexamples to specific meanings of ‘biodiversity’ but he focuses on three instances: genes, species, and ecosystems (Sarkar 2005, 180). So his counterexamples do point out an important but neglected dimension of biodiversity. However, counterexamples have multiple implications. I argue that they show that organism functionality is an important dimension of biodiversity. Sarkar argues that they justify us understanding ‘biodiversity’ in a deflationary sense and, Santana argues that they justify eliminating the concept altogether.

In brief, Sarkar is close to acknowledging that “biodiversity” means nothing at all, but if biodiversity is to be a useful concept, his definition needs more substance. On the other hand, if biodiversity, as I suggest, is not a useful concept, we should eliminate rather than deflate it. (Santana 2014, 765)

1.3 The Conceptual Case for Eliminating Biodiversity

In this section I will discuss the conceptual case for eliminating biodiversity. The case for elimination is motivated by the conceptual issues of biodiversity. The term has multiple uses and there is little consensus about the meaning of ‘biodiversity’. Several authors aim for a middle ground between general and specific meanings of ‘biodiversity’ by either identifying the general meaning with a specific dimension or by arguing that a specific dimension approximates more general features of biodiversity. Sarkar believes that these problems are sufficient to deflate biodiversity to a place-prioritisation procedure. But Santana argues that we should go further and eliminate the concept entirely. Biodiversity eliminativists such as Santana use a variety of arguments. Angermeier and Karr agree that the lack of consensus about the meaning of ‘biodiversity’ can mislead the goals of conservation by causing undue focus on a specific dimensions such as species richness (Angermeier and Karr 1994, 692). Santana presents a different argument. He builds on the work of Sarkar to argue that specific conceptions of biodiversity miss valuable biological elements and general conceptions are uninformative (Santana 2017, 87). I have constructed his conceptual argument for the elimination of biodiversity into a meaning-dilemma which argues that both specific and general meanings of ‘biodiversity’ are a poor conceptual fit for the role they must play in conservation biology.

1.3.1 The Lack of Consensus about Meaning Hampers Conservation Efforts

Angermeier and Karr’s main argument for the elimination of biodiversity focuses on how the concept misses valuable elements of the environment. So their work is more applicable to the chapters seven and eight on value than those on measurement and concepts. However, they do raise concerns that the conceptual issues affecting biodiversity mislead conservation efforts by equivocating the target of conservation and overlooking the importance of overall ecosystem integrity.
Current conceptions of biodiversity fall short of management needs, in part, because they fail to
distinguish between native (naturally evolved) and artificial (human generated) biotic diversity.
(Angermeier 1994, 600)

Conservation accommodates many world views (Callicott et al. 1999), but consensus on the
supremacy of natural elements is critical to precluding certain activities (e.g., introducing species to
enhance diversity) from being perceived as conservation. (Angermeier 2000, 377)

Further, because attributes of biological systems (e.g., species richness, relative abundances of
species, production, and trophic dynamics) vary geographically, measures of health or integrity of
streams must evaluate biological conditions against regional standards rather than against some
universal standard. (Karr 1993, 302)

Widespread use of single-species bioassays, complicated models, and impact-statement studies have
been singularly unsuccessful at predicting the effects of anthropogenic stress on biological systems.
(Karr 1991, 69)

The second distinction between integrity and diversity is that only integrity is directly associated
with evolutionary context. By definition, naturally evolved assemblages possess integrity but
random assemblages do not. Adding exotic species or genes from distant populations may increase
local diversity but it reduces integrity. (Angermeier and Karr 1994, 692)

In these passages, Angermeier focuses on the natural elements of diversity which he
argues add to integrity. Karr argues that the best standards for ecosystem health are a
matter of comparison with local similar ecosystems. Jointly they argue that integrity is a
better goal for conservation than diversity because integrity excludes non-native organisms
whilst diversity includes it.

The conceptual problem as construed by Angermeier and Karr is that there is some
equivocation over the meaning of ‘biodiversity’. We use the term to refer to the overall
value of the environment but treat it as species richness. So the efforts of conservation
focus on maximising species richness when they should focus on maintaining healthy
ecosystems and protecting native species. This concern is most clear when Angermeier
argues that importing new species into an ecosystem would lower biodiversity instead of
increasing it (Angermeier 1994, 600). They go on to argue that this conceptual confusion
has the potential to overlook important instances of biological value such as the mass
destruction of rainforests or the state of nutrient cycling (Angermeier and Karr 1994, 692).
For these reasons they argue that an integrity concept should replace biodiversity as the
goal of conservation. The focus for conservationists should be maintaining the health of an
ecosystem rather than on a general concept which has a strong focus on species but also
includes multiple other dimensions of biological elements.

1.3.2 Santana’s Meaning-dilemma Argument
In Save the Planet: Eliminate ‘Biodiversity’ and in Biodiversity Eliminativism Carlos
Santana argues that we should discard the biodiversity concept entirely (Santana 2014,
763; Santana 2017, 86). He presents two arguments against retaining the concept of
biodiversity. He claims firstly that defining ‘biodiversity’ is an impossible dilemma and
secondly that attempting to measure biodiversity only distorts our attempts to approximate
biological value (Santana 2014, 762 and 765). I will address Santana’s concerns about measurement and value in the relevant chapters four, five, and six. In this chapter I will restrict myself to his claim that “biodiversity is a poor conceptual fit for the role we want it to play in conservation biology” (Santana 2014, 761). In this sub section I will discuss his meaning-dilemma before justifying his crucial premises in the next two sections.

Santana begins his argument by drawing a distinction between general and specific meanings of ‘biodiversity’ but goes on to argue that this creates a dilemma.

This slipperiness is attributable in part to the fact the users of the biodiversity concept face a dilemma. Biodiversity is meant to serve as a reliable indicator of biological value, but given the vast variety of ways in which we value the biosphere, this requires us to employ a broad and open-ended definition of biodiversity. On the other hand, to serve reliably as a comparative measure, biodiversity needs to be observable and straightforwardly operationalisable. (Santana 2014, 762–63)

More formally his argument for the elimination of biodiversity may be understood in the following way.

**Santana’s Meaning-dilemma Argument**
1) ‘Biodiversity’ has either a general meaning or specific meaning but it cannot have both.
2) General meanings of ‘biodiversity’ are uninformative because they are synonymous with ‘all of biology’.
3) Specific meanings of ‘biodiversity’ have numerous counterexamples.
4) Conservation targets ought to be informative and lack numerous counterexamples.
5) Therefore: ‘Biodiversity’ is either uninformative or has numerous counterexamples.
6) Therefore: We ought not to use biodiversity as a conservation target.

This is my reconstruction of Santana’s argument, so I will justify my presentation of the meaning-dilemma argument with textual evidence. I begin with the justifications for premises one and four.

These two desiderata [general and specific meanings] pull in opposite directions: as our definition of biodiversity becomes more broad and open ended, it becomes more difficult to objectively quantify the amount of biodiversity in a particular unit of interest. (Santana 2014, 763)

This is Santana’s justification for the truth of premise one. In this quote he argues that while on a continuum, definitions of biodiversity lean towards either a general or specific meaning, both of which are problematic. The advantages of a general meaning necessitate the disadvantages of a specific meaning and vice versa.

As I discussed in section 1.2.1 and 1.2.2 the distinction between general and specific meanings is a vague one. Definitions of ‘biodiversity’ broadly fit under either one or the other. Because the category is vague, there are definitions which resist the distinction between general and specific meanings; but these still tend to lean to either side of the continuum. Maclaurin and Sterelny’s view appears to be specific because of its focus on species richness and phylogenetic diversity, but it leans towards general because
they argue that biodiversity also requires dimensions of disparity, a phylogenetic bias, and consideration of functions and ecosystems (Maclaurin and Sterelny 2008, 174). Santana argues that our current definitions of ‘biodiversity’ will be inevitably pulled towards either specific or general and that either outcome is unacceptable for defenders of biodiversity. I will spend much of chapters two and three challenging this assertion. For now, it is important to motivate the eliminativist’s position so that I can present a strong response to it.

Premise four that “Conservation targets ought to be informative and lack numerous counterexamples” is an analytic bridging premise for the purposes of constructing a valid argument. I take it as tacit that if Santana believes that biodiversity is a conceptually poor fit for its role in conservation due to a dilemma between uninformativeness and counterexamples, that he implicitly believes that uninformativeness and counterexamples make a concept a poor fit as a conservation target. Santana also has other concerns about the performance of biodiversity. He worries that biodiversity is not easily measureable and fails to approximate biological value (Santana 2014, 763).

If we were to replace the vague concept of biodiversity with the specific biological values we want to conserve, conservation would probably become more socially and politically appealing. But if we want to save pristine nature, untouched by human hands nature, it’s too late. We have the responsibility to decide what to prioritize and value, and taking shelter behind the vagueness of ‘biodiversity’ will not protect us from the consequences of shirking that responsibility. (Santana 2014, 778)

These are also reasons to reject biodiversity as a conservation target but, in as far as Santana believes that biodiversity is a conceptually poor fit for its role in conservation biology, the reasons he offers are concerns about counterexamples and uninformativeness. The justifications for premises three and four will be addressed in the next two subsections. They require dedicated space because Santana presents an extensive and compelling justification for the claims that specific meanings of ‘biodiversity’ have multiple counterexamples and general meanings are unininformative.

### 1.4 Specific Meanings of ‘Biodiversity’ Have Multiple Counterexamples

In this section I will motivate premise three of Santana’s meaning-dilemma argument that 3) “specific meanings of ‘biodiversity’ have numerous counterexamples”. There are multiple dimensions of biodiversity (Burch-Brown and Archer 2017, 981). There are too many possible specific meanings for Santana to present counterexamples to, so he uses a strategy of pessimistic induction. He presents counterexamples to several important specific conceptions of biodiversity and infers from those observations—and the work of biodiversity conservationists—that all specific meanings of ‘biodiversity’ have important counterexamples. His strategy here is philosophically interesting because, although he is a biodiversity eliminativist, he does not disagree with the analysis of Maclaurin, Sterelny, and Sarkar. Instead his pessimistic induction that specific meanings of biodiversity have numerous counterexamples relies on their critiques of specific conceptions of biodiversity.
In outlining the weaknesses of biodiversity, I drew on the same biologists and philosophers who attempt to rescue the biodiversity concept. The weaknesses of biodiversity, that is to say, are generally acknowledged. So why is biodiversity still central to conservation theory and practice? (Santana 2014, 773)

To motivate Santana’s pessimistic induction I will consider eight possible specific meanings of ‘biodiversity’: species richness, abundance, phenotypic diversity, phylogenetic diversity, functional diversity, genetic diversity, ecological diversity, and process diversity. Counterexamples to eight specific meanings of diversity drawn from both biodiversity eliminativists and conservationists justify the claim that “specific meanings of ‘biodiversity’ have numerous counterexamples”.

1.4.1 Biodiversity as Species Richness
Species richness is a count of the number of species in an ecosystem and is one of the most striking candidates for biodiversity. Of the 22 quotes discussed in section 1.2.1, 15 referred to some notion of species in their definition. In their book, Maclaurin and Sterelny tracked the fate of species richness as a core concept of biodiversity (Maclaurin and Sterelny 2008, 178). Species richness is an indispensable core of biodiversity because the term was coined in response to the modern extinction crisis. Species richness is also a strong candidate for the main meaning of ‘biodiversity’ because species are widely taken to be a natural kind rather than a purely human concept. If the proverbial visitor from Mars were to colonise earth millennia after the extinction of human beings and took an interest in biology, we would expect the visitor to roughly group the same organisms into species as we have. This is an important point, because while species are taken to be an objective unit in nature, other taxonomic categories such as genera and phyla are not (Boyd 1999b, 97). While the proverbial visitor from Mars would recognise the categorisation of species, it might not recognise the categorisation of genera or sub-species.

But it is these other taxonomic categories which present a real issue for any account of biodiversity which reduces it to species richness. The taxonomic ranking system is structured as follows: biota, domain, kingdom, phylum, class, order, family, genus, species, and sub-species. So the species *Colibri Thalassinus* (green violetear hummingbird) is a member of the genus *Colibri*, which is a member of the family *Trochilidae* (hummingbirds), which is a member of the order *Apodiformes*, which is a member of the class *Aves* (birds), which is a member of the sub phylum *Vertebrata* (animals whose spinal nerve is protected by bone or cartilage vertebrae), which is a member of the phylum *Chordata* (animals with notochords), which is a member of the kingdom *Animalia*, which is a member of the domain *Eukaryota* (organisms with a membrane-bound nucleus in their cell(s)), which is a member of the biota (superdomain containing all life on earth.) But species richness gives equal weight to all species. The deep sea angler fish *Bufoceratias Wedli* counts for the same as the earwig *Forficula Auricularia*.

Therein the problem lies because higher order taxonomic ranks do identify important differences in biological organisms, and treating all species as the same even if
some are aquatic and others are terrestrial misses an important element of diversity. How we cache out diversity of membership in higher order taxonomic ranks is the problem of disparity (Griffiths and Sterelny 1999, 287). It was the discovery of the burgess shale fauna which provided ecological evidence for this distinction. During the pre-Cambrian era we had fewer species than we do today but far more phyla and greater feature diversity (Gould 2000, 46). Species richness does not track feature diversity as well as disparity does. This is an important problem because there are twice as many marine phyla as terrestrial phyla but only half as many marine species (Angermeier and Karr 1994, 691). So marine biodiversity is more disparate than terrestrial biodiversity but it is only half as rich. Species richness cannot account for this important difference because it only counts the number of species and gives no further weighting to other dimensions of biodiversity.

Treating biodiversity purely as species richness forces conservationists to overlook other important dimensions of the biological world. As I will argue in the following subsections there are good reasons to think that: abundance, phenotypic diversity, phylogenetic diversity, functional diversity, genetic diversity, ecological diversity, and process diversity are all important elements of biodiversity but species richness by itself cannot account for these. Santana argues that we have overestimated how well species richness correlates with these other important elements. A focus on species richness encourages us to introduce as many new species to local ecosystems as possible, which can be bad for the species currently residing there (Lapointe et al. 2016, 221). Santana also argues that it is better for some species to be extinct. The eradication of smallpox was a benefit despite the reduction in species richness (Santana 2014, 769). The predator-free islands in the Bay of Plenty are another example of conservationists deliberately reducing species richness to protect a handful of other species. For these reasons biodiversity cannot be solely understood in terms of species richness. There are too many other important biological elements which it does not account for.

1.4.2 Biodiversity as Abundance
One response to the problems of species richness simpliciter is to supplement the concept with abundance. Species richness is a measure of the abundance of species types but it overlooks the abundance of the population within the species because species only need to be represented by a single individual. This is problematic because it means that a flourishing species is equally represented as a critically endangered one, which creates misleading values for conservation goals. One reason to think that abundance matters for diversity is the effect which poorly distributed abundance has on random sampling. Assume that in one ecosystem the population levels are balanced whereas the other has a very dominant species. Random sampling in the latter scenario is likely to only represent the dominant species, so while they are equally species rich, the ecosystem which is also equally abundant is more diverse (Vellend et al. 2011, 194). The two ecosystems described are vastly different in terms of their diversity but both score the same on species richness. To explain the problem another way the current Marvel cinematic universe is immortalisng its most popular superheroes in live action movies. Of the 20 films currently released (Ironman, Thor, Captain America, Antman, Spiderman, etc) the only story
focused on an African-American lead is *Black Panther.*\(^3\) So while the MCU does represent different ethnicities and genders in the sense of ‘richness’, it is not very diverse. Diversity is about more than having a group represented by at least one member.

The inclusion of population size into the concept of biodiversity aids the goals of conservation. Species diversity is species richness plus abundance. Species diversity is better at explaining why we should monitor population levels than a richness-only analysis. Despite difficulties with calculations of minimum viable population, abundance is an important factor in biodiversity. But it is not enough to explain what biodiversity is. Like species richness, species diversity struggles to accommodate disparity. Two species in the same phylum count for as much as two species in separate phyla. Stable ecosystems are also not structured with evenly distributed populations between species. Because of differing caloric requirements and the struggle for survival larger species are less abundant than smaller ones. Increasing the population of a particular species has the potential to severely disrupt the local ecosystem. A farmer who keeps 50 cattle to 50 blades of grass is headed for disaster. As a further example, much of the value which humans assign to biological entities is due to their rarity. One study found a direct correlation between the rarity of bird species and their desirability to birdwatchers (Santana 2014, 770). Biodiversity does include considerations of abundance but it is not the kind of evenly distributed species richness which is represented by maximum species diversity. In section 3.4 I will argue that we have good reasons to think that abundance should not be considered as a part of biodiversity.

**1.4.3 Biodiversity as Phenotypic Diversity**

Another candidate for the meaning of ‘biodiversity’ is phenotypic diversity (Burch-Brown and Archer 2017, 979). The phenotype of an organism is that organism’s observable characteristics, so phenotypic diversity should be understood as the total diversity of physical characteristics (Santana 2014, 770). When we attempt to preserve biodiversity we are conserving a maximal variety of physical characteristics. The difficulties with understanding biodiversity as phenotypic diversity have more to do with operationalisability than conceptual issues. Morphological measures of feature diversity identify mathematical relationships in nature and plot evolutionary adaptations on adaptive landscapes or morphospaces (McGhee 2007, 1). Morphospaces are logical or empirical explorations of the possible ways that a physical feature could be (McGhee 1999, 2). But there are infinitely many physical traits and no obvious way to aggregate them into a single morphological value for the purpose of conservation recommendations. The shared properties of leaf shape in *flora* do not commensurate well with the various wing shapes of *fauna.*

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So the problem with phenotypic diversity as a meaning of ‘biodiversity’ is developing a practical conservation strategy which can process the possible variations of multiple phenotypic characters into an operationisable conservation target. For this reason diversity of traits or forms such as morphological diversity cannot provide a complete account of biodiversity. While morphological diversity can be calculated with a small number of properties, attempting to perform such a calculation with all the properties is not “empirically or computationally tractable” (Maclaurin and Sterelny 2008, 77). Morphological diversity calculations can assist when we are interested in a few specific properties but it could never form the kind of global morphospace result that biodiversity requires (Santana 2014, 770).

1.4.4 Biodiversity as Phylogenetic Diversity
Phylogenetic diversity is an analysis of biodiversity through an evolutionary lens. It places organisms from an ecosystem on the tree of life and connects them with phylogenetic branches which map their evolutionary history (Vellend et al. 2011, 194). This mapping allows conservationists to measure the evolutionary distance between species (Faith 2002, 249). Phylogenetic diversity produces a calculable difference between diversity and disparity. An ecosystem with organisms who are members of higher order classes scores higher than an ecosystem with the same species richness represented by a narrower diversity of genera. PD also has the potential to overlap with other specific conceptions of biodiversity since the evolutionary history of an organism is tied to the selective pressures of the environment it evolved in. In turn there is a strong link between the evolutionary history of an organism and its physical features, functionality, and ecological niche (Faith 1996, 1287).

Phylogenetic diversity overlaps with many other specific meanings of ‘biodiversity’ but it struggles with the steady decline in populations. Since species only need one member to be represented on the tree of life, stable populations and critically endangered species produce the same value. This is problematic for issues such as the large-scale loss of ancient flora, which although not currently endangered still seem like they should be protected from human development (Takacs 1996, 1). Deforestation highlights the trouble phylogenetic diversity has with explaining why we should not bulldoze large sections of ancient rainforest or substantially reduce the population levels of species for the sake of human development. If we leave enough organisms alive to prevent a substantial increase in extinction rates then we could theoretically harvest the remaining natural resources for human benefit without suffering any loss of total phylogenetic diversity. If we are only interested in preserving phylogenetic diversity then harvesting ancient rainforest for coffee tables does not represent a decrease in biodiversity, provided that we leave enough trees alone to prevent any extinction events (Angermeier and Karr 1994, 692). Because phylogenetic diversity does not take into account population levels, it cannot justify our opposition to the deforestation of ancient flora, if such an act would not lead to species extinction (Santana 2014, 768). There are good reasons to resist deforestation but understanding biodiversity purely as phylogenetic diversity struggles to ground those intuitions.
1.4.5 Biodiversity as Functional Diversity

Functional diversity attempts to address the counterexamples to other specific meanings of ‘biodiversity’ by refocusing diversity on the functionality of organisms within the environment (Justus 2013, 345–46). A recurring objection to conceptions of biodiversity which focus on elements like species richness and abundance is that it overlooks important biological functions or interactions which we should preserve (Takacs 1996, 69). Nature is filled with fascinating biological phenomena such as simultaneous bamboo flowering in distinct geographical regions (Sarkar 2005, 180). Despite being 1500 km apart, the species flowers at identical times. Attention to functional diversity also explains why we might prefer organisms in the environment than in Zoos or botanic gardens (Sarkar and Margules 2002, 302). Keeping species in isolated conditions maintains species richness and phylogenetic history but it limits interaction and therefore functionality.

The conceptual issue with functional diversity is that despite the motivating examples of high level biological phenomena, in practice functional diversity is treated as feature diversity (phenetic diversity). Functional diversity is treated as a synonym for feature diversity, with the restriction that the focus is on functional traits rather than all traits (Weiher 2011, 175). However, since a functional trait is defined as one which impacts the survivability of other organisms and virtually all traits impact the fitness of other organisms, virtually all traits count as functional ones. So the main motivation for functional diversity, that we measure and conserve biological functionality, gives way to phenetic diversity by another name. Functional diversity as a concept is actually feature diversity, so it does not operationalise functionality in the way that it is supposed to.

1.4.6 Biodiversity as Genetic Diversity

A further candidate for a specific meaning of ‘biodiversity’ is genetic diversity. We can observe and monitor the total amount of unique genetic information contained in a local ecosystem and attempt to preserve it (Witting and Loeschcke 1995, 205). Focusing on the diversity of unique genetic information will also overlap species richness and phenotypic diversity. But this candidate is vulnerable to two counterexamples. Firstly, genomic size varies greatly from species to species, so a focus on unique genetic information would create unusual priorities for conservation (Santana 2014, 771). Secondly, placing diversity of genetic information as our conservation target has an unusual implication. A genetic soup could contain as much as, if not more, unique genetic material than a sizable chunk of the natural world. If biodiversity is understood as genetic diversity then we could boost biodiversity by replacing large sections of the natural world with genetic soup, provided that said soup contained more unique genetic material than the natural world (Santana 2014, 771).

As a hypothetical counterexample to genetic diversity, the details of genetic soup are problematic to cache out. For example, one issue is that it is unclear how anyone could extract useful genetic information from a bowl of genes. Mixing biological material together does not make it easy to itemise and quantify the genetic information represented by that sample. This thesis aims to defend biodiversity on the eliminativist’s ground as much as possible so I will presume the success of the genetic soup counterexample whilst discussing conceptual arguments for biodiversity’s elimination. However, during the
discussion of the value compass case for biodiversity’s elimination, in section 7.2.2 I will evaluate the plausibility of genetic soup in more detail.

1.4.7 Biodiversity as Ecological Diversity or Process Diversity
The final two candidates for a specific meaning of ‘biodiversity’ that I will consider in this section are ecological diversity and process diversity. Ecological diversity is a focus on preserving the greatest variety of ecosystems possible (Callicott 2017, 323). This instance of diversity has the potential to explain why we should preserve distinct ecosystems. For example, deserts tend to be overlooked for conservation because they are biodiversity coldspots (Durant et al. 2014, 114). A focus on preserving ecological diversity could explain why we should preserve wilderness as well as biodiversity hotspots. However, Santana rejects ecological diversity on the grounds that it simply returns us to the original meaning-dilemma for biodiversity. “Either we are back to square one, and ecological diversity reduces to “all of biology” or we have to choose a manageably small set of dimensions. Which dimensions of an ecosystem are relevant, however, depends on our goals.” (Santana 2014, 771).

Process diversity focuses on preserving the greatest variety of biological processes (Sarkar et al. 2006, 131). Functioning ecosystems involve multiple biological processes such as nutrient cycling in the soil, metabolic rates, carbon cycling, germination, and reproduction. But Santana questions the suitability of process diversity as a conception of biodiversity. First, he observes that focusing on protecting biodiversity hot spots (in terms of species richness), such as the west cape of South Africa, comes at the expense of endangered ecological processes in biodiversity cold spots, so process diversity and biodiversity come apart (Santana 2014, 772). Secondly Santana notes that conservation is not typically concerned with protecting as many different processes as possible. Rather we are concerned with a few major processes such as climate change or the persistent reduction of lake levels (Santana 2014, 773). Angermeier and Karr also argue that process diversity is better understood as a part of biological integrity because it is the rates of processes rather than the occurrence which varies (Angermeier and Karr 1994, 692). So process diversity will not serve as a specific meaning of ‘biodiversity’ because conservationists are less concerned with many distinct processes than they are with a few steady ones.

1.4.8 Lessons from the Counterexamples to Specific Meanings of ‘Biodiversity’
This completes my discussion of the counterexamples which face specific meanings of ‘biodiversity’. Species richness does not account for disparity and conservation based on abundance struggles because ecosystem diversity is different to the kind of evenly weighted populations which serve as the typical goal of diversity. Phenotypic diversity has operationalisable concerns which are also conceptual. We can conceive of a diversity of phenotypic characters, but amalgamating all possible phenotypic characters into a global morphospace is not computationally or conceptually tractable. Phylogenetic diversity overlaps with other dimensions of biodiversity but does account for population levels and operational requirements of functional diversity make it a synonym for phenotypic
diversity. A focus on genetic diversity implies that gene soup is as valuable as the natural world, ecological diversity returns us to the original meaning-dilemma, and process diversity incorrectly prioritises as many different processes as possible rather than a few stable ones.

As each specific meaning identifies an important dimension of biodiversity, many of them can be taken as counterexamples to one another. Phylogenetic diversity accounts for species richness but species richness does not account for phylogenetic diversity and neither fully account for process diversity. These eight specific meanings all have serious counterexamples and so this section has motivated Santana’s pessimistic induction. Since eight major candidates for a specific meaning of ‘biodiversity’ have serious counterexamples there is good reason to believe premise three of the meaning-dilemma argument that “specific meanings of ‘biodiversity’ have numerous counterexamples”.

One response to the weaknesses of a pessimistic induction is that Santana does not require an inductive justification for premise three. If biodiversity has multiple distinct dimensions which are strictly incommensurable then demonstrating that more than one dimension is required for biodiversity is sufficient to demonstrate that all specific meanings have counterexamples. Whether the strategy is inductive or relying on multiple incommensurable dimensions, Santana has justified premise three of the meaning-dilemma argument and he has done so by appealing to the conclusions of biodiversity conservationists such as Maclaurin, Sterelny, and Sarkar. The last premise for Santana to motivate is premise two that general meanings of ‘biodiversity’ are uninformative.

1.5 General Meanings of ‘Biodiversity’ are Uninformative

In this section I will motivate premise two of the meaning-dilemma argument that “general meanings of ‘biodiversity’ are uninformative because they are synonymous with ‘all of biology’”. This objection is raised in the first place by Sarkar and developed with more detail by Santana to justify his eliminativist conclusion. The claim can be understood in two ways; a concern that a general meaning of ‘biodiversity’ is not operationalisable or a concern that understanding biodiversity as ‘all of biology’ makes it uninformative. As concerns about the operationalisability of biodiversity will be addressed in the chapters on measurement my discussion about the conceptual case for biodiversity eliminativism will focus on the second interpretation of premise two, that general meanings of ‘biodiversity’ are uninformative.

Sarkar and Margules introduce the generality objection in Operationalizing Biodiversity for Conservation Planning. They argue that general meanings of ‘biodiversity’ reduce to ‘all of biology’ which make conservation impractical.

Conserving biodiversity, and construing the term intuitively to refer to all the biological diversity that there is at every level of both hierarchies, amounts to saying that “biodiversity” refers to all biological entities. “Biodiversity” in effect becomes all of biology. Conservation would be an impractical proposal if “biodiversity” is construed in this way. (Sarkar and Margules 2002, 137)
Santana develops this argument further in his own work. He agrees with Sarkar that general meanings of ‘biodiversity’ reduce to ‘all of biology’ and goes on to argue that for this reason we should reject general meanings as a conceptual candidate for ‘biodiversity’. One way to interpret this claim is as a concern about the operationalisability of general meanings of ‘biodiversity’.

**General Meanings of ‘Biodiversity’ are not Operationalisable**

1) Conservationists have limited resources.
2) Conservationists ought to preserve biodiversity.
3) If ‘biodiversity’ means ‘all of biology’ then conservationists ought to preserve all of biology.
4) The limited resources of conservationists are not sufficient to preserve all of biology.
5) Ought implies can.
6) Therefore: ‘biodiversity’ cannot mean ‘all of biology’.

Premises one and four are widely acknowledged. It is the reason that conservation is so frequently compared to a state of triage. Since Santana and his fellow eliminatists believe that we ought to eliminate *biodiversity* from our discourse, premise two should be understood as an assumption for the sake of the argument and premise three follows analytically because ‘biodiversity’ and ‘all of biology’ are treated as synonyms. In fact the only contentious premise in this argument is premise five that ought implies can. ‘Ought implies can’ is a Kantian constraint (Kohl 2015, 690). In this form it seems abstract but its converse, that ‘cannot’ implies ‘not the case that you ought’, is more straightforward. If it is not within your power to save a starving child then you bear no moral responsibility for failing to do so (Kohl 2015, 691). You could not, so it is not the case that you ought to have done it.

It is a contentious principle because it can be interpreted as either a logical law or a plausible moral principle. As a logical law it has possible counterexamples. If one doctor has three equally urgent patients they all ought to be treated, but resource constraints will only allow one to be treated at a time. Logical laws are not meant to have counterexamples because deductive logic is built on reasoning with certainty from the premises to the conclusion. For a rule to hold as a logical law, it must hold in all situations.

Rather than a logical law, ‘ought implies can’ is a better candidate for a moral principle. But as a moral principle, it also has counterexamples. A strength of the ‘ought implies can’ principle is that it argues against moral blame where circumstances were beyond an agent’s control (Walter Sinnott-Armstrong 1984, 250). A truly compulsive kleptomaniac is considered ill rather than evil because they exercise no agency over their actions (Graham 2011, 343). The strength of the principle is also a weakness because it can be used to devise counterexamples. In *Ought* and Ability Peter Graham describes the hypothetical example of a surgeon who can save her ten grandchildren if she kills and harvests organs from two healthy people. In the example the surgeon is as compelled to complete this action “as is the most severe kleptomaniac to steal”. He argues that despite the surgeon’s lack of control over his actions, she still ought not harvest organs from healthy people without their permission (Graham 2011, 346). He defends his argument
against objections with several variations of this example. In one such state of affairs, the surgeon is deluded and believes that she must kill the two healthy patients to prevent an apocalypse. Once she kills them, a second transplant surgeon discovers the bodies, notes that they had consented to be organ donors whilst alive, and uses their organs to save ten people (Graham 2011, 350). Despite saving lives, and the surgeon having no control over her actions, harvesting the organs is still wrong and the surgeon is morally blameworthy. So ‘ought implies can’ is better as a plausible moral principle which works some but not all of the time (Kuhler 2012, 181). We expect there to be some moral goals which we cannot accomplish but are still worth pursuing.

For this concern about operationalisability, conservationists cannot preserve all of biology so eliminativists argue that it is not the case that they ought to preserve biodiversity (Frank 2017, 106). Hence ‘biodiversity’ cannot mean ‘all of biology’ and we should reject general meanings of ‘biodiversity’ because they reduce to ‘all of biology’. This is a contentious premise, precisely because ‘ought implies can’ is a plausible moral principle rather than a logical law and as a moral principle is has problematic counterexamples.

Concerns about the operationalisability of biodiversity, such as how it can be measured and whether it can meet the goals of conservation, will be discussed in more detail in the chapters four, five, and six on measurement. However, this interpretation of premise two as a concern about operationalisability yields a weaker argument. To be successful it requires that ‘biodiversity’ literally refers to every single element which biologists study, which implies that there is nothing contained within the field of biology which biodiversity is not intended to represent. It is difficult to make sense of the study of extinct species as an immediate goal for conservation.

The role of the ‘ought implies can’ principle here means that it is not the case that conservationists ought to protect what they cannot conceivably protect. This is an odd view given that so much of the history of conservation has been fighting a losing battle. Conservationists still fight to preserve biological elements even when the odds are against them or they slowly lose over time to political flux. Using ‘ought implies can’ in this situation implies that the obligations of a conservationists are deeply tied to the probability of conservation efforts being successful. But I contend that even if they were penniless and politically powerless conservationists would still attempt to conserve things because of their underlying obligations. By analogy, it would be unusual to argue that conservationists have no obligations to conserve species because it is not possible for them to preserve all species. For these reasons the use of the ‘ought implies can’ principle here is inappropriate, but it is also the analytic bridge which Santana requires to reach a valid conclusion.

A better interpretation of premise two is as a conceptual concern about informativeness.

**General Meanings of ‘Biodiversity’ are Uninformative**

1) Conservationists ought to use biodiversity as a goal for the sake of preserving biodiversity.

2) The goal of conservation needs to be more informative than ‘all of biology’

3) If ‘biodiversity’ means ‘all of biology’ then the conservation goal is ‘all of biology’
4) Therefore: ‘biodiversity’ cannot mean ‘all of biology’.

Premise one is an assumption for the sake of argument and premise three follows analytically from premises one and two. Santana takes the truth of premise two as given because it is impractical for conservation to preserve all of biology. Whilst the ultimate goal of conservationists may be to save as much of biology as possible understanding biodiversity as ‘all of biology’ makes discussions of biodiversity considerably less informative. Consider the following abstract from ‘The Optimization of Biodiversity Conservation’ (Witting and Loeschcke 1995, 205), in which I have substituted ‘all of biology’ in place of ‘biodiversity’.

The conservation of [all of biology] is confronted with two major problems: how to define and measure [all of biology], and how to optimize the in situ conservation of [all of biology]. Here we outline a conceptual framework for the conservation of [all of biology] that is directed towards these problems. The framework combines a phylogenetic evaluation with a multi-species risk analysis and defines the objective of conservation biology as the minimization of the future loss of [all of biology].

By replacing ‘biodiversity’ with ‘all of biology’ the abstract becomes less informative. The claims make less of an original contribution to the literature. Precise claims tend to be more informative. Observing that we struggle to define or measure all of biology under a single category suggests the question of why we ought to in the first place, and ‘attempting to minimise the future loss of all of biology’ is an ambiguous statement. It could be interpreted as preventing the loss of any biology which would be incoherent because death and life are part of regular interactions between organisms. Or, it could be interpreted as minimising the loss of species, ecosystem reduction, prioritising native species, or any other dimension of biology discussed in the previous section on specific meanings. This is a deeply uninformative claim to make because it tells us little about which dimensions should be cared for. So, on pain of incoherence, ‘biodiversity’ with ‘all of biology’ in this abstract makes the claim far less informative.

This reduction of informativeness also happens when other uses of ‘biodiversity’ are exchanged with ‘all of biology’.

For example, economic growth—one of the highest priorities in the domestic policy arena—has been identified as posing a fundamental conflict with the conservation of [all of biology]. (Tear et al. 2005, 835)

Non-native fishes threaten aquatic [elements of all of biology] in North America by imperilling native fishes. (Lapointe et al. 2016, 221)

Here we analyzed local patterns of [all of biology] in a bird community to investigate effects of dispersal propensity on local species richness and the presence of rare species. (Møller and Mousseau 2011, 2789)

As noted in section two, there is also evidence that [all of biology] is correlated with a wide range of ecosystem services. (McLaurin and Lean 2016, 31)
These claims are less informative when ‘biodiversity’ is understood as ‘all of biology’. It is almost an analytical truth that conserving all of biology conflicts with economic growth. It is now unclear which elements of biodiversity non-native fishes threaten. ‘Local patterns of biodiversity’ is informative when it is treated as species richness or some other specific dimension of biology but ‘local patterns of all of biology’ requires more details on the kind of patterns which were analysed to be an informative statement. It also analytic that ecosystem services are a subset of all of biology, so observing that the two correlate does not provide new information to the reader. These examples demonstrate two things. Firstly it is unlikely in practice that these authors conceive of biodiversity in a general way, given how general it makes their claims. Secondly, treating biodiversity as ‘all of biology’ makes claims about biodiversity uninformative by increasing their generality. General claims are more vague and less informative than specific claims. So general conceptions of biodiversity such as “… biodiversity is the living resources of the planet.” (Ehrlich in Takacs 1996, 47) are vaguer and make uses of ‘biodiversity’ uninformative.

In this section I motivated premise two of the meaning-dilemma argument that “general meanings of ‘biodiversity’ are uninformative because they are synonymous with ‘all of biology’”. Santana argues that general meanings should be discarded because they are uninformative and not operationalisable (Santana 2017, 763). Understanding this premise as a concern about uninformativeness yields a stronger version of the argument than treating it as a concern about operationalisability. The difficulty of preserving all of biology is not a reason that we do not, or ought not, attempt to preserve it. However, understanding biodiversity as ‘all of biology’ does make the term uninformative. Treating the two as synonyms makes academic claims seem less precise and conservation work seems too widely targeted when an analysis is performed on all of biology rather than on a specific dimension such as species richness. This completes the motivation for Santana’s meaning-dilemma argument. Since specific meanings of ‘biodiversity’ have counterexamples and general meanings are uninformative, he argues that we should discard the concept entirely (Santana 2017, 94).

In this section I have examined several potential reasons for trying to repair the biodiversity concept despite its numerous weaknesses. Having found each reason wanting, I tentatively propose the retirement of biodiversity from conservation science and philosophy. (Santana 2014, 778)

1.6 Conclusion
In this chapter I discussed conceptual issues with biodiversity and motivated the conceptual case for eliminating its use from conservation biology. I outlined the conceptual issues largely by discussing the development of biodiversity as a concept. I started with its analytic meaning before discussing the sociological work of David Takacs who demonstrated that ‘biodiversity’ carried a diversity of meanings in academic work in the 90s. I then continued the methodology of Philosophies of Paradise by analysing uses of ‘biodiversity’ in modern academia. After surveying the different uses of ‘biodiversity’, I drew a distinction between general meanings of ‘biodiversity’ such as the richness of life
and specific senses which focus on a single dimension of biology such as the total amount of unique genetic information.

I used this conceptual ambiguity about the meaning of ‘biodiversity’ to motivate the conceptual arguments of biodiversity eliminativists. Angermeier and Karr argue that the conceptual ambiguity of biodiversity misleads the work of conservationists. Since ‘biodiversity’ could mean species richness to one person and native conditions to another, conservationists can preserve biodiversity (species richness) when they should be protecting native species over non-native species. Santana presents a compelling meaning-dilemma argument. He appeals to modern work on biodiversity to demonstrate that specific meanings of ‘biodiversity’ have empirical counterexamples. This point is not a contentious claim, as many academics who work on biodiversity discuss the same conceptual issues. He then argues that general meanings of ‘biodiversity’ are uninformative and not operationalisable (Santana 2017, 87). I will address concerns about operationalisability in chapters four to six but Santana’s concern about un informativeness is a compelling one. Substitutions of ‘all of biology’ for ‘biodiversity’ in academic papers made the authors’ claims seem less precise and uninformative. In the next chapter I will respond to the Santana, Angermeier, and Karr’s conceptual case for eliminating biodiversity by developing the underutilised possibility that biodiversity could be a homeostatic property cluster.
2 Biodiversity as a Homeostatic Property Cluster

2.1 Introduction

In this chapter I will discuss responses to the conceptual case for biodiversity’s elimination and outline a conception of biodiversity as a homeostatic property cluster. In section 2.2 I summarise the conceptual case for biodiversity eliminativism. In section 2.3 I discuss Burch-Brown and Archer’s (2017) general conception of biodiversity, which was developed as a response to Santana’s eliminativism. I will argue that their conception does not escape Santana’s meaning-dilemma. In section 2.4 I argue that biodiversity can be understood as a homeostatic property cluster—that is—biodiversity can be understood as a cluster of co-occurring properties of distinct diversities, the rise and fall of which is united by a homeostatic mechanism (Boyd 1991, 141). I introduce the conditions for a homeostatic property cluster and argue that biodiversity satisfies them. Then I discuss Santana’s objections to HPC conceptions of biodiversity and respond to them. In section 2.5 I argue that the success of HPCs in dealing with the species problem sets an important precedent for its potential with the biodiversity problem.

2.2 The Conceptual Case for Biodiversity Eliminativism

In the last chapter I motivated the conceptual case for eliminativism and argued that it had laid two challenges against biodiversity. Angermeier and Karr have argued that the concept misdirects the efforts of conservation by equivocating its meaning, and Santana argues that “biodiversity is a poor fit for the conceptual role we want it to play in conservation biology” (Angermeier and Karr 1994, 692; Santana 2014, 761). Angermeier and Karr’s main argument for the elimination of biodiversity focuses on how the concept misdirects conservation by equivocating biodiversity with species richness, despite species richness being unsuccessful at predicting the impact of human activity on ecosystems (Karr 1991, 69). They also argue that biodiversity fails to prioritise native over non-native elements, which implies that those who conserve biodiversity are often conserving the wrong thing (Angermeier 1994, 600; Angermeier 2000, 377; Angermeier and Karr 1994, 691). Thus the conceptual challenge raised by Angermeier and Karr is a concern about misdirection of conservation effort. Biodiversity leads conservationists to focus on species richness when they should focus on ecosystem integrity, and it treats native and non-native species as equally valuable when the integrity of an ecosystem is improved by native elements.

Santana’s conceptual case for eliminating biodiversity is more severe than Angermeier and Karr’s. Whilst Angermeier and Karr present an external critique of biodiversity by appealing to other important elements of ecosystems, Santana presents an internal critique of biodiversity. He argues that the concept cannot fulfil the role we need it to in conservation because it is pulled in separate directions. There are many valuable elements of the biosphere so our conception of biodiversity must be a very general one. However, we need a specific conception of biodiversity for it to be operationalisable (Santana 2014, 762–63). He then argues that specific meanings of ‘biodiversity’ fail to accurately capture the concept but general meanings are uninformative. So the concept requires both a specific and general meaning but neither is a good fit for conservation
biology. We are either left with a specific conception of biodiversity which falls short or a general one which is uninformative. Since both alternatives have serious problems, conservation would be better off eliminating biodiversity from discourse entirely. I have constructed Santana’s argument as follows.

Santana’s Meaning-dilemma Argument

1) ‘Biodiversity’ has either a general meaning or specific meaning but it cannot have both.
2) General meanings of ‘biodiversity’ are uninformative because they are synonymous with ‘all of biology’.
3) Specific meanings of ‘biodiversity’ have numerous counterexamples.
4) Conservation targets ought to be informative and lack numerous counterexamples.
5) Therefore: ‘Biodiversity’ is either uninformative or has numerous counterexamples.
6) Therefore: We ought not to use biodiversity as a conservation target.

So Santana’s conceptual challenge to biodiversity relies on a dilemma over its meaning. This is an internal critique because it examines biodiversity against its own conceptual standard. Biodiversity is meant to incorporate multiple biological diversities, but however we conceptualise it is either incomplete or too vague to be a good fit for the goals of conservation. In the next section I will discuss a recent challenge to Santana’s case for eliminativism which argues that general conceptions of biodiversity do not warrant elimination just because they have multiple dimensions.

2.3 Burch-Brown and Archer’s General Conception of Biodiversity

In this section I discuss Burch-Brown and Archer’s response to Santana’s arguments for eliminativism. In In Defence of Biodiversity Burch-Brown and Archer argue that the classical multidimensional concept of biodiversity plays an important explanatory role in ecology in terms of both informativeness and normativity (Burch-Brown and Archer 2017, 970–71). Burch-Brown and Archer’s response to Santana is philosophically interesting because they accept much of Santana’s meaning-dilemma argument but deny that a general multi-dimensional conception of biodiversity is uninformative.

Burch-Brown and Archer begin by identifying the steps in Santana’s argument. In a similar construction to my meaning-dilemma argument, they argue that conceptions of biodiversity can be either specific dimensions or general multidimensional concepts. But neither account will suffice for the role which is demanded of biodiversity in conservation biology. Santana is concerned about the ability of biodiversity to reliably predict biological value (Santana 2017, 86). However, many valuable biological features do not correlate well with aspects of biodiversity, and general conceptions are too multi-dimensional to play useful explanatory roles in science (Burch-Brown and Archer 2017, 974). “Biodiversity does not capture all of what Santana calls ‘biological value’, and not all forms of diversity are valuable; thus the concept is both too broad and too narrow to be the primary target of conservation.” (Burch-Brown and Archer 2017, 970). Burch-Brown and Archer do not challenge the possibility that biodiversity can be understood as a single
dimension such as species richness. Instead they identify the contentious premise of Santana’s conceptual case for biodiversity eliminativism as a claim of uninformativeness. Biodiversity is uninformative because as a concept it is too inclusive and ambiguous to be useful.

Burch-Brown and Archer respond to Santana’s meaning-dilemma on two fronts. They reject his observation that multidimensional conceptions of biodiversity are uninformative. They then assume that his argument is successful but argue that uninformative concepts can still play important explanatory roles in conservation biology (Burch-Brown and Archer 2017, 982). The purpose of their argument is to establish that conservation has good reasons to retain biodiversity even if ‘biodiversity’ does refer to every dimension of biological variation. Their strategy is philosophically interesting because they do not attempt to restrict the concept of biodiversity in the face of Santana’s arguments. In fact the multidimensional concept which they advocate for is more inclusive than that of Maclaurin and Sterelny (2008, 174). Where Maclaurin and Sterelny conceptualise biodiversity as a species-richness core with elements of phylogeny and morphology, Burch-Brown and Archer endorse biodiversity as an umbrella-concept for “all aspects of life’s variety” (Burch-Brown and Archer 2017, 982). So their conception of biodiversity is maximally general. It incorporates all dimensions of biological variance.

Burch-Brown and Archer then argue that their maximally general conception of biodiversity is still informative. They observe that Santana is concerned that general conceptions of biodiversity reduce to ‘all of biology’, then they point out elements of biological studies which are not a part of biodiversity.

For example, many parts of biology essentially focus on explaining how things work, such as how cells are replicated, how energy is produced, how genes function at a molecular level, and so on. It may be part of these studies to look at biological diversity (diversity in forms of cells, or forms of energy production, for instance) but the study of variation does not encompass the whole of these sciences. Biodiversity does not include ‘all of biology’, although the study of variety is clearly of central interest within biological science. (Burch-Brown and Archer 2017, 983–84)

Burch-Brown and Archer then assume that ‘biodiversity’ is no more informative than ‘all of biology’, but argue that biodiversity still has a useful role to play in conservation biology. Biodiversity functions as an explanans (a property which explains) because it explains important ecosystems behaviour and as an explanandum (a property which needs to be explained) because it is treated as an important property of ecosystems which needs to be described and explained (Burch-Brown and Archer 2017, 982 and 985). Burch-Brown and Archer also argue that biodiversity has normative importance in biology. Biodiversity does not track ecological value well but it does not need to. The biological variety of life ought to be a priority for conservation because it tracks ecosystem services (Burch-Brown and Archer 2017, 993). It is therefore one important element of the environment which should be valued and is not a surrogate for all the important elements of the environment.

This response to Santana’s conceptual case for eliminativism is important because it relies on excluding possibilities. Burch-Brown and Archer argue that ‘biodiversity’ is more informative than ‘all of biology’ because the concept of biodiversity does not include
studies of non-relational biological properties. In response to Santana’s arguments that biodiversity fails to track ecological value well, Burch-Brown and Archer exclude ecological value as a possible dimension of biodiversity. Instead they conclude that biodiversity “is one non-instrumentally valuable feature of the natural world” which tracks some elements of instrumental value (Burch-Brown and Archer 2017, 993). Burch-Brown and Archer’s response highlights two important strategies in the informativeness debate. A case can be made for informativeness if you demonstrate what biodiversity is not and separate some important conservational goals from biodiversity. Biodiversity has steadily incorporated more dimensions as time has passed so it will benefit from some restrictions.

Burch-Brown and Archer’s arguments are important for the strategy in this chapter but their conception of biodiversity is still vulnerable to Santana’s concern about uninformativeness. The problem is that their multidimensional concept is so broad that despite not reducing to ‘all of biology’ it is still not informative enough to advise conservation. They have excluded studies of non-relational properties but they also acknowledge that biologists are interested in the diversity of those properties (Burch-Brown and Archer 2017, 984). The problem is that Burch-Brown and Archer want biodiversity to include “any and all variation amongst biota” (Burch-Brown and Archer 2017, 981). Any concept which includes: species richness, abundance, phenotypic diversity, phylogenetic diversity, functional diversity, genetic diversity, ecological diversity, and process diversity, leaves little for biologists to study without studying biodiversity in some way. ‘Biodiversity’ is more informative than ‘all of biology’ but only marginally so.

Their response misses the heart of Santana’s concern. Good scientific concepts are precise, testable, and informative. Burch-Brown and Archer’s conception of biodiversity looks general, difficult to test, and uninformativeness. Since conservation decisions should be guided by good science, Santana is contending that we should eliminate the umbrella concept in favour of its more specific dimensions (Santana 2018, 13). In the case of Burch-Brown and Archer’s conception of biodiversity I find Santana’s concern about uninformativeness to be convincing. Biodiversity contains a constant tension between operationalisability for the goals of conservation and generality for the sake of capturing important biological elements. Burch-Brown and Archer’s account sacrifices too much operationalisability for the sake of generality. In the next section I will develop a different response to the conceptual case for biodiversity eliminativism. I develop a possibility discussed by Burch-Brown and Archer that biodiversity could be a homeostatic property cluster.

### 2.4 Biodiversity as Homeostatic Property Cluster

One possibility which Burch-Brown and Archer consider but do not develop is that biodiversity could be a homeostatic property cluster. Maclaurin also argues that biodiversity could be understood as an HPC but does not develop the possibility in detail (Maclaurin 2017, 63–66). Homeostatic property clusters identify kinds based on a cluster of co-occurring properties whose rise and fall is controlled by a homeostatic mechanism (Boyd 1991, 141). In the case of species the ‘species’ kind incorporates co-occurring properties over multiple conceptions of species but the mechanisms of external pressures
and genetic exchange between organisms keep the properties in sufficient homeostasis for the kind to be inductively successful (Boyd 1999b, 81). HPCs are an important conceptual possibility because biodiversity has similar conceptual problems to species and HPCs provide an excellent account of species-hood. Both are general concepts with multiple dimensions but any specific conception has serious counterexamples (Hull 1997). Despite this we have not —and I hope will not— eliminate ‘species’ from biology. Instead biologists have diverse views. Some are realist pluralists about species (Mishler and Donoghue 1982, 500) and some understand it as a homeostatic property cluster (Boyd 1989, 142)

Burch-Brown and Archer point out that a HPC conception of biodiversity escapes Santana’s meaning-dilemma.

One response would be to claim that this argument assumes too strong a standard for biological kinds. For instance, on the Homeostatic Cluster Properties conception of natural kinds, there may be no properties that all instances of a kind share, but if the important properties tend on the whole to cluster together, and if a mechanistic explanation can be given for this clustering (such as species boundaries), then there might be a biological kind. One strategy for replying to Santana, therefore, would be to seek to show that the dimensions of diversity do tend to be reasonably strongly clustered, and that there are underlying mechanisms for this clustering. (Burch-Brown and Archer 2017, 975–76)

However, as Santana observes in his reply, Burch-Brown and Archer do not develop this possibility further. “They don’t develop this suggestion at all, however, presumably because it is implausible that there is any mechanism maintaining homeostasis across the different dimensions of biodiversity.” (Santana 2018, 4) In this section I will argue that biodiversity can be understood as a homeostatic property cluster which escapes the conceptual case for its elimination. First I will explain the concept of homeostatic property clusters, and then I will argue that biodiversity is a homeostatic property cluster. Then I will argue that Santana’s objections to biodiversity as a HPC do not fully consider how well the HPC concept can address biodiversity’s problems. I further motivate this argument in section 2.5 with the example of species as an HPC.

### 2.4.1 Homeostatic Property Clusters
In this sub-section I will explain what a homeostatic property cluster is. I will argue that HPCs play an important role in biology at explaining biological kinds. Biological kinds are difficult to categorise because they sit on various continuums. The continual nature of species-hood—for example—leads to counterexamples. So while there are multiple concepts for species-hood, no individual concept correctly groups organisms by their species (Boyd 1999b, 72). Homeostatic property clusters provide an alternative account of species-hood which satisfies the demands of both scientists and philosophers. Likewise homeostatic property clusters can provide an alternative account of biodiversity which satisfies the conceptual demands of conservation biology. It is just a matter of outlining the property cluster conditions and arguing that biodiversity should be understood as a homeostatic property cluster.
Homeostatic property clusters are groups of properties whose connection is controlled by a homeostatic mechanism. A homeostatic mechanism is a mechanism which tends to make properties occur together (Boyd 1991, 141). It is the tendency rather than out right regularity which is of use to the conceptual challenges facing biodiversity. A key motivating observation in the conceptual case for biodiversity eliminativism is the observation that the individual dimensions of biodiversity do not co-vary in important ways (Santana 2014, 768). Under a HPC conception of biodiversity the various dimensions do not need to co-vary (Burch-Brown and Archer 2017, 976). For example, health is a homeostatic property cluster of normative biological function. Its various dimensions such as blood pressure, temperature, liver function, and heart rate, do tend to co-vary but they can also come apart in important ways. A broken arm may co-vary with an increased heart rate whilst liver function and mental health remain steady.

The ability to gather together properties which tend to co-vary—but can also behave independently—is why HPCs are a useful analytic tool for studies of biological kinds (Santana 2018, 4). Biology is a science of continuums which makes identifying necessary and sufficient conditions for group membership a difficult task. Special sciences such as psychology deal with multiply-realised categories. Pain may be understood as c-fibre firing in human beings but could also be realised by multiple distinct neural systems. HPCs can help with the conceptual difficulties in both these areas as well as with kind identification in the historical sciences (Boyd 1999b, 84). So a homeostatic property cluster analysis is well suited to the conceptual challenges facing biodiversity. It has been used before to solve a conceptual challenge in biology; the challenge of categorising species-hood.

Species are the paradigm case of the success of an HPC analysis. Whilst most academic work recognises that ‘species’ describes a natural kind, the attempt to carve nature at its joints was plagued with counterexamples (Boyd 1999b, 72). There are multiple ways to conceptualise species but each individual concept has counterexamples. In this thesis’s chapter on species, I will discuss the difficulties of conceptualising species-hood in more detail but the important point for this chapter is that a HPC conception of species can explain why multiple concepts are needed but can still defend the concept as a natural kind.

The paradigm cases of natural kinds - biological species - are homeostatic cluster kinds. The appropriateness of any particular biological species for induction and explanation in biology depends upon the imperfectly shared and homeostatically related morphological, physiological and behavioural features which characterize its members. The definitional role of mechanisms of homeostasis is reflected in the role of interbreeding in the modern species concept; for sexually reproducing species, the exchange of genetic material between populations is thought by some evolutionary biologists to be essential to the homeostatic unity of the other properties characteristic of the species and it is thus reflected in the species definition which they propose. (Boyd 1989, 17)

Boyd goes on to explicitly reject the possibility that there could be a single species concept because of the continual nature of species-hood and the different ways in which genetic information is passed on.
Any “refinement” of classification which artificially eliminated the resulting indeterminacy in classification would obscure the central fact about heritable variations in phenotype upon which biological evolution depends. More determinate species categories would be scientifically inappropriate and misleading. (Boyd 1989, 18)

So HPCs are a flexible concept with a successful history in biology. They are also highly relevant to the conceptual case for biodiversity eliminativism that the solution to the ‘species’ problem involved embracing its problem areas. A HPC account of species- hood requires that there are counterexamples and that some dimensions of species-hood such as reproductive isolation do not always co-vary with other dimensions such as cladistics (Boyd 1991, 142). The conceptual challenge to biodiversity has similar features. There are multiple ways to conceptualise biodiversity, no individual dimension gets everything correct, the dimensions co-vary but also vary independently of one another, and each dimensions seems indispensable to biodiversity.

Boyd provides the following conditions for homeostatic property clusters. t is a homeostatic property cluster if and only if:

1) There is a family F of properties which are contingently clustered in nature in the sense that they co-occur in an important number of cases.

2) Their co-occurrence is, at least typically, the result of what may be metaphorically (sometimes literally) described as a sort of homeostasis.

3) The homeostatic clustering of the properties in F is causally important.

4) There is a kind term t which is applied to things in which the homeostatic clustering of most of the properties in F occurs.

5) t has no analytic definition; rather all or part of the homeostatic cluster F together with some or all of the mechanisms which underlie it provide the natural definition of t.

6) Imperfect homeostasis is nomologically possible or actual: something may display some but not all of the properties in F; some but not all of the relevant underlying homeostatic mechanisms may be present.

7) In such cases, the relative importance of the various properties in F and of the various mechanisms in determining whether the thing falls under t - if it can be determined at all - is a theoretical rather than a conceptual issue.

8) Moreover, there will be many cases of extensional “vagueness” which are such that they are not resolvable even given all the relevant facts and all the true theories.
9) The causal importance of the homeostatic property cluster \( F \) together with the relevant underlying homeostatic mechanisms is such that the kind or property denoted by \( t \) is a natural kind.

10) No refinement of usage which replaces \( t \) by a significantly less extensionally vague term will preserve the naturalness of the kind referred to.

11) The homeostatic property cluster which serves to define \( t \) is not individuated extensionally. Instead, the property cluster is individuated like a (type or token) historical object or process. (Boyd 1989, 16–17)

Condition one in this definition requires that there exists a cluster of properties. Species, such as the kiwi have a cluster of recognisable properties. They have long narrow beaks, two legs, vestigial wings, nocturnal habits, etc which tend to instantiate together. The species concept distinguishes between a kiwi and an earth worm because the properties tend to cluster in different ways. Condition two requires that the clustering of those properties is determined by a homeostatic mechanism. There needs to be an underlying mechanism which tends to maintain clustering between the properties in \( F \). Without a mechanism to explain why kiwi properties and earth worm properties cluster differently, the clustering is coincidental. Condition three requires that the clustering is causally important. The clustering of the properties in \( F \) needs to produce an important effect. Speciation is a causally important effect because it impacts competition between organisms (among several other effects.)

Condition four requires that there is an identifiable kind. There must be a recognisable category which the properties cluster around. ‘Species’ is a recognisable category which picks out clusters of morphological, physiological, and behavioural properties. Other categories such as ‘all the objects within one meter of my knee’ are less recognisable. Condition five disqualifies analytic concepts as HPCs. Whilst ‘vixen’ picks out an important cluster of properties (female fox), the category is given by definition.

Condition six allows for the mechanisms of the homeostasis not to always co-vary. The morphological, physiological, and behavioural properties of species may vary independently of one another. Mistaking a honey bee for a wasp can be a painful mistake. Condition seven dictates that in cases of imperfect homeostasis, such as those described in condition six, membership in the HPC becomes a theoretical issue. Boyd emphasised the importance of definitions of scientific kinds to be determined by empirical observations and subject to theory-determined revisions (Boyd 1989, 10). In the case of species, the reproductive isolation of organisms alters the defining property clusters which pick out species (Boyd 1989, 18). Which organisms belong to which species is an ongoing discussion that is subject to revision based on the path that evolution takes. Condition eight requires that \( t \) have vagueness based counterexamples to its specific dimensions and allows for those dimensions to vary independently “There will be things which display some but not all of the properties in \( F \)” (Boyd 1989, 17). In section 2.5.1 I will discuss the multiple conceptions of species which includes discussion of how species may be categorised differently depending on the applied concept.
Condition nine requires that the HPC in question refers to a natural kind. The natural kind is the concept which is supported by the cluster of properties. There are many different ways to think of natural kinds. They are categories which pick out something real about the world or carve nature at the joints. ‘Gold’ picks out a natural kind but ‘the distance between my ear lobe and my big toe’ does not. Condition Ten states that attempting to understand \( t \) under a single dimension would be misleading because “Any such refinement would either require that we treat as important distinctions which are irrelevant to causal explanation or to induction, or that we ignore similarities which are important in just these ways” (Boyd 1989, 17). In section 2.5.2 I will argue that the biodiversity problem is similar to the species problem because understanding it along a single dimension means that we would fail to consider important biological phenomena.

The final condition, eleven, is a complex one which allows for the HPC to weather changes in specific properties over time. In a sense HPCs are bigger than any specific dimension. Evolution may discard one or more of the biological processes that are part of a homeostatic property cluster without loss of the cluster (Boyd 1989, 16–17). The biological species concept is a dominant model for many species but species did not always reproduce sexually. So that dimension has been added into species as sexual reproduction developed in organisms through evolution. The details of homeostatic property clusters are technical but it is the technical nature which leaves it uniquely suited to explain conceptually complex kinds like biodiversity. In the next sub section I will argue that the conceptually challenged property of biodiversity is actually a homeostatic property cluster.

2.4.2 Why Biodiversity is a Homeostatic Property Cluster

In the last subsection I explained what a homeostatic property cluster is. In this subsection I will argue that biodiversity is a homeostatic property cluster. I will argue that biodiversity satisfies the eleven conditions for a homeostatic property cluster set out by Boyd. Biodiversity satisfies all of Boyd’s (Boyd 1989, 16–17) conditions for a homeostatic property cluster. Where \( t \) stands for ‘biodiversity’, biodiversity is a homeostatic property cluster if and only if:

1) There is a family \( F \) of properties which are contingently clustered in nature in the sense that they co-occur in an important number of cases.

The family of properties which are contingently clustered in nature are the specific meanings of ‘biodiversity’ discussed in chapter one: species richness, phenetic diversity, phylogenetic diversity, etc. Santana has named this group of properties ‘SEGO’ for species richness, ecosystem services, genetic diversity, and others (Santana 2018, 6). Exactly which proposed specific meanings of ‘biodiversity’ are candidates for dimensions of biodiversity will be discussed in more detail in section 3.4. In that section I discuss what an HPC conception of biodiversity is not and argue that several proposed dimensions of biological variation such as evenly distributed abundance and ecosystem diversity are not dimensions of biodiversity. The other dimensions of biodiversity such as species richness, phenotypic diversity, and phylogenetic diversity constitute a family of properties because
they do co-occur in a number of cases. Species richness is a product of evolution, phylogenetic diversity is a product of the evolutionary relationships between those species, and phenotypic diversity is one of the important factors which allow us to determine one species from another.

2) Their co-occurrence is, at least typically, the result of what may be metaphorically (sometimes literally) described as a sort of homeostasis.

Homeostasis is the tendency of a common rise and fall among properties. In the case of biodiversity it is the tendency of dimensions such as species richness to co-vary with phylogenetic diversity and phenetic diversity. The role of ‘tendency’ is important here. Properties may vary independently while the other dimensions are maintained by the homeostasis. What is important for a HPC is that there is an overall homeostasis. This overall co-variance of properties is present for biodiversity because species richness increases with speciation. For two organisms to be considered distinct species they must possess different phenetic and phylogenetic characteristics.

There is sufficient homeostasis between the dimensions of biodiversity that our measurement strategy relies on using one dimension of biodiversity to approximate the other dimensions. This is called the surrogacy strategy and I discuss it in detail in chapter four. In that chapter, and chapters five and six, I argue that there is significant between-surrogate correlation of the dimensions of biodiversity. At times, accurately quantifying that correlation is difficult because of the different nature of the dimensions of the biodiversity. Despite the imperfect stasis between the dimensions, there is still sufficient homeostasis for us to use individual dimensions as key indicators of biodiversity. An excellent example of this is phylogenetic diversity. In section 5.5 I provide a detailed analysis of phylogenetic diversity and argue that it correlates highly with other dimensions of biodiversity such as: species richness, genus richness, habitat diversity, and functional diversity (Grenyer et al. 2007, 757 and Faith 1996, 1287). So there is a homeostatic relationship between the specific dimensions of biodiversity.

3) The homeostatic clustering of the properties in F is causally important.

The causal importance of property clustering is the relationship which Burch-Brown and Archer argue for. There is a relationship between high biodiversity and other important features such as ecosystem services and stability (Burch-Brown and Archer 2017, 985). A biodiversity ecosystem yields a variety of ecosystem services for human beings to thrive on. It provides greater options for adaptations, innovation, and alternative resources if preferred resources are depleted. Stability is another important cause of the clustering of the dimensions of biodiversity. The relationship between stability and biodiversity is complicated because it is not always the case that high diversity correlates with high stability (Maclaurin and Sterelny 2008, 121). In general though, we expect diverse ecosystems to weather change more successfully because ecosystems with all the same strengths have all the same weaknesses.
If Santana’s arguments against these relationships between biodiversity and its causally important effects were successful, there would still be other causally important biodiversity effects such as option value theory. Option value theory is the theory that future generations benefit from having as many environmental options as possible (Forsyth 2000, 414). We do not know exactly which biological resources will be important in the future so it behoves us to preserve the greatest biological diversity possible (Maclaurin and Lean 2016, 32). Preserving a diverse array of biological organisms essentially hedges our bets against multiple possible futures. There are common resources which we expect future generations of humans to need, such as clean air and water, but is not clear which organisms will be the most important to future generations. Unknown Flora or fauna may be important in the future for medical discoveries and we do not know which extinctions future generations may lament the most. Biodiversity is causally important because it preserves this option value (Maclaurin and Sterelny 2008, 154).

4) There is a kind term \( t \) which is applied to things in which the homeostatic clustering of most of the properties in \( F \) occurs.

The kind term \( t \) is ‘biodiversity’. Biodiversity is a cluster of its various specific dimensions such as species richness, phylogenetic diversity, genetic diversity, phenotypic diversity etc. The imperfect clustering of these dimensions together is the property of biodiversity. I say ‘imperfect’ because the clustering applies to most of the properties in \( F \) rather than all of them. Under condition 6, homeostatic property clusters allow for imperfect homeostasis.

5) \( t \) has no analytic definition; rather all or part of the homeostatic cluster \( F \) together with some or all of the mechanisms which underlie it provide the natural definition of \( t \).

‘Biodiversity’ has no analytic definition. I considered its analytic beginning in chapter one but argued that it quickly grew as a concept beyond species richness to accommodate other important dimensions. Concepts which are revised in the face of empirical evidence are not analytic. Instead they are \( a \ posteriori \) concepts which are revisable in the light of future experience. It is these kinds of theory-laden concepts, rather than analytic concepts, which Boyd has in mind when he developed the conditions for homeostatic property clusters (Boyd 1989, 10).

6) Imperfect homeostasis is nomologically possible or actual: something may display some but not all of the properties in \( F \); some but not all of the relevant underlying homeostatic mechanisms may be present.

Biodiversity demonstrates imperfect homeostasis. The motivating evidence for Santana’s conceptual challenges were the observations that its various dimensions come apart in important ways (Santana 2014, 768–73). Santana argues that there is not sufficient correlation between the dimensions of biodiversity for us to warrant considering it a property bundle (Santana 2014, 761). Two examples he uses are that species richness
increases as latitude decreases—but this effect is not consistent with other dimensions such as genetic diversity (Santana 2018, 4)—and that phylogenetic diversity and species diversity come apart on the South Africa Cape region. The eastern region of the cape has higher phylogenetic diversity while the western region has higher species richness (Santana 2014, 771). There is no contention between my arguments and those of eliminativists as to whether the dimensions of biodiversity demonstrate imperfect homeostasis. We only disagree on whether they demonstrate useful homeostasis as well as imperfect homeostasis.

7) In such cases, the relative importance of the various properties in F and of the various mechanisms in determining whether the thing falls under t - if it can be determined at all - is a theoretical rather than a conceptual issue.

Boyd’s seventh condition of HPCs states that it is a matter of current empirical theory rather than analytic analysis how important any particular dimension or mechanism is to the kind. This condition allows for specific dimensions or mechanisms to come or go from the kind. Reproductive isolation is an important dimension of the species concept, but given the possible ways in which species could have evolved there is some possible world in which the species concept does not have a dimension of reproductive isolation (Hull 1997). In the case of biodiversity it matters that the debate over which dimensions are included in biodiversity is a theoretical debate rather than a conceptual issue. Much of Burch-Brown and Archer’s paper—for instance—is dedicated to such a theoretical debate (Burch-Brown and Archer 2017).

That theoretical debate is important because biodiversity needs to adapt to new biological discoveries. If at some stage, human beings discover life on other planets, it may well be microbial. That planet would have biodiversity but the biodiversity concept for that planet would look quite different to that of Earth. The phylogenetic map between species would be much smaller if the life was (relatively) newly evolved. The species core would lack a biological species concept because the survival of genes is not reliant on sexual reproduction. Morphology would be a dominant dimension because it is a useful tool for studying microbial life forms. There would be lower functional diversity because of simpler interactions between organisms. The biodiversity concept adapts to evolution and biological discoveries, so theoretical debate is essential for its justification.

8) Moreover, there will be many cases of extensional “vagueness” which are such that they are not resolvable even given all the relevant facts and all the true theories.

Cases of extensional vagueness over membership in biodiversity are common in the literature. Angermeier argues that introducing non-native species into an ecosystem lowers biodiversity (Angermeier 1994, 600) whilst some authors argue that it increases biodiversity. The same problems occur for desert conservation. Some authors argue that biodiversity hotspots focus conservation away from biodiversity coldspots (Santana 2014, 772–73). Deserts are an important element of biodiversity, even if they are comparatively lower in biomass (Durant et al. 2014, 116). These are cases of extensional vagueness
because it is not clear if the dimensions they represent are a part of biodiversity or not. In chapters seven and eight of this thesis I dedicate much space to disentangling the concept of biodiversity from the concept of biological value. I argue that one of the reasons for the conceptual bloat that biodiversity has suffered is that dimensions of biological value have been added into it.

I will offer two further examples of extensional vagueness to justify the claim that biodiversity satisfies condition 8 of homeostatic property clusters: abundance and viruses. In section 3.4 I will argue that the abundance of species—in the sense that all species in an ecosystem have the same population— is not a dimension of biodiversity. Despite its importance for distinguishing species richness from species diversity, questions of abundance are a better dimension of ecosystem health than of biodiversity. That there is a strong argument both for including and excluding abundance as a dimension of biodiversity is a common feature of extensional vagueness.

Another extensionally vague element of biodiversity is the role that viruses occupy. Viruses are a quasi-species concept because, whilst they bear most of the properties of living organisms, they occupy an extensionally vague ground between living organism and chemical reaction (Van Regenmortel 1997, 18). Because of that vague middle ground, they also occupy an extensionally vague ground within biodiversity because ‘biodiversity’ fundamentally refers to the variation of biological organisms. In particular, the membership of viruses in biodiversity may not be resolvable given all the relevant facts and true theories. So, biodiversity satisfies condition 8 of homeostatic property clusters.

9) The causal importance of the homeostatic property cluster F together with the relevant underlying homeostatic mechanisms is such that the kind or property denoted by t is a natural kind.

Boyd has a realist preference for HPCs. In his ninth condition, he argues that they should be understood as natural kinds (Boyd 1991). In the case of biodiversity, there are a number of arguments that biodiversity is a natural kind, such as those by Maclaurin (Maclaurin 2017) who discusses biodiversity as a natural kind, natural quality, and HPC. These arguments are convincing. Biodiversity is a rapidly diminishing resource and conservationists are attempting to preserve it (Faith 2008, section 1). Biodiversity carves nature at the joints but is the task of conceptual analysis to explain how it does that. It is not surprising that such conceptual analysis would require much debate because by the very nature of homeostatic property clusters, biodiversity is an empirical concept which is subject to revision in the light of future experience. Biodiversity is a natural kind so it satisfies condition 9.

10) No refinement of usage which replaces t by a significantly less extensionally vague term will preserve the naturalness of the kind referred to.

Biodiversity satisfies condition ten because understanding biodiversity as one of its specific dimensions misses important elements of biological variation. Refining the usage of Biodiversity with a significantly less extensionally vague term is what happens if we
employ a specific meaning of ‘biodiversity’ which only refers to one or two dimensions of biological variation. We could replace biodiversity with a single dimension such as species richness but then we would have a conservation priority which overlooked other important biological properties such as phenetics, genetics, species diversity, and phylogenetic diversity. In sections 1.4.2 to section 1.4.7 I outlined several reasons to believe that there is more to biodiversity than species richness. Because of phylogenetic, phenotypic, and other differences two groups of 100 species can represent different amounts of biodiversity. Refining Biodiversity to just species richness will not preserve the naturalness of the kind; so too for the other dimensions of biodiversity. In section 1.4.8 I argued that the specific dimensions of biodiversity are counterexamples to any particular dimension of biodiversity which purports to represent all of biodiversity. That is because each dimension identifies an important element of biological variation. Thus it would not be an improvement to understand biodiversity along one or two dimensions.

11) The homeostatic property cluster which serves to define \( t \) is not individuated extensionally. Instead, the property cluster is individuated like a (type or token) historical object or process. (Boyd 1989, 16–17)

The homeostatic property cluster which distinguishes biodiversity from other parts of biology is not defined by a list of members. This is one way that a HPC concept is different from the classical multi-dimensional concept of Burch-Brown and Archer. Under the classical multi-dimensional concept biodiversity can be defined by a list of all its dimensions. Under a HPC concept biodiversity persists as individual dimensions are added or eliminated through historical processes. In a fictitious example, imagine that we discover a planet whose biological life was perfectly preserved in an instantaneous flash freeze. Such a planet still has biodiversity in the sense of species richness and evolutionary history but because none of the organisms are interacting with one another it has no functional diversity. If the planet thaws and the organisms survive then they will begin to interact and raise the functional diversity. The property cluster of dimensions which makes up biodiversity changes like a historical process.

Biodiversity satisfies all eleven conditions for a homeostatic property cluster. The conceptual challenges which biodiversity faces are not evidence that the concept should be eliminated. They are evidence that biodiversity is a homeostatic property cluster. Such challenges are normal for a HPC, and as such biodiversity is just another complex umbrella concept.

The conceptual challenges to biodiversity are less convincing when we consider them in relation to the conceptual challenges facing other complex properties like ‘gender’. Sex was once conceived of as a matter of biology for human beings (Ayala and Vasilyeva 2015, 730). A human being with an XX chromosome pair was female; a human being with an XY chromosome pair was male. Gender was then distinguished from sex to accommodate gender identity and counterexamples to the biological conception of sex (Mikkola 2009, 560; Stone 2004, 139). Now, some accounts of ‘gender’ make it a matter of placement along multiple continuums (Ayala and Vasilyeva 2015, 727; Mikkola 2009, 560). Biological sex is still a matter of chromosomes but the distinction struggles because
people’s chromosomes do not neatly group into binary categories (Ayala and Vasilyeva 2015, 727). They can have different combinations such as XXY. So, the gender concept also includes gender assigned at birth, the gender a person identifies with, the gender a person is attracted to, and the gender a person prefers to express themselves as.

Like biodiversity, gender also has multiple dimensions which tend to co-vary but also come apart in important ways. As an example, a person could be born with androgen insensitivity syndrome. In a normal pregnancy the Y chromosome detects androgens in the womb and triggers the development of male phenotypic characteristics. With androgen insensitivity syndrome the Y chromosome does not respond to androgens, so the foetus will develop female phenotypic characteristics whilst being a genetic male. They could identify as pan-gender whilst being attracted to males but express themselves as female. As with biodiversity, there has been a shift towards eliminating the concept of gender but that generated a push for retaining the concept (Stone 2004, 137). This was because, in part, social science benefits from having a concept which correctly identifies members of a vulnerable and oppressed group (Mikkola 2009, 561).

Biodiversity is just another sufficiently complex property in which multiple dimensions co-vary but can also act independently of one another. The conceptual case for biodiversity eliminativism cannot establish that biodiversity should be eliminated because of conflict between its dimensions. A homeostatic property cluster requires the clustering dimensions to conflict with one another. In this subsection I argued that biodiversity is a homeostatic property cluster. I argued that biodiversity satisfies the eleven conditions set out by Boyd. In the next subsection I will respond to Santana’s objections to the possibility that biodiversity could be a homeostatic property cluster.

**2.4.3 Santana’s Case against Biodiversity as a Homeostatic Property Cluster**

In this section I consider Santana’s objections to HPC conceptions of biodiversity. His arguments are a response to Burch-Brown and Archer’s suggestion that biodiversity could be understood as a HPC. He argues that biodiversity cannot be a HPC because there is no plausible underlying mechanism which could unite all the relevant properties. In response, I argue that speciation is a plausible homeostatic mechanism for the multiple dimensions of biodiversity. I also argue that Santana swiftly discounts the possibility that biodiversity is a homeostatic property cluster. He does not consider important similarities between the application of HPC to the *species* problem and the application of HPC to the *biodiversity* problem. I also argue that the counterexamples to specific meanings of ‘biodiversity’ which motivate Santana’s conceptual challenge are a normal feature of a homeostatic property cluster. Understood as a homeostatic property cluster, biodiversity is expected to have multiple dimensions which tend to co-vary but also come apart in important ways.

Santana considers Burch-Brown and Archer’s suggestion that biodiversity could be a homeostatic property cluster but argues that it is an implausible possibility. Burch-Brown and Archer point out that a HPC concept of biodiversity would avoid many of Santana’s objections because under a HPC concept multiple dimensions can vary independently of one another (Burch-Brown and Archer 2017, 976). In response Santana argues that there is
no plausible mechanism which could unite the different properties of biodiversity.

They don’t develop this suggestion at all, however, presumably because it is implausible that there is any mechanism maintaining homeostasis across the different dimensions of biodiversity. Primarily this is because different dimensions of biodiversity are not even properties of the same types of entities. (Santana 2018, 4)

The problem, as Santana portrays it, is that biodiversity is typically construed along three different hierarchies: genes, species or populations, and ecosystems. So, a plausible homeostatic mechanism needs to unite properties across different levels (Santana 2018, 4). As an example, Santana considers natural selection as a candidate for the homeostatic mechanism and rejects it.

. . . under most selective regimes it inhibits genetic diversity; mutation is the primary driver of genetic diversity, and the vast majority of genetic diversity created by mutation is quickly pruned away by selection. And selection’s effect on trait diversity is mixed, since it acts as a promotor by sustaining novel adaptations but also as an inhibitor through convergent evolution. (Santana 2018, 4)

Santana’s objections overlook important features of homeostatic property clusters. He argues that no single mechanism could unite the disparate dimensions of biodiversity. But Boyd’s seventh condition of HPCs allows for multiple mechanisms “. . . the relative importance of the various properties in F and of the various mechanisms in determining whether the thing falls under t.” (Boyd 1989, 16 emphasis added).

Santana also observes that the dimensions of biodiversity vary independently.

Species richness increases as latitude decreases, for instance (Hillebrand 2004), but whatever correlate of latitude causes this doesn’t seem to affect every dimension of diversity. Genetic diversity within species, for instance, is probably not affected, and even species richness within certain taxa, such as certain avian and planktonic groups, turns out to have the opposite relationship with latitude (ibid). (Santana 2018, 4)

But the conditions of a HPC allow for independent variation. Condition six states that “Imperfect homeostasis is nomologically possible or actual: something may display some but not all of the properties in F; some but not all of the relevant underlying homeostatic mechanisms may be present.” (Boyd 1989, 16). These oversights indicate that Santana is working with an idea of HPCs which is not fully fleshed out. An HPC concept which required a single homeostatic mechanism and perfect homeostasis would be inappropriate for biodiversity but the conceptual challenges facing biodiversity are not problematic for a pluralistic account of homeostatic property clusters.

The tension between a fully fleshed out account of homeostatic property clusters and the restricted notion that Santana is working with is evident when we consider the application of HPCs to the species problem. Santana uses the species problem to highlight why a HPC analysis could solve the biodiversity problem.

The virtue of the HPC account of kinds is that it doesn’t pick out any single property or set of properties as essential for kind membership, and thus tends to accommodate biological kinds better
than alternatives. Instead, it requires the presence of a mechanism which maintains similarity among kind members. Reproductive barriers, for instance, ensure that members of sexually-reproducing biological species tend to be more similar to each other than to other organisms. (Santana 2018, 3–4)

But Santana is misrepresenting how a HPC analysis addresses the species problem. Reproductive barriers only function as a homeostatic mechanism for species which reproduce sexually. That excludes micro-organisms, hybridisation, and ring species. In fact the homeostatic mechanism for species is much more complex because of the "imperfectly shared and homeostatically related morphological, physiological and behavioural features which characterize its members." (Boyd 1989, 17). Boyd later clarifies his position that he was not relying solely on Mayr’s biological species concept, as many commenters interpreted his position exactly as Santana did.

I didn't intend to subscribe to Mayr's biological species definition, but simply to refer to it, and to indicate that, for those cases in which it provides some insight into what defines a species, it validates the HPC conception. Every commentator I have read (or spoken with) about what I wrote has taken me to endorse roughly Mayr's conception, so obviously the problem lies in the unclarity of my exposition. (Boyd 1999b, 79)

The ‘species’ solution should be understood as an HPC with multiple homeostatic mechanisms which unite the morphological, physiological and behavioural features of distinct species. Santana uses species as an example of a successful HPC. Since SEGO (species richness, ecosystem services, genetic diversity, and others) can be united by a homeostatic mechanism in the case of species, it is difficult to see why—in biodiversity’s case—SEGO could not also be united by a homeostatic mechanism. A more detailed account of homeostatic property clusters indicates that a homeostatic mechanism which could unite the various dimensions of biodiversity is plausible. Santana is correct in arguing that the dimensions of biodiversity do vary independently of each other, but this kind of imperfect homeostasis is a feature of species as well as biodiversity. In fact Boyd explicitly rejects any changes to ‘species’ for the sake of eliminating the conceptual challenges.

Any “refinement” of classification which artificially eliminated the resulting indeterminacy in classification would obscure the central fact about heritable variations in phenotype upon which biological evolution depends. More determinate species categories would be scientifically inappropriate and misleading. (Boyd 1989, 18)

Homeostatic property clusters embrace conceptual complexity. So a more detailed analysis of HPCs indicates that they are well suited to the biodiversity problem. Important similarities between the species problem and the biodiversity problem indicate that a homeostatic mechanism can maintain similarity among the dimensions of biodiversity. It is just a matter of identifying it.

The homeostatic mechanism which maintains co-variance among the dimensions of biodiversity is speciation. I will not cover the relationship between speciation and every dimension of biodiversity but I will argue that speciation should satisfy Santana’s
concerns. Since species itself is a HPC, speciation already has a close relationship with morphological, physiological, and behavioural features. In the case of biodiversity, speciation affects species richness and diversity. It also affects phenotypic diversity because organisms must have distinct physical characteristics to be different species. Speciation therefore also affects genetic diversity because it is genetics which bring about phenotypic changes through mutation and selection. Speciation affects phylogenetics because the emergence of a new species is an adaptation to a new ecological niche or changing environmental pressures. Lastly, speciation also affects functional diversity because functions and other behavioural features are adaptations to ecological niches, and it is these adaptations which help to distinguish one species from another.

These examples satisfy Santana’s concern about the implausibility of a homeostatic mechanism for the first two levels of biodiversity. The diversity of genetic material, phenotypic features, evolutionary history, and functional adaptations are maintained in an imperfect homeostasis by the act of speciation. The third level, which contains ecosystem diversity, is more difficult to argue for because it is a property of ecosystems or sometimes groups of ecosystems (Santana 2018, 4). A possible response is to argue that ecosystem diversity is not a focus on a diversity of landscapes so much as on the unique functional adaptations which those landscapes produce. Whilst conservation might be concerned with rocky landscapes as well as deserts, biodiversity is a focus on the diversity of biological organisms. In that sense, biodiversity is concerned with the functional adaptations to rocky landscapes and the interactions between organisms which live in extreme desert temperatures. It is the functional diversity of organisms rather than a diversity of landscapes which are important targets for conservation. It just happens that preserving the landscapes is important for preserving the organisms.

One objection to this line of reasoning is to disagree with my argument and maintain the idea that maintaining a diversity of ecosystems is an important goal for conservation. In that situation the biodiversity theorist has the option of excluding ecosystem diversity from the biodiversity umbrella. One important difference between a HPC concept of biodiversity and the classical multi-dimensional concept advocated by Burch-Brown and Archer is that biodiversity does not include every dimension of biological variation. It only includes biological variations which are part of the homeostasis united by acts of speciation. If ecosystem diversity is not affected by speciation then the theorist is in a good position to argue that despite being an important goal for conservation it is not a part of biodiversity. One could object further and argue that ecosystem diversity should be included in biodiversity, but including too many dimensions takes the concept further down the slippery slope to Santana’s meaning-dilemma.

Excluding one or more dimensions from biodiversity is an important response to the conceptual case for its elimination. Santana’s concern about informativeness is motivated by the fact that we have folded so many dimensions into biodiversity that it has become too general. He echoes this concern in his objection to natural selection as a plausible candidate for a homeostatic mechanism. He argues that natural selection cannot be a plausible homeostatic mechanism for biodiversity because although it can increase functional diversity, it impedes genetic diversity instead of maximising it (Santana 2018,
4). He is correct that conservationists want species to flourish without maximising genetic diversity. There are many biological elements which are better for organisms and ecosystems when their diversity is not maximized. Scientists study the effects of nuclear fallout on mutation rates in birds. The meltdown at Chernobyl has increased rates of mutations, but the authors are concerned about this rather than excited about an increase in mutation diversity (Bonisoli-Alquati et al. 2015, 2). Therefore one response to Santana’s conceptual challenges is to exclude one or more dimensions of biodiversity. The advantage of a homeostatic property cluster concept of biodiversity is that it explains why certain dimensions should be excluded. I return to this topic in section 2.6.3 in which I argue that there are several important biological elements which are not a part of biodiversity.

In this section I considered Santana’s objections to HPC conceptions of biodiversity. Santana argued that biodiversity cannot be a HPC because there is no plausible underlying mechanism which could unite all the relevant properties of multiple levels. In response, I argued that speciation is a plausible homeostatic mechanism for the multiple dimensions of biodiversity. I also argued that Santana is too swift to discount the possibility that biodiversity is a homeostatic property cluster. He does not consider important similarities between the application of HPC to the species problem and the application of HPC to the biodiversity problem. The counterexamples to specific meanings of ‘biodiversity’ which motivate the Santana’s conceptual challenge are a normal feature of homeostatic property clusters. Understood as a homeostatic property cluster, biodiversity is expected to have multiple dimensions which tend to co-vary but also come apart in important ways. In the next two sections I will argue that a homeostatic property cluster conception of biodiversity avoids the conceptual case for biodiversity eliminativism.

2.5 The Success of an HPC solution for the species problem

In this section I will motivate the idea that the biodiversity problem is solvable by briefly discussing the species problem. Species are the canonical core of biodiversity and like the case of biodiversity their conceptualization and measurement are contentious (Santana 2014, 770). There are several important similarities between the biodiversity problem and the species problem. To highlight these similarities I will give a brief history of the multiple incommensurable conceptions of species. Then I will argue that that the biodiversity problem and the species problem share several important features. They both had multiple attempts at conceptualisation which identified important features of the concept. Since those features were important the different attempts could not be subsumed under one model so both concepts end up as multi-dimensional with strictly incommensurable dimensions. Then I introduce the species-the-category vs species-the-individuals objection to a homeostatic property cluster solution for the species problem. I argue that ultimately it is unsuccessful because, as Boyd argues, an HPC endorsement of species-the-individual tacitly requires an endorsement of species-the-category as a homeostatic property cluster (Boyd 1999a, 167). The solution to the species problem was to embrace its multidimensional nature. Given how many features the two problems share, it is therefore plausible to approach the biodiversity problem with a similar strategy
2.5.1 The Multiple Distinct Conceptions of Species

In this subsection I will give a brief account of the multiple distinct conceptions of species. Then I will discuss the biological species concept in detail as an example of the counterexamples facing the distinct conceptions of species. I discuss the biological phenomena of clonal species and asexual reproduction, before discussing the problems of hybridisation and ring species. I argue that this complexity is not a reason to eliminate the species concept. Instead the species problem and its solution set an important precedent for how to approach the biodiversity problem.

The problem with the species concept is that it is not clear how to justify the species classification. The classification of an atom is by the structure of its sub-atomic particles. This classification is justified because it divides up all the elements without any counterexamples. By contrast there are several different ways to classify species, and whilst they all have good justifications, they all also come with problem areas (Hull 1997). In What is Biodiversity? Maclaurin and Sterelny (2008, 32–33) discuss seven ways of conceptualizing species: biological, cladistic, cohesion, ecological, phylogenetic, phenetics, and typological. However, there are more than 22 species concepts currently in play in the literature and there seems to be little consensus about which is the best concept to use (Kocovsky, Ruffling, and Stauffer 2002, 143).

An ideal species concept would group organisms by similarity without counterexample, apply to all organisms, and be pragmatically maximal in terms of its operationalisability. But there is little agreement on the priorities for a species concept. Phenetic species concepts group organisms by clusters of properties, regardless of change over time. This is advantageous because it applies to extinct, extant, and yet to come species but there is no clear point when we can determine that a mutation has yielded a new species. The mate-recognition species concept claims that species are grouped by their disposition to recognize mates (Hull 1997). Organisms which mate together tend to be species. This idea works for species which mate but it is not universal. It struggles with clonal groups such as aspen trees, the brackern fern and asexually reproducing organisms such as bacteria (Mishler 1999, 309). Bacteriological species concepts have their own complex requirements (Chun, Goodfellow and Manfio 1997, 50) because they reproduce by binary fission, a process in which a mother cell splits into two daughter cells. As a group they maintain genetic variation by passing mutated genes between one another (Goodfellow, Manfio, and Chun 1997, 30).

Focusing on one species concept indicates how difficult it is to produce an ideal and comprehensive species concept. Consider the widely accepted biological species concept (Goodfellow, Manfio, and Chun 1997, 26). The biological species concepts claims that species are “groups of interbreeding natural populations that are reproductively isolated from other such species” (Hull 1997). Species of birds which cannot reproduce with one another are separate species. This is a highly intuitive idea for most organisms which mate with one another but it is not practically maximal for all of those organisms. Biologists as a whole seem to have adopted an instrumentalist response to this issue “The criteria that designates a ‘good’ species to cyprinid taxonomists may not be the same as those of salmonid researchers” (Kocovsky, Ruffling, and Stauffer 2002, 143).
The biological species concept does not group all organisms correctly. It cannot categorise clonal species or asexually reproducing species similar to the examples I have discussed in previous paragraphs. It also strongly requires supplementation with a further concept. Given that much of the early life on earth reproduced asexually, it would be odd to argue that there were no species on earth during this period (Hull 1997). It also cannot categorise viral species. After a great deal of debate viruses were recognised as species (Van Regenmortel 1997, 18). But the boundaries between unique strains are so fuzzy that categorizing them requires polyphetic classes which group organisms if they share most of the essential properties.

There are two further counterexamples to the biological species concept: hybridization and the ring species problem. Hybrids occur when two reproductively isolated species successfully mate with one another. The Grolar bear is a hybrid of the Grizzly and Polar bear which has occurred in both captivity and the wild. The problem is gene flow. Reproductive isolation is a useful way of categorizing species because gene flow typically occurs within a species rather than between them. The grolar bear and other hybrids are an important counterexample because they represent a mechanism for gene flow between species. So the notion of reproductive isolation which determines species in this case needs to be flexible, referring to organisms which are likely to breed together, rather than organisms which strictly have the capability of producing offspring (Maclaurin and Sterelny 2008, 32). But there is another mechanism for genes to transmit between species: the ring species.

A ring species problem occurs when there are two distinct species separated by terrain which is not traversable and whilst those species are reproductively isolated from one another, their sub-species can reproduce with one another (Cacho and Baum 2012, 1). The Eurasian greenish warbler has a range of sub-species living around the arid Tibetan Plateau as in figure 2.1 below.

![Figure 2.1: Distribution of Sub-species around Uninhabitable Terrain in a Ring Species. (Cacho and Baum 2012, 2)](image-url)
It cannot inhabit the plateau itself but it can inhabit the area around it. Two species of the warbler (Phylloscopus viridanus and Phylloscopus plumbeitarsus) live next to each other on the circumference of the plateau and are sufficient different that they cannot interbreed with each other (Irwin et al. 2005, 414). But a western sub-species of P. viridanus can reproduce with another sub-species which is further around the plateau, and that sub-species can reproduce with another sub-species which is slightly further to the east. Around the circumference of the plateau, various sub-species can reproduce with one another until P. viridanus has become P. plumbeitarsus. The two resulting species are still quite distinct from one another but they are not reproductively isolated because there is a continuum of sub-species between them.

This more detailed examination of the biological species concept has highlighted some of the difficulties faced by the species debate. The debate leaves us with a dilemma between species monism or pluralism. Monism (there is one correct species concept) will leave one field of study worse off whereas pluralism will falsely give the impression of a universal concept and leave us with less information to mitigate disputes between the concepts (Hull 1997). Hull’s famous paper ‘The ideal species concept and why we can’t get it’ identified the goals of an ideal species concept as universality, monism, and applicability (Hull 1997). He then scored seven species concepts on how they performed at these goals and concluded with some melancholy that they all perform similarly well. This concern can be alleviated if we remember that conceptual complexity does not imply no matter of fact about the property in question (Justus 2013, 367). Prejudice is an important concept in social science which can be measured in ways varied from rating images on a Likert scale (Aosved, Long, and Voller 2009, 2323) to how the introduction of double blind reviewing affects the rejection rate of submissions from female authors (Budden et al. 2008, 5). It is also conceptually complex, describing beliefs, actions, and subtle dispositions toward members of other groups, but like species-hood, prejudice is a real concept worth measuring.

In this subsection I gave a brief account of the multiple distinct conceptions of biodiversity. Then I focused on counterexamples to the biological species concept. I discussed clonal species and asexual reproduction hybridisation before moving on to the problems of hybridisation and ring species. I then argued that this is not a reason to eliminate the species concept. The best conception of species just is inherently multidimensional and complex. In the next subsection I will outline several important similarities between the species problem and the biodiversity problem to argue that there is an important precedent for treating biodiversity as a complex multidimensional concept.

2.5.2 Important Similarities between the Species Problem and the Biodiversity Problem
In this subsection I will argue that there are four important similarities between the ‘species’ problem and the biodiversity problem. In both cases there were a number of distinct attempts to explain the concept with a single set of necessary and sufficient conditions. No individual concept grouped all features correctly but most concepts identified an eliminable important feature of the concept. For both species and biodiversity
the concept bloated as more dimensions were added until the solution was pluralism. The species problem was solved by treating species as a multidimensional concept, so a multidimensional approach to the biodiversity problem is a plausible strategy.

The first major similarity between the species problem and the biodiversity problem is that both concepts have a number of alternative definitions. In the case of species the cladistic concept has to compete with the biological species concept which also competes with: genetic, ecological, phylogenetic, cohesion, typological, morphological, and polyphasic concepts (Maclaurin and Sterelny 2008; Hull 1997). In the case of biodiversity, species richness has to compete with species diversity, which also competes with: genetic diversity, phylogenetic diversity, phenetic diversity, ecosystem diversity and functional diversity. So both problems began with an important concept which needed to be adequately defined (Santana 2014; Burch-Brown and Archer 2017). In both cases pursuing that definition generated multiple definitions which performed very well for most examples.

Despite performing well for most examples, in both cases each definition has serious counterexamples. A cladistic concept implies the extinction of the old species when a new species arrives, biological concept fails with hybridisation, binary fission, and ring species, phylogenetic concept is better at describing than predicting, the cohesion concept is likewise a little too general for decisive prediction, and the ecological concept rests on the controversial concept of an ecological niche. In the case of biodiversity, species richness overlooks abundance, phenetic diversity glosses over genetic diversity, and phylogenetic diversity misses the importance of functional interaction between organisms. However, in both cases it is also clear that each competing concept has identified an important element of the concept which the others miss. So while the competing definitions disagree they are not also expendable. This implies that for both the species problem and the biodiversity problem both concepts have multiple dimensions which have counterexamples but are also not expendable.

In another important similarity the dimensions of both species and biodiversity are incommensurable and vary independently of one another. If we apply different concepts of species to the same group of organisms we will have conflicting results about the number of species represented by that group. If we apply different dimensions of biodiversity to a decision about introducing a new species we will have conflicting results about whether that act will change the biodiversity of the original group. So in both cases the individual dimensions vary independently of one another. In both cases those dimensions are strictly incommensurable with one another. We cannot make a conservation decision by comparing the genetic diversity of one ecosystem with the functional diversity of another. Analogously, if we are determining which ecosystem has the most species, we should use similar standards to do it.

The species problem has a number of similarities with the biodiversity problem. The solution to the species problem was to embrace the complexity of a multi-dimensional concept. So it is a plausible solution to approach the biodiversity problem in the same way. The most accepted view of species at the moment is that of realist pluralism such as Hull’s realist pluralism or Boyd’s homeostatic property cluster. That view persists despite problems such as incommensurability and independent variation among the dimensions.
Whilst Santana is legitimately concerned about incommensurability and independent variation, the species problem sets a strong precedent for successful multi-dimensional concepts. The key to success is to avoid looking for discrete boxes for the complex subject matter of the biological sciences and instead embrace its complexity.

2.5.3 The Species-the-Category vs Species-the-Individuals Objection and its Implication for a Conceptual Defence of Biodiversity

In this subsection I will introduce the species-the-category vs species-the-individuals objection to a homeostatic property cluster solution to the species problem and argue that is unsuccessful. I introduce a distinction between thinking of species-the-individual as a natural kind and species-the-category as a natural kind. I argue that a homeostatic property cluster framework can be used to justify either conclusion but the failure to distinguish between them is problematic for Boyd’s solution to the species problem. It is also problematic for my solution to the biodiversity problem because speciation plays an important role in my HPC account of biodiversity. Next I outline Boyd’s response that once we have accepted a homeostatic property cluster account of species, the best arguments for species-the-individual tacitly presume a species-the-category view. I consider an objection to this response but argue that Boyd is correct. Endorsing a homeostatic property cluster account of species-the-individual requires a homeostatic property cluster view of species-the-category.

The species-the-category vs species-the-individuals objection to Boyd’s solution to the species problem is that the homeostatic property cluster framework which Boyd supplies is ambiguous. It can be interpreted as a defence of species-the-category as a natural kind or it could be interpreted as a defence of species-the-individuals as natural kinds. The two views are distinct from one another (Boyd 1999a, 162). Under a species-the-category defence, there exists a natural kind named ‘species’ which picks out a taxonomic group of individuals which is a homeostatic property cluster of species concepts such as morphology and the biological species concept (Boyd 1999a, 165). Taken together, the HPC species is a natural kind as a category. By analogy, this is akin to justifying that Phylum is a natural kind rather than justifying that any particular Phyla such as Cnidaria picks out a natural kind.

Under a defence of species-the-individuals as a natural kind, each species is an individual natural kind (Boyd 1999a, 163). There is a homeostatic property cluster which justifies burrowing owls (Athene cunicularia) as a natural kind and there is a homeostatic property cluster which justifies staghorn coral (Acropora cervicornis) as a natural kind. But, there is no homeostatic property cluster which explains why burrowing owls, staghorn coral, and other organisms are species. The species problem is about finding a reasonable set of principles to justify a system of classification that accurately reflects existing species. A species-the-individuals response denies that there is such a set of principles and instead argues that individual taxa such as burrowing owls and staghorn coral are individual natural kinds. There is no species-the-category but there are species-the-individuals.
This objection matters for Boyd’s work because he seeks to solve the species problem by applying a homeostatic property cluster to it. He argues that the apparent conceptual incoherence of species is actually a cluster of various dimensions of specieshood correlating in an imperfect homeostasis (Boyd 1989, 17). Under a species-the-individuals interpretation of homeostatic property clusters, the species concept is conceptually incoherent and doesn’t pick out anything real about the world. Under a species-the-individuals interpretation, Boyd hasn’t solved the species problem because the solution to the species problem is that a species concept is inappropriate. So this objection requires Boyd to justify that his homeostatic property cluster justifies a species-the-category property cluster of speciation concepts rather than individual clusters of properties for species as individual natural kinds.

This objection matters for this project for several reasons. I have argued in section 2.4.3 that speciation is the homeostatic mechanism within biodiversity which is driving the imperfect homeostasis of its dimensions. I have also argued in this section that the success of homeostatic property clusters in addressing the species problem sets a strong precedent for the biodiversity problem. But if a species-the-individuals interpretation is correct, then homeostatic property clusters have not addressed the species problem and there is less precedent for applying the conceptual framework to the biodiversity problem. Lastly, adequately responding to the conceptual case for biodiversity eliminativism requires an application of the HPC framework which is much more like the species-the-category interpretation than the species-the-individuals interpretation. Similar to the species problem, Santana is accusing biodiversity of conceptual incoherence. The response requires establishing that biodiversity is a property cluster of various dimensions of biological variation. That requires demonstrating that the HPC solution the species problem is a property cluster of dimensions of specieshood and as such justifies a framework for species-the-category.

Boyd’s response to species-the-category vs species-the-individuals objection is to argue that if you believe in species-the-individuals as natural kinds, then you ought to believe in species-the-category as a natural kind. He does not need to argue for rationality of belief in the other direction because species-the-category dictates much of the structure of species-the-individuals. However, by arguing that a species-the-individuals interpretation also justifies a species-the-category interpretation, he argues that the two stand and fall together. It follows then that one cannot endorse one view and deny the other. In the case of biodiversity, this response addresses concerns about the species problem as a precedent for the biodiversity problem. This further insulates my account of biodiversity as a homeostatic property cluster against potential objections of biodiversity-the-category vs biodiversity-the-dimensions. It builds on the arguments in section 2.4.2 in which I have argued that it is the dimensions of biodiversity which cluster together to explain the conceptual coherence of biodiversity.

Boyd argues that once we accept a homeostatic property cluster account of species as natural kinds then it will apply to both species-the-category and species-the-individual. “I propose that biological species simply are HPC natural kinds. What is interesting is that the best arguments in favor of the alternative view that they are individuals rather than kinds actually support the thesis I am proposing” (Boyd 1999a, 167). This is because
species-the-category dictates species-the-individual and because endorsing a species-the-individual view requires accepting natural kind status about the ancestry and descent of that species.

When the residual positivist conception of kinds is stripped away, what the best arguments that species are individuals rather than kinds come down to, at least to a good first approximation, is that organisms which are in the same biological species must (a) be members of some initial population of that species or descendants of its members (so that a species cannot become temporarily extinct and then re-evolve) and (b) must, if contemporaneous, be members either of the same population or of populations which are relevantly reproductively integrated (so that the constituents of species have important internal relations with each other as constituents of paradigm individuals do). proposing (Boyd 1999a, 167)

So the view that the southern hairy-nosed wombat (Lasiorhinus latifrons) picks out an individual natural kind requires accepting two further propositions. Proposition a) that southern hairy nosed wombats are descended from the same initial population; and proposition b) that southern hairy nosed wombats are relevantly reproductively integrated with one another. In the case of the southern hairy nosed wombat this is isolated sexual reproduction. Boyd is being careful to phrase proposition b) so that it respects the variety of ways in which species pass on their genes.

Boyd then argues that propositions a) and b) tend organisms within species towards evolutionary unity.

The biologically serious arguments for (a) and (b) rest on the scientific claim that, without the operation of the factors they require, a family of populations will not possess the evolutionary unity characteristic of species level taxa. [Considerations of this sort are explicit in, for example, Hull 1978 and in Ghiselin, 1974.] (Boyd 1999a, 167)

The reason that the southern hairy nosed wombats are so similar to one another is because they come from a common ancestor and are reproductively isolated from other species. The twist, however, is that common ancestry and relevant reproductive integration also drive all speciation.

Let's suppose, for the sake of argument, that the considerations in favor of (a) and (b) are correct. Then common descent and reproductive integration of the sort they require are essential to establish the homeostatic evolutionary unity of biological species: the unity anticipated by inferences and explanations in evolutionary biology, and thus required for accommodation. But, as we have seen, the unity anticipated by such inferences and explanations is that appropriate to HPC kinds. Both species-as-individuals theorists and their opponents are tacitly treating biological species as HPC natural kinds. That's what they are. (Boyd 1999a, 167–68)

Common ancestry and relevant reproductive integration are required to justify a natural kind view of species-the-individual. But they are also sufficient to justify a natural kind view of species-the-category. The homeostatic property cluster account of species-the-category is just a framework intended to capture how common ancestry and reproductive integration drives imperfect homeostasis of phenotypic characteristics and adaptations etc.

Boyd then briefly considers an objection to his response. He considers whether it would be reasonable to argue that the natural kind status of species-the-individual are driven by one dimension of the species category rather than the whole thing. He gives the following example.

My favorite candidate for a programmatic definition of the species level in taxonomy is P. For any given species, S, the proper definition of S is provided by the formula 'the P which is instantiated in T', rather than by the associated homeostatic property cluster. [Where 'P' is some functional
He responds by arguing that this response fails because it retreats from an explanatory definition to a programmatic definition and programmatic definitions are far less useful for inference and explanation.

What the proposal fails to take account of however, is the distinction between programmatic and explanatory definitions. If we have an adequate programmatic definition of the species level (Good luck!) then we can indeed offer programmatic definitions of individual species in the way indicated. But such programmatic definitions would not be competitors with the explanatory definitions provided by the relevant homeostatic property clusters. (Boyd 1999a, 168)

The difference between these definitions is that a programmatic definition simply aims to meet the demands of its relevant discipline whereas an explanatory definition also explains why this particular definition meets this need (Boyd 1999a, 149). Defining a chemical element in terms of its position on the periodic table is a programmatic definition. Defining that same element in terms of its atomic number is an explanatory definition. Explanatory definitions are better than programmatic definitions because they are better suited to inference and explanation. Knowing the atomic number of a chemical element explains why it occupies the point on a periodic table that it does (Boyd 1999a, 150). “This conclusion is easy to see by reflecting on the fact that the programmatic definition "stuff which ...." (where .... specifies the role of gold in the periodic table of the elements) is not a competitor for the definition of gold as the element with atomic number 79” (Boyd 1999a, 168).

This is also true for definitions of species. A species-the-individual definition of a southern hairy-nosed wombat which relies only on the biological species concept and nothing else is only programmatic. It justifies the hairy-nosed wombat as a species because it is reproductively isolated from other species. It cannot seriously compete with a homeostatic property cluster account of species-the-category because that framework explains why the southern hairy-nosed wombat is a species. Species-the-category explains species-hood “in terms of common factors, relations of descent, gene exchange, etc.” (Boyd 1999a, 150). The response fails because defining species-hood in terms of one species concept is a much poorer explanation of species-hood than explaining it in terms of multiple dimensions such as ancestry, genetic exchange, and adaptations.

In this subsection I argued that the species-the-category vs species-the-individuals objection to HPCs as a solution to the species problem is unsuccessful. I outlined different interpretations of Boyd’s framework as arguing that either the category or the individuals are natural kinds. This was problematic for Boyd’s solution and this project because my solution to the biodiversity problem relies heavily on the species problem. Boyd’s response was that an HPC endorsement of species-the-individual tacitly requires an endorsement of species-the-category as homeostatic property clusters. This is because treating individual species as natural kinds requires natural kinds of common ancestry and relevant reproductive integration but the species category is a natural kind of how common ancestry and relevant reproductive integration drive speciation. I considered an objection that one could deny a species category but say that speciation is driven by one process such as the biological species concept. I agreed with Boyd that this response fails because it represents a programmatic definition and as such cannot compete with the explanatory definition which species-the-category as an HPC provides. This conclusion resolves the concern which the species species-the-category vs species-the-individuals objection raised for Boyd’s solution to the species problem and in turn my solution to the biodiversity problem.
2.6 Conclusion
In this chapter I discussed responses to the conceptual case for biodiversity’s elimination and outlined an account of biodiversity as a homeostatic property cluster. I summarised the conceptual case for eliminativism and discussed the work of Burch-Brown and Archer (2017) as an attempt to avoid Santana’s meaning-dilemma. I was sympathetic to Santana’s response to Burch-Brown and Archer, specifically his concern about the lack of informativeness of a classical multidimensional approach. I argued that the classic multidimensional concept of biodiversity does not escape Santana’s meaning-dilemma. Then I developed a conception of biodiversity as a homeostatic property cluster and addressed Santana’s objections to biodiversity as a HPC. Lastly, I argued that the success of an HPC analysis in dealing with the species problem makes it an excellent candidate to approach the biodiversity problem. There are a number of important similarities between the species problem and the biodiversity problem which set a precedent for the ability of an HPC to explain multi-dimensional concepts. In the next chapter I will argue that an HPC conception of biodiversity avoids the conceptual case for biodiversity’s elimination.
3 A Homeostatic Property Cluster Conception of Biodiversity Avoids the Conceptual Case for Elimination

3.1 Introduction
In this chapter I argue that a homeostatic property cluster conception of biodiversity avoids the conceptual case for elimination. The goal is not to present a compelling case for the correct way to understand biodiversity but rather to highlight that at least one conception of biodiversity avoids eliminativist challenges. In section 3.2 I argue that it avoids Angermeier and Karr’s concern about biodiversity misdirecting the goals of conservation because it embraces its multidimensional nature. Where biodiversity is more than species richness, maximising species richness is not the only priority for conservation. In section 3.3 I argue that an HPC conception of biodiversity also avoids Santana’s meaning-dilemma because general conceptions can still be informative. I justify this conclusion with the classical semantic measure of information (SMI) which measures the informativeness of propositions in terms of the possibilities which they exclude. In section 3.4 I protect an HPC account of biodiversity against Santana’s meaning-dilemma by identifying what biodiversity is not. According to the SMI biodiversity will be more informative as it excludes more possibilities. In section 3.5 I presume that my HPC analysis of biodiversity is unsuccessful and argue that there are still other reasons to retain biodiversity. Thus a HPC conception of biodiversity is general, informative, and avoids the conceptual case for eliminating biodiversity.

3.2 Understanding Biodiversity as a Homeostatic Property Cluster Reduces Misdirection
Understanding biodiversity as a homeostatic property cluster reduces misdirection in conservation because an HPC concept is multidimensional without incorporating all dimensions of biological interest. It focuses the efforts of conservation by excluding some biological elements from the set of goals but it also makes us engage with the multidimensional nature of the environment.

Understanding biodiversity as an HPC reduces misdirection because it sets a limit on the kind of dimensions which are a part of biodiversity. Homeostatic property clusters are united by a homeostatic mechanism (Boyd 1991, 141). Where the rise and fall of a dimension falls outside of that homeostatic mechanism it should not be considered part of that HPC. I have in mind here some of the dimensions which Angermeier and Karr are concerned about. Angermeier and Karr are both concerned about the presence of non-native species in ecosystems and a lack of focus on system integrity (Angermeier 2000, 377; Karr 1993, 302; Angermeier and Karr 1994, 692). They argue that biodiversity does not correlate well with these important features, so setting biodiversity as the goal of conservation misleads its efforts. Biological integrity is therefore a better goal for conservation than biodiversity (Angermeier and Karr 1994, 690). Their observation that biodiversity does not correlate well with either native conditions or ecological integrity is warranted. But treating biodiversity as a HPC explains this observation. Native conditions
and health do not correlate with biodiversity because they are not bound by a joint homeostatic mechanism. Native organisms and biological integrity are not dimensions of the umbrella concept. Biodiversity is operationalisable as a measure of biological diversities and not operationisable as a measure of health. So biodiversity is an important target for conservation but it is not the only important target (Burch-Brown and Archer 2017, 988).

Understanding biodiversity as an HPC also reduces misdirection because HPC’s are multidimensional, so focusing on a single dimension is erroneous. An analogy with ‘health’ is a useful example. Like biodiversity, health is an umbrella concept referring to many functions (in the case of ‘health’ they are normative but that need not be the case for ‘biodiversity’). It has general meanings such as ‘healthy’ and specific dimensions such as temperature, respiratory function, liver function etc. Like biodiversity, we measure health by sampling a number of specific dimensions and using them to approximate the umbrella concept of general health. During a visit with a general practitioner the doctor is likely to record your temperature, blood pressure, heart rate and a number of other specific dimensions. The best way to determine health is to measuring the normative function of multiple dimensions of health. Taken together, the results for multiple dimensions indicate the overall health of a patient.

Treating health as a complex umbrella concept reduces misdirection because it forces the patient to pay attention to the normative function of multiple individual dimensions of health. A diagnosis of ‘ill health’ forces us to engage with the specific dimension of health which is affected precisely because ‘health’ refers to a general umbrella concept which refers to multiple dimensions of normative biological functions. Likewise with biodiversity, a prognosis of biodiversity loss forces us to engage with the specific dimensions of biodiversity. Thus, it reduces misdirection because an undue focus on a single dimension is erroneous. Like biodiversity, health is a complex concept. Even if all biological functions are performing as they should, ill health can still occur if processes function as they should in an unfavourable environment (Matthewson and Griffiths 2017, 454). One of the causes of weight gain is spending adulthood in a high calorie environment, following a low calorie intake during foetal development (Matthewson and Griffiths 2017, 457). However, retaining health in its conceptually complex state provides a rich account of human health and more practical treatment advice. Knowing that obesity can be a product of a set metabolism in an unfavourable environment informs attempts to treat obesity. It reduces the likelihood of treatment being misdirected in a situation that we might have presumed a simpler model of health, one in which obesity is a result of a lack of will power.

Respecting the multidimensional nature of an HPC concept of biodiversity reduces misdirection in the same way. Saying ‘We measured the biodiversity of the region’ or ‘there has been a significant reduction in local biodiversity’ does not offer much information because biodiversity is an umbrella HPC concept which refers to multiple dimensions of biological diversities. Falling biodiversity should suggest further questions about which specific dimensions are affected. Treating species richness as interchangeable with richness of native organisms is fallacious reasoning because it exchanges one
dimension for another. It is as effective as concluding that an agent is ill because they have a headache and then treating them for a broken leg.

In this section I argued that understanding biodiversity as a homeostatic property cluster reduces misdirection of the efforts of conservation by setting limits on the dimensions which are included in biodiversity and embracing the multidimensional nature of conservation. In the next section I will argue that an HPC conception of biodiversity escapes Santana’s meaning-dilemma.

### 3.3 How Biodiversity as a Homeostatic Property Cluster Escapes Santana’s Dilemma

A homeostatic property cluster conception of biodiversity escapes Santana’s meaning-dilemma because biodiversity in the general sense is informative despite being multidimensional. The classical semantic measure of information measures the informativeness of propositions in terms of the possibilities they exclude (Bar-Hillel and Carnap 1953, 149). Santana is concerned that a general sense of biodiversity is uninformative because it reduces to ‘all of biology’. Under a S.M.I. analysis this is a concern that ‘biodiversity’ excludes no more possibilities than ‘all of biology’. In this section I will argue that this claim is false. A HPC cluster conception of biodiversity is informative because it excludes many possibilities which ‘all of biology’ does not. A strong response to Santana’s meaning-dilemma argument is to cease focusing on what biodiversity is and point out what it is not. By excluding possibilities I will argue that a HPC conception of biodiversity and other multi-dimensional versions are informative.

#### 3.3.1 The Classical Semantic Measure of Information

A recurring objection in the literature on biodiversity is that general meanings or umbrella concepts of biodiversity are uninformative because they reduce to ‘all of biology’.

Burch-Brown and Archer (2017) . . . focus on eliminativism as outlined in recent work by Santana (2014, 2016), who takes the position that biodiversity is neither a unitary natural entity nor justified by appeal to the normative goals of conservation biology. Similar arguments have also been made by Maier (2012), who doesn’t deny its natural existence but calls into question its normative and scientific utility, and Morar et al. (2015), who worry about both its ontology and its usefulness. (Santana 2018, 1–2)

Thus far the objection has relied on intuition rather than an analytic framework to motivate it. Work in the philosophy of information can elucidate this objection.

The classical measure of semantic information (hereafter S.M.I.) measures the informativeness of a proposition in terms of the possibilities it excludes (D’Agostino and Floridi 2009, 272). The sentence ‘I am walking to a movie or it is not the case that I am walking to a movie’ is less informative than ‘I am either walking to a movie or going home’ and both are less informative than ‘I am walking to a movie’. The propositions increase in informativeness as they exclude more possibilities. Given that I am walking, the proposition that ‘I am walking to a movie or it is not the case that I am walking to a movie’ truthfully describes all possible destinations. The proposition that ‘I am either
walking to a movie or going home’ is more informative because it excludes all possible further outcomes except for two destinations and the proposition that ‘I am walking to a movie’ is the most informative of the three because it excludes every possible destination except for one. In general, the more possibilities that a proposition excludes, the more informative it is.

An S.M.I. analysis has two implications for general conceptions of biodiversity. For biodiversity to be a more informative concept than the proposition ‘all of biology’ it must exclude more biological elements than ‘all of biology’. Also, the more biological elements which biodiversity excludes the more informative it will be. A general meaning of ‘biodiversity’ may exclude enough biological entities to be informative but it is only likely to be marginally more informative than ‘all of biology’. If biodiversity is an umbrella concept which includes at a minimum: species richness, abundance, phenotypic diversity, phylogenetic diversity, functional diversity, genetic diversity, ecological diversity, and process diversity, then there are few biological elements left to exclude and ‘biodiversity’ is at best marginally more informative than ‘all of biology’. In the next subsection I will apply the S.M.I. to the informativeness debate and argue that despite the generality of an HPC conception of biodiversity, it is still informative.

3.3.2 Biodiversity as a Homeostatic Property Cluster is General But Informative
A S.M.I. analysis of Santana’s objections shows that a homeostatic property cluster conception of biodiversity can be both general and informative. Santana is concerned about general notions of biodiversity being uninformative because they reduce to ‘all of biology’ (Santana 2014, 765). If ‘biodiversity’ excludes no more biological elements than ‘all of biology’ does, then it is no more informative than ‘all of biology’. Under a S.M.I. analysis Burch-Brown and Archer’s multidimensional concept is only marginally more informative than ‘all of biology’. Whilst the classical concept does exclude elements such as biodiversity effects, the inclusion of “any and all variation amongst biota” (Burch-Brown and Archer 2017, 981) excludes only a few biological elements which ‘all of biology’ does not. There is an inverse correlation between the informativeness of ‘biodiversity’ and the biological elements which it does not refer to. The more biological elements which are not covered by the concept’s umbrella, the more informative the concept is. These requirements are best satisfied by an HPC.

An HPC cluster is general because it includes multiple dimensions of biological diversities. Speciation creates a homeostatic mechanism which clusters together the relational properties of: species richness, phenotypic diversity, phylogenetic diversity, genetic diversity, and functional diversity. So an HPC concept of biodiversity is a general umbrella concept in the classical sense. ‘Biodiversity’ refers to a cluster of biological diversities. But it is still an informative concept because it excludes more biological elements than ‘all of biology’ does. Of the eight specific dimensions of biodiversity which I considered as candidates in chapter one I have excluded abundance, ecological diversity, and process diversity from the dimensions of my HPC concept of biodiversity. Under an HPC concept, membership in biodiversity is determined by how the particular property is affected by the homeostatic mechanism. If a dimension of biological diversity such as
ecosystem diversity is important to conservation but is not connected to the other dimensions of biodiversity via a homeostatic mechanism then it is not a part of biodiversity. It may be tempting to argue that it should be, but if we fold every element of biology into biodiversity then it becomes steadily more uninformative until it does reduce to ‘all of biology’

My HPC conception of biodiversity is distinct from Burch-Brown and Archer’s concept because it is not as multi-dimensional. Burch-Brown and Archer argue for a classical multidimensional concept which includes “any and all variation amongst biota” (Burch-Brown and Archer 2017, 981). Where Burch-Brown and Archer argue that biodiversity is an umbrella concept for all biological diversities, I have argued that some restrictions are important to increase its informativeness. Biodiversity eliminativists should prefer a restricted conception of biodiversity over the classical umbrella concept because it is more precise. Santana has argued that we should eliminate biodiversity in favour of its more specific dimensions (Santana 2018, 13). But this is unnecessary if we can maintain informativeness with a general conception of biodiversity. Restricted general conceptions of biodiversity such as an HPC conception achieve this. They are general concepts but they are still informative. So premise two of Santana’s meaning-dilemma argument is false. General conceptions of biodiversity do not reduce to ‘all of biology’. The key to avoiding uninformativeness in biodiversity is identifying biological elements which are not a part of biodiversity. In the next section I will identify several such elements and argue that they are not a part of a homeostatic property cluster conception of biodiversity.

### 3.4 What a HPC Conception of Biodiversity is Not

In this subsection I will justify my argument that a homeostatic property cluster conception of biodiversity is informative by identifying several biological elements and arguing that they are not a part of biodiversity. Since the informativeness of a concept is determined by the possibilities it excludes, arguing that a HPC conception of biodiversity excludes multiple biological elements demonstrates its informativeness. Under a homeostatic property cluster concept of biodiversity, this refinement of the concept makes it less extensionally vague. The debate over what biodiversity is has led to multiple dimensions of biological variety being subsumed under the biodiversity umbrella. At this point in the debate it will be useful to defend ‘biodiversity’’s informativeness by arguing what it is not. I will argue that the following are not a part of biodiversity: cellular diversity, chemical diversity, molecular biology, evenly distributed abundance, ecosystem diversity, biodiversity effects, or biological value. I begin with cellular diversity.

An HPC conception of biodiversity does not include cellular diversity. In *Ecological Hierarchy and Biodiversity* Chris Lean and Kim Sterelny argue that while biodiversity includes multiple dimensions of biological variety, authors do not pay attention to cellular diversity (Lean and Sterelny 2017, 110). Cellular diversity refers to the variation of cells in biological organisms at multiple levels. At a base level there is a difference between eukaryotic and prokaryotic cells. Eukaryotic cells have membrane-bound compartments, such as the nucleus, and appear in flora, fauna, fungi, and single-celled organisms. Prokaryotic cells are smaller, lack membrane-bound compartments, have
no nuclei and appear in bacteria and single-celled organisms without a nucleus. At a higher level cellular diversity refers to the different forms cells take. In human beings cells can function as metabolic storage, form part of a kidney, or become epithelial cells in the skin. Despite the wide biological variation of cells, cellular diversity has not been a focus for work on biodiversity and conservation efforts would not benefit from cellular ecosystem analyses. Lean and Sterelny reject cellular diversity as a dimension of biodiversity because a small number of building blocks can produce a great deal of diversity (Lean and Sterelny 2017, 110). So we needn’t focus on diversity of the smallest elements. Therefore cellular diversity is an interesting dimension of biological variety but it needn’t be a part of biodiversity.

Building on Lean’s work, biologists also study biochemical elements and molecular elements but these are also not typically treated as a part of biodiversity. Biologists also work on biochemical elements. Biochemists study the chemical processes within living organisms. Those chemical processes range from the energy transfer during metabolism to the roles of proteins and nucleic acids in organism growth. At a smaller level molecular biologists study the molecular causes of interactions between proteins and genes. Both fields of biology describe interesting dimensions of biological variation but neither are considered a part of biodiversity. This is likely due to the bottom level of biodiversity being treated as genetic diversity (Vira and Kontoleon 2012, 55). Molecular biologists do study genes but they are interested in the molecular causes which allow genetic function. Genetic diversity is the bottom level of biodiversity but biologists are also interested in lower levels of biology such as chemical processes and molecular causes of genetic properties. One could argue that molecular and chemical functions are a part of functional diversity but this claim would be at odds with conservational practice. Conservationists such as Witting and Loeschcke are concerned about the loss of unique genes (Witting and Loeschcke 1995, 206). They are not concerned with a diversity of biochemical reactions or a diversity of rates of cell division.

Biodiversity is not diversity in the sense of evenness. Organisations are evenly diverse when every group is represented by an equal number of members. A board with 12 members is more gender diverse if it is not dominated by men. The intuition about the relationship between abundance and biodiversity is often motivated in the same way.

Consider two hypothetical islands, each with only two species of vertebrate animals in equal abundance: two birds in one case and a bird plus a mammal in the other. Both islands have species richness = 2 (for vertebrates) and the same maximal value of species evenness. However, our intuition tells us that a bird plus a mammal represents more biodiversity than does two birds. (Vellend et al. 2011, 194)

But, in practice, evenness is not a feature of ecosystems or biodiversity because a healthy ecosystem food web requires large populations of prey to support smaller numbers of predators. If the reproductive cycle of the salmon yields 50 salmon to feed 50 brown bears then those brown bears are in trouble. Similar motivating examples suffer from analogous problems. Ecosystems with equal representations of tree species are maximally diverse in the classical sense but this proportion cannot carry on to every species in the ecosystem
(Vellend et al. 2011, 194). Limiting insect populations to one for every species of tree will have serious impacts on the survivability of trees and nutrient cycling in the soil. Ecosystems require greater abundance of smaller organisms, so whatever the relationship between biodiversity and abundance is, it excludes classical diversity in the sense of evenly represented groups.

One counterintuitive possibility is that biodiversity does not include ecosystem diversity. This is a contentious possibility because multidimensional concepts typically construe biodiversity as biological variation at three levels: genes, species, and ecosystems (Vira and Kontoleon 2012, 55). In the same way that biodiversity distinguishes between different species it should also incorporate a variety of ecosystems. Biodiversity is higher when our ecosystems include arctic tundra, wetlands, and desert. But Santana argues that ecosystem diversity is a problem for HPC conceptions of biodiversity because the multiple hierarchies make it more difficult to identify the homeostatic mechanism which controls the property cluster (Santana 2018, 4). One response to this objection is to accept that biodiversity does not include ecosystem diversity. The interest in ecosystem diversity can be also understood as an interest in a form of functional diversity such as adaptive diversity. Biodiversity would be lower without arctic tundra because we would lose the organisms which are adapted to survive in arctic tundra. However, biodiversity would not be obviously lower if we preserve the organisms from the arctic tundra whilst losing the tundra itself. Preserving the adaptations of the organisms seems to preserve most of what is biodiverse about arctic tundra. Preserving functional and phylogenetic diversity would therefore also preserve much of ecosystem diversity.

So we can eliminate ecosystem diversity as a dimension of biodiversity because its other dimensions already explain why we should conserve arctic tundra. Often we are not interested in preserving ecosystems until we discover living organisms within them. Submarine hydrothermal vents did not require conservation until we discovered that extremophile microorganisms could live in them. Pyrolobus fumarii is a microorganism which can survive at temperatures of up to 113 degrees Celsius (Hafenbradl et al. 1997, 19). Now hydrothermal vents warrant protecting if we want extremophiles to survive. So a case can be made that ecosystem diversity can be eliminated from biodiversity and subsumed under the other dimensions of biodiversity. It is not a conclusive case but it is an important possible element which can be excluded from biodiversity.

Biodiversity is also not the biological elements identified by Burch-Brown and Archer such as biodiversity effects. Where biodiversity is understood as a multidimensional concept, biologists are also interested in studying biodiversity’s effects, such as the relationship between a heterogeneous community and the patterns in their community processes (Burch-Brown and Archer 2017, 986). If the effects of biodiversity were a dimension of biodiversity then biodiversity would include its own effects, which would be conceptually odd. My HPC concept of biodiversity is different to Burch-Brown and Archer’s classic multidimensional concept because I exclude more possibilities from biodiversity than they do. However, I agree that biodiversity does not include biodiversity effects. These are of interest to biologists but they are not a part of biodiversity.

Lastly, biodiversity excludes multiple dimensions of biological value. The conceptual case for biodiversity eliminativism criticises biodiversity for failing to guide
conservation towards the environment’s valuable elements. Sarkar observes that protecting the holy trinity of genes, species, and ecosystems will not protect important biological phenomena such as the continental migration pattern of the monarch butterfly *Danaus plexippus*. *D. plexippus* has a migration pattern from Mexico to Canada but it takes multiple generations and wintering sites to cover the distance. This is an astounding example of biological phenomena because “the migratory instinct is hereditary and, yet, the precise geographical migration pattern is so specific” (Sarkar and Margules 2002, 301). Santana argues that focusing on biodiversity will miss the extensive loss of old growth forest so long as species richness is maintained (Santana 2014, 768). Angermeier argues that ‘biodiversity’ equivocates over “native (naturally evolved) and artificial (human generated)” conditions (Angermeier 1994, 600). Karr argues that biodiversity fails to adequately capture the health of an ecosystem (Karr 1993, 302; Karr 1991, 69).

These observations and arguments presume that the role of biodiversity is to preserve the valuable elements of the environment. In fact biodiversity has a very thorny relationship with biological value and in chapters seven and eight I will argue that biodiversity is a better guide to conservation normativity than biological value. Humans value the environment in multiple ways and there are multiple theories of biological value. A key response to Angermeier and Karr’s conceptual case for biodiversity eliminativism was arguing that biodiversity is one important part of the environment worth conserving but not the only part worth conserving. Biological value has a similar relationship to biodiversity because it also an important part of the environment but not a part of biodiversity. Santana’s smallpox example makes this mistake. He uses the extinction of smallpox as a counterexample to species richness because we are better off without smallpox (Santana 2014, 769). Smallpox falls under several dimensions of biodiversity but not under the instrumental value dimension of biological value, so it is perfectly sensible for us to prefer less species richness in this case. In chapters seven and eight of this thesis I will argue that biodiversity ought to be carefully distinguished from biological value. Biodiversity tracks some biological value but it does not track all of it.

In this section I argued that biodiversity is an informative concept by identifying the biological elements which the concept excludes. Santana has argued that general conceptions of biodiversity are uninformative because they reduce to ‘all of biology’. I provided an analytic framework for Santana’s argument by applying the classical semantic measure of information. The SMI measures the informativeness of a proposition in terms of the possibilities that it excludes. So I demonstrated that biodiversity is an informative concept by identifying the biological elements which the concept excludes. I argued that a homeostatic property cluster conception of biodiversity excludes: cellular diversity, chemical diversity, molecular biology, evenly distributed abundance, ecosystem diversity, non-relational properties, biodiversity effects, extinct species, and biological value.

I also used these biological elements to argue that biodiversity does not reduce to ‘all of biology’ because the concept excludes many more biological elements than the proposition does. Biology is a diverse field of study and biodiversity is only one object of study within it. This implies that premise two of Santana’s meaning-dilemma argument is false. General conceptions of biodiversity are informative. So we are not caught in a dilemma between specific and general meanings of ‘biodiversity’ because we can
demonstrate that general meanings are informative. Santana is correct to worry about lack of informativeness. As the concept of biodiversity has evolved to accommodate important biological elements we have rolled more and more dimensions into the concept. Under a SMI analysis concepts become less informative as they exclude fewer possibilities. Since an HPC concept of biodiversity excludes more possibilities than Burch-Brown and Archer’s classical multidimensional concept does, it is more informative. But an HPC concept is still multidimensional so it escapes Santana’s meaning-dilemma argument. It is both general and informative. In the next section I will argue that there would still be good reasons to retain biodiversity in conservation biology even if an HPC analysis were unsuccessful.

3.5 Other Reasons to Conserve Biodiversity in the Face of Eliminativism

In this section I will presume that the conceptual case for biodiversity eliminativism is successful, to argue that there are good reasons to retain biodiversity in conservation biology. This an important consideration given that, while an HPC account of biodiversity excludes a number of biological elements, it still incorporates a number of dimensions. Even if biodiversity is an uninformative concept which on occasion misleads conservation efforts we still lack a compelling case to eliminate the concept entirely. I will discuss Burch-Brown and Archer’s work in this area. They argue that in conservation biology biodiversity plays an important role as both an explanans and an explanandum. I consider Santana’s response to this observation and argue that he has not yet demonstrated that biodiversity is eliminable as an explanans or explanandum. Uninformative concepts which can be misleading can survive as analytic shortcuts for more complex ideas. Discussions which use ‘biodiversity’ are more efficient than those which list all the dimensions of biodiversity. In fact biodiversity is only one of a group of important cluster properties. Poverty, health, species, and stability are essential concepts, despite requiring multiple dimensions to adequately conceptually. The conceptual case for eliminativism is unsuccessful because eliminativism is a nuclear option. Scouring concepts from discourse requires a thorough justification.

As an explanans, Burch-Brown and Archer argue that biodiversity explains several other important environmental properties such as nutrient cycling and stability.

Seventeen ecologists write in Nature that ‘There is now unequivocal evidence that biodiversity loss reduces the efficiency by which ecological communities capture biologically essential resources, produce biomass, decompose and recycle biologically essential nutrients’ (Cardinale et al. 2012, p. 60). They also report agreement that current evidence supports the hypothesis that genetic, species and functional diversity tend to be associated with ‘insurance effects’, and that on average there is ‘greater temporal stability of a community property like total biomass at higher levels of diversity’ (2012, p. 60). (Burch-Brown and Archer 2017, 985)

The relationship between diversity and stability has a controversial history (Santana 2014, 776). The diversity-stability hypothesis was dominant until the mathematical models of Robert May predicted that too much diversity would lower an ecosystem’s stability (MacLaurin and Sterelny 2008, 121). Given the controversy, Burch-Brown and Archer have been careful to focus on consensus statements. These consensus statements give the
most up to date views of the relationship between biodiversity and ecosystem behaviour. Burch-Brown and Archer conclude that biodiversity plays an important role as an explanans in conservation biology because it explains ecosystem behaviour.

Burch-Brown and Archer also argue that in conservation biology biodiversity plays a role as an explanandum. Biodiversity plays an explanandum role in biology because scientists are interested in explaining the sheer variety of life. “biodiversity has an important role to play in science as an explanandum—which is to say that scientists often treat biodiversity as an aspect of living systems to be descriptively characterized and explained.” (Burch-Brown and Archer 2017, 982). Burch-Brown and Archer emphasise that this fascination with the sheer variety of life cannot be understood as a fascination with one of life’s dimensions.

For Wallace, the central object of scientific interest was the variety of life as such. His focus cannot be captured in any particular component such as species richness, nor certainly would he recognise the idea of biodiversity as reducible to a simple magnitude. Instead, he sought to characterise and explain the existence of innumerable forms, differing in innumerable ways, as well as the underlying processes by which these ‘variations on themes’ come to exist. (Burch-Brown and Archer 2017, 983)

Since all levels of biological variation are an object of study and Burch-Brown and Archer have argued that it would equivocate to treat all levels of biological variation as a single dimension such as species richness, it follows that multidimensional concepts of biodiversity are explananda. Scientists are interested in studying and explaining the sheer variety of life. They also focus on specific dimensions of biodiversity, but their characterisations of variation between organisms, communities, landscapes, and ecosystems are explanans which explain the explananda. The specific dimensions of biodiversity explain the multidimensional nature of biodiversity. “Amongst the central aims of biology, then (and particularly of branches like ecology, biogeography and conservation sciences) is the characterisation and explanation of biological diversity—what it is like and how it comes to exist.” (Burch-Brown and Archer 2017, 983).

In response, Santana considers Burch-Brown and Archer’s points but argues that biodiversity is still eliminable from conservation biology. He presents a formal schema for theory elimination but concedes that it does not account for the possibility of explanatory utility which Burch-Brown and Archer raise. He then adapts the schema in the following form (Santana 2018, 6).

**Santana’s Adapted Eliminativist Schema**

1) Biodiversity is a higher-level concept decomposable into distinct lower-level concepts species richness, ecosystem diversity, genetic diversity, and others [henceforth “SEGO”]

2) The objects picked out by SEGO don’t tend to share either
   a) A relevant cluster of properties, or
   b) A high degree of observable correlations

3) To support robust inductive generalizations across the group, a grouping must either share
a) A relevant cluster of properties, or
b) A high degree of observable correlations

4) [From (2) and (3)] The grouping picked out by SEGO doesn’t support robust inductive generalizations across the group

5) To be a natural kind or natural quality a grouping needs to support robust inductive generalizations across the group

6) Therefore, [from (1), (4), and (5)], biodiversity cannot be a natural kind or natural quality

7) To be a valid scientific kind a concept needs to either
   a) Be a natural kind or natural quality
   b) Or function ineliminably as an explanandum or explanans

8) Biodiversity doesn’t function ineliminably as an explanandum or explanans

9) Therefore, [from (6), (7), and (8)], biodiversity isn’t a valid scientific kind. (Santana 2018, 6)

Santana then argues for premise eight of his adapted schema. He contests that biodiversity is still eliminable from conservation biology as both an explanandum and explanans. In practice, biodiversity as an explanandum is often a stand in for a specific dimension of biological variation. Wallace was not curious about every level of biodiversity; he focused on the variety of form and adaptations. Likewise, MacArthur and Wilson seek to explain species richness, and Hubbel’s Unified Neutral Theory is about abundance and richness but not genetic, phenotypic, or functional diversity (Santana 2018, 7). Santana then argues that we are better off eliminating biodiversity as the explanandum in favour of its more specific dimensions because “Evolution and ecology explain the different aspects of biodiversity in different ways” (Santana 2018, 8). He concludes that ‘biodiversity’ is only eliminable in a very loose sense of linguistic shorthand. Strictly speaking and in practice biodiversity is eliminable as an explanandum.

Turning to the possibility of biodiversity as an explanans, Santana argues that we still have no reason to think that biodiversity is an explanans because the evidence provided by Burch-Brown and Archer is misrepresented. Burch-Brown and Archer have argued that biodiversity explains ecosystem behaviour such as nutrient cycling and stability but the empirical work identifies links between those effects and specific dimensions such as species richness (Santana 2018, 8).

For example: why are diverse communities more productive, where productivity is the rate of biomass production? According to Cardinale et al. they are more productive because “they contain key species that have a large influence on productivity, and differences in functional traits among organ- isms increase total resource capture” (2012). They aren’t appealing to biodiversity in all its multiple dimensions as an explanans, but only appealing to two dimensions— species and functional diversity. (Santana 2018, 8–9)

Santana’s other examples have a similar structure. Where Burch-Brown and Archer cite research on the link between biodiversity and productivity Santana argues that the explanans for productivity are actually complementarity and the selection effect. Both are properties of species richness and abundance, but crucially the explanation would not be
improved by appealing to phylogenetic distance or genetic diversity (Burch-Brown and Archer 2017, 9). Santana points out that this claim is not about mistaking a sampling method. He is not arguing that biologists are sampling species richness to indicate biodiversity and identify the relationship between biodiversity and productivity. He is arguing that including additional dimensions of biodiversity into our analysis adds no explanatory value. The *explanans* in these cases are specific dimensions of biodiversity rather than its multidimensional form so *biodiversity* is eliminable as an *explanans*.

The problem with Santana’s response is that he is using an inappropriate inference to the best explanation. His evidence is the set of academic studies of the effects of specific dimensions of biodiversity and his conclusion is the claim that scientists are interested in the dimensions of biodiversity rather than a high-level conception of biodiversity. However, there is an alternative explanation for the evidence and counter evidence to his conclusion. The large number of studies of specific dimensions of biodiversity is to be expected from modern academia which is becoming more and more specialised. Journals also set tight word limits which encourages narrow scopes in papers. It is a normal feature of scientific disciplines to find experts in one or two dimensions and few experts in everything. An expert who studies productivity is unlikely to be able to demonstrate a link between productivity and all of biology in 8,000 words or less. Biodiversity constitutes a big research project and tackling that project in small pieces does not indicate a lack of interest in biodiversity. By analogy, the fact that thousands of scientists work on aspects of climate change is not evidence that they doubt that climate change itself unites and explains other simultaneous effects.

There is also counter evidence to Santana’s conclusion. Santana concludes that the author is not discussing biodiversity because the details of the author’s work focus on one or two specific dimensions of biodiversity, (Santana 2018, 8). Whether Santana’s interpretation is correct is a decision for the author, but Burch-Brown and Archer pull examples from consensus statements of 17 collaborating authors. That kind of joint work looks like an attempt to give an up to date picture of biodiversity based on the scientific work on its specific dimensions. Conservation is particularly interested in a picture of biodiversity which is generated by multiple studies of the individual dimensions of biodiversity. Species richness can’t guide conservation triage alone because of the kind of problems which Santana points out (Santana 2014, 768–70). We need phylogenetic distance and genetic diversity to inform that decision so that we make the best conservation decision based on the current science.

A further issue with Santana’s response to Burch-Brown and Archer is his standard for eliminability. He outlines this in premises seven and eight of his revised eliminativist schema.

7) To be a valid scientific kind a concept needs to either
   a) Be a natural kind or natural quality
   b) Or function ineliminably as an *explanandum* or *explanans*

8) Biodiversity doesn’t function ineliminably as an *explanandum* or *explanans* (Santana 2018, 6)
For the sake of argument I will assume here that Santana has already demonstrated that biodiversity is neither a natural kind nor natural quality and is arguing that biodiversity is eliminable from conservation biology. However, Santana is unclear about why the eliminability of a concept is a reason to eliminate it. Just because we can do without a concept does not mean that we are better off without it. Maclaurin has argued that under Magnus’s account biodiversity can qualify as a natural kind by promoting inductive success (Maclaurin 2017, 64–65).

Concepts can have useful roles in science beyond the standard for eliminability which Santana uses. Analytic concepts are uninformative but play an important role in science. Biology is full of concepts such as ‘vixen’ which add no explanatory value but serve as linguistic shorthand. ‘Vixen’ is no more informative than ‘female fox’ and taxonomic ranks are flush with analytic concepts. The phylum ‘Chordata’ is an analytic concept which is no more informative than ‘organisms with notochords’. But we have not yet eliminated that concept in favour of its analytic meaning, despite it functioning eliminably. Santana himself finds a use for the ‘biosphere’ concept despite it being a polyphetic class of all other taxonomic ranks.

Biodiversity is meant to serve as a reliable indicator of biological value, but given the vast variety of ways in which we value the biosphere, this requires us to employ a broad and open-ended definition of biodiversity. (Santana 2014, 762–63 emphasis added).

Santana is concerned about ‘biodiversity’ reducing to ‘all of biology’ but uses ‘biosphere’ which is the name for the set of all biological organisms. An important function of kinds is to group other kinds. Such kinds are often eliminable in practice but the concepts survive in discourse as both language shortcuts and organisational tools.

Eliminability is not always a reason to eliminate. Concepts survive for all sorts of reasons. Santana is aware of these possibilities, which is why he is “happy to grant that, speaking loosely, biodiversity is a key explanandum in biological science” (Santana 2018, 7). My point is that ‘loosely eliminable explanandum’ are actually quite important. Boyd identifies loosely eliminable scientific concepts such as the classification of “elements into metals, semi-metals and non-metals” (Boyd 1999b, 83) which have endured as useful homeostatic property clusters. Even if there were nothing more to ‘biodiversity’ than a useful linguistic shorthand we should not eliminate it, because biology involves diagnosis and categorisation. Useful linguistic shorthand is essential for both of them.

Santana might object that he has other reasons for eliminating biodiversity than the observation that it is eliminable, but Santana’s conceptual standard for eliminability more generally would still eliminate several other important multi-dimensional concepts. Santana has already discussed problems with the stability concept (Santana 2018, 10). He observes that it has seven different conceptions which can vary fairly independently of one another (Santana 2018, 11). Weeds in a garden have low stability in the sense that they can be sprayed or pulled out but high stability in the sense that somehow, they always come back (Justus 2013, 360–61). So like biodiversity, stability can be conceptualised along multiple dimensions, and needs to be specific to be measured, but a general account might be incommensurable and uninformative. Stability has the same problems as biodiversity.
Biodiversity has those conceptual issues not because it is a concept stretched to breaking point but because biodiversity is an umbrella concept and many umbrella concepts have conceptual tensions. They group together multiple dimensions but are typically operationalisable one dimension at a time.

One example of this is health. It is a concept for normative biological function so it has multiple dimensions such as temperature, liver function, blood pressure, psychological distress, etc which can all vary fairly independently of one another. Blood pressure and temperature can be fine if a bone is broken. Digestion can be completely healthy whilst you have a headache. Poverty is another important complex concept. Your annual earnings can be high compared to some countries’ GDP whilst making it difficult to afford the basics in your country. You might have just enough money to survive week to week but not enough to create savings. You can have access to the material necessities but little disposable income. There are many complex cluster properties which appear eliminable in favour of their specific dimensions. But we group their dimensions together because the umbrella concepts highlight something important which we need to monitor. Conceptual complexity is not a good motivation for eliminativism (Justus 2013, 353). We need accounts of stability, poverty, health, and biodiversity. Even if they are complex, multidimensional and no more informative than the sum of their dimensions, concepts like biodiversity track an important collection of properties.

The conceptual case for biodiversity eliminativism struggles because eliminativism is a nuclear response. Concepts like ‘phlogiston’ are only eliminated from discourse once they have ceased to be useful. However, the conceptual case for eliminativism infers from conceptual difficulties to the claim that we should scour the concept from academic discourse. That kind of conclusion requires an enormous body of evidence. Biodiversity eliminativists correctly identify a number of problem areas for the concept, but motivating the elimination of biodiversity requires a very strong case. At this point a successful case has not been made. Biodiversity is only as problematic a concept as other umbrella multidimensional concepts, and if it is uninformative and misleading, it can still function as an: explanans, explanandum, linguistic shorthand, useful pragmatic concept, or the collective representation of multiple specific dimensions. Biodiversity eliminativists correctly identify a number of problem areas for biodiversity but more can be done to correct those problems before abandoning the concept. The conceptual case for biodiversity eliminativism requires more evidence than we currently have.

In this section I presumed that an HPC analysis of biodiversity was unsuccessful and argued that there were still good reasons to retain biodiversity in conservation biology. I discussed Burch-Brown and Archer’s arguments that biodiversity functions as both an explanans and explanandum. Biodiversity explains other ecosystem effects and biologists are interested in explaining the sheer variety of life. I considered Santana’s objection to these arguments and concluded that he has not been clear about the step from ‘we can eliminate a concept’ to ‘we ought to eliminate a concept’. He is correct that in practice scientists work with one or two specific dimensions of biodiversity but incorrect that this implies we ought to discard biodiversity. Santana’s standard for elimination would also cost us a great number of important multidimensional concepts such as: stability, health, and poverty. The problem with the conceptual case for elimination is that it is a nuclear
response to the problematic nature of multi-dimensional concepts. The tension between multiple dimensions, informativeness and operationalisability is not unique to biodiversity, so it is not a sufficient reason to eliminate it. ‘Biodiversity’ does have some conceptual issues but we need more evidence than we currently have to eliminate it from conservation biology.

3.6 Conclusion
In this chapter I argued that an HPC conception of biodiversity avoids the challenges raised by the conceptual case for eliminativism. It avoids the concerns of Angermeier and Karr because understanding biodiversity as a homeostatic property cluster reduces conceptual misdirection because it makes biodiversity more complex than species richness and allows for other important elements of the environment such as health. An HPC conception of biodiversity also avoids Santana’s meaning-dilemma because general conceptions can still be informative. The classical semantic measure of information (SMI) measures the informativeness of propositions in terms of the possibilities which they exclude so the key to a general conception of biodiversity which is also informative is to pay attention to what biodiversity is not.

To that end I identified biological elements which biodiversity should not incorporate, and argued that there were important differences between biodiversity and biological value. The exclusion of these possibilities from my HPC conception of biodiversity ensures that it is both informative and general. Therefore a homeostatic property cluster conception of biodiversity avoids the conceptual case for eliminating biodiversity. Furthermore even if his meaning-dilemma argument were successful there are other reasons to retain biodiversity. For these reasons, and my conclusion that a HPC conception of biodiversity reduces misdirection in conservation and escapes the meaning-dilemma argument, I conclude that biodiversity survives the conceptual case for its elimination. In the next chapter I shift my attention to the empirical case for eliminating biodiversity. I discuss Santana’s argument that biodiversity is an empirical poor fit for the goal we want it to play in conservation.
4 The Surrogacy Strategy for Measuring Biodiversity and the Empirical Case for Its Elimination

4.1 Introduction
In this chapter I will introduce the empirical case for eliminating biodiversity and begin an argument that it is unsuccessful. I say ‘begin’ because it will require three chapters to establish that the empirical case for eliminativism is unsuccessful. In section 4.2 I outline the empirical case for biodiversity eliminativism. The empirical case is an attack by Carlos Santana on the methodology for measuring biodiversity. Santana builds this empirical case on the work of biodiversity’s defenders, who also express concerns about the methodology of biodiversity measurement. Biodiversity is measured using the surrogacy strategy which uses individual dimensions as measurement surrogates. In section 4.3 I will explain how the surrogacy strategy works and demonstrate it with the example of using resilience as a measurement surrogate for Angermeier and Karr’s conception of biological integrity.

In section 4.4 I discuss and defend the surrogacy strategy against its limitations. I introduce the problem of strict incommensurability between dimensions of biodiversity. The various dimensions of biodiversity such as species richness and morphology cannot be measured as a single biodiversity value. I argue that the dimensions of biodiversity are not strictly incommensurable. Morphology is incommensurable with species richness, but we can still meaningfully compare the morphology diversity and species richness of two different ecosystems. Then I discuss concerns about multiple surrogates. Santana discusses Sarkar’s (2005) distinction between true and estimator surrogates. He argues that the relationship of estimator surrogate to true surrogate to biodiversity to biological value exacerbates imprecision in the surrogacy strategy. In response I argue that including biodiversity in this surrogate chain does not weaken the correlation between estimator surrogate and biological value.

In section 4.5 I argue that the empirical case for biodiversity eliminativism is misrepresenting the state of biodiversity measurement. I draw a distinction between within-surrogate operationalisability—how operationalisable the specific dimensions of biodiversity are—and between-surrogate operationalisability—how operationalisable biodiversity is as a single property. I argue that Santana’s arguments overlook this distinction. He shifts between criticizing the operationalisability of specific dimensions of biodiversity and criticizing the correlation between dimensions. I also argue that imperfect correlation between biodiversity surrogates is an important feature for measuring an umbrella concept. I conclude that the plausibility of the empirical case is incompatible with the details of biodiversity’s measurement methodology. Chapters five and six outline the details of how specific dimensions of biodiversity are measured and will establish two propositions. The expanding multiplicity of biodiversity measures is overblown and the empirical case for biodiversity eliminativism is unsuccessful.
4.2 The Empirical Case for *Biodiversity* Eliminativism

The empirical case for *biodiversity* eliminativism has two components, Santana’s poor fit argument and current methodological debate over biodiversity measures. I construct Santana’s poor fit argument by appealing to the textual evidence of his many claims about the empirical shortcomings of *biodiversity*. His remarks are general but serious. He argues that biodiversity is not straightforwardly operationalisable, lacks surrogate correlation, exacerbates imprecision in the conservation process, and that the true surrogates of biodiversity do not track their goals well (Santana 2017, 86; Santana 2018, 6; Santana 2014, 765–68). The current debate over how to measure biodiversity is not an argument for eliminating *biodiversity*, but it does motivate the argument. Fierce debate over the correct way to measure biodiversity, coupled with concerns about incommensurability and the number of available measures, give the impression that there is little consensus on how to measure biodiversity. The poor fit argument relies on this impression to be plausible. It will be the task of this chapter to demonstrate that this impression is misleading. Despite healthy debate as to whether this is so, measures of biodiversity are empirically rigorous.

4.2.1 Empirical Case I: Santana’s Poor Fit Argument

In this section I will formalize Santana’s poor fit argument. I begin by presenting a summary of Santana’s main claims that biodiversity is a poor empirical fit for conservation biology through textual evidence. Santana does not summarise his objections into a single formalised argument against *biodiversity*. He does present a formal argument that *biodiversity* is eliminable as a scientific kind but the conclusion of that argument is focused on biodiversity’s conceptual role (Santana 2018, 6). Compared to the conceptual case, Santana’s empirical case against *biodiversity* is just as important. I will assemble his empirical objections into a single argument and formalise it into premise-conclusion format. Next I will outline my strategy for disagreeing with his conclusion in this chapter and chapters five and six. I outline five key propositions which I will present evidence for. The truth of these propositions implies the falsity of the main premises in Santana’s poor fit argument and give us good reason to believe that biodiversity is an empirically good fit for use in conservation biology.

Santana has argued that on empirical grounds biodiversity is a poor fit for the role we want it to play in conservation biology. He argues that biodiversity is not straightforwardly measurable.

> The principle role played by the concept ‘biodiversity’ in conservation biology is as a comparative measure of value. Biodiversity does not fulfil that role well, in part because it is not a straightforwardly measurable quantity. (Santana 2017, 86)

He argues that the dimensions of biodiversity which we measure do not correlate enough for us to consider biodiversity as a property bundle.

> Against pluralists, who hold that biodiversity consists of distinct but correlated properties of natural systems, I argue that the supposed correlations between these properties are not tight enough to warrant treating and measuring them as a bundle. (Santana 2014, 761)
He argues that those dimensions of biodiversity do not support robust inductive generalisations. “The grouping picked out by SEGO [species richness, ecosystem diversity, genetic diversity, and other] doesn’t support robust inductive generalizations across the group” (Santana 2018, 6). He argues that the inclusion of biodiversity in our methodology from estimator surrogate to biological value makes the approximation less precise than if we had just approximated biological value from the estimator surrogate without biodiversity.

“I agree with Sarkar that biodiversity is a placeholder, but while Sarkar sees it as a useful placeholder, in fact the placeholder itself unnecessarily complicates the picture . . . As normative descriptions of the practice of conservation biology, series B is more economical than series A [the methodology which employs biodiversity as a proxy], and less prone to errors due to misrepresentation of one member by another.” (Santana 2014, 765 my emphasis)

He also argues that the true surrogates around which biodiversity is thought to orbit either fail to approximate biodiversity, fail to approximate biological value, or fail the pragmatic requirements of conservation biology.

“It has been frequently pointed out that [Species] richness does not even capture intuitive ideas about what diversity is, such as abundance and disparity.” (Santana 2014, 768)

“But the relative abundance of species also fails to represent biological value well . . . for one thing . . . it could be that a larger population of that species would impact other populations adversely . . . and in terms of value to humans, rarity itself might sometimes be preferable.” (Santana 2014, 770)

“So although mathematically described local morphospaces could provide insight into the evolution of a lineage, local morphospaces do not meaningfully do not capture a broad notion of biodiversity.” (Santana 2014, 770)

“Genetic diversity, however, is nearly a non-starter. A “gene soup” containing a random sample of genetic material from a given place would furnish little useful in the way of important information for several reasons.” (Santana 2014, 771)

“So ecological diversity, like the measures we have examined fails to correlate reliably with other types of biological diversity.” (Santana 2014, 772)

“And although a variety of functional roles must be occupied to keep biological processes in place, we can explain those roles and those process without needing to call on a biodiversity concept.” (Santana 2014, 773)

Santana argues that taken together these observations justify the claim that biodiversity is a poor empirical fit for conservation biology. Consider the following formalization of Santana’s poor empirical fit argument.

The poor empirical fit argument

1) General conceptions of biodiversity are not straightforwardly measureable.
2) There is not sufficient correlation between properties for biodiversity to be considered a property bundle.
3) The dimensions of biodiversity do not support robust inductive generalisations across the group.
4) The inclusion of biodiversity in the conservation process exacerbates imprecision between the measured target and the conservation goal.
5) Individual dimensions of biodiversity are either:
   a. Not operationalisable
   b. Do not accurately track biodiversity
   c. Or do not accurately track biological value
6) If premises one to 5) accurately describe biodiversity then biodiversity is a poor empirical fit for its role in conservation biology.
7) Therefore: Biodiversity is a poor empirical fit for its role in conservation biology.

This argument collects Santana’s empirical objections to the use of biodiversity as a conservation goal. It is philosophically valid, but the truth of premise six in particular is contentious because the goals of conservation biology can be justified for other reasons. A goal is a good empirical fit if it is more empirically suitable than the available alternatives. However, Santana argues that premises one to five are a sufficient reason to eliminate biodiversity.

“While taken individually these arguments must be tentative, relying as they do on uncertain empirical claims as well as tendentious assertions of what is worth conserving, taken as a whole they are strong enough to cast serious doubt on the usefulness of biodiversity as the primary target of conservation.” (Santana 2014, 768)

It will be the task of this chapter and the next two to demonstrate that biodiversity is not a poor empirical fit for its role in conservation biology.

I will address the individual premises of Santana’s argument at different stages. In section 4.3 I will explain how biodiversity is measured with the surrogacy strategy. Understanding the surrogacy strategy is important to understanding why an empirically suitable conservation goal should not satisfy premises one to five. After outlining the surrogacy strategy I respond to Santana’s argument by defending the strategy against its limitations. I discuss the problem of strict incommensurability between dimensions of biodiversity in section 4.4.1 and 4.4.2. In those sections I discuss premises one and three since it is incommensurability which drives difficulties with operationalisability and robust inductive generalisations. In sections 4.4.3 and 4.4.4 I discuss problems with multiple surrogates. In these sections I discuss premises two, four, and five since lack of correlation, increased imprecision, and concerns about the individual dimensions of biodiversity are problems of multiple surrogates. In section 4.6 I discuss premise six that “If conditions one to five accurately describe biodiversity then biodiversity is a poor empirical fit for its role in conservation biology”. In the next section I explain how the debate over the best way to measure biodiversity has unintentionally motivated Santana’s poor fit argument. This is the second part of the empirical case against biodiversity.
4.2.2 Empirical Case II: How Biodiversity Conservationists Unintentionally Motivate the Empirical Case for Biodiversity Eliminativism

Biodiversity conservationists are academics who wish biodiversity to retain its place as a goal of conservation. Understandably, there is considerable debate between academics about the best way to measure biodiversity. This debate often takes the form of arguing against other measures of biodiversity whilst promoting the author’s newer, preferred measure (Maclaurin 2017, 56). The net effect of this debate over time has been a large increase in the number of ways to measure biodiversity. Biodiversity is a complex property and the ways to measure it seem to be exponentially increasing (Maclaurin 2017, 56). Given that each measure produces different results and that selecting a measure is at a conservationist’s discretion, the expanding multiplicity of available measures give the impression that biodiversity calculation is imprecise. It appears as if there are large numbers of measures with varying results so it is possible to select the measure which best advances an author’s conclusion. Consider the following comments on the state of biodiversity measurement methodology.

Several developments are needed to provide a truly firm foundation to the measurement of diversity. First, more attention to and development of methods to account for the fact that collected data are sampled data are needed . . . Second, rather than developing new measures of diversity by ad hoc processes we hope to see a further focus on fundamental ideas like variance and information (Maurer and McGill 2011, 64)

Our current understanding of biodiversity is a mess. It is a fortunate, productive, and useful mess but a mess none the less. This can be traced to the lack of a guiding set of standards from which to assess the value of proposed biodiversity measures. Although measures are tested, the testing has often been piecemeal across conservation biology and related disciplines leading to conflicts over whether a metric has been proved. (Maclaurin and Lean 2016, 20)

The problem is that the rigorous discussion of the best way to measure biodiversity gives the impression that there is little consensus and that biodiversity values are still up for grabs. Biodiversity conservationists exacerbate this impression by discussing the strict incommensurability of biodiversity’s dimensions, without explaining how biodiversity might still be operationalisable.

Perhaps this wish bundles together dimensions of biodiversity that are strictly incommensurable. Certainly we do not as yet have a translation of this imperative into any simply applicable measure of biological difference, and perhaps we will never have one. (Maclaurin and Sterelny 2008, 177)

There are innumerable dimensions along which living things can be compared, so it is impossible to describe biodiversity as a simple magnitude (Gaston 2011) . . . To fully describe a region’s biodiversity would be impossible. (Burch-Brown and Archer 2017, 971)

It is not surprising that there is a bewildering array of tools available to those who would measure biodiversity. There are of course countless respects in which organisms and ecosystems vary. (Maclaurin and Lean 2016, 19)
A related problem with broad definitions, discussed by Sarkar (2002, 2005), Norton (2006), and recently Maier (2012), is that multiple “dimensions” or biological diversities at different scales are incommensurable. This makes it seem impossible to develop an additive “index” of biodiversity to rank areas in terms of their overall diversity. (Frank 2017, 98)

The empirical case for biodiversity eliminativism seems more plausible when we consider it in the context of these comments. Scientific measures need to be as precise as possible, but biodiversity has an expanding multiplicity of measures to choose from. Biodiversity conservationists speak of the strict incommensurability of biodiversity’s dimensions, but comparing the biodiversity of multiple ecosystems requires some commensurability. The debate over biodiversity’s measurement methodology gives the impression that the measurement problem is at an impasse. Santana’s empirical poor fit argument uses this impression to motivate the empirical case for biodiversity eliminativism. Santana points out that his conclusions rely heavily on the work of biodiversity conservationists.

In this chapter and the following two I will argue against the impression that the measurement problem is at an impasse. In section 4.4.2 I will argue that despite incommensurability between specific dimensions we can still use them to make meaningful comparisons between the biodiversity of distinct ecosystems. In chapters five and six I outline the detail of measurement methodology for several biodiversity surrogates. I will argue that this detail shows that measures of biodiversity are in a better state than the poor fit argument presumes. The expanding multiplicity of biodiversity measures is overblown and biodiversity is empirically suitable for its role in conservation biology. It simply has a very rich tool kit. I begin in the next section by explaining how the surrogacy strategy is used to measure biodiversity.

4.3 The Surrogacy Strategy for Measuring Biodiversity

In this section I will explain the surrogacy strategy for measuring the biodiversity of an ecosystem. The detail of how biodiversity is measured is essential to understanding the empirical poor fit argument. Because general conceptions of biodiversity are not operationalisable, conservationists measure biodiversity using biodiversity surrogates. These surrogates are key elements of biodiversity such as species richness, phylogenetic diversity and its other dimensions. Scientists measure one or more key elements of biodiversity in an ecosystem and use this figure to approximate the total biodiversity of an ecosystem and how it has been affected (Sarkar 2005, 153–54). Thus a key element of biodiversity such as species richness serves as a useful surrogate for the biodiversity of an ecosystem. The selection of a specific surrogate for an area is based on what is the most appropriate for the area. Species richness weighted for abundance is usually the dominant surrogate but genetic diversity, or diversity of physical characteristics could be better for ecosystems containing large numbers of closely-related species (Sarkar 2005, 169). In this section I will explain the role of specific dimensions of biodiversity in the surrogacy strategy.
4.3.1 The Role of Specific Dimensions of Biodiversity in the Surrogacy Strategy

Specific dimensions of biodiversity have an important role in measuring biodiversity because they act as different surrogates in a chain of approximation. In its simplest form a conservationist may approximate the biodiversity of an area by measuring a single dimension such as species richness. In this case the surrogacy strategy can be represented in the following way.

Species Richness \(\rightarrow\) Biodiversity

This is the practice in studies which identify biodiversity hot spots. Biodiversity hot spots are ecosystems which contain species richness that is disproportionally higher than typical species richness. 34 biodiversity hotspots represent 2.3% of the world’s land mass but contain 50% of vascular plant species and 42% of terrestrial vertebrates (Burch-Brown and Archer 2017, 992).

Sarkar gives a more complicated picture of how biodiversity is measured. Sarkar discusses the issue of how we assess biodiversity by separating the problem into two distinct concerns: a question about which property is to be measured, and a concern about the pragmatic possibility of gathering data on that property.

Two problems must be solved: (i) a relatively theoretical one – what is to be measured?, and (ii) a practical one – can the required data realistically be collected? The former is the problem of quantification; the latter is the problem of estimation. Jointly, these two problems comprise the problem of assessing biodiversity. (Sarkar 2005, 168)

Before discussing the concern about which surrogate should be measured he draws attention to the distinction between true surrogates and estimator surrogates (Sarkar and Margules 2002, 140). The difference between true and estimator surrogates is determined by their place on the surrogacy chain. True surrogates are representative of general biodiversity whereas estimator surrogates are taken to be representative of true surrogates (Sarkar 2005, 169). In this case the surrogacy strategy can be represented in the following way.

Estimator Surrogate \(\rightarrow\) True Surrogate \(\rightarrow\) Biodiversity

Estimator surrogates are important because of the difficulty of measuring the true surrogate. True surrogates are operationalisable but it takes time to measure them. We have limited time to make conservation decisions because conservation work often resembles triage (Takacs 1996, 8). For instance one of the most popular true surrogates for biodiversity is species diversity, which is species richness weighted for abundance (Santana 2014, 763–64). But species diversity is difficult to accurately determine. This is shown by how often our estimates of species numbers and daily extinction rates change (Takacs 1996, 83–84). As Sarkar notes:
It should be clear that complete distributions of all species for any region will never be available: even leaving aside microbial species, complete distributions of many other taxa, including insects (which are believed to show more diversity than any other taxon), are never available in practice. (Sarkar 2005, 169)

Ecosystems simply have too many inhabitants for measures of species richness to be efficient. Identifying some larger organisms is easier but species of flora and insects represent a disproportionately large amount of the species richness of a local ecosystem. Terry Erwin’s work demonstrated that the unique species of beetle can vary significantly as you travel just from one tree to the next (Takacs 1996, 83–84). Species richness is operationalisable, but conservationists do not have time to check the species in every single tree.

Estimator surrogates are both operationalisable and efficient measures. They are used as surrogates for the true surrogate through the assessment of representative samples. This is how much of current biodiversity assessment is carried out (Sarkar 2005, 171). True surrogates tend to be the specific dimensions of biodiversity such as species richness, morphology, and genetic diversity. Sarkar provides a list of candidates for estimator surrogates, stating that “There are at least six plausible candidates for estimator-surrogates: (i) environmental parameter composition, (ii) soil type composition, (iii) dominant vegetation composition, (iv) life-zone composition, (v) subsets of species composition, and (vi) subsets of genus or other higher taxon composition.” (Sarkar 2005, 171). The advantage of an estimator surrogate is that we can obtain data on it within a short time frame. In general we have large amounts of weather data for environmental parameter composition, soil composition can be easily measured and the dominant vegetation can be identified via satellite images (Sarkar 2005, 168–71).

Surrogate selection is dependent on the ecosystem we are studying. Sarkar believes that selection is based on which true surrogate is the best explanatory and predictive tool for the ecosystem’s biodiversity (Sarkar 2005, 160). We should begin by compiling existing geographical data on the ecosystem in question whilst remaining aware of any problems with the existing data. Then we should select the true surrogate based on which one is most appropriate for the ecosystem (Sarkar 2005, 153). If we are studying a biodiversity hotspot then species diversity may be the best true surrogate to use. Next we select an estimator surrogate on the basis of its accuracy and efficiency. Once we have finishing selecting the estimator surrogates we then take representative samples from the ecosystem and use it to approximate the system’s biodiversity (Sarkar 2005, 153). So the surrogacy strategy uses specific dimensions of biodiversity as the measurement surrogates for biodiversity. The purpose of the surrogacy strategy is to operationalise biodiversity in a way which meets the demands of conservation biology.

One objection to Sarkar’s account of the surrogacy strategy is that it is not clear that we need a distinction between estimator and true surrogates. The problem is that Sarkar has not yet explained the difference between estimating the prevalence of a true surrogate and sampling it. If the surrogacy chain only identifies stages at which we infer the value of the next step then we could extend the chain like this:
Observed Soil Composition → Soil Composition → Species Richness → Biodiversity

But a good reason to reject this chain is that the first step looks like sampling. Surrogates require measuring a different property to the target and using it as a proxy. The first step is not a surrogate because the target properties are the same. In practice this occurs with studies of species richness. Moller (et al. 2007) study species richness but focus on the avian class so their surrogacy chain is like this:

Avian Richness → Species Richness → Biodiversity

Santana characterises avian richness as an estimator surrogate in this kind of chain (Santana 2017, 87). But, in this case avian richness is just a sampling method rather than an estimator surrogate. Long surrogacy chains are difficult to justify because they require a justification for why the middle stages are important. Sarkar has yet to tell us why we ought not to simply use soil composition as the true surrogate for biodiversity. There is some vague ground in Sarkar’s surrogacy strategy over the distinction between estimator surrogates and true surrogates but it is this account of measuring biodiversity which Santana directly engages. Since the measurement chapters focus on Santana’s arguments, I will use Sarkar’s account of the surrogacy strategy in this thesis. In the next section I discuss and defend the surrogacy strategy against its limitations.

4.4 Limitations of the Surrogacy Strategy and Their Defence

In this section I will discuss methodological limitations of the surrogacy strategy and defend the strategy against them. I focus on two limitations of the surrogacy strategy: surrogate incommensurability, and the problem of multiple surrogates. The individual dimensions of biodiversity which are used as surrogates are strictly incommensurable with one another (Maclaurin and Sterelny 2008, 177). This prevents measures of biodiversity from producing a final biodiversity value for an ecosystem (Frank 2017, 98). Without a final biodiversity value conservation triage is difficult because there are no easy comparisons between the biodiversity of different ecosystems. In response to this problem I argue that only certain dimensions of biodiversity are strictly incommensurable. Other dimensions such as species richness and phylogenetic diversity still allow for meaningful comparisons between distinct ecosystems.

The problem of multiple surrogates has to do with the issues that arise from the high number of specific dimensions of biodiversity. Because biodiversity has so many specific dimensions there is a large number of surrogates and combinations of surrogates in the surrogacy strategy. Since they measure distinct dimensions, this implies that measures of biodiversity summarise biological properties which do not highly co-vary. Santana argues that the use of multiple surrogates in the surrogacy strategy makes the process more prone to error (Santana 2014, 765). Three steps of surrogacy is less precise than one or two. The number of surrogates also implies that there is latent flexibility in the results of the surrogacy strategy. With multiple surrogates to choose between, we could choose the surrogates which provide the most favourable data. Against these problems I
argue that correlation between dimensions of biodiversity is higher than Santana argues, that multiple surrogates do not make the strategy more prone to error, and that biased selection of measures would not pass peer review.

4.4.1 The Problem of Incommensurability
In this subsection I will outline the problem of incommensurability between the specific dimensions of biodiversity. It is incommensurability which drives premises one and three of Santana’s poor fit argument. To support his conclusion that biodiversity is a poor empirical fit for conservation biology Santana claims that general conceptions of biodiversity are not straightforwardly measurable and that the dimensions of biodiversity do not support robust inductive generalisations. Assuming he is correct, the cause of these issues is the incommensurability of the specific dimensions of biodiversity. Specific dimensions of biodiversity, such as species richness, genetic diversity, and phenetic diversity can be calculated individually, but the results cannot be combined into a single value for general biodiversity.

It is an important limitation of the surrogacy strategy that we cannot produce a single quantity for calculating biodiversity. Since we have no single value, biodiversity is not straightforwardly measurable and premise one of the poor empirical fit argument is true. Premise three that “the dimensions of biodiversity do not support robust inductive generalisations across the group” is ambiguous. It can be understood as a concern about correlation between the specific dimensions of biodiversity or as a concern about how well the dimensions track biodiversity. The former concern is more explicitly expressed in premise two that “there is not sufficient property correlation for biodiversity to be considered a property bundle”, so I will interpret premise three in the latter sense. We cannot inductively generalise from dimensions of biodiversity to biodiversity values.

I accept the truth of premise one that “biodiversity is not straightforwardly measurable”. There is no single biodiversity value and we require a surrogacy strategy to measure it. That is, we must employ other surrogate measures to approximate biodiversity. So it follows that biodiversity is not straightforwardly measureable. The truth of premise three is more complex. Whilst it is true that specific dimensions of biodiversity cannot be inductively generalised to biodiversity values; that is because there currently is no biodiversity value to generalise towards. Conservationists do not currently produce a single quantity to represent biodiversity. Instead they provide a quantity of one of its dimensions to indicate how much biodiversity there is. We don’t have empirical data of an ecosystem with low species richness but high biodiversity because we don’t yet have values to assign biodiversity. We should not expect a single value for biodiversity because it needs to be multi-dimensional and complex to track the disjunctive nature of biological phenomena.

Premise three is motivated by conceptual concerns. Santana is using his conceptual arguments from his 2014 paper to motivate an empirical premise in his 2018 paper (Santana 2018, 6). If there is more to biodiversity than species richness, species richness will not track biodiversity well. But this inference is problematic for two reasons. Conceptual counterexamples rely on intuition. If I’m not convinced that abundance is an important element of diversity then I won’t think that evenly-weighted populations are
more biodiverse than ecosystems with a few dominant species. Secondly, counterexamples only tell us that specific dimensions such as species richness have an imperfect correlation with biodiversity. They do not tell us how well the specific dimension and biodiversity correlate. Establishing poor correlation requires a large body of statistical evidence which is difficult to come across with a single quantity for biodiversity. So premise three of the poor fit argument is true. Specific dimensions of biodiversity do not support robust inductive generalisations from the dimensions to biodiversity value because there currently is no quantity for the biodiversity of an ecosystem. There is no single quantity, because the dimensions of biodiversity are incommensurable. In the next subsection I will defend the surrogacy strategy against the incommensurability problem.

### 4.4.2 A Reply to the Incommensurability Problem

In this section I will offer two replies to the incommensurability problem. I will argue that the incommensurable dimensions of biodiversity can still be used for meaningful conservation comparisons. I will also argue that measures of biodiversity would not be better represented by a single straightforwardly measureable quantity. Beginning with incommensurability, it is true that the dimensions of biodiversity are strictly incommensurable with each other (Burch-Brown and Archer 2017, 974) but they are only incommensurable in the sense that there is no cross comparison. Most measures of true surrogates can be converted into measures of other true surrogates with a small transformation. Transformation is possible because most measures of biodiversity use species identification as a common data point.

Consider the following example. Imagine that we have two different ecosystems A and B and we have to select one for conservation based on the best use of our resources. We have a measure S of the species richness of ecosystem A and P of the phylogenetic diversity of ecosystem B.

<table>
<thead>
<tr>
<th>Ecosystem A</th>
<th>Ecosystem B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species Richness</td>
<td>Phylogenetic Diversity</td>
</tr>
</tbody>
</table>

The problem then is that we need to decide between ecosystem A and B but we cannot compare S with P. The true surrogates, species richness and phylogenetic diversity, are incommensurable. As David Frank puts the problem, “There is no natural metric of “overall biodiversity” to determine whether, say, an additional species in one area (more species diversity) and a certain loss in heterozygosity in that area (less genetic diversity) would make that area more, less, or equally biodiverse.” (Frank 2017, 98). In chapters five and six I will discuss measurement methodology of biodiversity’s true surrogates in more detail but there is a solution to Frank’s problem because so many metrics of biodiversity use species as a common data point.

Species are a common point of data collection for many different metrics. Measures of species richness require a list of species. Species diversity applies counts of abundance to a list of species (Maclaurin and Lean 2016, 25). Phylogenetic diversity maps
the evolutionary relationship between lists of species (Faith 1996, 1286). Morphology and functional diversity map the variation of physical traits of species. So the quantity of most true surrogates can be calculated with a list of species and abundance data. Difficulties apply for a focus on traits or genetic diversity, but for the most part the gaps can be filled in for both ecosystems and we can cross compare the same dimensions to get an idea of which ecosystem has the most biodiversity.

In the case of ecosystems A and B we can generate a measure of phylogenetic diversity from the data set because we have its species richness. In the case of ecosystem B we can reverse engineer the species richness from the species list generating phylogenetic diversity.

**Ecosystem A**

Species Richness<sup>1</sup>

Phylogenetic Diversity<sup>1</sup>

**Ecosystem B**

Species Richness<sup>2</sup>

Phylogenetic Diversity<sup>2</sup>

So we can’t compare species richness with phylogenetic diversity but we can easily compare $S_1$ with $S_2$ and $PD_1$ with $PD_2$. Conservationists can do a lot with a list of species and abundance data because many true surrogates of biodiversity can be understood as transformations of the same data set. Incommensurable dimensions can still be used to compare ecosystems and inform conservation decisions. The mean, median, and mode of a data set jointly give an important impression of data despite being incommensurable values. The incommensurability of the specific dimensions of biodiversity is a barrier to straightforward measurability but that barrier can be overcome. We can still perform comparative analyses of biodiversity straightforwardly without a single biodiversity quantity.

A single quantity for biodiversity seems attractive, but it would severely misconstrue the status of an ecosystem. It is an important limitation of the surrogacy strategy that we cannot reduce our multidimensional results to a single biodiversity quantity. Santana presumes that this is a weakness of the surrogacy strategy. He argues that a lack of a straightforwardly measureable quantity and the inability for specific dimensions of biodiversity to track a biodiversity quantity are empirical reasons to eliminate biodiversity (Santana 2017, 86). But a multidimensional incommensurable measure is more appropriate for a multidimensional concept like biodiversity. This is because properties such as species richness, disparity, resilience and functionality are all important elements of biodiversity but no single dimension captures all the important elements of biodiversity. A focus on species richness can overlook the importance of resilience, or the ecosystems which the species inhabit. Focusing on disparity can overlook the importance of unique genetic information or functional interactions (Angermeier and Karr 1994, 692). Processing the data of multiple dimensions into a single quantity will require transforming results in a way which could cause us to overlook an important result along a single dimension. Using the analogy with another complex multidimensional
concept, a single value for health would be misleading. If there were a single quantity for good health then that result could easily overlook critical failure along one specific dimension. It is possible for a patient to have a fractured bone whilst many of their other bodily functions are still healthy. An average score for health will not lower much when there is a serious problem with a single dimension because there are many dimensions of health and they can rise and fall independently of one another. Likewise for biodiversity, a single measure would gloss over distinct dimensions whose performance should be considered individually. A key piece of motivating evidence in Santana’s arguments is the independent variation of properties. When properties vary independently of one another we should measure them individually instead of processing them into a single value. The specific dimensions of biodiversity are incommensurable but that is not a good reason to eliminate biodiversity. Complex multidimensional concepts are served best by complex multidimensional measures. The surrogacy strategy accomplishes this well.

In this subsection I defended the surrogacy strategy against the problem of incommensurability. I argued that the incommensurability of specific dimensions of biodiversity does not prevent meaningful comparisons of ecosystems. I also argued that measures of biodiversity are more informative as complex and multidimensional than as a single quantity. Premises one and three of the poor fit argument are therefore true. Biodiversity is not straightforwardly measureable and the specific dimensions of biodiversity do not support robust inductive generalisations across the group. Values for true surrogates cannot accurately predict quantities of biodiversity because there is no single quantity for biodiversity.

The search for a single unified measure of the biodiversity value of an ecosystem seems appealing but on closer inspection it is inherently flawed. Generalising biodiversity into a single value would be a mistake because it would inevitably gloss over the subtle but important biodiversity features of an ecosystem. Measuring specific dimensions of biodiversity individually enables us to give them due consideration when making important conservation decisions. The incommensurability of the specific dimensions of biodiversity is therefore not a flaw of the surrogacy strategy. We are better off treating biodiversity as a cluster of distinct but important properties, rather than trying to process them all into a single value. As Maclaurin and Sterelny note

Identifying a single quantity is clearly an attractive goal. It would prevent us talking past one another. It would maximise the collection of useful data. It would present a clear and unified picture of the natural world, useful to those promoting action in the face of ecological threats. But can such a one-size-fits-all measure adequately depict biodiversity? We doubt it. (Maclaurin and Sterelny 2008, 173)

In the next subsection I will discuss problems with multiple surrogates in the surrogacy strategy and how they motivate premises two, four, and five of the poor empirical fit argument.
4.4.3 Problems with Multiple Surrogates

In this subsection I will discuss how the surrogacy strategy generates problems with multiple surrogates. Santana appeals to three such problems to motivate his empirical poor fit argument. In premise two he claims that there is not sufficient property correlation for biodiversity to be considered a property bundle. This premise is important because it also informs premise three that the specific dimensions of biodiversity do not support robust inductive generalisations across the group. In premise four he claims that including biodiversity in the surrogacy strategy exacerbates imprecision between the measured target and the conservation goal. In premise five he claims that the multiple surrogates of biodiversity either are not operationalisable, do not accurately track biodiversity, or do not accurately track biological value. I begin with premise two.

Santana argues that there is not sufficient property correlation for biodiversity to be considered a property bundle. In part this is a conceptual argument but he also supports his conclusion with empirical work.

Species richness increases as latitude decreases, for instance (Hillebrand 2004), but whatever correlate of latitude causes this doesn’t seem to affect every dimension of diversity. Genetic diversity within species, for instance, is probably not affected, and even species richness within certain taxa, such as certain avian and planktonic groups, turns out to have the opposite relationship with latitude (ibid). (Santana 2018, 4)

Unfortunately, evolutionary diversity and species diversity are often distinct, as demonstrated, for example, by Mooers (2007), who describes a case study on the flora of South Africa’s cape region showing that the eastern region of the cape has higher diversity on a clade-based measurement, while the western region has higher species richness. (Santana 2014, 771)

So the argument has a strong empirical component. In his 2018 paper Santana takes these empirical conclusions to support his claim that the specific dimensions of biodiversity do not support robust inductive generalisations across the group (Santana 2018, 6). In the previous subsections I discussed the interpretation of premise three, that Santana was concerned about the ability of specific dimensions of biodiversity to predict quantities of biodiversity. However, Santana is also concerned about the ability of specific dimensions of biodiversity to predict other true surrogates.

In premise four of the poor empirical fit argument Santana expresses concern about the accuracy of the surrogacy strategy. He argues that including biodiversity in the surrogacy strategy exacerbates the imprecision between the estimator surrogate and biological value. Measurement surrogates are most effective when there is a very high correlation between the surrogate measure and the actual measure. A thermometer is an accurate gauge of temperature because the expansion of mercury in the glass tube correlates very highly with the mean kinetic energy of particles in the measured substance (Maclaurin and Sterelny 2008, 134). However, because the surrogacy strategy involves multiple surrogates, Santana argues that the chain is more prone to error.

I agree with Sarkar that biodiversity is a placeholder, but while Sarkar sees it as a useful placeholder, in fact the placeholder itself unnecessarily complicates the picture:

A estimator surrogate → true surrogate → biodiversity → biological value
B estimator surrogate \(\rightarrow\) true surrogate \(\rightarrow\) biological value

As normative descriptions of the practice of conservation biology, series B is more economical than A, and less prone to errors due to misrepresentation of one member by another. (Santana 2014, 765)

Santana considers the biodiversity concept to be an ineffectual theoretical link which makes the final value vaguer (Santana 2014, 762).

Imprecision along a surrogacy chain is generated when the quantity for each additional step is determined by the quantity of the previous step. For this example imagine that each step in the surrogacy strategy predicts the next step with 95% accuracy. In a two-step surrogate chain the true surrogate approximates biodiversity. If the true surrogate has a value of 100 then the biodiversity value has a range of 95-105. The range increases with every additional surrogate step. Santana’s account of the surrogacy chain has four steps.

Estimator surrogate \(\rightarrow\) true surrogate \(\rightarrow\) biodiversity \(\rightarrow\) biological value

Every stage increases the range. In this example the range is not exceptionally large but that is because I have presumed a 95% correlation between surrogates. However, the conceptual analysis of biodiversity discussed in chapters one to three indicate that the specific dimensions of biodiversity diverge more than this. Features of biodiversity vary independently of one another and less correlation between surrogates significantly increases the imprecision of the surrogacy strategy over multiple stages. So, according to Santana, the surrogacy strategy is more precise without biodiversity in the surrogacy chain.

Santana’s other concern about the use of multiple surrogates in the surrogacy strategy is that despite the surrogacy strategy using multiple surrogates, these surrogates all have major shortcomings. Individual dimensions of biodiversity are not operationalisable, do not accurately track biodiversity, or do not accurately track biological value (Santana 2017, 86; Santana 2018, 6; Santana 2014, 765–68). These claims are an attack on the ability of specific dimensions of biodiversity to serve as true surrogates. If those dimensions are not operationalisable, or do not track biodiversity, or do not track biological value then the surrogacy strategy is a poor fit for its role in conservation biology. Santana’s solution to this problem is to eliminate biodiversity in favour of its specific dimensions (Santana 2018, 8). If there is no such thing as biodiversity than we needn’t worry about how well species diversity or genetic diversity track it.

Debating premise five of the empirical poor fit argument will require more evidence than I have discussed thus far. The conceptual arguments which I set out in chapters one to three are sufficient to demonstrate that specific dimensions of biodiversity do track biodiversity. They just also vary independently of one another (Burch-Brown and Archer 2017, 974). Empirical evidence of high correlation between true surrogates and biodiversity is unavailable because we do not measure biodiversity as a single quantity. However, demonstrating that specific dimensions are operationalisable requires an analysis of their measurement methodology. In chapters five and six I present the methodology of species richness, species diversity, phylogenetic diversity, morphology, and functional
diversity. I will argue that the former three are straightforwardly operationalisable but the latter two are not. The relationship between specific dimensions of biodiversity and biological value is contentious partially because Santana is not clear on what type of biological value he appeals to. I will discuss that relationship in chapters seven and eight which focus on the role of biological value in biodiversity eliminativism. In the next subsection my responses to the problems of multiple surrogates will focus on between-surrogate correlation and the risk of imprecision in the surrogacy strategy.

4.4.4 A Reply to the Problem of Multiple Surrogates
In this subsection I will defend the surrogacy strategy against the problems of multiple surrogates. I will argue that premise two of the poor empirical fit argument is false because the within-surrogate correlation of biodiversity’s dimensions is higher than Santana gives it credit for. I will argue that premise four of the empirical poor fit argument is false because the number of surrogates in the surrogacy chain is not as important as the correlation between the measured property and the target property. I also argue that biodiversity eliminativism is not the only response to his argument. We could also shorten the surrogacy chain by removing biological value or denying the distinction between true and estimator surrogates. I begin with Santana’s concern about how well the specific dimensions of biodiversity correlate between each other.

The correlation between specific dimensions of biodiversity is better than Santana indicates. Santana’s conceptual analysis indicated that the specific dimensions of biodiversity come apart in important ways (Santana 2014, 768). His empirical evidence collects numerous examples from biology studies in which the specific dimensions of biodiversity fail to co-vary (Santana 2014, 774; Santana 2018, 4). The problem with this strategy is that correlational claims require large bodies of evidence but Santana has focused on specific empirical examples. Those empirical examples aren’t problematic for proponents of biodiversity because the multi-dimensional concept of biodiversity allows for its dimensions to vary independently of one another. Independent variation is a positive feature. Phylogenetic diversity is as important as species richness because it picks out a feature of biological diversity which species richness glosses over. Santana’s examples demonstrate independent variation rather than systematic poor correlation.

Santana’s examples give the impression that the specific dimensions of biodiversity are poor predictors for one another, but the correlation between them is higher than he suggests. Santana does not provide a standard for poor correlation but instead presents a large volume of evidence that the specific dimensions of biodiversity come apart in important ways. However, there is further evidence that the specific dimensions of biodiversity do not come apart as far as Santana argues. Grenyer (et al. 2007) performed a case study on the biodiversity of the south cape of Africa. They find that phylogenetic diversity has a 77% correlation with species richness and a 96% correlation with genus richness (Grenyer et al. 2007, 757). There are other similar claims of correlation in the literature because proponents of specific dimensions of biodiversity argue that their specific dimension is the best surrogate for other dimensions and biodiversity. In Conservation Priorities and Phylogenetic Pattern, Daniel Faith argues that phylogenetic diversity correlates with both feature diversity and habitat diversity (Faith 1996, 1287). In
his own discussion of objections to his arguments Santana (Santana 2014, 769) notes that species richness correlates well with ecological diversity, diversity of higher taxa, and phenetic diversity (provided that the species richness of the ecosystem is high enough). There are counterexamples to correlations between surrogates because the specific dimensions of biodiversity vary independently of one another. However, there is still sufficient correlation between the specific dimensions of biodiversity to deny premise two of the empirical poor fit argument. Therefore, there is sufficient property correlation for biodiversity to be considered a property bundle.

In premise four of the empirical poor fit argument Santana claims that including biodiversity in the surrogacy chain increases imprecision in the surrogacy chain. This claim is false because Santana is discussing the wrong kind of surrogacy chain. Santana’s account of the surrogacy chain has four steps, each of which is used to calculate the quantity in the next step.

Estimator surrogate \(\rightarrow\) true surrogate \(\rightarrow\) biodiversity \(\rightarrow\) biological value

But that isn’t how the surrogacy strategy works. We can’t use a true surrogate to calculate a quantity of biodiversity because we don’t have single quantities for biodiversity. We also don’t have single quantities for biological value, so the only step of quantity calculation is between estimator and true surrogate, or in other cases between empirical sample and true surrogate.

Sarkar resists the idea that the surrogacy strategy should be understood as one stage approximating another. His resistance is difficult to justify, as the results which the surrogacy strategy yields differ when tested in different regions. At the very least we do not yet possess sufficient evidence to think that patterns of estimator surrogates can accurately predict patterns of true surrogates (Sarkar 2005, 171). Sarkar argues that the more accepted view of the empirical relationship between estimator and true surrogate is that they share an important biological element (Sarkar 2005, 171). The places which the estimator surrogate selects for conservation are selected not just because they are high in the true surrogate but because they are high in whatever important element of biodiversity the true surrogate contains.

Under this interpretation of the surrogacy chain we should be less concerned with the number of surrogates than with the final correlation between the measured property and the target property. So, in the case of the surrogacy strategy we should not be as concerned with the number of surrogates as we should be with how well the measured property correlates with the target property. As an example, consider a simple surrogacy measure such as a mercury thermometer measuring the temperature of a liquid. The surrogacy chain could be presented as mercury expansion approximating liquid temperature. However, the dissipation of heat throughout a substance during the process of conduction is rarely uniform so the mercury at the top of the tube is slightly colder than the mercury which is being directly heated by the measured substance. That same chain can be understood as individual layers of mercury approximating the temperature of the next layer. The reason that nobody worries about multiple mercury surrogates widening the range of results is that the effect is so minimal. The number of surrogates in the measuring
process is irrelevant because of the high correlation between the initial measured property and the target property which it approximates. Therefore the number of surrogates is not as important as the correlation between measured property and target property.

In the case of biodiversity the number of surrogates in Santana’s surrogacy chain is not as important as the correlation between estimator surrogate and biological value. For example Grenyer (et al. 2007, 757) argue that phylogenetic diversity generally has a 77% correlation with species richness and a 96% correlation with genus richness. So their surrogacy chain looks like this:

```
Species Richness

Estimator surrogate  →  Phylogenetic Diversity  →  Biodiversity  →  Biological Value

Genus Richness
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Santana’s case for imprecision relies on the assumption that the quantity of a surrogate is always used to calculate the quantity of the next surrogate in the chain. However, this is not always the case. Temperature, blood pressure, and heart rate are surrogates for health, but they are not used to calculate a health quantity because health is a complex multidimensional property, like biodiversity. Santana cannot motivate his concern about imprecision via empirical data of poor correlation because there isn’t any. Premise one of his empirical poor fit argument tells us that biodiversity is not straightforwardly measureable. Since there is no single quantity for biodiversity we cannot measure it to empirically check how well it correlates with its surrogates.

Santana might object that without an option to measure correlation defenders of biodiversity are no more entitled to argue that these surrogates do track biodiversity. Sarkar expresses a similar concern about the difficulty of justifying correlational claims empirically (Sarkar 2013, 142). But there is a solution to this problem. We can demonstrate that multiple measures are picking out an important property if their results correlate highly with one another. Consider an example which I call the scale calibration thought experiment.

**The Scale Calibration Thought Experiment**

Imagine that Maya has invented the first scales and wishes to know how accurate they are. She cannot test them with standard weights to see how well measured weight correlates to actual weight since weight has not been assigned a value yet. She knows that there is a value to be identified (objects on earth have weight); she simply lacks a method to check how accurate our measurement of that weight is. One solution is to create multiple scales and check to see if they all yield the same value for a single object. The probability that all the scales yield the same incorrect answer decreases as the number of scales increases.
The problem of calibrating the first scales is analogous to the problem of checking how accurate our scores are for biodiversity. In the case of biodiversity it is unlikely that phylogenetic diversity has a 77% correlation with species richness and a 96% correlation with genus richness but that those three dimensions are not surrogates for a common property. We have empirical justifications that biodiversity surrogates track biodiversity because we can test true surrogates against one another and demonstrate that they are all picking up on some important biological element. And, as I have argued in this subsection, the correlation between biodiversity surrogates is higher than Santana gives it credit for.

A final response to Santana’s concern about imprecision in the surrogacy strategy is to accept his critique of long chains for the sake of argument and argue that there are better things to eliminate than biodiversity. Santana’s surrogacy chain has four components: estimator surrogate, true surrogate, biodiversity, and biological value. Santana wants to eliminate biodiversity to increase precision but we could also increase precision by denying the distinction between estimator surrogate and true surrogate or eliminating biological value as the target property. In section 4.3 I discussed the problematic nature of Sarkar’s distinction between estimator and true surrogate. Sarkar goes on to argue that estimator surrogates are successful because they pick out the same element of biodiversity which the true surrogate does (Sarkar 2005, 170). So we could increase precision by treating the estimator surrogate as a direct surrogate for biodiversity. We could also increase precision by eliminating biological value as the target property. In chapter three I argued that biodiversity should be understood as one valuable element of the environment rather than a surrogate for biological value. The relationship between biological value and biodiversity is a complicated one which will be addressed in chapters seven and eight. However, in terms of measurement strategy, determining vegetation composition via satellite imagery seems like a complex surrogacy chain for determining how valuable an ecosystem is.

In this subsection I defended the surrogacy strategy against the problems of multiple surrogates. In the poor fit argument Santana claimed that the multiple surrogates of biodiversity do not correlate sufficiently well for biodiversity to be treated as a bundle property (Santana 2014, 761). He also argues that the number of surrogates in the surrogacy chain made it more imprecise and prone to error (Santana 2014, 765). I argued that premise two of the poor empirical fit argument is false because the correlation between biodiversity surrogates is higher than Santana suggests. I argued that premise four of the poor empirical fit argument is false because Santana is analysing the wrong kind of surrogacy chain. The surrogacy strategy only predicts a quantity once. It does not determine quantities for biodiversity or biological value because there are no single quantities for those properties. When measuring biodiversity the number of surrogates is not as important as the correlation between measured property and target property. Furthermore we could accept Santana’s claim but eliminate other elements from the surrogacy chain. The distinction between estimator and true surrogate could be rejected and we could eliminate biological value as the target property. In the next subsection I will argue that the empirical case for biodiversity eliminativism has misrepresented the state of biodiversity measurement. This argument will challenge premise six of the empirical poor
fit argument that “If conditions 1) to 5) accurately describe biodiversity then biodiversity 
is a poor empirical fit for its role in conservation biology”.

4.5 The Empirical Case for Biodiversity Eliminativism is wrong about the State of Biodiversity Measurement

In this section I will argue that the empirical case is wrong about the state of biodiversity measurement. This argument will falsify premise six of the poor empirical fit argument which claims that satisfying conditions one to five of the argument justifies elimination. The empirical case gives the impression that measures of biodiversity are less empirically suitable than they actually are.

While taken individually these arguments must be tentative, relying as they do on uncertain empirical claims as well as tendentious assertions of what is worth conserving, taken as a whole they are strong enough to cast serious doubt on the usefulness of biodiversity as the primary target of conservation. (Santana 2014, 768)

Measures are empirically suitable for conservation when there is a common methodology and agreement on which measures should be applied in which situation. In the case of biodiversity the surrogacy strategy allows for a great multiplicity of different methodologies and there is much debate over which measures should be applied to which situations. I argue that the empirical case is misleading because it focuses on the problem areas of biodiversity measurement. Whilst focusing on problems is important for refining measurement methodology, only discussing the problems is a misleading way to determine empirical suitability. Considering the successes of measures of biodiversity along with its failures gives a different impression of the state of its methodology. I will argue in this section that in particular, the empirical case overlooks two important points. It focuses on between-surrogate operationalisability but overlooks within-surrogate operationalisability. Secondly, Santana does not realise that the imperfect correlation between biodiversity surrogates is essential for the surrogacy strategy. I go on to argue that the plausibility of the empirical case for biodiversity eliminativism is incompatible with the details of biodiversity’s measurement methodology. When the details of biodiversity measurement are laid out, it will be clear that the empirical case is wrong about the state of biodiversity measurement.

4.5.1 Between-Surrogate Operationalisability is distinct from Within-Surrogate Operationalisability

One mistake of the empirical poor fit argument is that it does not distinguish within-surrogate operationalisability from between-surrogate operationalisability. In his arguments Santana questions how straightforwardly biodiversity can be measured, or how well one surrogate can predict another (Santana 2017, 86; Santana 2018, 6). These are criticisms of between-surrogate operationalisability. They argue that there is no straightforward way for one surrogate to approximate another or measure biodiversity. Santana rarely discusses within-surrogate operationalisability, which is how well we can
measure individual biodiversity surrogates. This is a problematic oversight for two reasons.

The first reason is that the empirical suitability of a multidimensional complex is a function of both its between-surrogate operationalisability and its within-surrogate operationalisability. The within-surrogate operationalisability of biodiversity measures is empirically rigorous. Demonstrating this requires outlining details of the measurement methodology of specific dimensions of biodiversity. In chapters five and six I will outline the measurement methodology for species richness, species diversity, phylogenetic diversity, morphology, and functional diversity. Premise six of the poor empirical fit argument claims that conditions one to five are a sufficient reason to eliminate biodiversity. However, biodiversity’s measurement methodology seems far more empirically rigorous when we also consider within-surrogate operationalisability.

Secondly, there are biodiversity surrogates whose within-surrogate operationalisability gives rise to the same problems which Santana uses to justify eliminating biodiversity. The measurement methodology which I discuss in chapters five and six will make this clearer. Some surrogates such as morphology are not straightforwardly measureable, lack high within-surrogate correlation of results, and struggle to support robust inductive generalisations across their measures. But Santana cannot afford to eliminate many of these dimensions because he needs them to replace biodiversity as the goal of conservation. Distinguishing between within and between-surrogate-operationalisability will show that in many ways biodiversity is no more complex than the specific dimensions which Santana would use as biodiversity’s replacement. The poor empirical fit argument is misrepresenting the state of biodiversity measures because it does not make that distinction. But the within-surrogate operationalisability of biodiversity is empirically rigorous and in some cases indicates that between-surrogate operationalisability is better than the poor fit argument suggests.

4.5.2 Imperfect Correlation between Biodiversity Surrogates is Important
The empirical poor fit argument also misrepresents the state of biodiversity measures because the complex correlation of biodiversity’s surrogates is important for accuracy. Premise six of the empirical poor fit argument claims that satisfying conditions one to five are a good reason to eliminate biodiversity. This is false in part because measures of biodiversity are better with imperfect correlation between its specific dimensions. Santana is correct that biodiversity surrogates do not always correlate highly with one another. “Unfortunately, evolutionary [Phylogenetic] diversity and species diversity are often distinct.” (Santana 2014, 771). It is possible to have high species richness but low species diversity if the abundance of species in an ecosystem is uneven, and, it is possible to have high phylogenetic diversity with low species richness if there is an ecosystem containing few species which are evolutionarily distinct. But the between-surrogate correlation of specific dimensions of biodiversity is no lower than we should expect it to be.

This kind of imperfect between-surrogate correlation is normal for a complex multidimensional property. Dimensions which perform distinctly from one another can often be very helpful in identifying causal relationships. A patient who is healthy in every respect except for their blood pressure has a much smaller set of possible causes to
investigate than one who has high blood pressure, cholesterol, heart rate, and blood sugar. The property of health would not be a better fit for science if all these properties rose and fell together and neither would biodiversity. If species richness, diversity and phylogenetic diversity all rose and fell at the same rate, we would have little need for them all. Biodiversity would just be species richness, and considering the evolutionary relationship between species or their abundance would provide us with little more information than performing a species count.

Imperfect correlation does not mean that measures of biodiversity are an empirically poor fit for the goals of conservation biology. The independent variation of biodiversity’s dimensions informs our conservation decisions. Conservation is about prioritising which places need to be protected (Sarkar 2005, 160). An ecosystem with high species richness, diversity, and phylogenetic diversity has higher biodiversity and may therefore be given a higher priority than one with just high species richness. Such an argument is an important scientific justification for a difficult conservation decision, so the multidimensional nature of biodiversity measures is an advantage for conservation rather than a hindrance. Multidimensional measures of biodiversity are appropriate because biodiversity is a multidimensional concept. This entails low correlation between biodiversity’s surrogates at times but it is not a good reason to eliminate biodiversity. Premise six of the empirical poor fit argument is therefore misleading because low between-surrogate correlation is not a good reason to eliminate biodiversity. In the next subsection I discuss how the measurement methodology of biodiversity makes the empirical poor fit argument seem implausible.

4.5.3 The Plausibility of the Empirical Case for Biodiversity Eliminativism is Incompatible with the details of Biodiversity’s Measurement Methodology

Thus far I have argued against several key premises of the Santana’s empirical poor fit argument. I have argued that there are solutions to incommensurability, that multiple surrogates do not increase imprecision in the strategy, and that Santana’s standards for the goals of conservation are inappropriate. However, more work remains to be done on premise five that “individual dimensions of biodiversity are either not operationalisable, do not accurately track biodiversity, or do not accurately track biological value”. Santana blends together empirical arguments against the operationalisability of biodiversity with empirical arguments against the operationalisibility of individual dimensions. In this chapter I have pointed out several problems with his poor fit argument, but the best defence of the empirical suitability of biodiversity is in the detail of the measurement methodology.

The plausibility of the empirical case for biodiversity eliminativism is incompatible with the details of biodiversity’s measurement methodology. It seems plausible because the dimensions of biodiversity seem incommensurable and because there is concern in the literature about the expanding multiplicity of biodiversity measures. The detail of measurement methodology suggests the opposite. The expanding multiplicity of biodiversity measures is overblown and the empirical case for biodiversity eliminativism is unsuccessful. Chapters five and six will focus on outlining the detail of biodiversity surrogates. I will use the measurement methodology of species richness, species diversity,
and phylogenetic diversity to argue that the expanding multiplicity of biodiversity measures is overblown. I will use the measurement methodology of morphology and functional diversity to argue that conservation biology would not be empirically better off eliminating biodiversity in favour of its specific dimensions. The detail of the methodology will be technical but that detail will show that biodiversity is empirically suitable for its role in conservation biology.

4.6 Conclusion

In this chapter I introduced the empirical case for biodiversity eliminativism and began an argument that it is unsuccessful. In the previous two chapters I discussed the work of Santana, Angermeier, and Karr. In this chapter and the next two I focus on the work of Santana. Angermeier and Karr’s arguments for eliminativism are focused on conceptual and value based challenges but Santana argues for biodiversity’s elimination by appealing to conceptual, value-based, and empirical reasons. Appealing to methodological reasons and recent work on biodiversity Santana argues that it is a poor empirical fit for the role we need it to play in conservation biology (Santana 2014, 761). His argument is persuasive because it builds on the measurement debate by biodiversity conservationists. Although biodiversity conservationists are not intentionally motivating biodiversity eliminativism, their vigorous debate over the best way to measure biodiversity gives the impression that there is little consensus on measurement methodology.

To provide context for the empirical case for eliminativism, I explained how biodiversity is measured using the surrogacy strategy. According to Sarkar we select specific dimensions of biodiversity such as species richness to use as both estimator and true surrogates for biodiversity. Then I introduced the limitations of the surrogacy strategy and defended the strategy against them. Whilst the apparent incommensurability of biodiversity surrogates makes conservation triage difficult, in practice it is only certain dimensions of biodiversity which are incommensurable with other dimensions. Other dimensions such as species richness and phylogenetic diversity are loosely commensurable, at least in the sense that we can use them to make meaningful comparisons between the biodiversity of different ecosystems.

Santana has also expressed concern about the use of multiple surrogates in the surrogacy strategy. In response I argued that the correlation between surrogates is higher than Santana concludes and that multiple surrogates do not make the strategy more imprecise because Santana has misread where in the surrogacy strategy the values are. I go on to argue that the surrogacy strategy does not allow for the kind of flexibility in results that would preclude it as empirically suitable. I concluded that the empirical case for biodiversity eliminativism is misrepresenting the state of biodiversity measurement. This is in part because it does not distinguish between within-surrogate operationalisability and between-surrogate operationalisability. I also argued that it has misunderstood the requirements of conservation biology. Imperfect correlation between dimensions is essential if additional dimensions add more value to our analyses. Lastly, I argued that the plausibility of the empirical case for biodiversity eliminativism is incompatible with the details of biodiversity’s measurement methodology. In the next two chapters I will outline
this methodology and use it as evidence to argue that the empirical case for *biodiversity* eliminativism is unsuccessful.
5 Implications of Measurement Methodology I: The Expanding Multiplicity of Biodiversity Measurement is overblown

5.1 Introduction
This chapter is the second part of a defence of the biodiversity concept against Santana’s poor empirical fit argument. In this chapter I will outline the measurement methodology of three true surrogates for biodiversity: species richness, species diversity, and phylogenetic diversity. The purpose for outlining the technical detail of these measures is twofold. Firstly I will challenge a concern which motivates the poor empirical fit argument from chapter four. I will argue that the expanding multiplicity of biodiversity measures is overblown. Secondly I will continue my argument against the poor empirical fit argument. Premise five of the empirical poor fit argument claims that individual dimensions of biodiversity are either not operationalisable, do not accurately track biodiversity, or do not accurately track biological value. Premise six claims that the truth of premises one to five is a sufficient reason for eliminating biodiversity. The measurement methodology outlined in this chapter will challenge premises five and six. I will use the detail of the measurement methodology to argue that biodiversity surrogates are operationalisable and that by implication biodiversity is a good empirical fit for its role in conservation biology. Premise six overlooks the possibility that the empirical suitability of a multidimensional measure is a function of both its between-surrogate operationalisability and its within-surrogate operationalisability. In this chapter I will distinguish between-surrogate operationalisability from within-surrogate operationalisability. If the within-surrogate measurement methodology is empirically rigorous then we have good reason not to eliminate the measure.

In section 5.2 I summarise the problem of the expanding multiplicity of biodiversity measures and how it motivates the poor empirical fit argument. Then I will outline the methodology of calculating the species richness of an ecosystem in section 5.3. I explain the role of discovery curves and the different metrics of species richness before arguing that species richness is an operationalisable measurement surrogate. In section 5.4 I outline the methodology of measuring the species diversity of an ecosystem. I discuss the role of abundance in diversity before outlining different metrics of diversity and arguing that species diversity is an operationalisable measurement surrogate. In section 5.5 I will outline the methodology for measuring phylogenetic diversity. I explain the use of phylogenetic trees and discuss different metrics of phylogenetic diversity before arguing that phylogenetic diversity is an operationalisable biodiversity surrogate. I draw on analyses of all three biodiversity surrogates in section 5.6 to argue that the expanding multiplicity of biodiversity measures is overblown. That is, I will argue that the number of biodiversity measures is not an indication of the empirical suitability of biodiversity for conservation biology. The technical detail of these measures is significant evidence that biodiversity is a good empirical fit for its role in conservation biology.
5.2 The Importance of the Expanding Multiplicity of Biodiversity Measurement for Motivating the Empirical Case for Biodiversity Eliminativism

In section 4.2.2 of chapter four I argued that biodiversity conservationists unintentionally motivate the case for biodiversity eliminativism. Biodiversity eliminativism is more plausible when the state of biodiversity measurement seems controversial and undecided. The apparent lack of consensus is a by-product of the expanding multiplicity of biodiversity measures. Given an ecosystem and the surrogacy strategy for measuring it we have a great multitude of options. There are many true surrogates and estimator surrogates for biodiversity including: species richness, feature diversity, phylogenetic diversity, genetic diversity, historical weather patterns, and satellite imagery. These are some of the surrogates that Sarkar, Santana, and I have discussed but in practice there are a great deal more. Biodiversity after all, is a multidimensional concept for many different dimensions of biological variety.

Each surrogate for biodiversity has multiple methods of calculation and each calculation produces a different result. In the instance of functional diversity, Weiher discusses 17 such calculations (Weiher 2011, 178–85). Multiple surrogates with multiple options for calculation produce a great range of biodiversity values for conservation triage. So the biodiversity value which a conservationist arrives at depends as much on the calculation selection as it does on the ecosystem’s biodiversity. Measurement is the most reliable when the value is determined by the property rather than determined by a preference for a particular calculation. So the expanding multiplicity of biodiversity measures is a problem for its empirical suitability as a goal of conservation.

Whilst this problem is well known, much of the discussion takes the expanding multiplicity problem for granted rather than contesting it. ‘Biodiversity’ conservationists in particular use the issue of expanding multiplicity to motivate new measures of biodiversity or concerns about the ontological status of biodiversity. In section 4.2.2 I outlined examples of this in the literature from Archer, Burch-Brown, Frank, Lean, Maclaurin, Maurer, McGill, and Sterelny. I will use the analysis of biodiversity surrogates in this chapter to argue that the expanding multiplicity of biodiversity measures is overblown. That is, I will argue that the number of biodiversity measures is not an indication of the empirical suitability of biodiversity for conservation biology. For species richness, species diversity, and phylogenetic diversity, I will explain how the surrogate works, discuss different metrics, and argue that they are operationalisable. The detail of their individual methodologies also forms a body of evidence for an inference to the best explanation. After analysing the evidence I will argue in section 5.6 that the multiplicity of biodiversity measures does not make biodiversity a poor empirical fit for its role in conservation biology. There are fewer measurement options than it appears and the options which conservationists possess indicate a rich and nuanced tool kit.

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4 The full list of citations was: (Burch-Brown and Archer 2017, 971; Frank 2017, 98; Maclaurin and Lean 2016, 19–20; Maclaurin 2017, 56; Maclaurin and Sterelny 2008, 177; Maurer and McGill 2011, 64)
5.3 The Methodology of Measuring Species Richness

The first true surrogate for biodiversity which I will discuss is species richness. Species richness is a measure of the total number of species in an ecosystem. In this section I will introduce discovery curves as a tool for measuring species richness. Then I will discuss different metrics of species richness before explaining two calculations in detail: Abundance Coverage Estimate and Chao2. A focused response to the empirical case for eliminativism requires that not all metrics will be covered but the methodological detail I outline is sufficient to answer challenges of the expanding multiplicity of biodiversity measures and concerns about operationalisability. That detail is technical but familiarity with the methodology supports two important claims; species richness is an operationalisable measurement surrogate and the expanding multiplicity of measures of species richness is overblown.

5.3.1 Discovery Curves

In this subsection I will explain the methodology of discovery curves for calculating the species richness of an ecosystem. I discuss the difficulty of counting the total number of species in an ecosystem before discussing how discovery curves address that problem. I outline different sampling methods and draw a distinction between species richness and species density. Lastly, I discuss the predictive challenges facing the use of discovery curves.

It is difficult to determine the number of species in an ecosystem because of the sheer number of species. Despite a great deal of effort we have catalogued very few of the extant species. Mora (et al. 2011, 2) predict that 86% of terrestrial species and 91% of ocean species still await description. The issue in part is that it is difficult to detect species as they get smaller. So our sampling is not genuinely random as we are limited to what we can see, trap, or gas (Colwell and Gotelli 2011, 43). To help with this calculation we use discovery curves. A discovery curve begins with a rapid growth in the number of new species (indicated by point A on the figure below) obtained with each sample and naturally curves off into a plateau (indicated by point B on the figure below) as fewer and fewer new species are discovered with repeated sampling (Colwell and Gotelli 2011, 42).

![Discovery Curve Graph]
Imagine that you have a large container of Lego bricks in front of you. You reach in and retrieve a handful of bricks and inspect them. On this occasion you have identified 56 Lego bricks which have appeared for the first time in your sample. When you reach in for another handful you identify 45 new bricks, as a few of the bricks in this handful were also present in the previous handful. As you retrieve more and more handfuls you identify fewer and fewer new bricks until eventually the discovery curve reaches its plateau. This is known as the asymptote (Colwell and Gotelli 2011, 43). Discovery curves are a useful tool because the curves which they produce are mathematically predictable, so we can calculate where the curve will plateau based on our current position on that curve (Colwell and Gotelli 2011, 49). With an empirical sample much smaller than the total number of species in an ecosystem we can calculate the ecological sample (the actual number of species in an ecosystem) (Colwell and Gotelli 2011, 62).

Discovery curves have limitations. Firstly we must choose between our sampling methods. We can catch and remove species from an ecosystem by releasing gas under trees or setting traps or we can catch and release those species (Colwell and Gotelli 2011, 41). This is the difference between sampling a handful of Lego bricks but removing them from the container, and sampling a handful but replacing them. The discovery curves will function in the same way (Colwell and Gotelli 2011, 46). The discovery curve will still plateau, using sample and replace, but the difference in methodology matters because removing species from an ecosystem frequently to calculate the species richness is destructive but replacing them makes it more likely that we will encounter them again in future sampling.

A second problem with discovery curves is that the methodology makes a false assumption. The methodology presumes that the ecosystem which we are sampling is a closed one. The Lego bricks are all inside a single container. In reality there is no static number which represents the species richness of an ecosystem because it fluctuates. Birds fly through ecosystems, organisms migrate through them, and predators have large ranges which they hunt over because they have a more general ecological niche (Maclaurin and Sterelny 2008, 35). Ecosystems are not closed, they are open because the number of organisms which reside within them fluctuate regularly (Colwell and Gotelli 2011, 141). And once we have marked off an area as the ecosystem to test, its species richness will fluctuate over time. A key assumption in discovery curves, then, is that while the species richness of an ecosystem fluctuates, it does not fluctuate enough to seriously hamper our calculations of discovery curves.

There is also a predictive problem with the ability of discovery curves to predict species richness. The problem is the sheer height of the discovery curve. Estimates of total species richness world wide range from 5 to 100 million although more recent work has narrowed the estimate to 8.7 million give or take 1.3 million (Mora et al. 2011, 2). For a large ecosystem the total species richness is high enough to make accurately approximating it somewhere between difficult and impossible. The problem is the margin of error in curve calculations. Because the curve alters very little in the beginning we need
to be a certain height on the curve to calculate where it will plateau with accuracy. As shown on this figure:

![Graph showing species richness over sample size with points A, B, R, and R* indicating margins of error for asymptote calculations from varying points along the rarefaction curve.](image)

*Figure 5.2: Margins of error for asymptote calculations from varying points along the rarefaction curve. (Adapted from Neeson (et al 2013)*)

The lower the point on the curve which the data will reach, the greater the margin of error for the predicting when the curve will plateau. Predicting the asymptote from point A would yield a margin of error similar to R* whereas predicting asymptote from point B would have a margin of error similar to R. The margin of error increases significantly when the prediction is made from an earlier point on the curve. Given the high number of species in an ecosystem, for many ecosystems we could sample for years before we can accurately predict the species richness of the ecological sample. One such team in the rainforest has been cataloguing ant assemblages for 30 years without approaching the asymptote. They began this task when the term ‘biodiversity’ was coined and they are still sampling (Colwell and Gotelli 2011, 43). The accuracy of inferring from the empirical sample to the ecological sample is an ongoing problem for biodiversity calculations and most of science. Progress on this problem is promising as testing with known samples shows that calculations such as Chao2 can find the curve plateau much faster than other calculations of species richness (Colwell and Gotelli 2011, 51).

In this subsection I discussed the methodology of using discovery curves to determine the species richness of an ecosystem. I explained how discovery curves work and the different sampling methods which are used. Then I discussed the predictive challenges facing discovery curves. I mentioned that certain measures are addressing this problem. In the next subsection I will explain the methodology of different metrics of species richness.

### 5.3.2 Metrics of Species Richness

In this subsection I will discuss the different metrics of species richness. I give an overview of the most common metrics before discussing abundance coverage estimate...
(ACE) and Chao 2 in detail. I briefly argue that Chao 2 is an excellent estimator of species richness. Given the difficulty of accurately calculating the plateau of a discovery curve it should not be surprising that there are many different ways to calculate the species richness of an ecosystem. In *Biological Diversity: Frontiers in Measurement and Assessment* Colwell and Gotelli (2011, 40–41) discuss 8 different measures of species richness viewable in the table below.

<table>
<thead>
<tr>
<th>Formula for Abundance Data</th>
<th>Formula for Incidence Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total number of individuals in Sample: [ n = \sum_{k=1}^{S_{\text{obs}}} f_k ]</td>
<td>Total number of Samples: [ m = \sum_{k=1}^{S_{\text{obs}}} q_k ]</td>
</tr>
<tr>
<td>Chao 1 (with doubleton species): [ S_{\text{chao1}} = S_{\text{obs}} + \frac{f_1^2}{2f_2} ]</td>
<td>Chao 2 (with duplicate species): [ S_{\text{chao2}} = S_{\text{obs}} + \frac{q_1^2}{2q_2} ]</td>
</tr>
<tr>
<td>Chao 1 (any species combination): [ S_{\text{chao1}} = S_{\text{obs}} + \frac{f_1(f_1 - 1)}{2(f_2 + 1)} ]</td>
<td>Chao 2 (any species combination): [ S_{\text{chao2}} = S_{\text{obs}} + \left( \frac{m - 1}{m} \right) \left( \frac{q_1(q_1 - 1)}{2(q + 1)} \right) ]</td>
</tr>
<tr>
<td>First-order jackknife richness estimator: [ S_{\text{jackknife1}} = S_{\text{obs}} + f_1 ]</td>
<td>First-order jackknife richness estimator: [ S_{\text{jackknife1}} = S_{\text{obs}} + q_1 \left( \frac{m - 1}{m} \right) ]</td>
</tr>
<tr>
<td>Second-order jackknife richness estimator: [ S_{\text{jackknife2}} = S_{\text{obs}} + 2(f_1 - f_2) ]</td>
<td>Second-order jackknife richness estimator: [ S_{\text{jackknife2}} = S_{\text{obs}} + \left[ \frac{q_1(2m - 3)}{m} - \frac{q_2(m - 2)^2}{m(m - 1)} \right] ]</td>
</tr>
</tbody>
</table>
ACE:

\[ S_{ACE} = S_{abund} + \frac{S_{rare}}{C_{ACE}} + \frac{f_1}{C_{ACE}} \gamma^2_{ACE} \]

Where:

\[ S_{abund} = \sum_{k=1}^{s_{obs}} f_k \]

\[ S_{rare} = \sum_{k=1}^{10} f_k \]

\[ C_{ACE} = 1 - \frac{f_1}{n_{rare}} \]

\[ n_{rare} = \sum_{k=1}^{10} k f_k \]

And:

\[ \gamma^2_{ACE} = \max \left[ \frac{S_{rare}}{C_{ACE}} \frac{\sum_{k=1}^{10} k(k-1) q_k}{(n_{rare})^2(n_{rare} - 1) - 1,0} \right] \]

ICE:

\[ S_{ICE} = S_{freq} + \frac{S_{infr}}{C_{ICE}} + \frac{q_1}{C_{ICE}} \gamma^2_{ICE} \]

Where:

\[ S_{freq} = \]

\[ S_{infr} = \]

\[ C_{ICE} = 1 - \frac{q_1}{n_{infr}} \]

\[ n_{infr} = \sum_{k=1}^{10} k q_k \]

And:

\[ \gamma^2_{ICE} = \max \left[ \frac{S_{infr}}{C_{ICE}} \frac{m_{infr}}{m_{infr} - 1} \frac{\sum_{k=1}^{10} k(k-1) q_k}{(n_{infr})^2} - 1,0 \right] \]

Symbol Guide: ‘S’ stands for species and ‘S_{obs}’ for the observed species. Then for abundance calculations ‘f_k’ is the number of species represented by k individuals. For incidence calculations, ‘q_k’ is the number of species present in k samples over repeated sampling and ‘m’ is the total number of samples.

**Table 5.1: Calculations of Species Richness**

Formulae for species richness are divided in the first instance by the data collection method, either by abundance or replicated incidence. In data collection by abundance I sample an area and record how many individuals there are in each species. In which case f_0 is the number of undetected species, f_1 is the number of species with only one individual present, f_2 the number of species with two individuals present, and so forth to f_k. With replicated incidence data I sample an area and only record the presence or lack thereof of a species. In which case q_0 is the number of species which are never recorded, q_1 is the number of species which are only present in a single sample, q_2 are the duplicate species (those which are present in two samples), and so forth to q_k (Colwell and Gotelli 2011, 40). Chao, jackknife, ACE, and ICE are then used to predict the total species richness of an area based on the observed sample. I will outline ACE and Chao2 in detail.

Abundance Coverage Estimate or ‘ACE’ is a calculation of species richness from abundance data which separates individuals in samples by their rarity and uses this distinction to predict the total number of species in an ecosystem. It is given by the formula \(S_{ACE} = S_{abund} + \frac{S_{rare}}{C_{ACE}} + \frac{f_1}{C_{ACE}} \gamma^2_{ACE}\), where \(S_{abund}\) is the total number of species in a sample with more than ten individuals, \(S_{rare}\) is the total number of species in a sample with less than ten individuals, and \(n_{rare}\) is the total number of individuals considered to be
of rare species. Then $C_{ACE}$ is the proportion of all individuals in rare species which are represented by more than one individual and $y_{ACE}^2$ is the coefficient of the variation which is used to calculate the margin of error. The ACE formula will not work if every rare species in the sample is only represented by a single individual because in that case $C_{ACE} = 0$. In such an instance the version of Chao1 which works for any species combination will work (Colwell and Gotelli 2011, 40). The analogous formula for data gathered by replicated incidence is ICE which works in a similar fashion to ACE.

Chao2 is a greatly simplified asymptote calculation which works on a principle discovered by Alan Turing during the cracking of the enigma coding machine (Colwell and Gotelli 2011, 51). The presence of rare occurrences can be used to predict the total number of events. Imagine I am trying to work out the total number of Lego bricks in a container, and I know that I only have a 1:1000 chance of finding a brown two by one flat tile. Then while sampling a handful I discover three brown two by one flat tiles. I could extrapolate that there should be at least 3000 bricks in the container. The simplified version of Chao2 given by the formula $S_{chao2} = S_{obs} + \frac{q_2}{2q_2}$ focuses on the number of duplicate species in repeated incidence sampling, where $q_2$ is the number of duplicate species present in repeated sampling. If repeated incidence sampling does not reveal duplicate species then a more complex form of Chao2 which works for any combination of species is required. This is given by the formula $S_{chao2} = S_{obs} + \left(\frac{m-1}{m}\right)\left(q_1(q_1-1)/2(q+1)\right)$ where $m$ is the summation of $q_1$ as the number of species which are only present in a single sample, $q_2$ as the duplicate species (those which are present in two samples), and so forth to $q_k$ for the entire set of observed species $S_{obs}$. Chao2 can only be calculated for repeated incidence data but it has an analogous measure in Chao1 which can calculate the asymptote for abundance data in both a simplified and more complex form if no doubleton species are present in the sample (Colwell and Gotelli 2011, 40).

Chao 2 is one of the highest performing predictors of species richness in an ecosystem. By ’highest performing’ I mean that it is able to accurately predict the height of the asymptote from much lower down the rarefaction curve than other formulae such as ICE and ACE (Colwell and Gotelli 2011, 51). The performance of these calculations is tested against existing ecosystems in which the species richness is already known. Then the ecosystems are resampled and the formula is tested to see how quickly they can predict the asymptote with accuracy (Colwell and Gotelli 2011, 52). Under these conditions Chao2 outperforms its counterparts quickly establishing the prediction and narrowing it as we move further along the asymptote. Typical instances of sample based rarefaction plot as a smooth curve whereas Chao2 plots a steep almost linear initial gradient until it reaches the asymptotes level (Colwell and Gotelli 2011, 51). So Chao2 is an excellent predictor of species richness which addresses concerns about the operationalisability of large discovery curves.

In this subsection I explained the measurement methodology for calculating species richness. I outlined several different metrics before discussing ACE and Chao 2 in detail. I then argued that Chao2 is an excellent metric for calculating species richness. In the next
subsection I will argue that the detail of the measurement methodology for species richness indicates that species richness is an operationalisable surrogate.

5.3.3 Species Richness is an Operationalisable Measurement Surrogate

‘Operationalisability’ is a pragmatic constraint for quantifying and measuring a property. When I describe a property as operationalisable I mean that if an agent needed to know, they could go out and determine its quantity by measuring it. Weight is an operationalisable surrogate. If an agent wishes to know how many grams of bananas they have before they purchase them then they can place them on scales. Santana appeals to operationalisability frequently in his arguments but he is not clear what the standard for operationalisability is. This is problematic because we can always assign a number to a changing property and develop measures, which based on the change in the property, generate a value. Well-being is operationalisable because we can generate a value for well-being based on income levels. But that value would be misleading because there is more to well-being than financial security. So there is more to operationalisability than the pragmatic constraints of quantification and measurement. Accuracy is also important. A biodiversity surrogate is operationalisable if it is accurately quantifiable and measurable.

Another problem though, is that operationalisability is also a vague constraint. There is no clear point at which a property ceases to become pragmatically measurable. This is because pragmatism is relative to more than the empirical suitability of a measurement method. It is also relative to time constraints, resources, and person power. With a large enough team, sufficient time, and funding we could accurately measure the species richness or phylogenetic diversity of an ecosystem but conservation requires triage. A biodiversity surrogate may then be operationalisable in the sense that we can accurately quantify and measure an important element of biodiversity but not operationalisable given the time constraints of triage. Science works around time constraints with sampling. Sampling difficulties are not a good reason to reject a measure because it is difficulty shared by all scientific methodology. However, lack of operationalisability is a good reason to reject a measure. Good scientific measures are accurately quantifiable and measure important properties. So there is a vague boundary between operationalisability and challenges such as sampling which face all measurement methodology.

Species richness is an operationalisable surrogate for biodiversity because it is accurately quantifiable and measureable. There is an issue with the height of the discovery curve but that is an issue with sampling rather than with operationalisability. Beginning with quantification, there is no controversy over how species richness should be quantified. Species richness is a numerical count of the number of species in an ecosystem. Species richness is also straightforwardly measureable. Conservationists go to an ecosystem and repeatedly sample groups of species. Once the data has been collected a method of calculation is selected to determine the asymptote of the discovery curve.

The height of the discovery curve is a barrier to the operationalisability of species richness but it is caused by sampling problems. Ecosystems can contain thousands of species so repeated sampling can continue for some time before a conservationist is far enough along the discovery curve to accurately predict the asymptote (Colwell and Gotelli 2011, 52). This is a challenge for the empirical suitability of species richness as surrogate
but is a sampling challenge. Sampling issues need to be taken seriously but they do not disqualify systems of measurement from informing conservation decisions because sampling is a common challenge facing all scientific methodology. This particular sampling issue is not universal for all classes or families. Finding the asymptote gets harder as the species get smaller and more mobile. Determining the height of the discovery curve for birds, mammals and flora species is not as difficult.

Determining the operationalisability of a surrogate also requires considering how that surrogate addresses its problem areas. In the case of species richness, the diversity of methods for calculating the asymptote is a response to that problem. The different calculations can determine the height of the discovery curve from different data sets with different efficiencies. For example, Chao2 has two variants, one which is intended to work for any combination of species and one which is intended to work solely from the duplicate species present. It can usually find the asymptote from a smaller data set because it focuses on the relative incidence of rarer species (Colwell and Gotelli 2011, 51). Species richness is therefore accurately quantifiable and measureable. There is a sampling issue with determining the asymptote but it does not apply to all classes of species and different calculations have been developed to address it. So, species richness is an operationalisable surrogate for biodiversity.

5.4 The Methodology of Measuring Species Diversity

The second true surrogate for biodiversity which I will discuss is species diversity. A calculation of species diversity takes the data for species richness and weights it for abundance (Maurer and McGill 2011, 56). The aim of measures of diversity is to identify ecosystems with misleading high species richness. Species richness may be high but diversity is low if there are a small number of dominant species. We tend to think that diversity is highest when different groups are represented evenly in a sample. In this section I will discuss the role of abundance in diversity and then discuss some different metrics of species diversity. I will use this analysis to then argue for two claims; that species diversity is an operationisable surrogate and in section 5.6 I will argue that the expanding multiplicity of species diversity measures is overblown.

5.4.1 The Role of Abundance in Diversity

Species diversity takes the value of richness and weights it by how even the populations of those species are (Maurer and McGill 2011, 56). The motivation for the idea that there is more to species diversity than simple richness is generated by thought experiments. Considering the Lego bricks again, now instead of one container with a random assortment of Lego bricks, there are two. They both have the same number of bricks (10,000) but container B is 50% randomly assorted bricks and 50% one by four red bricks whereas container A is 100% randomly assorted bricks. The intuition here is that container A with its randomised contents is more diverse than container B because if I sampled them both at the same rate then the discovery curve for A would plot much faster and the samples of B would nearly always contain multiples of the same one by four red brick. Hill (1973, 427)
puts it in the following way.

When we say that the humid tropics are more diverse than the tundra, we mean that there are more species there. More precisely, we mean that the species in the humid tropics have on average lower proportional abundances than those in the tundra a fact which is amply visible to the naked eye and which can be demonstrated by the use of any measure of diversity we care to devise. But there is little point in merely confirming the obvious. . .

Applying this thought experiment to ecosystems, consider the illustration below.

![Figure 5.3: Ecosystems with identical populations and species richness but different evenness (McGee 2016).](image)

Ecosystem A is more diverse than B because the populations of the species in the ecosystem are all relatively even to one another. Repeated sampling of A would produce varied results and that is a good reason to think that A has a more diverse ecosystem than B. If I have a container of Lego bricks and I can repeatedly sample it with fewer repeated bricks each time then the contents of the container are more diverse than if a quarter of every sample is the same red, four by one, Lego brick. Abundance matters for diversity because in a diverse group, random sampling should produce different results. That kind of even representation is important for conservation because it provides insight into an ecosystem’s stability. If a single species has become dominant and is threatening the populations of numerous many other species, conservationists want to know. Abundance helps identify those threats.

In chapter three I have also argued that abundance in the sense of equal representation for all species is not a part of biodiversity. Population levels are an important element of biodiversity but biodiversity is not at its best when every species has an equal population. The number of workers in an individual ant colony can range from a handful to 5000 (Burchill and Moreau 2016, 291). 5000 elephants in the same ecosystem are sufficient for those animals to be considered pests because large mammals such as elephants or whales have large dietary requirements. In Iceland, the conservation of minke whales became a threat to the sustainability of fishing cod stocks (Einarsson 1993, 76). Furthermore, there are a great number of ecosystems like the one shown in B from figure A. These ecosystems are reasonably stable despite a single dominant species which has a disproportionately large population. We call them urban cities. It wasn’t human flourishing that was a problem for biodiversity, it was the effect that flourishing had on the rest of biodiversity.
Abundance has a complex relationship with biodiversity because flourishing biodiversity requires a variation in population levels. High populations for dominant species aren’t as important for biodiversity as the effects of those populations. Many species such as ants can have disproportionately high populations without threatening the rest of the local biodiversity (Way and Khoo 1992, 482). There is an international mega colony of ants with super colonies in Argentina and Europe (Giraud, Pedersen, and Keller 2002, 6078). They are all uni-colonial because they refuse to fight one another (Giraud, Pedersen, and Keller 2002, 6077). That mega colony does not lower biodiversity. Biodiversity is threatened by a disproportionately high population accompanied with multiple extinctions because of that high population. However, population levels do matter for the goals of conservation. Much of our concern about impending extinction is because of rapidly declining populations. So abundance has a complex relationship with biodiversity. In the next subsection I will discuss metrics for measuring species diversity.

5.4.2 Metrics of Species Diversity
In this subsection I will discuss the methodology for measuring species diversity. I discuss two of the most successful measures in detail: Simpson’s index and the Shannon-Weiner diversity index. Then I outline the large total number of diversity indices but do not identify them individually. The technical detail of measures of species diversity is similar to that of species richness so it will suffice to give the reader an impression of the total number of measures and discuss two calculations in detail. I also briefly discuss the additional metrics of evenness which allow us to separate species diversity back into richness and evenness.

Two of the most common measures of species diversity are Simpson’s Index and the Shannon Wiener Diversity Index. Simpson’s index is a diversity index based on the inversion of the probability involved in sampling species from an even population (Maurer and McGill 2011, 56). It is given by the formula \( D_{Simpson} = \frac{1}{D} \) where ‘D’ refers to the probability that any two individuals drawn from a population will belong to the same species and is given by the formula \( D = \sum p_i^2 \) (Maclaurin and Sterelny 2008, 136). The inversion is required because in an ecosystem with even species populations the probability of any two individuals being from the same species is very low. A high probability of any two individuals being from the same species would indicate an extremely dominant species in that ecosystem.

An example makes the nature of the diversity index clearer. Imagine that there exists a board of 13 members and we already know that one of them is named John. What then, is the probability that a randomly sampled member from the remaining 12 is also named John? If the probability is high then board diversity for member’s names is low because its membership is dominated by people named John. Now imagine that the target of the calculation was randomly selected. One board member is chosen at random and the probability that their name is represented by a second person is calculated. If the probability is low then that same dimension of board diversity is high because no individual member has a name which is dominantly represented. Thus the final diversity
value is obtained by inverting the result of D and dividing 1 by D is the most common way to do it even if it is not the only way (Maurer and McGill 2011, 56).

The Shannon Wiener Diversity Index is more strictly speaking a mathematical measure of information which can be applied very successfully to calculations of species diversity. It measures the informational disorder of the sample which is equivalent to there being a group with many different individuals with the same population for each type of individual (Maclaurin and Sterelny 2008, 136). So if I have a group with 100,000 organisms containing 1000 species, each of which has an abundance of 100 individuals, then the informational disorder of this group will be very high. That same informational disorder will decrease as more species leave the group or the abundance of individual species becomes uneven proportional to one another. The calculation is given by the formula \( D_{\text{shannon}} = \sum_{i=1}^{s} p_i \ln(p_i) \) where the act of summation ranges over the probability that information drawn from multiple sources will be identical or alternatively those two individuals will have an identical genetic makeup (Maurer and McGill 2011, 56).

Informational disorder is a complex idea. It works on the relationship between variation in data and predictability. The more variation in a group, the harder it is to accurately predict a randomly selected member of that group. If our hypothetical board of directors only contains people named John and Sandra then there is a high probability of correctly predicting the name of a randomly selected member. Likewise, there is a high probability of correctly predicting the name of a randomly selected member if half the members are named John, even if the remaining six members all have different names. Accurate prediction is the most difficult when there is a large number of groups and each group is represented evenly. So accurately predicting which species will be selected at random from a group is hardest when species diversity is highest. Therefore, diversity can be calculated in terms of how unpredictable (or disordered) the group is.

Maurer and McGill (2011, 56–57) also present a further four richness focused diversity calculations, two measures of species diversity which take evenness into account and six additional metrics intended to calculate evenness. I will briefly discuss the additional metrics of evenness but I will not go into detail. There are numerous calculations of species diversity, nearly three times as any as discussed by Maurer and McGill (2011, 64). However, the Shannon Weiner diversity index and Simpson’s diversity are two of the oldest and most popular measures of diversity (Maurer and McGill 2011, 64).

The additional metrics of evenness are of interest because they allow a conservationist to separate evenness from species diversity. If species diversity is equivalent to richness plus evenness then by untangling species richness from species diversity we should be left with species evenness. Consider the calculation for Simpson evenness given by the formula \( E_{\text{Simpson}} = \frac{D_{\text{Simpson}}}{s} \) where \( D_{\text{Simpson}} \) refers to Simpson’s Diversity Index and ‘S’ refers to the number of observed species. Shannon’s measure of evenness works in an analogous manner and is given by the formula \( E_{\text{Shannon}} = \frac{D_{\text{Shannon}}}{\ln(s)} \) (Maurer and McGill 2011, 57). In both cases the calculations express the evenness of a population as the function of the diversity index over the number of observed species. Diversity is equivalent to richness weighted by evenness so evenness is equivalent to
diversity inversely weighted by species. Both of these formulae allow an agent to easily convert a calculation of species diversity into one of evenness by removing the richness from the final value.

In this section I outlined the detail of the measurement methodology for calculating species diversity. I outlined Simpson’s diversity index and the Shannan-Weiner diversity index in detail before giving the reader an impression of the large number of diversity indices available. I finished by discussing metrics of evenness which pull the evenness out of diversity scores. In the next subsection I will argue that the detail of the measurement methodology for species diversity indicates that species diversity is an operationalisable surrogate.

### 5.4.3 Species Diversity is an Operationalisable Measurement Surrogate

Species diversity is an operationalisable surrogate if it is accurately quantifiable and measureable. Species diversity is accurately measureable but its quantification is problematic because of the relationship between abundance and diversity. Beginning with measurability, species diversity is straightforwardly measureable. Diversity is a function of richness and evenness. Evenness is a measure of how equally individual groups are represented by a sample. Populations in ecosystems are maximally even when all species are equally abundant. So measuring the species diversity of an ecosystem requires richness and data on the abundance of the collected species. The methodology of species diversity calculations shows that species diversity is straightforwardly measureable. With data on abundance and richness, Simpson’s index is the probability that the second organism you sample is from the same species as the first organism you sampled. There is a higher probability of randomly selecting two larch trees from a sample when larch trees are the dominant flora in the ecosystem.

The accuracy of quantifying species diversity is more complex. In one sense measures of species diversity are accurate. They quantify what they are supposed to. They measure how evenly populations of species are distributed. In another sense the quantification is not accurate because species diversity is not at its best when all species are equally represented. A thriving ecosystem requires an uneven distribution of predators to prey. Increasing the populations of certain species to maximize evenness is a poor use of conservation resources if the population in question is already highly stable (Santana 2017, 92). Maximising evenness can be a very bad thing for an ecosystem (Santana 2014, 770). Whilst equal representation of gender and race in a board of directors is maximally diverse, a farm with one blade of grass for every cow would be a disaster.

More work is required on the role of abundance within biodiversity. Abundance is an important part of biodiversity because it is linked to resilience, stability, and patterns of extinction. 1000 Maui dolphins would be better than the population of <100 that currently exists because the species is an extinction risk (Baker et al. 2013, 229; Hamner et al. 2014, 87). One of the causes of toxic algae blooms in the ocean is rapid changes in abundance over a short period of time. Because of overfishing by humans the organisms which eat plankton are suddenly low in abundance (Jackson et al. 2001, 631). Lack of predators and the benefits of nutrient flow off into the water mean those phytoplankton are thriving (Heisler et al. 2008, 3). Phytoplanktons now have such high abundance that they die of old
age. Then they fall to the ocean floor and decompose. During this composition the bacteria thrive but use up most of the oxygen. That creates an anaerobic ecosystem which is toxic for any organism which can’t migrate away. We have large scale toxic algal blooms primarily because of changes in abundance. Overfishing prevents the fished species from interacting with the other organisms in its environment (Jackson et al. 2001, 629). If the abundance of plankton were low in proportion to the abundance of species which eat plankton such as the sea urchin Diadema Antillarum then we wouldn’t have as many toxic algal blooms.

The controversy is not about whether species diversity is an operationalisable surrogate but whether abundance should be a part of biodiversity. Species diversity is straightforwardly measureable and accurately quantifies what it aims to quantify. But it is not clear if quantifying abundance informs our view of biodiversity. Abundance is an important element in an ecosystem but it may be better understood as a dimension of ecosystem health or stability. Santana briefly criticises maximal evenness for threatening an ecosystem’s stability (Santana 2014, 770). A strong motivation for measures of species diversity is that they distinguish between a flourishing species and an imperilled one. However these can also be understood as concerns about health. Richness tells us how much biological diversity exists, evenness tells us how likely biological diversity is to stay at that level. Regardless of whether abundance is better understood as a dimension of biodiversity or something like stability, it is an operationalisable surrogate. We can straight-forwardly measure it and it accurately quantifies the evenness of an ecosystem so it is operationisable. In the next section I will discuss the methodology of measuring phylogenetic diversity.

5.5 The Methodology of Measuring Phylogenetic Diversity

The third true surrogate for biodiversity which I will discuss is phylogenetic diversity. Phylogenetic diversity is a measure of the evolutionary variation of the organisms in an ecosystem. Two ecosystems can have similar species richness but one can better represent biodiversity if it has greater feature diversity or unique evolutionary adaptations. Phylogenetic diversity measures this relation by mapping organisms onto a phylogenetic tree in terms of their common evolutionary ancestors. In this section I will introduce phylogenetic trees and explain how they are used to calculate the phylogenetic diversity of a group of organisms. Then I will discuss the different metrics of biodiversity. I will use this analysis to argue for two claims; phylogenetic diversity is an operationisable surrogate and in section 5.6 I will argue that the expanding multiplicity of phylogenetic diversity measures is overblown.

5.5.1 Why Phylogenetic Diversity Matters

In this subsection I will explain why measures of phylogenetic diversity are important for conservation decisions. I will argue that phylogenetic diversity tracks an important element of biodiversity which species richness overlooks, feature diversity. I explain why feature diversity matters and present three sources of evidence for species richness’ inability to
track it: counterexamples from the literature, the burgess-shale fauna, and the different proportion of phyla to species for marine and terrestrial organisms.

Phylogenetic diversity matters because it captures an important element of biodiversity which species richness overlooks. Species richness treats all species as equal so it overlooks how complementary that species is. Species are complementary to the extent that including them in a group brings novel features to that group (Faith 1994, 49). If I have a group of two avian species and a choice about adding a floral species or a third avian species then the floral species is more complementary because adding it instead of a third avian species will introduce more novel features. Feature diversity is an important element of biodiversity but species richness overlooks it (Frank 2017, 97). Phylogenetic diversity tracks feature diversity because speciation is caused by natural selection isolating organisms. Survival of the fittest favours certain adaptations over others. So, over time speciation tends to diversify phenotypic characteristics. So there is a phylogenetic pattern between all species on the tree of life. The branching patterns on the tree of life are used in phylogenetic calculations to track overall feature diversity (Faith 1996, 1286).

Demonstrating that phylogenetic diversity is important requires demonstrating that species richness does not track feature diversity well. In the literature this is typically motivated with a hypothetic counterexample of two groups of organisms such as the following passage.

Consider two hypothetical islands, each with only two species of vertebrate animals in equal abundance: two birds in one case and a bird plus a mammal in the other. Both islands have species richness \( r = 2 \) (for vertebrates) and the same maximal value of species evenness. However, our intuition tells us that a bird plus a mammal represents more biodiversity than does two birds. (Vellend et al. 2011, 194)

Feature diversity is important. The brown spotted kiwi of New Zealand is a more worthwhile conservation target than the snail darter because there are only a few species of kiwi and the snail darter is a “thoroughly unremarkable minnow.” By contrast the kiwi has a number of unique features. Kiwis, which are native to New Zealand, are a group of flightless birds with nostrils at the end of their extended beaks. Their highly developed sense of smell allows them to detect food such as worms long before seeing them and their long beaks allow them to root prey out of the ground (Martin et al. 2007, 198). They burrow in the ground instead of nesting and proportionate to its body size, lay the largest egg for any avian species at approximately 20% of the mother’s body mass. Species richness treats the snail darter and the kiwi as of equal value to conservation. Phylogenetic diversity distinguishes different degrees of complementariness because of the kiwi’s unique features.

Aside from hypothetical motivations for the value of feature diversity, the failure of species richness to track feature diversity is shown by important ecological discoveries. The burgess shale fauna were discovered by Charles Walcott in Canada during the second decade of the twentieth century. These fossils were unusual. They were members of the metazoan kingdom from the pre-Cambrian era but work on these fossils in the 1970s by Whittington, Briggs, and Conway revealed that these creatures did not fit into existing
Stephen Gould hypothesised that these creatures belonged to phyla which had since gone extinct. He argued that the physical characteristics of the fossils precluded them from membership in modern phyla. The fossils are radically different from any surviving lineages of metazoans which are alive today. Some are arthropods and some of those arthropods are trilobites but most of them are significantly different in physical character to the groupings of trilobites or arthropods (Griffiths and Sterelny 1999, 287).

Gould argued that the burgess-shale fauna indicate that diversity does not always increase with time. Greater species richness does not indicate greater diversity because during the Precambrian era, there were more families and orders with fewer species (Sepowski 2017, 35). The burgess shale fauna bear the features of the metazoan kingdom but they are phenotypically distinct enough that they do not belong in modern phyla (Gould 2000, 47). Gould illustrates his hypothesis in the following way:

![Figure 5.4: Increasing diversity over time and Greater Diversity in the Precambrian Era (Gould 2000, 46).](image)

The tree in the left of figure B indicates fewer phyla with more species. The burgess-shale indicate a time period with more disparity but fewer species. So during that time period species richness was lower but feature diversity was higher. This indicates that species richness does not track feature diversity as well as phylogenetic diversity.

In this subsection I argued that phylogenetic diversity matters because it tracks feature diversity in a way that species richness does not. Species richness treats all species as equal despite organisms being complementary in different degrees. This conclusion is supported by hypothetical counterexamples, the burgess-shale fauna, and the difference in proportions of phyla to species for marine and terrestrial species. In the next subsection I will outline the detail of phylogenetic trees and how they represent the evolutionary pattern which tracks feature diversity.

### 5.5.2 Phylogenetic Trees

In this subsection I will outline the detail of phylogenetic trees for calculating phylogenetic diversity. I will cover the common elements of all trees and the different kinds of trees
which are used. The first stage of phylogenetic calculations is mapping organisms onto a phylogenetic tree. Since any two existing species share a common ancestor somewhere in their lineage, entire ecosystems can be represented on evolutionary maps like this one.

![Figure 5.5 Simple Phylogenetic Tree](image)

This tree depicts the phylogenetic pattern of the organisms in the group. It is simplified because it is agnostic as to whether the lengths of the branches indicate any information. It represents evolutionary history and can be used to track feature diversity for conservation. The phylogenetic pattern is represented by the common features of phylogenetic trees: tips, branches, nodes, and roots. The tips of each tree represent individual species. The branches represent the evolutionary development. A node is a point at which one branch splits into two (in the case of more than two they are referred to as polytomies) so it represents the act of speciation. The root node is the single common ancestor which is shared by all organisms on the tree. These are the common features of phylogenetic trees (Vellend et al. 2011, 196).

There are different kinds of phylogenetic trees so as well as common features, there are unique features. Trees differ in branch length and whether or not the branches indicate distance. Distance is typically indicated either by time or standard for similarity in features. Consider the following phylogenetic trees.

![Figure 5.6 Ultrametric Phylogenetic Tree (Faith 1992, 6) and Non-Ultrametric Phylogenetic Tree (Faith 1996, 1287)](image)
The branches of these phylogenetic trees are quantifiable. That is the phylogenetic pattern presented represents not only the relations of ancestry and descendants but also quantifiable information about phylogenetic distance. In these trees the length of the branch indicates either the time between acts of speciation or the number of novel features developed. The tree on the left is ultrametric because all of its tips end at the same place. It is also additive because its branch length is quantifiable. The scale used is time and all tips represent extant species. The tree on the right is non-ultrametric because its tips end at different places (Vellend et al. 2011, 196). This is because it is an additive tree with a scale of physical difference. Physical difference can also be indicated in an ultrametric tree with dash for difference or parallel speciations (Faith 1992, 3; Faith 1994, 48; Faith 1996, 1287). The details of the distance metrics will be discussed in the next subsection. In this subsection I explained the methodology of phylogenetic trees which represent the evolutionary relationships between organisms.

5.5.3 Metrics of Phylogenetic Diversity

In this subsection I will explain the methodology for calculating phylogenetic diversity. I explain the detail of three groups of metrics. First I discuss the quantification of branch length in distance based trees. Next I outline metrics for node based trees. I discuss taxonomic distinctiveness, species originality, and pendent edge in detail. Then I outline the metrics for distance based trees and discuss phylogenetic diversity and mean phylogenetic distance in detail.

Branch lengths along phylogenetic trees can be quantified using different metrics. The different metrics are important because phylogenetic diversity tracks feature diversity. A problem with quantifying the diversity of features is that it requires a measure of similarity between organisms (Maclaurin and Lean 2016, 28). Similarity is notoriously difficult to quantify (Goodman 1972, 437). It is easiest to quantify in restricted groups but living organisms are extremely phenotypically diverse with more distinct traits than shared ones. So much of the operationalisability of phylogenetic diversity relies on how well the trees represent similarity and difference between organisms. There are at least four common methods for quantification. One common method is to make the tree ultrametric, use time for a scale and place the nodes along branch lengths according to the date of speciation. A second method is to proportion branch length to the total change from ancestor to speciation. A third method is to rely solely on the phylogenetic pattern for distance. These calculations only factor into account the branching pattern and do not consider branch length.

For node based phylogenetic trees, there are five main metrics: taxonomic distinctiveness, species originality, pendent edge, species evolutionary history, and originality of species within a set (Vellend et al. 2011, 198). I will explain two metrics in more detail: taxonomic distinctiveness, and pendent edge. The methodology of the metrics is shown by applying them to a single simplified phylogenetic tree.
Taxonomic distinctiveness is calculated as the reciprocal of number of nodes between species and the root of the tree. The result for an individual species can be standardised by dividing by the sum of these scores across species and multiplying by 100.

Figure 5.7 Taxonomic Distinctive Values for Species on a Simplified Phylogenetic Tree

Figure 5.8 Pendent Edge Values for Species on a Simplified Phylogenetic Tree
Pendent edge calculates the length of the branch connecting a species to the rest of the regional tree. It focuses on how few members belong to a clade. This is not a distance measure. Metrics for node based trees do not rely on quantifiable distance in the branch length. Instead, they determine phylogenetic diversity based on the phylogenetic pattern made by the organisms in the ecosystem.

The metrics for distance based trees rely on a quantifiable distance in branch length. The calculation typically relies on an ultrametric tree with time as the scale. Four such measures are shown in the following table adapted from (Vellend et al. 2011, 199).

<table>
<thead>
<tr>
<th>Distance Based Metric</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phylogenetic Diversity</td>
<td>$PD = \sum_i^B L_i$</td>
</tr>
<tr>
<td>Mean Phylogenetic Distance</td>
<td>$MPD = \frac{\sum_m \sum_n d_{mn}}{\frac{S(S - 1)}{2}}$</td>
</tr>
<tr>
<td>Sum of Phylogenetic Distances</td>
<td>$SPD = \sum_m \sum_n d_{mn}$</td>
</tr>
<tr>
<td>Mean Nearest Neighbour Distance</td>
<td>$MNND = \sum_m \sum_n \min(d_{mn})$</td>
</tr>
</tbody>
</table>

Symbol Guide: ‘B’ stands for ‘branch’ where the act of summation ranges over the length ‘L’ of all branches. ‘S’ stands for the total number of species and $d_{mn}$ is the distance between two points ‘$m$’ and ‘$n$’. ‘$\min(d_{mn})$’ is then the minimum distance between those two points.

Table 5.3 Metrics of Phylogenetic Diversity for Distance Based Trees

I will explain phylogenetic distance in more detail. The methodology is shown on the following simplified phylogenetic tree. The following tree is assumed to be additive for the sake of simplicity.
Figure 5.10 Phylogenetic Distance Scores for a Simplified Additive Phylogenetic Tree

Phylogenetic diversity is calculated as the sum of all branch lengths in the phylogenetic tree. After calculating the length of the individual branches, the results are added together to yield a score of 29.

Metrics for distance based trees like phylogenetic distance rely on a quantifiable distance in branch length. So the results which they produce are a function of both the phylogenetic pattern and branch length. Because branch length affects the phylogenetic value which a species adds to overall phylogenetic diversity, distance based trees can be more easily weighted for abundance. Node based trees record presence or absence for a species but since each tip of the tree is represented by a pathway length, distance based trees assign a quantity to species. Each branch represents a quantity which can be weighted for abundant populations of pairs of species (Vellend et al. 2011, 199). In this subsection I explained the methodology for calculating phylogenetic diversity by grouping the metrics according to distance, node based trees, and distance based trees. In the next subsection I argue that phylogenetic diversity is an operationalisable measurement surrogate.

5.5.4 Phylogenetic Diversity is an Operationalisable Measurement Surrogate

In this subsection I will argue that phylogenetic diversity is an operationalisable surrogate for the goals of conservation biology. To argue that phylogenetic diversity is accurately quantifiable and measureable, I present evidence from a principle component analysis by Vellend (et al. 2011). The results show a high redundancy between metrics for node based trees, and between metrics of distance based trees. I argue that phylogenetic diversity has made the problem of similarity operationalisable for the goal of tracking feature diversity. Other studies also indicate that there is a consensus of results between node and distance based trees for triage decisions in conservation biology. I conclude that phylogenetic diversity is operationalisable because it is accurately quantifiable, pragmatically measureable, and correlates highly with other true surrogates of biodiversity.

Phylogenetic diversity is an operationalisable surrogate if it is accurately quantifiable and measureable. The values which it assigns must be accurate and the true surrogate needs to be measureable within the time constraints of conservation biology. One way to test for accuracy is with a principle component analysis. A PCA calculates all
metrics on the same group of organisms to test how highly the results of different metrics correlate. The PCA performed by Vellend (et al. 2011, 201) demonstrates that the different metrics of phylogenetic diversity which I discussed in section 5.5.3 correlate highly with one another. The mean correlation for any two metrics of node based trees was 0.88 which indicates high redundancy among metrics. That is, the different measures of phylogenetic topology correlate so well that they are almost equivalent.

Correlation was also high for metrics of distance based trees. Two versions of the four metrics I discussed in section 5.5.3 were tested against one another; one which weighted for abundance and one which was not (Vellend et al. 2011, 202). The results of the PCA indicated that they had an overall correlation of >0.9 (Vellend et al. 2011, 205). This result is high but there is a greater range of scores which are represented by the mean. Correlation scores could be increased by restricting certain measures of phylogenetic diversity such as imbalanced trees but this is not necessary for the goals of conservation. Conservation biology most frequently uses the higher correlating node based trees. Distance based trees are favoured by community ecology (Vellend et al. 2011, 192).

There is also some evidence that node and distance based trees make the same conservation recommendations. In Conservation Evaluation and Phylogenetic Diversity, Faith compares conservation recommendations for bumble bees of the *sibiricus* group to demonstrate that phylogenetic diversity is a better measure than taxic diversity (Faith 1992). Given the decision of selecting one place of three for conservation, he arrives at the following data.

<table>
<thead>
<tr>
<th></th>
<th>R1</th>
<th>R2</th>
<th>R3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species Number</td>
<td>9</td>
<td>8</td>
<td>10</td>
</tr>
<tr>
<td>Phylogenetic Diversity</td>
<td>66</td>
<td>71</td>
<td>50</td>
</tr>
<tr>
<td>Taxic Diversity</td>
<td>21.1</td>
<td>15.1</td>
<td>12.7</td>
</tr>
</tbody>
</table>

*Table 5.4: Values for species richness, phylogenetic diversity and taxic diversity for each of the three reserve areas, R1, R2, and R3 (Faith 1992, 6)*

So taxic diversity suggests protecting reserve area 1 but phylogenetic diversity suggests protecting reserve area 2. Faith considers if the results could be a product of branch length assumptions and so repeats the process with a node based analysis. The node based analysis also indicated that reserve area 2 should be selected for conservation. “When all the terminal branches were simply set to unit length, it remained the case that R2 had greater PD than R1, though the difference between the two was now greater (38 versus 19).” (Faith 1992, 7).

This conclusion is supported by the findings of Vellend (et al. 2011, 206) who note that weighting branches by abundance had little impact on the results for distance based trees. Abundance has little effect on the results because it is obscured by the phylogenetic pattern. The redundancy of weighting for abundance supports the operationalisability of
phylogenetic diversity because the extra step for weighting has no serious impact on the conservation recommendation. Part of the constraint of operationalisability for conservation biology is time constraints so not having to weight for abundance or use a distance based tree speeds up the process. More work is required to demonstrate node based and distance based trees do not have an impact on place selection in conservation but some precursory evidence exists. Deciding between node trees, distance trees, and weighting for abundance has little impact on the final conservation recommendation because the greatest factor is the phylogenetic pattern.

This high redundancy between metrics is an impressive result for phylogenetic diversity because of the difficulty of quantifying similarity and difference. The redundancy is between metrics rather than for the surrogate. Phylogenetic diversity is not a redundant surrogate but the different ways in which it is calculated correlate so highly in their results that metrics are redundant against one another. This meets the requirements of conservation biology because metric selection has little impact on results. This is an impressive result because phylogenetic pattern tracks feature diversity and quantifying similarity and difference is meant to be an almost insurmountable problem. In Seven Strictures Against Similarity, Nelson Goodman argues against relying on similarity to solve problems. “Similarity, ever ready to solve philosophical problems and overcome obstacles, is a pretender, an impostor, a quack. It has, indeed, its place and its uses, but is more often found where it does not belong, professing powers it does not possess.” (Goodman 1972, 437)

The strictures, which Goodman argues for, make the problem more approachable. He notes that similarity can be addressed in restricted domains with a small number of important properties (Goodman 1972, 444,446). It is easier to quantify how tomatoes are different to one another than how different a tomato is from a human being. But this restriction is not available to feature diversity because the features of biological organisms are so diverse (Vellend et al. 2011, 194). The high redundancy between metrics of phylogenetic diversity is such an impressive result because it demonstrates that feature diversity can be accurately quantified.

Because metrics of phylogenetic diversity are accurately quantifiable, their operationalisability turns on whether they are pragmatically measureable. Phylogenetic diversity is pragmatically measureable because conservationists can measure the phylogenetic diversity of an ecosystem with limited resources in a small time frame. Because species are already placed on the tree of life, and considering abundance is optional, conservationists only need to identify the species present in an ecosystem to calculate phylogenetic diversity. Some information on extant species in an ecosystem is already available. For this reason, phylogenetic diversity can make quick recommendations from complex data sets. In Conservation Evaluation and Phylogenetic Diversity, Faith shows how a cladogram of the taxa in a group can accurately predict which species would preserve the greatest feature diversity without having to directly observe any features (Faith 1992, 3). In his example, individual species do not need to be checked for novel features before deciding which to preserve. Preservation of the greatest feature diversity is accurately tracked by the phylogenetic pattern of the organisms. The
option to easily construct a visible pattern to inform conservation is a strong pragmatic advantage.

Lastly there is a high correlation between phylogenetic diversity and other true surrogates for biodiversity. In their PCA Vellend (et al. 2011, 201) found a 0.91 correlation between species richness and node based phylogenetic trees. Grenyer (et al. 2007, 757) phylogenetic diversity has a 77% correlation with species richness and a 96% correlation with genus richness. Faith has also argued that phylogenetic diversity correlates with habitat diversity and functional diversity (Faith 1996, 1287). The high correlation between phylogenetic diversity and other true surrogates is a pragmatic advantage for conservationists because it limits the number of other surrogates which need to be measured. The correlation is imperfect because the specific dimensions of biodiversity vary independently of one another. However, perfect correlation would not be beneficial to conservation. If phylogenetic diversity had a perfect correlation with species richness then the two metrics would be redundant for one another. There would be no point in calculating phylogenetic diversity because it would not give us any information that species richness could not. High but imperfect correlation between surrogates is the pragmatic goal for conservationists. Phylogenetic diversity meets that goal. It is accurately quantifiable and pragmatically measureable so it is operationalisable for the goals of conservation biology.

In this subsection I argued that phylogenetic diversity is an operationalisable surrogate for the goals of conservation biology. I first argued that metrics of phylogenetic diversity are accurately quantifiable by appealing to the results of a PCA of the metrics I discussed in section 5.5.3. The high redundancy between metrics indicated accurate quantification. This conclusion is supported by the low impact of distance based trees and weighting for abundance on conservation recommendations. The most important factor in tracking the feature diversity of organisms in an ecosystem is the phylogenetic pattern.

Then I argued that metrics of phylogenetic diversity are pragmatically measureable. I argued that metrics of phylogenetic diversity require little information to be performed, that they can easily make sense of complex data sets, and that they correlate highly with other true surrogates for biodiversity. I concluded that phylogenetic diversity is operationalisable for conservation biology. In the next section I will use the detail of the measurement methodology which I have outlined in sections 5.3, 5.4, and 5.5 to argue that the expanding multiplicity of biodiversity measures is overblown.

5.6 The Expanding Multiplicity of Biodiversity Measures is Overblown
In this section I will use the analysis of measurement methodology which I have outlined in this chapter to argue that the expanding multiplicity of biodiversity measures is overblown. That is, the number of biodiversity measures is not an indication of the empirical suitability of biodiversity for conservation biology. The expanding multiplicity of biodiversity measures is a problem because it gives the impression that biodiversity calculation is in a worse state that it actually is. There are enough measures to choose from that in “Is biodiversity a natural quality?” Maclaurin (Maclaurin 2017, 56) use the expanding multiplicity to motivate the debate over the ontological status of biodiversity.
Contra to that impression, I will advance several points to argue that the expanding multiplicity of biodiversity measures is overblown. I will argue that there are fewer options for measuring species richness because each calculation is catered to a different data set. In the case of species diversity, I argue that the total number of diversity measures do not impact the success of Shannon’s diversity index and Simpson’s diversity index. The detail of phylogenetic diversity shows a high within-surrogate correlation of results. I explain that the apparently large number of biodiversity calculations is actually a product of multiple decisions with a small number of options. I consider the objection that surrogate selection still does negatively impact the expanding multiplicity of biodiversity measures but argue that a range of choices does not make all options equal. A misleading focus on an inappropriate biodiversity surrogate will not pass academic scrutiny. I conclude that the expanding multiplicity of biodiversity measures is overblown and so cannot motivate the empirical case for biodiversity eliminativism.

The apparent expanding multiplicity of species richness’ measures is overblown because the disjunction of measures represents a rich and nuanced tool kit. Every calculation in that tool kit determines the height of the discovery curve using a prediction. The predictive success of those calculations is dependent on collected data. So there is a multiplicity of measures because there are different kinds of data collection. Conservationists eliminate half the possible measures when they decide to record species via incidence or abundance. Following data collection, the different metrics are then available because they cater to different data sets but all are focused on identifying the height of the discovery curve. The multiplicity of measures seems large because it is the product of a small number of choices. The biodiversity tool kit is a rich and nuanced one precisely because it can cater to diverse needs.

Imagine that Sandra collects incidence data in a study on species richness. Sandra could employ the ICE calculation to determine the height of the asymptote but all the infrequent species in her sample are singletons. If all the infrequent species in a sample have an abundance of one then ICE will not work (Colwell and Gotelli 2011, 41). Instead Sandra is better off calculating the asymptote with Chao2. She then has two further options based on her data set. Chao2 has two variants, one which is intended to work for any combination of species and one which is intended to work solely from the duplicate species present. It can usually find the asymptote from a smaller data set because it focuses on the relative incidence of rarer species (Colwell and Gotelli 2011, 51). Sandra has multiple calculations to choose from because they are optimised for different kinds of data sets.

We need multiple calculations of species richness because there are multiple possible data sets and we need the fastest way of determining the height of the discovery curve. By analogy, a cheese knife, bread knife, and a paring knife can all carve a block of cheese. One will do the best job and the others will not perform as well because they are intended for different materials. We still need all three knives but the available number of knives does not make them a poor fit for the role of carving food. Instead it makes them collectively better at the task. Likewise with calculations of species richness, the expanding multiplicity of measures represented a rich and nuanced tool kit.

The expanding multiplicity of species diversity’ measures (the large number of
available measures to choose from) is overblown because despite the large number of calculations available there are still dominant measures of species diversity. There is a large number of different methods for calculating species diversity but Shannon’s diversity index and Simpson’s diversity index are still two of the best performing, most straightforward, and most used (Maurer and McGill 2011, 64). The expanding multiplicity of biodiversity measures is not solely a function of biodiversity’s conceptual complexity. It is also a function of the academic focus on publication. Publications require an original contribution to literature which can be achieved by developing a new measure of biodiversity and demonstrating that it outperforms other measures at some task. No individual measure of biodiversity captures every important element of biodiversity. It can’t because biodiversity is a complex multidimensional concept. So, it is normal for systems of measurement to appear which capture those important elements. The expanding multiplicity is overblown because despite multiple measures to capture as many important elements as possible two of the oldest measures are still two of the best.

The expanding multiplicity of phylogenetic measures is overblown because there is high within-surrogate correlation of phylogenetic measures. The different distance metrics have a 90% correlation with one another (Vellend et al. 2011, 205). That is an impressive result because biological organisms are so phenotypically diverse and quantifying difference and similarity seems like an intractable problem outside of restricted domains (Goodman 1972, 437). There are scenarios in which we can accurately quantify difference. A spinal column with six vertebrae is minimally different to the same spinal column with seven vertebrae. Facial recognition software uses points of comparisons to determine identity. It can do this because it focuses on a small number of important properties in a general setting (Goodman 1972, 444, 446). The problem is more complex when quantifying the difference between a house fly and a thistle. Despite this, the mean correlation between two metrics of phylogenetic diversity is 90%.

The expanding multiplicity of phylogenetic measures is also overblown because like species richness the large numbers of metrics is a product of a small number of decisions. Conservationists must choose between node and distance based trees. If there is a preference for distance based trees then they have the option of different scales and whether to weight branch lengths by abundance. What is interesting in the case of phylogenetic diversity is that the correlation between metrics is so high that preference can determine the easiest metric to calculate. “Within node-based and distance- based metrics, redundancy is quite high (r > 0.9 for most pairs of metrics across all tree types). As such, an appropriate criterion for choosing among metrics is their conceptual and mathematical simplicity.” (Vellend et al. 2011, 205). The expanding multiplicity of phylogenetic measures is a product of a small number of decisions, most of which do not have a serious impact on conservation recommendations.

The analysis of the measurement methodology of biodiversity surrogate outlined in this chapter indicates that the large number of measures is a factor of a small number of choices. During biodiversity calculation several decisions are made between a small range of options. A true surrogate is selected. An estimator surrogate is selected. The importance of abundance in the results is considered. Sampling strategy is decided. A calculation is selected based on the collected data. In the case of phylogenetic calculations a distance
metric is decided. Each decision step has a small number of options but multiple stages increases the total outcomes exponentially. Three true surrogates with ten measurements and five options for distance metrics is already 150 options. A small number of choices exponentially increase the expanding multiplicity of biodiversity measures. For example in the next chapter I will discuss measures of trait diversity. Since those measures require focusing on a common trait, there are as many possible trait diversity calculations as there are common traits.

The expanding multiplicity of biodiversity measures gives the impression of thousands of possible results. But in practice there are a handful of distinct ways to calculate biodiversity with a great number of subtle variants. Because the expanding multiplicity increases exponentially for each decision, it also narrows exponentially once a decision is made. The decision with the biggest impact on the results isn’t the decision between chao2 and first-order jackknife richness estimator, it’s the selection of true surrogate. Species richness, species diversity, and phylogenetics are all distinct measures so once one true surrogate has been selected, two thirds of the possible results are eliminated. By analogy with temperature the expanding multiplicity of measures is less a problem of 100 ways to measure temperature and more a product of there being a few ways to measure a temperature with many brands of thermometer. Temperature can be measured via digital, mercury, internal or surface but there are many competing brands which perform slightly differently. Like temperature, once a conservationist selects a true surrogate for biodiversity they drastically narrow the possible range of results.

An objection might be that a source of the expanding multiplicity of biodiversity measures is surrogate selection. Whilst measurement preference cannot heavily skew final results, surrogate selection can. A score of species richness is very different from a score of species diversity which weights results for abundance. This concern conflates the number of choices with no matter of fact about the best choice. But, the multiplicity of diversity measures does not imply that all calculations are equally valuable for all ecosystems. Using a straight-forward measure of species richness to assess the taxonomy of an ecosystem containing ancient species such as the tuatara, is a poor choice of surrogate because an ancient unchanged species and a relatively recently evolved species count for the same. In this case a phylogenetic score is better because it gives greater value to species which have remained unchanged over a long period of time.

The expanding multiplicity of biodiversity measures should not motivate the empirical case for eliminativism because poor choices do not pass critical evaluation. In NZ there is an issue with child poverty and in 2015 a nationwide study on the depth of the problem yielded 13 measures indicating that the problem was severe. The government of 2015 opted to focus on the measure which presented the problem as least severe. The opposition of 2015 were quick to argue that this single measure misrepresented the state of child poverty in NZ (Parliament 2015, question 11). Likewise, while a poor selection of surrogate may be misleading it is unlikely to go unnoticed by critical academic work. A large proportion of Santana’s academic work is built on pointing out where biodiversity surrogates fall short. Their limitations are clear and so a biased surrogate selection intended to mislead the taxonomic state of an ecosystem is unlikely to convince anyone. A
conservation biologist who uses the ‘ACE’ calculation \( S_{ACE} = S_{abund} + \frac{s_{rare}}{c_{ACE}} + \frac{f_1}{c_{ACE}} \gamma_{ACE}^2 \) from a set of incidence data is likely to have the same amount of academic credit as a doctor who checks a patient for diabetes by taking their temperature. The ACE calculation is intended for abundance data rather than incidence data.

There is a great multiplicity of biodiversity measures but more often than not those measures share a great deal in common both conceptually and empirically. Species richness, species diversity, and phylogenetic diversity all measure different dimensions of biodiversity but they are also all transformations on the same data set. For any ecosystem, if a conservationist has a list of species and their abundance, they can calculate that ecosystem’s species richness, species diversity, and phylogenetic diversity. Like mean, median, and mode biodiversity surrogates are often transformations on the same data set. They process the data in different ways to calculate different features. Those distinct features give us important insight into the properties of the data set but they are not meant to be the only aspect of the data set worth considering. Deciding which transformation of a data set is the most important is made on a case by case basis. Species richness may work well for biodiversity hotspots but ecosystems with unique selective pressures such as islands may be better served by calculations of phylogenetic diversity.

In this section I argued that the analysis of measurement methodology which I have outlined in this chapter shows that the expanding multiplicity of biodiversity measures is overblown. I argued that the apparent expanding multiplicity of species richness’ was actually a case of a rich and nuanced tool kit. I argued that the apparent expanding multiplicity of species diversity’ measures was a case of diverse competition with a few dominant competitors. In the case of phylogenetic diversity, I argued that despite the apparent expanding multiplicity, phylogenetic measures have a high within-surrogate correlation of results. I explained that the large range of available biodiversity calculations is a function of a small number of options at several decision points. I argued that these decision points do not increase imprecision because poor measurement choices do not survive academic scrutiny. Because the expanding multiplicity of biodiversity measures is overblown it cannot motivate the empirical case for biodiversity eliminativism. Familiarity with the detail of the measurement methodology of biodiversity surrogates indicate that biodiversity is a good empirical fit for the role it plays in conservation biology. Its surrogates are operationalisable and the large number of options for measurement is a normal feature of complex multi-dimensional concept.

**5.7 Conclusion**

In this chapter I presented a detailed analysis of three measurement surrogates for biodiversity, focusing on their measurement methodology: species richness, species diversity and phylogenetic diversity. I argued that the technical detail of the methodology supported two claims about the state of biodiversity measurement. The expanding multiplicity of biodiversity measures is overblown and measurement surrogates are operationalisable. First I summarised the role of the expanding multiplicity of biodiversity measures in motivating the poor empirical fit argument. Then I outlined the measurement
methodology for three true surrogates of biodiversity: species richness, species diversity and phylogenetic diversity. For each surrogate I discussed its unique approach to measuring biodiversity. Species richness uses discovery curves to solve the problem of counting the thousands of species in an ecosystem. Species diversity weights richness results by abundance to detect how evenly species in an ecosystem are represented. Phylogenetic diversity maps species on to phylogenetic trees to measure the evolutionary variation of in an ecosystem.

Next, for each surrogate I outlined different metrics and explained how they work. I used this technical detail to argue that each surrogate was operationalisable for conservation biology. This conclusion contradicted premises five, six and the conclusion of the empirical poor fit argument. Premise five claimed that “individual dimensions of biodiversity are either not operationalisable, do not accurately track biodiversity, or do not track biological value. In chapters one to four I argued that the true surrogates of biodiversity track biodiversity conceptually and empirically. In this chapter I argued that they are also operationisable. Premise six claimed that satisfying conditions one to five was a sufficient reason to eliminate biodiversity but in chapter four I argued that it overlooked the importance of within-surrogate operationalisability.

Within-surrogate operationalisability is as important for a multidimensional measure as between-surrogate operationalisability. So demonstrating that measurement surrogates for biodiversity are operationalisable shows that premise five is false, premise six has overlooked an important ‘good fit’ element, and produces important evidence that the conclusion of the empirical poor fit argument is false. Lastly I used the detail of the surrogate’s measurement methodology to argue that the expanding multiplicity of biodiversity measures is overblown. Whilst it may appear that measures of biodiversity are numerous with little consensus on how biodiversity ought to be measured, the large number of measures is the product of a small number of options. The inference to the best explanation is not that the biodiversity measures are in a poor state but rather that conservationists have a highly nuanced tool kit. In the next chapter I will continue my analysis of measurement methodology and conclude that the empirical case for biodiversity eliminativism is unsuccessful.
6 Implications of Measurement Methodology II: The Empirical Case for Biodiversity Eliminativism is Unsuccessful

6.1 Introduction
This chapter is the final part of an extensive defence of the biodiversity concept against Santana’s poor fit empirical argument. In this chapter I will outline the measurement methodology of two true surrogates for biodiversity: morphology, and functional diversity. The purpose of outlining the technical detail is to demonstrate that some biodiversity surrogates are not operationalisable. This implies that premise five of the empirical poor fit argument that “individual dimensions of biodiversity are either not operationalisable, do not accurately track biodiversity, or do not accurately track biological value” is true for some surrogates. I will use this conclusion to argue that the empirical poor fit argument fails because it has an internal contradiction.

First, I will summarise the importance of within-surrogate operationalisability for the empirical case against biodiversity. Then I will outline the measurement methodology of morphological calculations. I explain why phenotypic diversity is an important element of biodiversity and outline adaptive landscapes and morphospaces as empirical tools. I call attention to the mathematical relationships in nature before arguing that morphology is not an operationalisable surrogate for biodiversity. Next I outline the measurement methodology of functional diversity. I explain why functional diversity is an important element of biodiversity before discussing several different metrics of functional diversity. I use this detail to argue that measures of functional diversity are not functional enough and that functional diversity is not an operationalisable surrogate for biodiversity. Lastly, I argue that the empirical poor fit argument for biodiversity’s elimination fails because it contains an internal contradiction. Santana’s intended replacement for biodiversity fails his own empirical standard for a conservation goal.

6.2 The Importance of Within-Surrogate Operationalisability for the Empirical Case against Biodiversity
In this subsection I will argue that within-surrogate operationalisability (how operationalisable specific dimensions such as species richness are) is important for the empirical case against biodiversity. The empirical case would eliminate biodiversity in favour of its surrogates so the operationalisability of those surrogates is important. I give examples of theory replacement in the history of science before arguing that eliminating biodiversity shifts the burden of operationalisability to its surrogates. I consider and defend against the possible objection that Santana does not need his attack on the specific dimensions of biodiversity to motivate the empirical poor fit argument.

Within-surrogate operationalisability is important for the empirical case against biodiversity because Santana wants conservation to eliminate biodiversity without a new replacement. Theory eliminativism in the history of science is either an instance of
replacement or hard eliminativism. Replacement eliminativism occurs when a more successful theory replaces an older one. This is a case of Kuhnian paradigm shift, or Lakatosian research program replacement. The oxygen theory of combustion replaces phlogiston theory and the theory of moving tectonic plates replaces biblical catastrophism. In cases of hard eliminativism a theory or concept is eliminated without replacement. There are no seriously competitive theories for the transmutation of iron into gold because chemistry eliminated the theory of chryosperia in the late seventeenth century (Principe 2014, 97). Santana’s eliminativism is a case of hard eliminativism because biodiversity is being removed from the surrogate chain rather than replaced. Angermeir and Karr, by contrast, want to replace biodiversity with biological integrity. Santana simply wants it gone.

Eliminating biodiversity rather than replacing it with something like biological integrity will shorten the surrogacy chain so that conservationists infer biological value from the specific dimensions of biodiversity such as species richness. So if dimensions such as species richness are not operationalisable then conservationists lack a practical goal for conservation. Within-surrogate operationalisability matters for the empirical case against biodiversity because Santana expects biodiversity’s surrogates to pick up the work which biodiversity was doing. The surrogacy chain goes from ‘Surrogate → Biodiversity → Biological Value’ to ‘Surrogate → Biological Value’. So if conservationists are relying on surrogates to guide conservation decisions then they need those surrogates to be operationalisable.

The importance of within-surrogate operationalisability is a problem for the empirical case against biodiversity because Santana does not distinguish between within-surrogate operationalisability and between-surrogate operationalisability in his arguments. He presents arguments against both as an attack on biodiversity. Consider the poor empirical fit argument.

The poor empirical fit argument

1) General conceptions of biodiversity are not straightforwardly measureable.
2) There is not sufficient property correlation for biodiversity to be considered a property bundle.
3) The dimensions of biodiversity do not support robust inductive generalisations across the group.
4) The inclusion of biodiversity in the conservation process exacerbates imprecision between the measured target and the conservation goal.
5) Individual dimensions of biodiversity are either:
   a. Not operationalisable
   b. Do not accurately track biodiversity
   c. Or do not accurately track biological value
6) If conditions 1) to 5) accurately describe biodiversity then biodiversity is a poor empirical fit for its role in conservation biology.
7) Therefore: Biodiversity is a poor empirical fit for its role in conservation biology.
In my construction of his argument I have distinguished between-surrogate methodology from within-surrogate methodology. Premises one to three target the between-surrogate operationalisability of biodiversity. According to Santana, general conceptions of biodiversity are not straightforwardly measurable because they gather together strictly incommensurable dimensions. We don’t have good reasons to treat those dimensions as a property bundle. We cannot inductively generalise from one dimension to another. However, premise five that “individual dimensions of biodiversity are either not operationalisable, do not accurately track biodiversity, or do not accurately track biological value” is a concern about within-surrogate operationalisability. Santana needs premises one to five to motivate the conclusion.

One objection is that Santana could dispense with premise five and motivate the conclusion with premises one to four. This is not an option because Santana has already used premise five in his conceptual argument for biodiversity’s elimination. A key premise in his conceptual dilemma was that no specific dimension of biodiversity captures all the important biological elements which we ought to preserve. There is more to conservation than maximising species counts so there is more to biodiversity than species richness. Santana uses these conceptual arguments to motivate his empirical case. If biodiversity in the general sense is not operationalisable and its specific dimensions are either not operationalisable or do not accurately track biodiversity then biodiversity is a poor empirical fit for its role in conservation biology. Santana is using within-surrogate operationalisability to motivate between-surrogate operationalisability.

Because Santana doesn’t distinguish within-surrogate operationalisability from between-surrogate operationalisability he doesn’t consider important problems with the former. Only a small number of biodiversity surrogates are fully operationalisable. In chapter five I argued that species richness, species diversity, and phylogenetic diversity are operationalisable. In this chapter I will argue that morphology and functional diversity are not operationalisable. Santana needs a large number of operationalisable biodiversity surrogates because eliminating biodiversity implies that the surrogates are better indicators of biological value. If conservationists only have a small number of surrogates and those surrogates fail to track biological value then Santana has no viable alternative to using biodiversity as a goal of conservation. In this chapter I will argue that the empirical case against biodiversity fails because Santana has no viable alternative to biodiversity. I use the detail of the measurement methodology of morphology and functional diversity to argue that there are few operationalisable true surrogates for biodiversity. Santana requires additional surrogates beside species richness and phylogenetic diversity to accurately track biological value but those surrogates are not operationalisable for the demands of conservation biology. I begin with morphology.

6.3 The Methodology of Measuring Morphology
The fourth true surrogate for biodiversity which I will discuss is morphology. Morphology is a method for calculating phenotypic diversity. Phenotypic diversity is the variety of observable physical characteristics contained in an ecosystem (Santana 2014, 764). In this section I will argue that phenotypic diversity is an important dimension of biodiversity. Then I explain how adaptive landscapes and morphospaces work before I draw attention to
other mathematical patterns in nature. I will argue that morphology is not an operationalisable surrogate for biodiversity because of a problem I will call ‘the trait dilemma’. Calculations of morphology must select a range of traits to represent the phenotypic diversity of an ecosystem. Unique traits such as wing length are informative but are not operationalisable because they are not features of all organisms. Common traits such as mass are operationalisable but uninformative because they do not detect unique phenotypic features. I conclude that morphological calculations offer interesting biological insight but are not suited to the demands of conservation.

6.3.1 Why Phenotypic Diversity Matters
Phenotypic diversity refers to the variation of physical characteristics present in an ecosystem (Santana 2014, 764). It focuses on the physical attributes of organisms: their colour, shape, how many limbs they have, and what their internal structure is like. Phenotypic diversity is an important dimension of biodiversity because ecosystems are more biodiverse when they have a greater variation of physical characteristics. One of the reasons that there is more to biodiversity than species counts is that species can be quite similar. Ladybird beetles may seem similar but they are actually part of family named “Coccinellidae”. “Coccinellidae” contains 6000 distinct species of ladybird. Groups which contain ladybird beetles and house sparrows are more biodiverse than those which just contain ladybird beetles. Phenotypic diversity can quantify this example more accurately than species richness by assigning greater values to unique phenotypic traits.

Calculating the variation of physical characteristics is difficult because of the number of distinct physical traits and the problem of quantifying difference between those traits. Simple physical traits such as mass range widely from charismatic megafauna to microorganisms but are shared. Complex traits are often not shared or multiply realisable. Traits such as wingspan are not shared by all organisms in an ecosystem so wing variation will not tell us much about the total phenotypic diversity of an ecosystem. Wings are also multiply realisable. Something is multiply realisable if it can be instantiated in multiple distinct ways. Mouse traps are multiply realisable because they are defined by function; they can be made of steel or wood and still be mousetraps. Wings are multiply realisable because a fly, a sparrow, and a penguin all have wings but that module is phenotypically distinct for each organism. Fly wings have chitin over a vein structure. Sparrows’ wings have feathers and hollow bones. Penguin wings are vestigial limbs because they are now used for swimming.

Multiple realisability, along with lack of shared traits and a large number of total traits makes quantifying phenotypic diversity difficult (Vellend et al. 2011, 194). The problem is not unsurmountable. Nelson Goodman argues that similarity is a more tractable problem when it is confined to a specific domain with a limited number of important properties (Goodman 1972, 444,446). We can quantify how similar one human face is to another better than how similar it is to a pumpkin. Morphologists tackle the quantification of phenotypic diversity by mapping the diversity of physical traits on to morphospaces.
6.3.2 Morphospace Methodology

A morphospace is a map of the variation of physical traits within a group of organisms. This enables us to visualise the relationship between multiple ranges of traits. There are two kinds of morphospaces, empirical morphospaces and theoretical morphospaces. Empirical morphospaces map physical traits against an appropriate scale. In subsection 6.4.2 I will discuss calculations of functional diversity which use empirical morphospaces. Theoretical morphospaces map physical traits against a scale of all logical possibilities so they indicate how much space of biological possibility is currently occupied by the organisms in an ecosystem. For instance this hypothetical morphospace shows all of the biological possibilities for planispiral bivalved shell morphology.

Morphospaces are not the only way to quantify the variation of physical characteristics. Morphology aims to reduce multiple physical characteristics down to their mathematical relationships (McGhee 1999, 2).

One reason for the success of theoretical morphology is the way in which morphospaces visualize the relationship between phenotypic traits. On a morphospace, ranges of traits can be plotted against one another to visualize an important pattern (McGhee 2007, 60). There is a dimensional limitation to visualising morphospaces. We cannot map five traits against one another because we cannot create a five dimensional morphospace. We can map up to three properties against one another visually. True morphological spaces are hyper-dimensional (McGhee 2007, 45). These cannot be visualized but they can be analysed with clustering algorithms.

Raup’s cube which explores the possible forms of shell coiling in univalve mollusks is an example of a three dimensional morphospace.

Figure 6.1: Complete morphospace (contains all possibilities) of planispiral bivalved shell morphology. (Adapted from (McGhee 1999, 122–24))
Figure 6.2: Raup’s three dimensional morphospace of shell coiling in mollusks (Raup 1966, 1184).

The cube plots all theoretical combinations of shell coiling. Visualising the relationship between these traits allows for some interesting observations. It shows us certain correlations but it also shows us that much of the possible space is unoccupied. These empty volumes on a morphospace represent non-existent organisms (McGhee 2007, 59). This could be due to local environmental pressures or the impracticality of certain coiling shapes but it highlights unrealised evolutionary potential.

Mapping properties on morphospaces can also give us insight into important changes in phenotypic diversity. During the cretaceous/tertiary extinction the ammonites became extinct which emptied an existing ecological niche. During this period the nautilids evolved to become more like the ammonites.
Figure 6.3: Change in Nautilid Shell Morphologies Following the Ammonite Extinction. $S$ represents its shape, $D$ represents the distance of the generating curve (Ward 1980, 32).

By plotting the nautilids over morphological space, we can see them evolving to fill an empty ecological niche. This is important evidence for the ecological rule of competitive exclusion. Competitive exclusion is important for biodiversity because it drives the ability of phylogenetic pattern to track feature diversity. Species with the same features occupy the same niche and species which require the same ecological niche cannot co-habit (Justus 2013, 356). Here in this morphological cube, we can see how the ammonites’ survival was constraining the nautilids’ evolutionary potential. The role of ecological niches in biodiversity is contentious because the concept of an ecological niche is controversial (Maclaurin and Sterelny 2008, 35). This morphospace is an interesting example of understanding the organisms of biodiversity in terms of their ecological niches.

Despite the insight which morphospaces can provide to biology I will argue in section 6.3.4 that morphology is not an operationalisable surrogate for biodiversity. The problem with the methodology of morphology is that it is better suited to investigating specific hypotheses such as the impact of ecological niches on evolution than generating phenotypic diversity values for conservation decisions. It is not possible to create a single morphospace because of the sheer number of total traits and the lack of shared traits. Three-dimensional morphospaces can accommodate three traits, whereas a global morphospace is hyper-dimensional (McGhee 2007, 47–49). It must be hyper-dimensional because of the staggering number of possible traits (McGhee 2007, 45).

Clustering algorithms are used for processing large numbers of traits. Whilst we cannot visualise multiple ranges of variables on a single morphospace, we can apply algorithms to determine the relationship between the ranges of phenotypic traits. Despite their use with processing enormous volumes of data, clustering algorithms cannot generate a global morphospace because of the lack of common traits between organisms. If we have the complete theoretical morphology of a Devil’s Fingers fungus (*Clathrus archeri*) and the complete theoretical morphology of a duck-billed platypus (*Ornithorhynchus anatinus*) then we can still not usefully calculate the relationship between those data points on a single morphospace. The Devil’s Fingers fungus does not have enough traits in common
with a duck-billed platypus. This suggests that the operationalisability of morphology is limited to testing specific hypotheses (Maclaurin and Sterelny 2008, 75).

6.3.3 Mathematical Patterns in Nature
This section should not be understood as a case for eliminating morphology. Morphological work is impressive and important. At its heart morphology is about identifying mathematical relationships in nature and there are many such relationships to discover. One example of this is the work on reducing the branching patterns of flora to formulae. Whilst the images below all appear to be fairly natural branching patterns they are in fact computer simulations of branching patterns producing by the formula beneath each picture.

Mathematical relationships are everywhere in a nature. Nature’s apparent randomness often yields surprising regularities. The Fibonacci sequence is a sequence of numbers in which each successive numeral is the sum of the previous two numerals: 1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144, etc. Surprisingly, that sequence appears in nature in unusual places such as breeding cycles with pairs of rabbits and the leaf arrangements in plants (McGhee 1999, 259). In The Geometry of Evolution McGhee argues that an adaptive evolutionary landscape shows a convergent evolution among marine mammals, marine reptiles, cartilaginous fishes, and bony fishes. Ichthyosaurs and porpoises resemble sharks and swordfishes because each group has individually evolved organisms with a streamlined morphology for fast swimming (McGhee 2007, 33). These morphological results are interesting and important. The morphological results which we have thus far

\[ \text{Figure 6.4: Computer produced branching patterns (McGhee 1999, 258)} \]
can inform our conservation decisions. Morphology is operationalisable but as I will argue in the next section, it just isn’t operationalisable for the demands of conservation biology. Morphological methodology cannot analyse two ecosystems and tell us which one to preserve.

### 6.3.4 Morphology is Not an Operationalisable Surrogate

Morphology is not an operationalisable true surrogate for biodiversity because we cannot produce an accurate value for the overall phenotypic diversity of an ecosystem. A biodiversity surrogate is operationalisable if it is accurately quantifiable and measureable. In this subsection I will argue that specific morphological features are accurately quantifiable and measureable but overall phenotypic diversity is not. To motivate this conclusion I consider the plausibility of a global morphospace and a global morphospace library. I argue that the resource demands of conservation and lack of established theoretical morphological work make both options implausible. I argue that the main obstacle to the operationalisability of morphology is an internal problem with the nature of phenotypic traits. Phenotypic traits are widely diverse and there is a lack of shared traits between organisms. I argue that morphological calculations face a dilemma. They must select a range of traits to indicate the ecosystem’s overall phenotypic diversity but general traits gloss over important morphological features and specific traits—those which are unique to a few species—do not accurately track phenotypic diversity. I conclude that morphology is not an operationalisable true surrogate for biodiversity.

Specific morphological features are accurately quantifiable and measureable. Raup’s cube of shell coiling in mollusks produces accurate morphological maps of the specific morphological feature of shell coiling. That cube, and other specific morphological features do not offer much insight into the overall phenotypic diversity of an ecosystem. So whilst specific morphological features are operationalisable morphology in the sense of phenotypic diversity is not. For morphology to be operationalisable for the demands of conservation biology it needs to either produce a global morphospace library or identify a common range of functional traits to use as an estimator surrogate for phenotypic diversity. I will argue that neither is an operationalisable possibility.

A global morphospace could produce an overall score for phenotypic diversity. A global morphospace is the idea of morphology applied to every phenotypic trait in an ecosystem with the aim of producing a final value for the total phenotypic variance of the ecosystem in question (McGhee 1999, 13). The prospect of such a morphospace is grim because of several methodological difficulties. The first of which is the number of phenotypic traits in an ecosystem. Morphosphaces can successfully compare many phenotypic traits at a time but phenotypic diversity is the variation of every phenotypic trait in an ecosystem. There is no single morphospace which could map all the data.

A global library of morphosphaces for specific morphological features may be a suitable replacement for a single global morphospace. It could not process the phenotypic diversity of an ecosystem into a single value but it could highlight the unique organisms within an ecosystem to inform conservation decisions. Such a library will not meet the time constraints of conservation because of the number of phenotypic characteristics and the morphological work which remains to be done. Applying the work of Nelson
Goodman on similarity, we could constrict the number of phenotypic characteristics to those which biologists are interested in (Goodman 1972, 444, 446). However, there is still a wide diversity of phenotypic traits which warrant study and few traits which are shared by many species (Vellend et al. 2011, 194). It would be a long time before such a library would be close to complete. The time constraint does not meet the demands of conservation because conservation work requires triage (Durant et al. 2014, 120). With the increasing impact of human habitation on biodiversity, the goal is to swiftly preserve as much as possible with the resources we have left.

Triage concerns are a bigger problem for theoretical morphology than for other surrogates because in any given conservation scenario, we do not just need to sample the species/access the weather patterns but also finish identifying the mathematical relationships in the species we are studying. Nearly all species on the planet remain unstudied from a theoretical morphological stand point. In *Theoretical Morphology: The Concept and its Applications* McGhee notes that work in theoretical morphology has only been undertaken on a fraction of the total species. Of the 56 phyla in the super domain, 41 currently have no theoretical morphological work completed on them at all. Within the 15 phyla which have been studied, work has only been completed on a handful of species (McGhee 1999, 282). We have morphological data on practically all discovered species because all known species have been documented. However, very few species have had their morphological features quantified and mapped and the known species are a small fraction of the total species (Mora et al. 2011, 5). The triage requirement is more pressing for theoretical morphology than for other estimator surrogates because the mathematical groundwork still needs to be completed for millions of remaining species. It is possible that a global morphospace library could provide a decisive biodiversity value but it is just as likely that by the time we are finished with the mathematical groundwork, there won’t be much biodiversity left to apply it to.

The obstacle facing the operationalisability of morphology is more than just a sampling issue. The time constraints of conservation affect all true surrogates for biodiversity. Reliable conservation recommendations require large volumes of accurate data which takes time to collect but conservation decisions need to be made swiftly. In practice conservationists solve this dilemma through a combination of sampling methods and use of historical data. Whilst studying the impact of radioactive fallout on the biodiversity in Chernobyl, Moller (et al. 2007) calculated the biodiversity of the area using species richness as their true surrogate. They conducted standard census point counts of birds (their estimator surrogate) in 254 locations. For each standard point count the authors stood in place for five minutes and recorded every bird species which was seen or heard. This methodology produces a reliable estimate of species richness and abundance (Moller et al. 2007, 483). The sampling is combined with adjustments to the data for confounding variables such as weather. Weather conditions affect bird activity which can impact the census data. So weather conditions were recorded and these can be compared to historical weather patterns to determine if the census point data was gathered on a typical day. By employing a combination of sampling and historical data the authors concluded that the radioactive fallout in Chernobyl negatively impacted the species richness of the area and health of local organisms in a severe manner (Moller et al. 2007, 485).
The main obstacle to the operationalisability of morphology is not a sampling issue such as the number of species which are required to accurately predict species richness. Instead, the problem is that there is no trait (or collection of traits) which can accurately predict the phenotypic diversity of an ecosystem. This is due to the problems with the great range of phenotypic diversity and the lack of common traits. Phenotypic traits cover everything from petal number to eye colour. They are so distinct that there is little reason to think that mollusk coiling or leaf shape indicates much about the rest of phenotypic diversity. There is a causal relationship between the empirical sample of species in an ecosystem and the ecological sample. There is not a strong causal relationship between wing diversity and branching patterns. The great variance of phenotypic diversity makes sampling impractical because there are few common traits between distinct organisms. Mammals have no chlorophyll and flora have no blood. Petals, teeth, and claws are not present in all biological organisms.

The wide diversity of phenotypic characteristics and lack of common traits force morphological calculations into a trait dilemma. A calculation of phenotypic diversity should accurately indicate the variation of phenotypic characteristics in an ecosystem but the calculation can only use a small range of traits. So a range of traits must be selected to serve as an estimator surrogate. Those traits can be shared or specific. If the traits are shared then they will be a very general phenotypic trait such as colour or mass. They will also tell us little about the variation of the other phenotypic traits in the ecosystem because they generalise over important differences. For example the diversity of mass per organism tells us little about the form or function of those organisms. If the range of traits is a specific such as shell coiling then it will accurately map the diversity of that specific morphological feature but it will be a misleading indication of the overall phenotypic diversity in the ecosystem. As I argued previously, the diversity of specific traits implies that they cannot reliably indicate overall phenotypic diversity. Morphology is therefore not an operationalisable true surrogate for biodiversity. Specific morphological features are accurately quantifiable and measureable but morphological work cannot accurately predict the overall phenotypic diversity of an ecosystem.

In this subsection I argued that based on its measurement methodology, morphology is not an operationalisable true surrogate for biodiversity. I drew a distinction between the morphology of an ecosystem and specific morphological features before considering if morphological calculations could accurately predict the phenotypic diversity of an ecosystem. I considered the possibility of a global morphospace but argued that there are too many phenotypic traits to process in a single morphospace. I considered the possibility of a global morphospace library but argued that the triage requirements of conservation and lack of theoretical morphological work make it implausible. I then argued that the obstacle to operationalisability was not a sampling issue but a deeper problem to do with phenotypic traits. There is a wide variation of phenotypic traits and few common traits. This creates a trait dilemma for operationalisability. Common traits are uninformative but specific traits predict phenotypic diversity poorly. I concluded that morphology is operationalisable for specific morphological features but not as a true surrogate for the demands of conservation biology. In the next section I move my analysis on the detail of calculations of functional diversity.
6.4 The Methodology of Measuring Functional Diversity

The final true surrogate for biodiversity which I will discuss is functional diversity. Functional diversity shifts the focus of conservation away from the number of organisms in an ecosystem and towards the functional interactions between those organisms. In this section I will explain the importance of functional diversity with case studies on three organisms. Then I will outline different metrics of functional diversity. For those metrics I draw a distinction between calculations which use morphospaces and calculations which use phylogenetic trees. I then argue that functional diversity is not functional enough because measures of functional diversity do not prioritise rare biological functions. I conclude that functional diversity is not an operationalisable true surrogate for biodiversity because of the trait dilemma and because the standard for functional trait is too liberal.

6.4.1 The Importance of Functional Diversity

In this section I explain the importance of functional diversity as a true surrogate of biodiversity. I motivate this claim with three case studies of complex biological phenomena: the tiger moth (*Arctia caja*), *P. Carnivora*, and *X. Vesparum*. I introduce the zootopia thought experiment and briefly defend it. In all three cases I argue that functional diversity captures an important dimension of biological variation which other surrogates miss because it focuses on how organisms interact.

Functional diversity is an important dimension of biodiversity because it shifts the focus of conservation away from static elements of an ecosystem like species counts and towards the interactions and behaviours of those organisms. Complex biological phenomena are a high priority for conservationists. Functioning butterflies tell us more than those preserved in glass cases because we can also preserve their behaviour and interaction with other organisms. Interactions between organisms matter to conservation but species counts and phylogenetic analyses aren’t the best guide to those interactions. The monarch butterfly has an inter-continental migration pattern but scores of species richness or phylogeny only consider an organism as an equal species or in terms of how complementary it is to the ecosystem. Species richness treats the monarch butterfly as an equal species. If there is a species in the ecosystem with recent common ancestors with the monarch butterfly then phylogenetic diversity will not prioritise it for conservation. Functional diversity is important because it pays attention to important functional biological phenomena. Here I present three case studies which highlight such phenomena: the tiger moth and its ability to mislead sonar, the predatory bagmoth larvae, and the parasitic fly *xenos vesparum*.

The tiger moth (*bertholdia trigona*) is an insect which has evolved a sophisticated adaptation against the predation of the big brown bat (*eptisicus fuscus*) (Corcoran, Barber, and Connor 2009, 325). Like most other bats, the brown bat of Central America hunts insects for its primary food source. Known commonly as sonar, bats hunt their prey using a system of echolocation. The bat makes a clicking noise which travels into the world and bounces off objects. Based on the time it takes for the click to return, the bat is able to determine the shape of objects and their proximity to it. The use of sonar makes the big
brown bat a formidable hunter because unlike focused vision, sonar is omni-directional. The big brown bat does not have to look at an insect to know it is there.

As a defence mechanism, the tiger moth has evolved the ability to jam the sonar of approaching bats. As the bat approaches the moth, it makes a series of high duty cycle ultrasonic clicks which prevent the bat from successfully killing its prey. One such study aimed to discover if the ultrasonic clicks produced by the tiger moth startle the bat, warn it, or functionally jam the predator’s sonar. Researchers trained three naïve and one adult *eptisicus fuscus* to hunt tethered moths over the course of several days and then tested them against tethered tiger moths for several more days (Corcoran, Barber, and Connor 2009, 326). If the clicks produced by the tiger moth startled the attacking bats then over time the bats would habituate to the noise and learn to ignore it. If the clicks served as a warning the bats would initially capture the moth then drop the distasteful insect and learn to abort future attacks upon hearing the warning click. If the clicks jammed the radar, then the bats would be unable to capture the tethered moth and would continue to do so.

In this study, the bats successfully hunted control moths four times as much as a clicking tiger moth. The same bats had a 100% contact rate with tiger moths which had been silenced. They also persisted in their attacks against the tethered moth despite failing multiple times which suggests that the clicks do not serve to startle or warn the bats. The tiger moth is actually jamming the sonar of the big brown bat. Roughly one third of the time the bats would suddenly change their attack pattern shifting their focus from the moths’ location to a new unoccupied location. This was an immediate response to the high cycle clicks of the tiger moth which suggests that the jamming function of the tiger moth may be to alter the location in which its predator perceives it to be (Corcoran, Barber, and Connor 2009, 327). The evolutionary arms race between *bertholdia trigona* and *eptisicus fuscus* has led to the tiger moth evolving an organic jamming function.

My second example of complex biological phenomena is *perisceptis carnivore*. *P. carnivore* is a bagworm moth, which means that its larvae are safely contained within a case made of golden abdominal hairs called setae (D. R. Davis et al. 2008, 689). Like most bagworm moths, *P. carnivore* lays a single egg inside a protective case. As the larva outgrows its case it forms a portable structure in which all larval stages and pupation will take place. Unlike most bagworm moths, the larva of *P. carnivore* is actually predatory. The species thrives on so many different plants because it hunts other organisms around those plants. This particular species of bagworm moth launches itself out of one end of its bag to capture prey and devour them before adding undigested items to the outside of its enclosure (D. R. Davis et al. 2008, 698–99). The larval bag of a *P. carnivore* prefers ants but its bag is also commonly decorated with pieces of beetles, flies, grasshoppers, katydids, and wasps.

*Perisceptis carnivore* is an important example of the interaction between organisms. As a bagworm moth it is unique because of its diet and predatory nature (D. R. Davis et al. 2008, 689). As a functioning part of an ecosystem it interacts heavily with many other organisms in the ecosystem. *P. carnivore* constructs its home and hunting disguise from the undigested remains of its prey. *P. carnivore* is just as important for biodiversity conservation as any member of the charismatic megafauna group because the structure of its case changes based on which prey are around it. If we were to move *P.*
carnivore to a reserve then the structure of its protective casing would change to reflect the other organisms in the reserve. P. carnivore demonstrates a preference for ants but has a fairly wide diet ranging from crickets to other predatory larvae. If we keep it in a reserve with ants for food then its protective casing would only be decorated with ant parts. If we leave it in its native environment then its protective casing will be decorated by a wide range of prey.

My third case study is xenos vesparum. Xenos vesparum is a parasitic organism which has evolved the ability to burrow into a paper wasp and affect its neuro chemical instincts (Manfredini, Benati, and Beani 2010, 254). The common European paper wasp (polistes dominulus) first contracts xenos vesparum in its larval form from the underneath of foliage or a deposit inside its own colony. X. vesparum burrows into the paper wasp through its abdomen and lodges itself there. Whilst there, it exerts a unique effect on the behaviour of its host. The host paper wasp begins to reject its colony role idling and pursuing its own interests at a time when other members of the colony gather food and defend the colony. The host grows but much less than uninfected wasps and when the hive is at its busiest the host wasp leaves the colony for good. Presumably under the influence of X. vesparum, the host wasp flies to a location at which multiple infected wasps meet so that their parasites may mate.

At this mating site, the males burrow out of their hosts and abandon them, leaving them to die from massive infection. Female X. vesparum, however, remain in their hosts and extend their rears from the host for mating. The parasitic effects of X. vesparum are powerful. The infected paper wasps are incapable of reproducing. Their shrunken ovaries are non-functional because the negative effect of their parasites on growth and development. Despite this infected, P. dominulus which are now carrying a pregnant X. vesparum will now treat themselves as queens. They fatten themselves on any food they can find before flying to resting sites with other uninfected paper wasp queens to wait out the winter. When spring comes, the other queens go off to build nests whilst the infected queens either find foraging sites to deposit their host’s larvae or transport the larvae directly to another queen’s colony. So, the complex life cycle begins again (Manfredini, Benati, and Beani 2010, 253). It is a cycle which highlights the importance of interaction between species and the functions they perform in our concepts of biodiversity. Functional diversity captures such interactions better than static elements of biodiversity such as species richness.

One motivating thought experiment for the importance of interaction between organisms is what I will call the ‘zootopia thought experiment’. This thought experiment is based on Sarkar’s observation that botanic gardens often preserve species without preserving complex biological phenomena.

In 1970–71, there was simultaneous flowering of spiny bamboo (Bambusa arundinacea) throughout India after a lapse of 45 years. Clearly, a very precise biological clock exists in these species. In these cases, extinction of the species would also lead to the extinction of the phenomenon of synchronous flowering. More interesting, in this context, is that in extended habitats consisting of forests of a single bamboo species, flowering occurs in waves, starting at one end and propagating to the other. This unique phenomenon would disappear if these habitats do, even if the species
Sarkar argues that botanic gardens miss some important biological elements because they isolate a species from a functioning ecosystem. Botanic gardens are still ecosystems but all the interactions have changed because the survival of each species is managed by human beings.

The zootopia thought experiment applies Sarkar’s reasoning on a grander scale. Imagine that we could conserve all extant species by shifting them into tightly managed futuristic enclosures. We conserve all our species but we have also lost biological elements in the process. Species richness, diversity, disparity, morphology, and genetic diversity are all protected but we will have lost a number of important biological interactions. Placing endangered eagles in an aviary does protect them but that eagle cannot soar and it will never spot a rabbit from a distance of three kilometres before snatching it off the ground. Zoos, which are small scale Zootopias, have a place in conservation. Often, if a species is critically endangered, it needs to have its population managed in some way. Zoos also draw attention to the efforts of conservation and why they are important. However, Zootopias are an imperfect solution for conservation because they drastically alter the interactions and behaviours of the conserved organisms.

Functionality and interaction matter. The Darwin bark spider can build webs over rivers up to 25 metres in diameter (Kuntner and Agnarsson 2010, 351). But it can only do that if there is a river to bridge, and it will only continue to build webs across rivers if that method catches prey for it to feed on. So to for tiger moths which jam bat sonar, a bag worm moth which hunts prey from a protective casing of undigested prey, and a parasitic fly which can use a European paper wasp as a personal mode of transport. Organisms which are preserved but lose important functions or interactions with other species represent a lower biodiversity value than if both the organism and its function or interactions were preserved. In this section I explained the importance of functional diversity as a true surrogate of biodiversity. I motivated this claim with three case studies of complex biological phenomena: the tiger moth, *P. Carnivora*, and *X. Vesparum*, and the zootopia thought experiment.

### 6.4.2 Metrics of Functional Diversity

Metrics of functional diversity approximate the functional variance in an ecosystem by measuring the degree that the functional traits of co-existing species vary (Weiher 2011, 175). In this subsection I will explain the notion of a functional trait and argue that it sets a general standard. Then I will outline the measurement methodology of calculations of functional diversity. The calculations themselves are separated by their methodology. I will outline the metrics which use morphological methodology first and then I will outline the metrics which use phylogenetic methodology.

Calculations of functional diversity rely on a general conception of functional trait. A functional trait is understood as “observable or operationally defined phenotypic characteristics that influence species performance and/or ecosystem processes” (Weiher 2011, 175). Whilst the case studies that I presented earlier in this section focused on
unique biological phenomena such as the ability of the tiger moth to jam bat sonar with high frequency ultrasonic clicks, this notion of a functional trait is not limited to such complex interactions between species. Any observable trait which influences the performance of a species or an ecosystem’s process is a functional trait. Not all traits are functional ones. There are other traits such as genetic ones which do not qualify as observable or operationally defined phenotypic traits. Recessive genes are only realised when there is no dominant gene to compete with so organisms can have genetic traits without them becoming functional traits. However, so many traits are functional that in practice functional diversity is treated as a synonym for trait diversity (Weiher 2011, 175).

Morphological calculations of functional diversity are based on morphospace methodology. They apply morphospace calculations to functional trait space to determine the functional diversity of a set of organisms. A selection of the trait space based calculations of functional diversity are shown in table 6.1

<table>
<thead>
<tr>
<th>Selection of Trait Space Based Formula for Functional Diversity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Convex Hull Volume (CHV)</td>
</tr>
<tr>
<td>Calculation of the overlap in trait space occupied by more than one species.</td>
</tr>
<tr>
<td>Functional Attribute Diversity (FAD)</td>
</tr>
<tr>
<td>$FAD = \sum_{i=1}^{S-1} \sum_{j=i+1}^{S} d_{ij}$</td>
</tr>
<tr>
<td>Modified FAD (MFAD)</td>
</tr>
<tr>
<td>$MFAD = \frac{1}{F} \sum_{i=1}^{F-1} \sum_{j=i+1}^{F} d_{ij}$</td>
</tr>
<tr>
<td>Functional Dispersion (FDis)</td>
</tr>
<tr>
<td>$c = [c_k] = \frac{\sum_{i=1}^{S} a_i t_{ik}}{\sum_{i=1}^{S} a_i}$</td>
</tr>
<tr>
<td>$FDis = \frac{\sum_{i=1}^{S} a_i z_i}{\sum_{i=1}^{S} a_i}$</td>
</tr>
<tr>
<td>Functional Divergence (FDiv)</td>
</tr>
<tr>
<td>$g_k = \frac{1}{V} \sum_{i=1}^{V} t_{ik}$</td>
</tr>
<tr>
<td>$dG_i = \sqrt{\sum_{k=1}^{T} (t_{ik} - g_k)^2}$</td>
</tr>
<tr>
<td>$dG = \frac{1}{S} \sum_{i=1}^{S} dG_i$</td>
</tr>
<tr>
<td>$\Delta d = \sum_{i=1}^{S} p_i (dG_i - \bar{dG})$</td>
</tr>
<tr>
<td>$\Delta</td>
</tr>
<tr>
<td>$FDiv = \frac{\Delta d + dG}{\Delta</td>
</tr>
</tbody>
</table>

Functional Divergence (FDiv) will serve as an example of how morphological calculations of functional diversity work. It is a complex calculation which corrects for a weakness in calculations of functional dispersion (Weiher 2011, 180). Conceptually FDiv is a measure of dispersion across trait space. Tight clustering of species over trait space indicates low FDis whilst loose spacing indicates high FDis. The problem is the background scale which the clustering is measured against. Loose spacing across trait space appears as tight clustering if the scale on the figure is extended far enough (presuming the respective traits are presented on a non-finite scale.) The results of FDiv are independent of both functional evenness and the volume of trait space. The measure accomplishes this by calculating the tendency of the most common species to be on the periphery of the convex hull which is the overlap between mapped species in trait space, but also weights the distance by the abundance of that species.

There are several steps to calculating FDiv. The formula for FDiv is $\frac{\Delta d + dG}{\Delta|d| + dG}$. It appears straightforward but involves several steps of substitution. When viewed as a single formula the calculation is given by the following expression.

$$
\left( \sum_{i=1}^{S} p_i \left( \left( \sum_{k=1}^{T} (t_{ik} - \frac{1}{V} \sum_{i=1}^{V} t_{ik})^2 \right) - \left( \frac{1}{S} \sum_{i=1}^{S} \sqrt{\sum_{k=1}^{T} (t_{ik} - \frac{1}{V} \sum_{i=1}^{V} t_{ik})^2} \right) \right) \right)
$$

$$
+ \left( \frac{1}{S} \sum_{i=1}^{S} \sqrt{\sum_{k=1}^{T} (t_{ik} - \frac{1}{V} \sum_{i=1}^{V} t_{ik})^2} \right)
$$

$$
\left( \sum_{i=1}^{S} p_i \left( \left( \sum_{k=1}^{T} (t_{ik} - \frac{1}{V} \sum_{i=1}^{V} t_{ik})^2 \right) - \left( \frac{1}{S} \sum_{i=1}^{S} \sqrt{\sum_{k=1}^{T} (t_{ik} - \frac{1}{V} \sum_{i=1}^{V} t_{ik})^2} \right) \right) \right)
$$

In this calculation $V$ is the taxon on the periphery of the convex hull, $t,i$ and $k$ are identical to their use in functional dispersion, $T$ stands for the total number of traits, $S$ the total number of taxa and $p$ is the relative abundance for the species $i$. The calculation is performed in several steps. First we calculate the trait space centroid which is the mean
value of the trait scores using only the taxa on the convex hull. This is given by the formula $g_k = \frac{1}{V} \sum_{i=1}^{V} t_{ik}$. Next, for each individual species, we calculate the mean distance from the trait space centroid and then calculate the mean of the distances. Given by the following formulas in which $dG_i = \sqrt{\sum_{k=1}^{r} (t_{ik} - g_k)^2}$ calculates the Euclidian distance and $dG = \frac{1}{S} \sum_{i=1}^{S} dG_i$ calculates the mean of the distances. With the values for $dG_i$ and the mean of $dG$ calculated we are now in a position to calculate the abundance weighted difference between each taxon’s distance to the trait space centroid. This is given by the expression $\Delta d = \sum_{i=1}^{S} p_i (dG_i - dG)$. We then sum the total of the weighted differences (given as absolute values). This is calculated as $\Delta |d| = \sum_{i=1}^{S} p_i |dG_i - dG|$. And then we can calculate the functional divergence of our data set by substituting the results into our original formula.

Functional divergence is a complex calculation but it is also valuable because it is independent of the volume of occupied trait space. The kind of trait space affects results of functional diversity because dispersion may be measured over an empirical morphospace or a hypothetical morphospace. On a hypothetical morphospace, how tightly clustered the data points are indicates high or low functional diversity. On an empirical space apparent clustering is affected by how the scales are set. Consider the following figure:

Figure 6.6: Identical clustering of functional traits over trait space with different scales

The plotted clustering is identical in both cases but it appears tighter when the scale is spread out. This is not a problem for hypothetical morphospaces because the scale indicates all logical possibilities. But it is an issue for empirical morphospaces so it is useful to have a calculation which is independent of the volume of occupied trait space.

Phylogenetic based calculations of functional diversity construct dendrograms of the evolutionary relationships between ranges of functional traits (Weiher 2011, 179). Original calculations of FD sum the branch lengths of a dendrogram similarly to those used for phylogenetic diversity. The modified dendrogram is closer to phylogenetic methods. It uses a species based dendrogram which presents the species which have the relevant traits in terms of the evolutionary position to one another and then sums the distance. The main difference between dendrogram based calculations of functional
diversity and a straightforward phylogenetic analysis is that it restricts itself to species which possess the salient functional traits. A selection of the phylogenetic based calculations of functional diversity are shown in table 6.2

<table>
<thead>
<tr>
<th>Selection of Phylogenetic Based Formulae for Functional Diversity</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Functional Diversity (FD):</strong> Sum of the accumulative branch lengths represented by the phylogenetic tree.</td>
</tr>
<tr>
<td><strong>Minimum Spanning Tree (MST):</strong> Shortest possible combination of branches representing all species.</td>
</tr>
<tr>
<td><strong>Functional Evenness (FEve)</strong></td>
</tr>
<tr>
<td>Without abundance:</td>
</tr>
<tr>
<td>$FEve = \frac{\sum_{i=1}^{S-1} \min \left( \frac{l_{ij}}{MST}, \frac{1}{S-1} \right) - \frac{1}{S-1}}{1 - \frac{1}{S-1}}$</td>
</tr>
<tr>
<td>With abundance:</td>
</tr>
<tr>
<td>$EW_i = \frac{l_{ij}}{p_i + p_j}$</td>
</tr>
<tr>
<td>$FEve = \frac{\sum_{i=1}^{S-1} \min \left( \frac{EW_i}{\sum_{i=1}^{S-1} EW_i}, \frac{1}{S-1} \right) - \frac{1}{S-1}}{1 - \frac{1}{S-1}}$</td>
</tr>
<tr>
<td><strong>Alpha MST ($\alpha_{MST}$):</strong> Rank branches by length then ($\alpha_{MST}$) is the slope of the relationship between the cumulative branch length and its rank on a log scale.</td>
</tr>
<tr>
<td><strong>Quadratic Entropy (FDq)</strong></td>
</tr>
<tr>
<td>$FD_q = \sum_{i=1}^{S-1} \sum_{j=i+1}^{S} d_{ij} p_i p_j$</td>
</tr>
<tr>
<td><strong>Variance Based Functional Diversity (FDvar)</strong></td>
</tr>
<tr>
<td>$FD_{var} = \frac{2}{\pi \arctan \left[ 5 \sum_{i=1}^{S} (lnt_i - \sum_{i=1}^{S} p_i lnt_i)^2 \right]}$</td>
</tr>
<tr>
<td>Where $\sum_{i=1}^{S} p_i lnt_i$ is the logarithmic mean value of the trait weight by relative abundance.</td>
</tr>
</tbody>
</table>

Symbol Guide: In phylogenetic based calculations of functional diversity ‘S’ stands for species and ‘p’ is the abundance of the species S. ‘$d_{ij}$’ is the distance of the branch length between species $i$ and $j$ except for Feve which uses the notation ‘$l_{ij}$’.

*Table 6.2 Phylogenetic Calculations of Functional Diversity* (Weiher 2011, 179–84).

Functional evenness (FEve) will serve as an example of how dendrogram based calculations of functional diversity work. It is a measure of the consistency of branch lengths in the minimum spanning phylogenetic dendrogram which connect all the species with salient property (Weiher 2011, 181). It is an index between 0 and 1 which measures the MST by weighting branch length against the abundance of the species represented by that branch. The index approaches 1 as species in the ecosystem approach equal abundance and branch length. FEve may be calculated with or without taking species abundance into account. If calculated without species abundance the formula is:
\[ FEve = \frac{\sum_{i=1}^{S-1} \min \left( \frac{l_{ij}}{\text{MST}}, \frac{1}{S-1} \right) - \frac{1}{S-1}}{1 - \frac{1}{S-1}} \]

However, without abundance data, the measure only expresses the similarity of the branch lengths for individual species. If taking abundance into account then FEve may be calculated with the following formula:

\[ FEve = \frac{\sum_{i=1}^{S-1} \min \left( \frac{EW_i}{\sum_{i=1}^{S-1} EW_i}, \frac{1}{S-1} \right) - \frac{1}{S-1}}{1 - \frac{1}{S-1}} \]

where \( p \) is the abundance of the species \( S \) and \( l_{ij} \) is the branch length from species \( i \) to \( j \).

\( EW_l \) is calculated as \( EW_l = \frac{l_{ij}}{p_i + p_j} \).

In this subsection I analysed the measurement methodology of functional diversity. I drew attention to the general notion of a functional trait before moving on to the detail of the metrics. Calculations of functional diversity either use morphospaces or phylogenetic trees. I presented 13 calculations in tables and I explained two in detail. I explained how calculations of functional divergence work as an example of morphological calculations of functional diversity. Then I explained how functional evenness works as an example of a phylogenetic calculation of functional diversity. In the next subsection I use the detail of this measurement methodology to argue that functional diversity is not an operationalisable true surrogate.

### 6.4.3 Functional Diversity is Not an Operationalisable Surrogate

A biodiversity surrogate is operationalisable if it is accurately quantifiable and measureable. Similarly to morphology, functional diversity is accurately quantifiable and measureable for specific functional traits but not for overall functional diversity. Despite high within-surrogate operationalisability, functional diversity is not functional enough because it cannot track overall functional diversity. The problem is twofold. Firstly, the conception of a functional trait is too general because functional diversity is virtually a synonym for trait diversity (Weiher 2011, 175). The general notion of a trait is a product of the trait dilemma. Like morphology, calculations of functional diversity select a range of functional traits to use an estimator surrogate. Specific traits highlight important functionality but are not operationalisable. Shared traits are general so they tell us little about the functional diversity of an ecosystem. Secondly, because of the methodology of functional diversity calculations, the results are often incommensurable with one another. I conclude that functional diversity is not an operationalisable true surrogate for biodiversity.

Calculations of functional diversity have high within-surrogate operationalisability. That is, the thirteen measures which I presented in section 6.4.2 all have similar results when applied to the same functional trait of the same ecosystem. Weiher tested multiple measures of functional diversity over 16 different conditions in a principle component analysis (Weiher 2011, 188). He performed the functional diversity calculations for two
traits: height and leaf dry matter content in different conditions. The conditions covered 66 different plant species with richness ranging from 3 to 15 species on an experimental grassland and artificial data on a theoretical grassland with random richness from 3 to 20 species with random species abundances and two random traits. The calculations required the rescaling of results to a value between 0 and 1 where applicable.

The results indicated a high correlation of results within calculations of functional diversity. The results differ somewhat for artificial data on random assemblages but the tight clustering from the observational data indicates high within-surrogate operationalisability for specific functional traits. The authors argue that there is no single perfect measure of functional diversity and we should employ the one which is most appropriate to our goals. In most cases we can accurately approximate the diversity of a shared functional trait diversity in an ecosystem with around four measures of functional diversity (Weiher 2011, 191). We should select a measure focused on the occupation of trait space such as: CHV, FDis, FDpg, FDq, FDvar, MFAD, or MST. Then we should also calculate the functional evenness, functional divergence and the density of species packing. Taken as a package these four methods will provide a reliable approximation of the functional diversity of an ecosystem. However, the authors also stress that “there are few, if any, bona fide standard practices at this point in time” (Weiher 2011, 191).

This result is positive but it is evidence for the operationalisability of the functional diversity of a small number of traits rather than for the operationalisability of an ecosystem’s functional diversity. This is because the employed concept of a functional trait is too broad. In section 6.4.1 I motivated the importance of functional diversity by discussing three case studies of complex interactions between organisms in an ecosystem. An excellent metric of functional diversity would assign a high score of functionality diversity to biological phenomena such as the parasitic life cycle of xenos vesparum but the measures currently available to us do not. At the very least functional diversity should distinguish functional traits as a proper subset of phenotypic traits. I argued in chapter two that concepts become more informative as they exclude possibilities. In practice, functional diversity is treated as a synonym for trait diversity because there are no phenotypic traits which do not impact the survival of other species. Evolution has little use for phenotypic traits which do not give an organism an advantage over the competition.

The definition of a functional trait is so inclusive that functional diversity is not functional enough. This is problematic because calculations of functional diversity will not account for complex biological phenomena. An example such as the jamming of bat sonar by tiger moths highlights the way that species or morphological accounts of biodiversity do not give enough weight to complex biological interactions. But the current understanding of a functional trait is far too general to pick out those interactions. The definition requires just that the trait influence the performance of another species. If we understand a functional trait as any observable trait which affects the fitness of another species then we must accept that functional diversity is a synonym for trait diversity. While it can be sensible to be wary of overly restrictive definitions, our current definition is so general that it fails the counterexamples which were used against species focused concepts of biodiversity in the first place. There was dissatisfaction with existing accounts of biodiversity because they overlooked complex interactions between organisms such as
the migration pattern of the monarch butterfly (Sarkar and Margules 2002, 301). These calculations of functional diversity are more similar to morphological measures or phylogenetic calculations some cases than measurements of high-level functionality.

The reason that the definition of a functional trait is so general is that there is a trait dilemma. Like morphology, calculations of functional diversity require a range of traits to use as an estimator surrogate for the ecosystem’s functional diversity. Those traits can be shared or specific. A specific functional trait such as creation of high frequency clicks highlights functionality but cannot indicate ecosystem functional diversity because it is only shared by a few species. A general trait such as height is shared but doesn’t represent the kind of functional interaction which calculations of functional diversity aim for. However, calculation constraints limit us to generic shared traits such as height. The trait dilemma can be seen in Weiher’s analysis of within-surrogate correlation. For the sake of a common trait, the calculations focus on height and dry leaf matter (Weiher 2011, 188). They also have to be performed on artificially controlled ecosystems because in a full ecosystem, most organisms do not shed leaves. The variation of height and dry leaf matter tells us much about the trait diversity of plant assemblages. But, it tells us little about how those plants interact or the variation of other biological functions in a full ecosystem. Specific functional traits are not shared, shared functional traits are not good predictors of functional diversity and often not good examples of organism interaction.

A final concern with the operationalisability of functional diversity is that many of its results are incommensurable with one another. This is a problem because for a biodiversity surrogate to be operationalisable for the demands of conservation biology, it needs to be able to compare values for different ecosystems. Values for functional diversity cannot be compared between ecosystems unless they refer to the same trait. Like calculations of biodiversity, calculations of functional diversity use a surrogate. A range of common traits is used as a surrogate for the functional diversity of the ecosystem (Weiher 2011, 188). Functional diversity scores which use different traits as surrogates are not commensurable because they can refer to different ranges of traits. A score of 0.78 is not comparable with a score of 0.82 if the former refers to the dry leaf matter and the latter refers to mollusk coiling. They are incommensurable because we have no good reason to think that these trait ranges are accurate surrogates for the overall functional diversity of an ecosystem. The scores also cannot be compared with the method I outlined in section 4.4.2. Scores for phylogenetic diversity and species richness can be reverse engineered from one another. Scores for functional diversity cannot.

In this subsection I argued that functional diversity is not an operationalisable true surrogate for biodiversity. Similar to morphology, functional diversity is accurately quantifiable and measureable for ranges of specific functional traits but not for overall functional diversity. The various metrics of functional diversity have high within-surrogate operationalisability but they cannot accurately predict an ecosystem’s overall functional diversity. This problem is caused by the inclusive standard of a functional trait and the trait dilemma. ‘Functional trait’ is defined in such a way that functional diversity is a synonym for trait diversity, so it does not track the diversity of interactions between organisms well. Even if it did, calculations face a dilemma when selecting a range of functional traits to use as estimator surrogate. Specific functional traits track some functional variation but are
not common enough for use as a general data point. General functional traits are shared but are poor examples of functionality. Given that there are also issues with cross comparing functional diversity’s results between ecosystems, functional diversity is not an operationalisable true surrogate for biodiversity. In the next section I will draw on the detail of measurement methodology which I have discussed in chapters four, five, and six to argue that the empirical case for biodiversity eliminativism is unsuccessful.

6.5 Why the Empirical Case for Biodiversity Eliminativism is Unsuccessful

In this section I will argue that the empirical case against biodiversity is unsuccessful for two reasons. Firstly the evidence and arguments which I have presented in chapters four, five, and six indicate that the premises of the empirical poor fit argument are either false or not problematic. That is, if a premise of the empirical poor fit argument is true then it is still not a good empirical reason to eliminate biodiversity. Secondly there is an internal contradiction in the poor empirical fit argument. If premises one to six are true and biodiversity ought to be eliminated for empirical reasons then biodiversity’s true surrogates ought to be eliminated for the same empirical reasons. The surrogates which will take on biodiversity’s role fail the empirical standard which Santana uses to justify eliminating biodiversity. I conclude that the empirical case for biodiversity eliminativism is unsuccessful.

The first reason that the empirical case for biodiversity eliminativism is unsuccessful is that Santana’s empirical poor fit argument is unsound. Consider the truth of the following premises.

The poor empirical fit argument

1) General conceptions of biodiversity are not straightforwardly measureable.
2) There is not sufficient property correlation for biodiversity to be considered a property bundle.
3) The dimensions of biodiversity do not support robust inductive generalisations across the group.
4) The inclusion of biodiversity in the conservation process exacerbates imprecision between the measured target and the conservation goal.
5) Individual dimensions of biodiversity are either:
   a. Not operationalisable
   b. Do not accurately track biodiversity
   c. Or do not accurately track biological value
6) If conditions 1) to 5) accurately describe biodiversity then biodiversity is a poor empirical fit for its role in conservation biology.
7) Therefore: Biodiversity is a poor empirical fit for its role in conservation biology.
In chapter four I argued that premises two and four are false. Premise four is false because including biodiversity does not exacerbate the imprecision between the measured target and the conservation goal. The number of surrogates in the surrogacy chain does not increase the imprecision because in the case of biodiversity values are only calculated for the first or second stages. Those values are used to inform a broader picture rather than determine a precise value for biodiversity or biological value. There were also other options for elimination. If Santana is right about the number of steps increasing imprecision then we could deny the distinction between estimator and true surrogate or eliminate biological value as the final goal of conservation.

Premise two is false because there is sufficient correlation between the specific dimensions of biodiversity for them to be treated as a property bundle. Empirical results show correlations between species richness, phylogenetic diversity, genus richness, and feature diversity correlation of (Grenyer et al. 2007, 757; Vellend et al. 2011, 201; Faith 1996, 1287). Further arguments have also been made for correlations between phylogenetic diversity, functionality, and habitat diversity (Faith 1996, 1287). Furthermore instances in which the specific dimensions of biodiversity do not co-vary are important. Phylogenetic diversity does not co-vary perfectly with species richness because it tracks a distinctly important element of biodiversity. This casts doubt on the truth of premise six because the lack of between-surrogate correlation is not a good empirical reason to eliminate biodiversity. Imperfect homeostasis is an important feature of homeostatic property clusters (Boyd 1991, 142).

In chapter four I also argued that premise six of the empirical poor fit argument is false because whilst premises one and three are true they are not good empirical reasons to eliminate biodiversity. Premise two cast doubt on the truth of six because if premise two were true then it would not be a good empirical justification for elimination. Premises one and three confirm that suspicion. Complex multidimensional properties are not straightforwardly measureable but the difficulty of measuring them does not imply that we should not do it. Also, the lack of robust inductive generalisations between surrogates is an important feature. We can’t inductively generalise across the dimensions of biodiversity because they are strictly incommensurable. They are strictly incommensurable because each dimension tracks a distinct important biological feature of the natural world. Like other important multidimensional concepts such as health and poverty, conceptual complexity is not a good reason for elimination.

In chapter four I concluded that the state of biodiversity measures is not as bad as the empirical poor fit argument suggested and that familiarity with the detail of the measures’ methodology would make this clearer. This technical detail also demonstrated that premise five of the empirical poor fit argument, that “individual dimensions of biodiversity are either not operationalisable, do not accurately track biodiversity, or do not accurately track biological value”, was false. In chapters five and six I outlined the measurement methodology of five true surrogates for biodiversity: species richness, species diversity, phylogenetic diversity, morphology, and functional diversity. I used the detail of that methodology to determine if those surrogates were operationalisable for the demands of conservation biology and whether the expanding multiplicity of biodiversity measures should motivate the empirical poor fit argument. The technical detail of these
measures indicated that the expanding multiplicity of biodiversity measures is overblown and that some but not all true surrogates for biodiversity are operationalisable.

This conclusion implies that premise five of the empirical poor fit argument is true for some surrogates of biodiversity but not others. Premise five is disjunctive with three disjuncts so satisfying at least one component makes it true. The conceptual arguments which I presented in chapters one to five demonstrate the specific dimensions of biodiversity do track biodiversity. The relationship between biodiversity and biological value will be discussed in chapters seven and eight but we can take it for granted at the moment that surrogates for biodiversity do track biological value. At least they track sufficient normative importance for us to be convinced that they should be a part of biodiversity. If phylogenetic diversity, for example, did not highlight an important biological feature which species richness glossed over then it would not be a useful dimension of biodiversity.

So the truth of premise five for each surrogate turns on whether that surrogate is operationalisable. Premise five of the empirical poor fit argument is therefore false for species richness, species diversity, and phylogenetic diversity but true for morphology and functional diversity. But the truth of premise five is not a good reason to eliminate biodiversity because the empirical suitability of its surrogates has been evaluated on a sliding disjunctive scale. In his analysis, Santana changes his justification for disqualifying biodiversity surrogates. Species richness fails because it does not track value well but ecological diversity fails because it is not operationalisable (Santana 2014, 768, 772). The problem with a disjunctive standard is that it is reasonable for a biodiversity surrogate to succeed at two out of three disjuncts. A surrogate such as species richness which is operationalisable and tracks biodiversity is still useful even if it does not also track biological value. Species richness should not be expected to succeed at all three disjuncts or we would not need the other dimensions of biodiversity such as functional diversity and phylogenetic diversity to inform our conservation decisions.

Not every dimension of biodiversity needs to be operationalisable. Only a small number of operationalisable dimensions of biodiversity are required to make the surrogacy strategy work. Between-surrogate operationalisability will always be complicated because not every dimension has within-surrogate operationalisability. It is normal for complex multidimensional concepts to have specific dimensions which are not operationalisable. In the instance of health it is very difficult to operationalise pain. In the case of poverty it is very difficult to operationalise social mobility. Premise five is true for some surrogates of biodiversity but false for others. That mix is sufficient for the surrogacy strategy to meet the demands of conservation so it is not a good reason to eliminate biodiversity. The empirical poor fit argument fails because most of its premises are false. The premises which are true are not a good reason to eliminate biodiversity so premise six which justifies the elimination of biodiversity based on conditions one to five is also false.

The second reason that the empirical poor fit argument is unsuccessful is that the empirical standard which eliminates biodiversity as a goal of conservation would also eliminate its surrogates. The surrogates cannot be eliminated for the poor fit argument to work because Santana needs them to be conservation’s new goal.
If we keep our lens zoomed out at the general level of multilevel biodiversity and stability, we should expect decades of seesawing on the relationship, because there is no unitary relationship. But if we tackle the complexity of ecosystems by zooming into examine specific dimensions of diversity, as the best experimental and theoretical work does, we have compelling and understandable explanations. (Santana 2018, 13)

Santana argues that we should remove biodiversity from the surrogacy chain and use true surrogates as a direct approximation of biological value.

Using biodiversity’s specific dimensions as surrogates for biological value is problematic because no individual surrogate perfectly tracks biological value. Broad surrogates such as environmental diversity track it well but are not operationalisable. Narrow surrogates such as species richness are operationalisable but do not track biological value well. If that dilemma sounds familiar it’s because it is. It is the same dilemma that Santana used to motivate conceptual eliminativism.

This slipperiness is attributable in part to the fact the users of the biodiversity concept face a dilemma. Biodiversity is meant to serve as a reliable indicator of biological value, but given the vast variety of ways in which we value the biosphere, this requires us to employ a broad and open-ended definition of biodiversity. On the other hand, to serve reliably as a comparative measure, biodiversity needs to be observable and straightforwardly operationalisable. (Santana 2014, 762–63)

Eliminating biodiversity in favour of its specific dimensions leads to an analogous empirical dilemma. Conservationists must select a true surrogate for biological value but the operationalisable surrogates are misleading and the accurate surrogates are not operationalisable.

The empirical dilemma is tougher than the conceptual dilemma because of the empirical standards which Santana has set. He implies that for a surrogate to serve as the goal of conservation it should be both operationalisable and track biological value. However one implication of Santana’s analysis of the specific dimensions of biodiversity is that there are no such surrogates. In chapter one I considered possible specific meanings of biodiversity which I later argued in chapter two were part of a single homeostatic property cluster. I will now argue that the following true surrogates for biodiversity do not pass Santana’s empirical standard: species richness, species diversity, phenotypic diversity, phylogenetic diversity, functional diversity, genetic diversity, ecological diversity, and process diversity.

Phenotypic diversity and functional diversity cannot be true surrogates because neither is operationalisable. The detail in this chapter demonstrated that there is a trait dilemma which prevents these surrogates from being both accurately quantifiable and measureable. Likewise ecological diversity and process diversity are disqualified because Santana has argued that they are also not operationalisable.

So ecological diversity, like the measures we have examined fails to correlate reliably with other types of biological diversity. (Santana 2014, 772)
And although a variety of functional roles must be occupied to keep biological processes in place, we can explain those roles and those process without needing to call on a biodiversity concept. (Santana 2014, 773)

The remaining four candidates for true surrogates are genetic diversity, species richness, species diversity, and phylogenetic diversity. Santana has argued that genetic diversity does not track biological value well.

Genetic diversity, however, is nearly a non-starter. A “gene soup” containing a random sample of genetic material from a given place would furnish little useful in the way of important information for several reasons. (Santana 2014, 771)

In response, I argued that his gene soup example is unconvincing for various reasons. However, genetic diversity is unlikely to be operationalisable because genetic barcoding is expensive and time consuming. Shortcuts have been developed such as relying on mitochondrial sections of DNA but studies have questioned the accuracy of such shortcuts (Will, Mishler, and Wheeler 2005, 844; Elias et al. 2007, 2881).

Another problem is that genetic barcoding requires making physical contact with the organisms in an ecosystem. Outside of insect collections and flora cuttings much of the documentation involved in conservation is via distance. Avian species richness is determined using census point data. Aquatic species are documented visually and various recording devices are used to capture the behaviour of nocturnal organisms and other species. If a true surrogate only represents organisms which can be physically sampled then it will miss many more organisms in the ecosystem. Genetic diversity is operationalisable for the demands of biology but not for the demands of conservation biology because of the difficulty of making physical contact with organisms in an ecosystem. By Santana’s standard then, genetic diversity cannot be a true surrogate for biological value.

The remaining three candidates of species richness, species diversity, and phylogenetic diversity are strong candidates because they are operationalisable. However, Santana has already argued that they do not track biological value well.

It has been frequently pointed out that [Species] richness does not even capture intuitive ideas about what diversity is, such as abundance and disparity. (Santana 2014, 768)

But the relative abundance of species also fails to represent biological value well . . . for one thing . . . it could be that a larger population of that species would impact other populations adversely . . . and in terms of value to humans, rarity itself might sometimes be preferable. (Santana 2014, 770)

Disparity might include genetic or evolutionary difference, such as Faith’s proposal (1994) that phylogenetic distance can represent true biodiversity. It could also be morphological or phenotypic, since an organism that has a unique trait like the tuatara’s third eye is intuitively more diverse. Unfortunately, the intuitive appeal of these types of disparity is not always matched by their tractability as measurement tool. (Santana 2014, 764)

This implies that, by Santana’s standards there are no suitable true surrogates for biological value. Phenotypic diversity, functional diversity, ecological diversity, process
diversity, and genetic diversity are not operationalisable. Species richness, species diversity, and phylogenetic diversity are operationalisable but do not track biological value well.

The purpose of this argument is not to demonstrate that no true surrogate can track biological value but rather to demonstrate that the empirical poor fit argument has a strong internal tension. Several dimensions of biodiversity do track biological value but Santana has argued that they do not. Santana motivated concerns about between-surrogate operationalisability by attacking within-surrogate operationalisability. But, criticising the dimensions of biodiversity implies that they cannot serve as replacements for biodiversity because they are either not operationalisable or do not track biological value well. Without a better alternative, Santana cannot argue that eliminating biodiversity would leave conservation biology better off. The empirical poor fit argument is unsuccessful because the empirical difficulties which face biodiversity also face its specific dimensions. Santana wants to eliminate biodiversity in favour of its specific dimensions but he cannot justify its elimination by appealing to its empirical difficulties.

In this section I argued that the empirical case against biodiversity is unsuccessful for two reasons. The first reason is that several premises of the empirical poor fit argument are false. Premises two and four which focus on between-surrogate operationalisability are false. Premise five which focuses on within-surrogate operationalisability is false for some but not all surrogates. Premises one and three which focus on between-surrogate operationalisability are true but they are not good reasons to eliminate biodiversity. They are normal features of operationalising a complex multi-dimensional property. A weakness of the argument is premise six which justifies eliminating biodiversity if the first five premises are satisfied. This is a false premise because features such as imperfect homeostasis among dimensions, strict incommensurability between dimensions, and lack of within-surrogate operationalisability are valuable features. The second reason why the empirical case against biodiversity is unsuccessful is that biodiversity shares empirical difficulties with its specific dimensions. Santana cannot use the empirical difficulties of biodiversity to justify its elimination because they would also justify eliminating Santana’s intended replacement. Conservation requires triage so without a substitute target, Santana cannot argue that conservation biology is better off without biodiversity.

6.6 Conclusion
In this chapter I argued that the empirical poor fit argument for biodiversity’s elimination fails. This conclusion relies on evidence and arguments produced in chapters four and five as well as this one. In this chapter I summarised the importance of within-surrogate operationalisability for the empirical case against biodiversity before presenting a technical analysis of the measurement methodology of two surrogates: morphology and functional diversity. In the case of morphology, I motivated its importance as a dimension of biodiversity before explaining the use of morphospaces and highlighting the mathematical relationships in nature. I used the detail of my analysis to argue that morphology is not an operationalisable surrogate for biodiversity. In the case of functional diversity, I also motivated its importance as a dimension of biodiversity before discussing several different metrics of functional diversity. Used the detail of my analysis to argue that measures of
functional diversity are not functional enough and that functional diversity is also not an operationalisable surrogate for biodiversity.

In the final section I drew on material presented in this chapter as well as four and five to argue that the empirical poor fit argument for biodiversity’s elimination is unsuccessful. In chapter four I accepted that premises one and three of the poor fit argument are true but argued that premises two and four are false. I argued that the truth of premise five required a large body of evidence and concluded that familiarity with the detail of how biodiversity surrogates are measured would demonstrate that the empirical poor fit argument fails. In chapter five I outlined the measurement methodology of species richness, species diversity, and phylogenetic diversity. I defended them as true surrogates for biodiversity and argued that they are operationalisable because they are accurately quantifiable and measureable. In this chapter I outlined the measurement methodology of morphology and functional diversity. I defended them as dimensions of biodiversity but argued that they are not operationalisable. That is, they do not satisfy the empirical demands of conservation triage. Taken together, the arguments and evidence of chapters four, five, and six imply an internal contradiction in the empirical poor fit argument. The empirical standard which Santana uses to justify eliminating biodiversity would also eliminate most biodiversity surrogates. However, Santana has already argued that the remaining biodiversity surrogates do not track biological value well so by his own standards he has no viable conservation goal which could replace biodiversity. Since the empirical case for biodiversity eliminativism is unsuccessful, in the next chapter I move my focus to the value compass case against biodiversity eliminativism.
7 The Value Compass Case for *Biodiversity*’s Elimination and its Equivocations of ‘Value’

7.1 Introduction

In this chapter I will introduce the value compass case for *biodiversity*’s elimination and argue that *biodiversity* eliminativists are equivocating in their appeals to biological value. The value compass case treats the goal of conservation as a compass which ought to point towards biological value. *Biodiversity* eliminativists appeal to biological value to argue that biodiversity is not a suitable goal for conservation because it is a poor indicator of biological value. Conservation ought to protect the valuable elements of the environment, so a conservation goal should approximate biological value well. The value compass argument of eliminativists is that biodiversity is an ineffective surrogate for biological value; protecting biodiversity does not protect the important pieces of an ecosystem (Santana 2017, 86). Eliminativists motivate their arguments with examples of biodiversity correlating poorly with biological value.

Nor does preserving richness reliably preserve biological value. Because richness is nothing more than a count of the number of species in an area, value on the richness scale increases with speciation and decreases with extinction but this misrepresents common values. Not all species are equally valuable, so the extinction of a pollinator like a honeybee would be more lamentable than the extinction of a species of leech. (Santana 2014, 769)

This incomplete view fails to recognize that elimination of extensive areas of old growth forest, dramatic declines in hundreds of genetically distinct salmonid stocks in the Pacific Northwest, and the loss of chemically distinct populations from different portions of a species represent significant losses of biodiversity, regardless of whether any species become extinct. (Angermeier and Karr 1994, 692)

However eliminativists do not identify the type of biological value which biodiversity is required to approximate. This is problematic because without a clearly defined target the argument for low correlation between biodiversity and biological value is difficult to motivate. It is also problematic because of the different ways that the environment may be valued. If biodiversity is intended to be a surrogate for economic value then protecting biodiversity may not protect rare biological phenomena or value nature in an undisturbed state. Eliminativists believe that preserving biodiversity often fails to preserve biological value so the type of value they are appealing to needs to be laid out.

The goal of this chapter is to identify the type of biological value which eliminativists use as the correlation goal for biodiversity. I will consider three candidates: instrumental value which values as a means to an end, three different uses of intrinsic value, and non-anthropocentric value which forms an overlapping continuum with intrinsic value. There are instances of intrinsic value such as Calicott’s which are anthropogenic because they do not obtain without an agent to value them (Svoboda 2011, 27). There are also instances of non-anthropocentric value such as Paterson which reject the instrumental-intrinsic distinction entirely (Paterson 2006). For each candidate I will outline the nature of
The value system and present textual evidence that eliminativists are appealing to it. From this textual evidence I conclude that the type of biological value which eliminativists are appealing to is pluralistic biological value. I use this conclusion to argue that eliminativist arguments equivocate over ‘biological value’.

7.2 The Importance of Biological Value in the Value Compass Case

In value compass eliminativism, biological value has an important role because it is treated as the goal of conservation. Eliminativists argue that protecting biodiversity does not protect the valuable parts of the environment. So the value compass argument for biodiversity eliminativism relies on a claim of low correlation between the properties of biodiversity and biological value. One danger with this strategy is that it overlooks important research on biological value by treating it as a single category. There are many distinct types of biological value such as economic instrumental value or intrinsic value in the sense of value independent of agents. So if value compass eliminativism argues that biodiversity ought to approximate instrumental value but appeals to examples of biodiversity failing to approximate intrinsic value then the argument is equivocating in its appeal to biological value.

7.2.1 The Value Compass Case for Biodiversity’s Elimination

The value compass case for biodiversity’s elimination argues that biodiversity should be eliminated because it correlates poorly with biological value. It treats the goal of conservation as a compass which ought to point towards biological value. Since conservation ought to preserve the valuable elements of the environment, a good conservation goal needs to approximate biological value well. Formalised, the argument looks like this.

The Value Compass Case for Biodiversity Eliminativism
1) Conservation ought to preserve pluralistic biological value.
2) Biodiversity does not reliably track pluralistic biological value.
3) Biodiversity is the goal of conservation.
4) The goal of conservation ought to reliably track pluralistic biological value.
5) If the goal of conservation does not reliably track biological value then it ought to be eliminated.
6) Therefore: Biodiversity ought to be eliminated as the goal of conservation.

The value compass case argues that biodiversity ought to be eliminated as the goal of conservation because it fails to reliably track pluralistic biological value. It treats the goal of conservation as a value compass. Biodiversity ought to point conservationists towards the valuable elements of the environment. Since biodiversity does not reliably perform this function, Santana, Angermeier, Karr argue that we ought to eliminate it in favour of a different conservation goal. Eliminativists appeal to different types of value to justify elimination but the consensus between them is that biodiversity prioritises the wrong biological elements for conservation. It overlooks more valuable biological elements such as native species or important functional phenomena. I will critically
analyse the value compass case for biodiversity eliminativism in chapter eight. The purpose of this chapter is to inform that critical analysis by determining what eliminativists mean when they appeal to biological value.

Individual eliminativists appeal to different types of biological value to motivate premise two of the value compass case. Angermeier and Karr appeal to health and sustainability with their preference for biological integrity; “Two visionary phrases in the act dealt with a 'fishable and swimmable goal' and the charge to 'restore and maintain the physical, chemical, and biological integrity of the Nation's waters.'” (Karr 1991, 68). By contrast Santana does not identify the type of biological value which he believes fails to effectively correlate with biodiversity in his original work. In his 2017 paper he identifies ecological value as the goal of conservation where ecological value is “the aggregate of values we place in the environment” (Santana 2017, 86). So Santana uses the aggregate of all values we place in the environment as the standard for both the goal of conservation and the target which biodiversity fails to approximate.

7.2.2 How the Value Compass Case Risks Equivocating ‘Biological Value’

The value compass case for biodiversity’s eliminativism risks equivocating in its uses of ‘biological value’ for two reasons. Eliminativists do not explicitly state what type of biological value biodiversity is meant to approximate. It is unclear from textual evidence if biodiversity is meant to approximate instrumental value or less anthropocentric types of value. This lack of clarity is exacerbated by the motivating examples which appeal to specific but distinct theories of biological value. Santana for example describes a fictional gene soup as a counterexample to genetic diversity. “Genetic diversity, however, is nearly a non-starter. A “gene soup” containing a random sample of genetic material from a given place would furnish little in the way of useful information for several reasons.” (Santana 2014, 771).

Santana’s example can be interpreted in a number of different ways which is a red flag for equivocation. By ‘gene soup’ Santana could mean some kind of genetic ark or just a literal soup of biological material. The former interpretation is more charitable because conservation has little interest in genes which are not realised by genomes and less interest in a contaminated bucket of DNA. Charity is required to engage with the gene soup thought experiment because it is problematic in its current form. Genes cannot be easily quantified because they are strings of base pairs amongst other strings of base pairs. There is also an element of structural novelty to genetic information. Blood samples are not equivalent to living biological organisms any more than a word scramble is equivalent to a novel.

For the sake of argument, this project will be charitable and presume a genetic ark interpretation of gene soup with additional science fiction technology which could de-extinct a species based on information extracted from that genetic ark. Santana’s argument then, can be understood as point that if diversity of genetic information is what matters about biodiversity then we would have no good reason to claim that extant species represent higher biodiversity than a genetic ark. But this example equivocates in its appeal to value. The uninformativeness of gene soup looks like an appeal to the value of genetics
for human beings but the soup example suggests a preference for biological organisms in their natural state. An argument could be made for either interpretation.

Equivocation is likely when multiple distinct types are treated as one category. One reason for the multiple distinct theories of biological value is that ‘value’ is a verb (Svoboda 2011, 27). So there as many theories of biological value as there are ways for agents to value the environment and—as I will argue in the following sections—just as many theories of value which don’t require agents. Identifying the type of biological value which eliminativists appeal to is essential to discussing the value compass argument for biodiversity eliminativism. I will not consider every type of biological value as the eliminativist target but I will discuss three staples of value theory: instrumental value, intrinsic value, and non-anthropocentric value which is often understood as equivalent to intrinsic value but forms a complex relationship with it. For value compass eliminativism to avoid equivocation, eliminativists need to appeal to the same type of biological value in their examples as the type that conservation is meant to prioritise. I begin by considering instrumental value as the type of biological value that eliminativists appeal to in their arguments against biodiversity.

### 7.3 The Instrumental Value Compass Interpretation

In this section I will consider if the type of biological value which eliminativists are appealing to in the value compass argument is instrumental value. My analysis has two stages. First I explain why eliminativists would appeal to instrumental value in their arguments. To this end I will explain what instrumental value is and discuss different kinds of instrumental value drawing attention to economic and aesthetic instrumental value. Then I will discuss the relationship between using objects instrumentally and value to show that this concept yields a great diversity of values for many objects. This diversity is operationalisable for the goals of conservation in so far as we can quantify values but leads to disagreement when one agent values a biological element but the other agent does not. I consider the argument that instrumental value makes the environment a second class citizen and respond that instrumentalists have the tools to treat various sentient beings as moral agents worthy of consideration. After motivating instrumental value as a candidate for biological value I present textual evidence to argue that eliminativists are appealing to instrumental value in the examples they use to motivate the value compass argument. I conclude that the value compass argument should be understood as instrumentally laden.

#### 7.3.1 The Nature of Instrumental Value

In this subsection I will explain the nature of instrumental value with an emphasis on its diverse applications. Instrumental value is the value of means to an end. An object which can be used to achieve some beneficial goal has instrumental value (Ronnow-rasmussen 2002, 25). Movies and art have instrumental value because they may produce a variety of emotions in us. A hammer has instrumental value because we may use it to drive in nails more effectively or flatten dents in metal. But instrumental value is not limited to human interactions. An object has instrumental value just so long as it useful in achieving some beneficial goal. In one experiment scientists introduced the concept of money to a society
of capuchin monkeys by introducing silver coin like discs and teaching them to trade them for food rewards (Chen, Lakshminarayanan, and Santos 2006, 519). These discs quickly gained instrumental value for the capuchins who re-budgeted their allowance to purchase more food when the price of apple slices was decreased (Chen, Lakshminarayanan, and Santos 2006, 528).

There are different types of instrumental value because there are many ways to value an object. One important type in conservation biology is economic instrumental value; the many ways in which the environment help human beings to prosper (Kaufmann 1980, 35). New Zealand has a reputation for being a very green country which brings in millions of dollars of tourism to our GDP every year. The environment has also yielded many important medications and although the prospects of a biological gold rush were overestimated (Maclaurin and Lean 2016, 31), the products we derive from the environment are an important source of economic instrumental value. Aesthetic instrumental value is another important form of instrumental value (Kaufmann 1980, 35). We experience great beauty whilst travelling through the environment and we may find aesthetic beauty in everything from biodiversity hot spots to desert wilderness. Leopold’s well known Sand Country Almanac extolled the virtues of untouched wilderness and the importance of preserving it in its natural state (Callicott, Crowder, and Mumford 1999, 30). Leopold’s descriptions of nature capture an irreplaceable source of beauty (Leopold 1949, 89). Leopold was a champion of intrinsic value but reservations about intrinsic value are no obstacle to the instrumental value which the aesthetics of nature provide.

There are problems with our romanticised conception of wilderness (Cronon 1996, 51). Apparently barren dessert terrains teem with life (Durant et al. 2014, 116) and there are few true wilderness ecosystems in the sense that they are actually untouched by human beings (Odenbaugh 2014, 94; Takacs 1996, 42). But we can also be amazed by complex organisms flourishing under harsh conditions, or scarcity.

Biodiversity hotspots understandably attract considerable conservation attention. However, deserts are rarely viewed as conservation priority areas, due to their relatively low productivity, yet these systems are home to unique species, adapted to harsh and highly variable environments. (Durant et al. 2014, 114)

We find great aesthetic value in desert wilderness and our romanticised conception of wilderness is another source of instrumental value.

The total instrumental value of the environment is diverse because there is a multitude of different ways for organisms to use the environment. For a long time humans have taken great pride in reshaping the environment and its products (Kaufmann 1980, 36). But the same tree which is valued as raw material for household furniture is also valued as part of ancient forest in its natural state. That tree is also the home to many organisms which rely on it for life, and it competes with smaller plant life for survival. Because instrumental value is the value of using an object to achieve a goal and there are many goals that the environment could fulfil, there are many kinds of instrumental value. That diversity leads to conflict between valuations.
Economic instrumental value forms a complex relationship with the environment. The snail darter is such a remarkable case because it seemed to bear so little instrumental value. It was not phenotypically distinctive, it was phylogenetically uninteresting, it had no cultural history, apparent economic importance or potential, and its small population meant that its extinction was unlikely to disrupt the local ecosystem. But it was an endangered species so people campaigned against the construction of the Tellico dam to preserve it (Nash 1989, 178–79). While the environment is a source of economic value through tourism, intellectual property, and the off-setting of carbon emissions, conserving it requires commitment from entire societies (Angermeier 2000, 378). The prospect that the Tellico dam might not be built just to save an unremarkable minnow from extinction is the wrong decision if you are an agent counting on the job which dam construction will provide. Often the people we ask to sacrifice economic value for the sake of the environment are those who are the most dependent on it (Cronon 1995, 20).

One objection to instrumental value is that it relegates the environment to the status of a second class citizen (Kaufmann 1980, 37). Human beings and the various ways in which we value the environment take priority. The environment is valuable in so far as it continually supports our survival and entertains us. The Pando aspen grove at Fishlake National Forest looks like a forest of aspen trees. It is in fact a single 43.6 hectare clonal biological organism with an interconnected root system (DeWoody et al. 2008, 495). The genetic material in one aspen tree at one edge of the colony is identical to the genetic material in a different aspen at the other edge of the colony. If we apply an instrumental analysis to this grove we would conclude that this particular grove has great instrumental value including aesthetic and economic but we would also conclude that our obligations to protect this grove stem from self-interest. The grove is valuable and we should protect it so long as it benefits human beings. But Hargrove might argue that a single organism of this size on our planet has its own value as well as the potential for human use (Hargrove 1992, 199).

Utilitarian responses to this problem have revolved around the goal of expanding our circle of moral obligations to include the environment. Much of our development as a species has occurred alongside a slow expansion of our circle of moral obligation (Nash 1989, 5). We know to take care of ourselves and then we extend care to our family and friends. As societies form we gain obligation to our groups, our countries, and then people in other countries. An important question for Utilitarians has been how to ground our expansion of that moral circle out to other biological organisms. Peter Singer has proposed the quality of sentience (Paterson 2006, 146). Comparisons of outcomes often weigh up happiness with unhappiness, pleasure with suffering, prosperity and fulfilment with impoverishment and dissatisfaction. Humans share these qualities with other sentient creatures so we can expand the moral circle to include any creature with the capacity to suffer. Conservation decisions which weigh instrumental value must also take into account their impact on the instrumental value for other sentient species.

This response by Utilitarians is an important improvement but it does not avoid the objection because much of the biological world such as plants, fungi, and single celled organisms are still excluded from the moral circle (Paterson 2006, 146). Bear in mind that this does not mean that we have no obligation to rest of the biological world. We retain
some obligations; the problem for Utilitarians who wish to explain the value of the natural world is just that the worth of the biological world is grounded entirely in its value to sentient creatures. The circle can be extended further by considering if the interests of biological organisms carry moral weight. Organisms which lack sentience can still demonstrate interests (Callicott 1984, 301). Plants grow towards sunlight, insects adapt protection from predators for survivability, every living thing attempts to pass on its genes, and prey prefers not to be eaten (Rolston 1992, 253). Though not strictly instrumentalists, Paul Taylor and Tom Regan both argue for an expansion of the moral circle. Taylor argues that moral rights are incompatible with animals and plants in some senses but that our general moral duties justify strong protections for much of the environment which are structurally very similar to moral rights. We must respect their preservation, protect their good, and make restitution if a group of organisms are wronged (Taylor 1986, 253, 245). Regan argues that many organisms including mammals, birds, and fish are ‘subjects-of-life’ in the sense that they have rights to liberty, bodily integrity, and life. As such, those organisms bear moral rights.

But, the justification for extending the circle is contentious. By contrast DeGrazia also argues for an expansion of the moral circle but limits its expansion far more severely, based on current evidence of the mental activity of biological organisms. He argues that the moral impermissibility of confining great apes (excluding . . . ) and organisms of the dolphin family is absolute. But he also argues that we have less moral obligation to birds, and most species of fish. Despite these difficulties, endorsing an expansion of the moral circle allows theories of instrumental value to more successfully ground moral obligations to protect the environment. This does leave the issue of discerning the interests of non-sentient biological organisms. It is not clear that the moral circle can expand to include all of biological diversity. Much of an ecosystem depends on the very small organisms which keep an ecosystem functioning. Aside from the vested interest all species have in survival, the interests of mites or bacteria are unclear. The value of those organisms require further justification similar to Taylor’s who, for example, argues that all humans have a moral interest in ecosystem services. So substantially harming the environment also harms those interests and decreases instrumental value (Taylor 1986, 236).

The strength of instrumental value is also problematic for the efforts of conservation. Instrumental value identifies value wherever there is means to an end but because all agents desire different ends those values conflict. The poaching of endangered species and destruction of the rain forest represents unreplaceable losses of aesthetic instrumental value to some but to others it represents survival: food on the table, employment, and financial security. I am concerned about the possible extinction of the panda bear. But when villagers from Africa who had never heard of pandas were shown a picture of them, they asked where it could be found and if it could be eaten (Einarsson 1993, 74). This conflict of values is exacerbated if we take into account future generations. We can understand economic, aesthetic and other interpretations of instrumental value as a-temporal (Kaufmann 1980, 34). That is, the aesthetic or economic value of the environment for current generations counts equally with the aesthetic or economic value for future generations. The valuations conflict because it is difficult to predict how
instrumental valuations will change. Cronon observes that the preference for wilderness is a modern one. Once it was considered savage, barren, and desolate (Cronon 1995, 8).

Theories of instrumental value meet the goals of conservation well because they identify a diversity of ways to value the environment. Considering value as a means to end identifies types of instrumental value such as economic value, aesthetic value, cultural value and others. One objection to instrumental value is that it treats the environment as a second class citizen. The instrumental tool kit responds by expanding our moral circle of consideration to take into account the interests of sentient organisms. However we are still left without a reason to care for the smallest pieces of biodiversity other than some further benefit which it may provide to sentient species. The advantage of identifying value wherever there is a means to an end is also a drawback because it leads to conflicting valuations. There is conflict between economic and aesthetic value, conflict between humans and other biological organisms, and conflict between current and future generations. In the next subsection I will argue that eliminativists are appealing to instrumental value in their examples of biodiversity failing to approximate biological value.

7.3.2 Eliminativists’ Appeals to Instrumental Value

To motivate premise two of the value compass case for biodiversity eliminivism, eliminativists present examples in which protecting biodiversity would fail to protect valuable parts of the environment. Some of these examples appeal to instrumental value.

Healthy fish stocks feed us, extensive forests remove carbon dioxide from the atmosphere, and flourishing vegetation feeds livestock, prevents erosion, and directs the flow of water. (Santana 2017, 88)

Only in the presence of a functioning biological system are other resources (for example, energy, minerals) useful to man. (Karr and Dudley 1981, 56)

The total worth of biodiversity to society comprises a broad array of values, including aesthetic, ecological, and utilitarian values. Some of that value is inherently dependent on the variety of biotic systems. (Angermeier 1994, 601)

Santana points out that fish stocks feed us, Karr and Dudley acknowledges the importance of the resources to man, and Angermeier highlights the importance of aesthetic value. These are all conceptions of value which focus on a means to an end. Fish are a means to nourishment, natural resources are a means to flourishing, and the variety of biotic systems is a means to aesthetic enjoyment. These are examples of appeals to instrumental value because they understand the value of the environment in terms of their ability to satisfy a further goal. Based on these examples the value compass argument for eliminativism should be understood as focused on anthropocentric instrumental value. Conservation should preserve the instrumental value of the environment, so because biodiversity correlates poorly with instrumental value it is a not suitable goal for conservation. However I will argue in the following sections that eliminativists are not just appealing to
instrumental value. They also appeal to a combination of intrinsic and non-anthropocentric types of value.

7.4 The Intrinsic Value Compass Interpretation
In this section I will consider if eliminativists’ arguments are appealing to intrinsic value. In this two-stage analysis I first explain why eliminativists would appeal to intrinsic value by discussing the nature of intrinsic value. I will outline the distinction between three different uses of ‘intrinsic’ in academic literature: intrinsic in the sense of non-instrumental, intrinsic in the sense of a non-extrinsic property, and intrinsic in the sense of value independent of agents’ beliefs. I argue that intrinsic value in the first sense creates moral obligations to organisms in the environment analogous to the moral obligations humans bear to one another. I discuss the tension between instrumental and intrinsic value and argue that value theorists often want the best of both worlds and attempt various ways of importing features of intrinsic value into instrumental systems or vice versa. I argue that intrinsic value provides strong protection for the environment and can defend itself against objections provided that attention is paid to the different types of intrinsic value. After arguing that eliminativists have good reason to appeal to intrinsic value in the value compass argument I move on to textual evidence of their appeals to intrinsic value. In the case of Santana these appeals are tacit rather than explicit so I argue that his examples do at least appeal to intrinsic intuitions to motivate value compass eliminativism. Angermeier and Karr demonstrate a clear preference for naturalness which is a clear appeal to intrinsic value. I conclude that as well as an argument for instrumental value compass eliminativism there is also an argument for intrinsic value compass eliminativism.

7.4.1 The Multiple Meanings of ‘Intrinsic Value’
In this subsection I explain the nature of intrinsic value and draw attention to its differing uses in academic literature. I argue that the primary use of ‘intrinsic value’ for conservationists is in the non-instrumental sense but it also supplemented by the senses of ‘intrinsic property’ and agent independent value. ‘Intrinsic value is a single term but in the literature it is used with different meanings. This is problematic because our conclusions are at risk of equivocating meaning (O’Neill 1992, 120). O’Neill has identified at least three senses of ‘intrinsic value’: non instrumental value, intrinsic properties, and the possession of objective value. These different meanings are important because of the conclusions we draw about moral obligations from claims of intrinsic value. The inference from ‘x has intrinsic value’ to ‘x must be protected’ is only a valid one if ‘intrinsic’ is used in the sense of some kind of value. Other senses of ‘intrinsic’ may commit a fallacy of equivocation. We are morally obliged to respect an organism if it possesses intrinsic moral worth but not obliged to respect it if it possesses intrinsic properties.

The first sense that ‘intrinsic value’ is used within the literature is the sense of non-instrumental value. As I discussed in the previous section ‘Instrumental Value’ is a term which is used to refer to objects which have value in terms of their further use. Movies have instrumental value in that they may create enjoyment when they are experienced or given as gifts. This is distinct from the intrinsic value of an autonomous agent. An organism with intrinsic value in this sense cannot be used as a means to an end without
informed consent. If an organism lacks the means to provide informed consent then there is still a moral duty that we never treat that organism merely as a means. We must always treat them as an end in themselves. Thus to have intrinsic value in this sense is to be valuable regardless of any potential benefit or use which you may bring to another agent (O’Neill 1992, 119).

In the second sense, ‘intrinsic value’ refers simply to the intrinsic properties of an object in the sense that they are not extrinsic properties. These are properties which are inherent to the object rather than those properties which are relational between objects. ‘Intrinsic’ in this sense is the claim that the value of an organism is a primary quality in the same way that shape is intrinsic to an object. This distinguishes it from an extrinsic property such as weight which relies on the relation between two or more objects which have mass. While mass is intrinsic to an object, weight is extrinsic because it is a gravitational relation between two or more objects. Applying this analogy to value, intrinsic value supervenes on the properties of an object. That is, when A supervenes on B, any alteration of A is also an alteration of B. This is in contrast to extrinsic value such as rarity or difference. Rarity and difference are relational properties in that they are a function of multiple objects. Being rare can make an object such as gold valuable but it is a function of supply of and demand for that object. In the second sense of ‘intrinsic value’ then, ‘intrinsic’ refers to the intrinsic properties of an object rather than an extrinsic kind of value such as rarity (O’Neill 1992, 120).

In the third sense ‘intrinsic value’ refers to the value which biodiversity possesses independently of any autonomous valuers. An analogy with art is useful here. Most people would agree that the music of Beethoven is a rare fusion of beauty and genius which has created a timeless piece of art. But a problem remains about the value his symphonies would possess if there were no agents around to enjoy it. While it is contentious, some people argue that Beethoven’s symphonies would still be beautiful even if no agent had ever experienced them. This is the third sense of ‘intrinsic value’. Rather than being valuable because of its use to humans, biodiversity has an independent value (Elliot 1992, 151). This is subtly different to the second sense. Value does not need to be intrinsic to an object for it to persist without a valuer around. We hold that the intrinsic value of a human being persists even if there were no other agents around to value her (and was in a coma so could not value herself) but it does not follow that value is a primary quality.

The first sense of intrinsic value, the traditional Kantian interpretation of non-instrumental value, is supplemented by the second and third senses in various ways. Callicott, for instance, argues that organisms have intrinsic value (in the first sense) but that this value does not persist without valuers (third sense) because ‘value’ is a verb and so must require a subject to act (Svoboda 2011, 27). Whatever the further combination, using the first sense of intrinsic value implies very strong moral obligations to the environment because the organisms have intrinsic moral worth. If biodiversity and the organisms which inhabit it cannot be ethically treated as a means to an end then we have an obligation to the environment not to use it as a means to an end. It is true that agents do use each other as a means to an ends on a regular basis. The normal interactions of everyday life require that I perform tasks for money but these interactions are permissible because agents obtain informed consent from one another and consent in arrangements are
how we ensure that our ends are considered. The first sense of intrinsic value creates strong protection for the environment because we may not use it merely as a means to an end whilst the second sense acknowledges the unique value of biodiversity but is more flexible with its uses.

Santana worries that intrinsic value cannot aide in conservation triage because assigning intrinsic value to organisms makes it impossible to compare values for conservation decisions. If one endangered organism has intrinsic moral worth and another organism has intrinsic moral worth then deciding which to conserve is an impossible moral dilemma. So, intrinsic value makes no difference to the outcomes of triage decisions. Since all organisms have moral worth we must appeal to instrumental value to decide which one to preserve.

If intrinsic value is ubiquitously distributed, or incommensurable with other values, or of infinite worth, —all features often attributed to intrinsic environmental value— it will not allow us to use quantitative decision-making tools to prioritise conservation efforts. (Santana 2017, 89)

Additionally, if a response to biodiversity eliminativism is going to be grounded in an appeal to intrinsic value, units will not differ in any meaningful way in the intrinsic value they possess. They will however, differ significantly in the non-intrinsic value attributed to them. Consequently, in situations of conservation triage, decisions between different units must be made on the basis of non-intrinsic value. (Santana 2017, 89)

But it is only the first sense of non-instrumental value which provides strong protection for the environment but struggles with triage dilemmas. That is the sense which confers inherent moral value on organisms. The second sense of a value as an intrinsic property and the third sense of value without an observer provide weaker protection for the environment but allow for agents to use it as a means to an end without requiring informed consent.

Intrinsic value in the sense of non-instrumental value provides strong protection for the environment because it mimics the trumping power of moral rights by implying a moral duty not to treat organisms merely as a means. To have non instrumental value is to be valued as an end in itself. Any organism which is valued as an end in itself bears moral rights which protect it from the interference of other agents (Regan 2013, 119). This is deeply problematic because moral rights bear a trumping value (Hargrove 1992, 200). Agents are not entitled to violate moral rights just because the outcomes would be beneficial. If I need to obtain permission to use my friend’s car then it does not matter how much I need the vehicle or even if I can burrow it in a way that does not inconvenience my friend. I still need to obtain permission before I can use it because otherwise I treat my friend merely as a means. There are extreme counterexamples in which the positive outcomes are so important that they appear to justify infringing on a right (Nili 2017, 322; Taylor 1986, 243). No friend of mine would consider me to have wronged them if I borrowed their car without permission because I needed to drive a dying person to the hospital. The trumping power of rights is so strong that some authors worry that it entails a right to do wrong (Waldron 2006, 107). After all it seems well within my rights to spend
money on what I wish rather than donating it to a needy cause or to set fire to my property if it should please me to do so.

If organisms bear intrinsic value in the Kantian sense then it is problematic for conservation because this implies strong moral duties with an accompanying trumping feature (Regan 2013, 119). So the benefit the environment provides to us does not justify us harvesting it for resources. This reasoning is explicit in David Degrazia’s work who argues in Taking Animals Seriously that we have inalienable moral duties to certain non-human animals. He goes onto argue that because of our duty not to cause unnecessary suffering and our duty to only confine when it is required, both factory farming and much of rural farming is unethical (DeGrazia 1996, 288). Intrinsic value grants strong protection to organisms such that even free farming rural methods may not be sufficiently ethical to respect that organisms’ wellbeing.

If multiple species are intrinsically valuable then even issues of survival become ethically complicated (Callicott 1984, 301). If a biological organism bears intrinsic value in the first sense then I am no more entitled to kill that organism for food than I would be to kill another human for food. In Animal Rights and Environmental Value Regan responds to the predatory and prey objection to intrinsic value (Regan 2013, 121). Roughly, this is the argument that if predator and prey both have intrinsic value then predators violate the rights of prey when they hunt. He argues that only moral agents have the capacity to violate rights and that we have a moral duty to organisms in the environment to let them be as much as possible. The latter he takes to explain why we would be obliged to save a human child from a lion but not a wildebeest. In effect he attempts to solve this problem by stripping out some of the protection of intrinsic value (Regan 2013, 122). Wildebeests have a right to protection from human beings but not from lions.

We cannot strip out the protection of intrinsic value in the Kantian sense. Intrinsic value in the Kantian sense without an accompanying prefect moral duty simply isn’t intrinsic value in the Kantian sense. Non-instrumental value systems are such that they do not permit the use of others merely as a means. Whilst Kant did not have non-rational animals and other biological organisms in mind as bearers of non-instrumental value, if authors argue that biological organisms bear intrinsic value in the Kantian sense then that implies strong moral duties to those organisms. In his framework, Regan restricts those duties but needs to explain why the predator prey relation between biological organisms does not warrant interference when the relation between serial killer and human victim does warrant it.

The problem for Santana is that his conclusion rests exactly upon a non-instrumental interpretation of ‘intrinsic’. The non-instrumental Kantian sense of intrinsic does bear moral rights but a non-intrinsic property or value independent of agents needn’t bear any moral rights. This is problematic for Santana’s example because he requires a non-instrumental sense of intrinsic value for his incommensurability objection to work. But that interpretation makes little sense because normal interactions between organisms for survival become so ethically contentious. Santana makes a mistake in treating all intrinsic value as the same and I will argue in the next sub section that despite his scepticism about intrinsic value, he is appealing to it in his examples of biodiversity failing to approximate biological value.
7.4.2 Eliminativists’ Appeals to Intrinsic Value

To motivate premise three of the value compass argument for biodiversity eliminativism, eliminativists present examples in which protecting biodiversity would fail to protect valuable parts of the environment. Some of these examples appeal to intrinsic value. Angermeier’s and Karr’s appeals to intrinsic value are transparent because they prioritise ecosystems in an undisturbed state. For Santana’s work I will argue that his appeals to intrinsic value are tacit rather than explicit. I say tacit because Santana is sceptical of the idea of intrinsic value (Santana 2017, 89). However at the very least his examples appeal to intuitions about intrinsic value.

Additionally it seems to be the case that many people value keeping ecosystems as close as possible to the state of nature. But a richness scale suggests that we can improve a system by deviating from the state of nature and importing species by, say, adding a fish to a lake. (Santana 2014, 769)

The trend in conservation biology of prioritising biodiversity “hot spots” distracts from attending to biodiversity “cold spots”. (Santana 2014, 770–71)

Even if Santana is not convinced by intrinsic value theory, he argues that maximising biodiversity will not help conservationists maintain the natural state of an ecosystem. But arguing that biodiversity misleads conservation because the concept does not prioritise nature in an unspoilt state is appealing to intrinsic intuitions. This tacit use of intrinsic is echoed in his concern for biodiversity cold spots. Biodiversity cold spots have less species and biological phenomena than biodiversity hotspots so it is unusual for a pure instrumentalist who is focused on conservation triage to express the kind of concern for them shown by Durant (et al. 2014, 115).

Angermeier and Karr both demonstrate a more transparent appreciation for intrinsic value as they include naturalism as an important aspect of biological integrity.

The inadequacy of current conceptions of biodiversity recently was made clear to me in several independent discussions with natural resource managers and scientists, where I asserted that introductions of exotic species into the wild diminish rather than enhance biodiversity. (Angermeier 1994, 660)

Conservation biology exists because conservationists believe that biotic diversity, ecological complexity, and evolution are intrinsically good (Soulé 1985) and ought to be conserved. It is not diversity, complexity, and evolution, per se, that warrant conservation, but natural components and levels of diversity and complexity and natural rates of evolution. The cornerstone value judgment of conservation is that naturally evolved biotic elements—genomes, communities, landscapes—are fundamentally more valuable than artificial ones. (Angermeier 2000, 377)

Biological Integrity — The capability of supporting and maintaining a balanced, integrated, adaptive community of organisms having a species composition and functional organisation comparable to that of natural habitat of the region. (Karr 1990, 285)

Despite the difficulties of a distinction between artificial and natural ecosystems, the belief that ecosystems have greater integrity if they are in a natural state only seems justifiable if
it rests on the idea that natural ecosystems have greater intrinsic value. The type I meaning of intrinsic value was that of non-instrumental value. Where instrumental value identifies a means to an end, intrinsic value identifies an end in itself (Norton 1992, 214). If ecosystems are more valuable in an undisturbed state they will continue to possess value even if they remain completely untouched by human beings. Intrinsic value in the sense of an intrinsic property or agent independent value should also not be affected by the presence of humans. It could be affected by destruction at the hands of humans but the appeal to intrinsic value in these examples is very much non-relational value. The environment has value in its own state rather than as a use for human beings.

Based on this textual evidence I conclude that the value compass argument for eliminativism should also be understood as focused on intrinsic value. Conservation should preserve the intrinsic value of the environment, so because biodiversity correlates poorly with intrinsic value it is a not suitable goal for conservation. This conclusion increases the risk of equivocation in the value compass argument for biodiversity eliminativism. If the goal of conservation were instrumental value but biodiversity was eliminated for failing to approximate intrinsic value then there is a serious equivocation in the value compass argument. Eliminativists must therefore carefully distinguish between instrumental value compass eliminativism and intrinsic value compass eliminativism. This task becomes more complex because non-anthropocentric value forms a complicated relationship between instrumental and intrinsic value. I will argue in the next section that eliminativists’ examples can also be understood as appeals to non-anthropocentric value in a way that is not captured by either instrumental or intrinsic value. Non-instrumentalism correlates highly with non-anthropocentricity but value in the sense of an intrinsic property can still be conceived in an anthropocentric manner. The ascription of interests and moral rights to other sentient beings is an anthropocentric method of justifying conservation efforts because interests and moral rights are human-centric frameworks.

7.5 The Non-Anthropocentric Value Compass Interpretation

In this section I will consider if eliminativists’ arguments are appealing to non-anthropocentric value in a way that is not accurately captured by either instrumental or intrinsic value. This analysis has three stages. First I discuss the nature of non-anthropocentric value to explain why biodiversity eliminativists would appeal to it in their arguments. I discuss anthropocentric motivations and briefly chart the aim of deep ecology which attempts to identify value in the environment on its own terms. Secondly I argue that non-anthropocentric value differs from intrinsic value in important ways. I discuss examples of: instrumental value with a non-anthropocentric slant, intrinsic value with an anthropocentric slant, and a form of non-anthropocentricism which rejects the instrumental-intrinsic distinction entirely. I use these examples to motivate a continuum of anthropocentricity along which instrumental value and intrinsic value sit in their various formulations. Lastly I present textual evidence to argue that biodiversity eliminativists are appealing to non-anthropocentric value. I argue that if the textual evidence is not sufficient to justify an intrinsic value interpretation of the value compass case, then it is still sufficient to justify a non-anthropocentric interpretation of the value compass case. This
conclusion implies that if eliminativists object to my arguments for interpreting the value compass argument as intrinsically motivated they still risk equivocating instrumental value with non-anthropocentric value.

### 7.5.1 The Nature of Non-Anthropocentric Value Theories

The non-anthropocentric movement is motivated by the distinction between deep ecology and shallow ecology. Where shallow ecology values the environment in human terms, deep ecology attempts to value the environment on its own terms. This distinction emerged because many of our systems have attempted to find value in the environment in a human centred way. Does this resource benefit us more out of the ground than in it? Can the conservation of this species benefit us financially in the long run? Even our attempts to protect the environment are often more human centred than we would like to admit. Conservation campaigns to protect whales and native birds are far more prevalent than campaigns to save frogs or insects. This is due in some part to the greater ease of identifying with the rationality of a whale than with a frog (Paterson 2006, 146).

We have caught the whale butchers red-handed in the act of taking an undersized whale. Riding out on a Zodiac, I leap from the inflatable craft onto the slain whale, its skin warm and oily, the blood flowing from the gaping wound in its side, hot on my hand. I stroke the flipper, reach down toward the vacantly staring open eye and close the eyelid. I am lost and lonely upon the ocean with that dead whale child. (Paul Watson quoted in Einarsson 1993, 78)

It is also due to the charisma of certain fauna. The charismatic megafauna group is just that because it shifts the focus of conservation to relatable mammals from the many smaller species which maintain the ecosystems that those mammals inhabit (Karr 1993, 301). These are instances of shallow ecology because they tend to conceive of environmental value in very anthropocentric ways, either by directly linking the value of the environment to its benefit for humans or by failing to consider the interests of biological organisms on their own terms.

Deep ecology attempts to reconceive of environmental value in a non-anthropocentric way. This is a complicated task because we are attempting to remove implicit bias from our inferential reasoning. However, we aren’t always aware of our bias. Work in psychology has shown that unconscious bias affects our decision making even when we are made aware of and struggle against our bias. One such study demonstrated that a Judge’s sentencing is most lenient immediately following a meal break, despite the Judge deciding when the meal break should occur (Danziger et al. 2011, 6890 and 6892). As human beings we are also limited to converse in human concepts. So the goal of deep ecology is a worthy but ambitious one. Unsurprisingly then it has yielded a great diversity of theories with differing levels of non-anthropocentric commitment. Intrinsic theories of environmental value are non-anthropocentric in that they consider the moral worth of organisms in the environment on their own terms. A further non-anthropocentric step is to reject the instrumental / intrinsic distinction all together and attempt to reinterpret the role of human beings as participants in the ecosystem rather than as external entities in competition with it (Paterson 2006, 148). An even further non-anthropocentric step is an
attempt to conceptualise biological value with a minimal reliance on human concepts and traditions. The next subsection will focus on these varying levels of deep ecology to explain how the distinction between deep and shallow ecology comes apart from the distinction between instrumental and intrinsic value.

### 7.5.2 How Deep Ecology and Intrinsic Value Come Apart

In this subsection I will argue that the continuum of anthropocentric theories comes apart from the distinction between instrumental and intrinsic value. I will do this by outlining non-anthropocentric theories of biological value to highlight the difference between deep ecology and deeper ecology. ‘Deeper ecology’ is the name I give to the continuum of non-anthropocentric theories which vary in their commitment to an anthropocentrism-free theory. Whilst I discussed intrinsic value in its own section, intrinsic value is a non-anthropocentric commitment in so far as it extends the moral duties which agents hold to one another out to non-human organisms in the environment (Callicott 1984, 299). Anthropocentric theories such as instrumental value can also extend our moral duties out to non-human organisms but they ground those duties in very different ways. Instrumental value may ground an obligation to protect the environment but it is does so because the environment has a further use to us or because certain organisms in the environment suffer in the same way that we do. Theories of intrinsic value ground those moral duties in very different way. Organisms and the environment have their own value independent of us which we are morally obliged to respect (Svoboda 2011, 26). There is the notable exception of Callicot who believes that there is never value without someone to value it, even if that value is intrinsic (Svoboda 2011, 27). But most theories of intrinsic value assign non-anthropocentric value to differing aspects of the ecosystem, some to sentient creatures and some to more.

A further non-anthropocentric commitment is to reject the distinction between instrumental value and intrinsic value entirely. Whilst intrinsic value does ground moral obligations to other organisms it still brings some anthropocentric ideas to the table. The framework of intrinsic value is built on a foundation of moral rights which is a thoroughly human-appropriate framework. With various extensions it captures some of the organisms in the environment but still excludes most of them (Callicott 1984, 301). Interestingly, some further deontological analysis seeks to distance itself from these anthropocentric elements. Rights based ethical analyses dictate when an agent is permitted to act, and when they can waive their rights (Wenar 2005, 230). Neither is a good fit for non-sentient instinctual organisms such as flora, insects, or bacteria. Taylor is acutely aware of this issue when he argues that biological organisms require a modified system of rights. He advocates for a modified system because the traditional moral rights framework relies on notably human features such as the will to decide if one should exercise a right and second order powers over rights (the right to alter our rights) (Taylor 1986, 241, 251). He concludes that plants and animals are not right-holders but argues that it is less confusing if we simply put the language of rights to one side and, instead, focus on their inherent worth (Taylor 1986, 254).
For Kant moral evil occurred when an agent made an exception for themselves from a moral law; but insects and flora don’t make exceptions for themselves any more than they can respect one another’s interests or waive their rights.

Barbara Patterson has argued that we should reject the instrumental-intrinsic approach because it perpetuates a western and deeply anthropocentric approach to life: development and competition (Paterson 2006, 149). One of the enduring trends of human civilisation is our passion for taking the environment and reshaping it for our needs or according to our vision (Kaufmann 1980, 36). In the western world we also have a cultural glorification of competition (Paterson 2006, 147). We compete and the strong emerge, those who have yet to emerge need to fight harder. Patterson argues that we should abandon systems of intrinsic value because they echo these anthropocentric assumptions. They place us in conflict with the environment. Rights theory still places us in competition because the right of human beings to flourish conflict with the right of the environment to survive. Patterson argues that we would be better off to understand environmental value as a Buddhist land ethic, one which sees human beings as part of the ecosystem which they inhabit. Under this interpretation for human beings to irreparably consume the environment is as much an act of self-destruction as it is the harvesting of resources (Paterson 2006, 148). The details of Patterson’s proposal for this thesis are not as relevant as what it represents; a non-anthropocentric system of environmental value which rejects intrinsic value as an anthropocentric concept.

A final extra step towards non-anthropocentrism is to divorce ethical analysis from human preferences as much as possible (Grey 1998, 98–100). This is a punishing standard for non-anthropocentrism. It is difficult to conceive of analysis or conversation about environmental value between humans without employing at least some human concepts. This extreme form of non-anthropocentrism appears as a conceptual challenge to the goals of non-anthropocentrism.

This approach is said to produce non-anthropocentric value, rather than anthropocentric value, because the human self is only a small part of nature as a whole, which is the Self with a capital S. Nevertheless, an alternative interpretation is available, according to which Self-realization is anthropocentric and nothing more than Cartesianism commandeered for environmental purposes. Note that nature acquires (or borrows) its intrinsic value from the human self, which is established on supposedly noncontroversial traditional grounds (the uncritical belief that humans have intrinsic value). (Hargrove 1992, 194)

It is an obscure version of non-anthropocentrism because it represents the very far end of the continuum of non-anthropocentric theories of value. It is the point on the continuum at which we recognize that we cannot completely separate ethical analysis from anthropocentric ideas.

Non-anthropocentric theories of biological value range in diversity from intrinsic theories which extend human considerations to other sentient species to theories which attempt to analyse environmental value with as few anthropocentric assumptions as possible. Deep ecology is a broad continuum which interacts with instrumental and intrinsic value in different ways. Singer extends moral consideration out to non-human animals (Paterson 2006, 146). So the application of his theory to biological value is
instrumental with a non-anthropocentric slant because it applies instrumental value to non-humans. Callicot recognises intrinsic value but denies it can occur without an agent to value it (Svoboda 2011, 27). Callicot’s intrinsic value has an anthropocentric slant because it requires agents. Patterson argues against the instrumental-intrinsic distinction entirely so her view of biological value is non-anthropocentric without appealing to intrinsic value. So the relationship between anthropocentrism and the instrumental-intrinsic distinction is understood as a perfect overlap between the instrumental/intrinsic distinction and the anthropocentric/non-anthropocentric distinction (Paterson 2006).

![Figure 7.1 The received relationship between instrumental, intrinsic, and anthropocentric value](image)

Instead of the above figure, instrumental and intrinsic value should be viewed as interacting with a continuum of anthropocentric commitment like this.
Figure 7.2 The proposed relationship between instrumental, intrinsic, and anthropocentric value

In this figure zones A and B represent the standard view of instrumental value as anthropocentric and intrinsic value as non-anthropocentric. Zone C is Singer’s extension of interests to non-human organisms. Zone D is the overlap of instrumental and intrinsic theory since intrinsically valuable organisms are also an instrumentally valuable means to an end. Zone E is Callicott’s theory of intrinsic value which has an anthropocentric slant and zone F is Patterson’s Buddhan Land ethic that rejects the instrumental, intrinsic divide. There are many non-anthropocentric theories of value but they have a diverse interaction with other theories of value. What unites them is a core belief that the environment bears its own value, independent of anthropocentric concerns.

In this subsection I explained the distinction between deep ecology and deeper ecology. The goal of deep ecology is to rethink our approach to biological value by removing anthropocentric assumptions. Instead of thinking of the value of the environment in human terms, we should focus on the value of the environment in its own terms. I began with a discussion of intrinsic value which is non-anthropocentric in so far as it confers value on the environment independent of whether humans are around to value it. I discussed a Buddhan land ethic which attempted to reinterpret the role of human beings as caretaking participants rather than in a state of competition with the environment. Finally I discussed the extreme deepest ecology in which as little recourse is made to human concepts as possible. I then used these examples to justify interpreting types of value along an anthropocentric continuum between shallow ecology, deep ecology, and deeper ecology. This picture differs from the traditional categorisation of instrumental value as anthropocentric and intrinsic value as non-anthropocentric. The relationships are more complex and require careful attention when appealing to biological value in examples. In the next subsection I will argue that biodiversity eliminativists are appealing to non-
anthropocentric value in their examples to motivate premise three of the value compass argument. This serves as a back up to my claims made about intrinsic value. If eliminativists wish to argue that they are not appealing to intrinsic value they will also have to argue that they are not appealing to non-anthropocentric value to avoid the risk of equivocation.

### 7.5.3 Eliminativists’ Appeals to Non Anthropocentric Value

To motivate premise three of the value compass argument for biodiversity eliminativism, eliminativists present examples in which protecting biodiversity would fail to protect valuable parts of the environment. Some of these examples appeal to non-anthropocentric value. I argued in the previous section that the value compass argument is intrinsically focused but eliminativists do diverge in how they appeal to intrinsic value. Angermeier’s and Karr’s preference for naturalness is a less contentious appeal to intrinsic value than Santana’s appeal which openly rejects intrinsic value. “Therefore, appeals to the intrinsic value of biodiversity, or to how well the broad nature of biodiversity captures the broad distribution of intrinsic value, don’t ground an objection to biodiversity eliminativism” (Santana 2017, 90).

Using textual evidence I will argue in this sub section that eliminativists are appealing to non-anthropocentric biological value in their examples. So if eliminativists disagree with their appeals being labelled as intrinsic then I will still have a strong case for equivocation in the value compass argument. Eliminativists will have to demonstrate that the value compass argument appeals to biological value without equivocating instrumental, intrinsic, or non-anthropocentric value. The distinction between intrinsic and non-anthropocentric value is important because they are distinct conceptions of value. As I have argued in the previous subsection, it is possible for: an instrumental theory to lean towards non-anthropocentrism, for an intrinsic value theory to lean towards anthropocentrism, and for a non-anthropocentric theory to reject the instrumental-intrinsic value theory completely.

As with intrinsic value Angermeier and Karr appeal to non-anthropocentric value more explicitly than Santana. Both argue that keeping ecosystems in a natural state should be the goal of conservation.

When a river is dammed, integrity is reduced, resulting in declines of populations adapted to the natural hydrological regime.

Such a change may be interpreted as either a gain or loss in diversity, but integrity is clearly reduced because of the shift away from native conditions.

*Artificial* elements reduce integrity through widely documented effects on *native* elements and processes and *should be excluded* from evaluations of biodiversity. (Angermeier and Karr 1994, 693–94)

This preference for a natural state works into their concept of ecological integrity. Angermeier defines ecological integrity as the completeness of evolved elements and in
one joint author study, measures the introduction of nonindigenous species as a reduction of biological integrity.

Thus, ecological integrity reflects the completeness of evolved elements and processes over a broad range of organizational levels and spatiotemporal scales. (Angermeier 1994, 601)

Percent nonindigenous individuals measures the degree to which nonindigenous species and hybrids have reduced biological integrity in the Ohio River. (Angermeier, Emery et al. 2003, 800)

Angermeir and Karr are appealing to non-anthropocentric value theories in their arguments for the elimination of biodiversity. They have a preference for the natural state of an ecosystem and they view nonindigenous species as greater threat to biological integrity than indigenous species. The most prevalent nonindigenous species is Homo Sapiens so tying biological integrity to a lack of nonindigenous species is a deeply non-anthropocentric commitment.

Santana’s appeal to non-anthropocentric value is contestable because he words most ascriptions of value in terms of what they mean to an agent. “Some ecological values are none of these, but are merely existence value, which is the satisfaction derived merely from knowing that an object persists in a desired form.” (Santana 2017, 88). The ascription of value to an object merely for persisting is intrinsic value in the sense of agent independent value but Santana’s description as the “satisfaction . . . from knowing” presents it in an instrumental way. Putting aside questions of whether intrinsic value understood through an instrumental lens is no longer intrinsic; Santana is appealing to the non-anthropocentric intuitions of his readers. “Genetic diversity, however, is nearly a non-starter. A “gene soup” containing a random sample of genetic material from a given place would furnish little in the way of useful information for several reasons.” (Santana 2014, 771). One of the reasons that gene soup is a compelling example is that it describes a state of affairs with comprehensive genetic diversity but without species interacting with one another in any sort of ecosystem. It argues that genetic diversity is better when the organisms which carry them are active and interacting. Valuing organisms in their own ecosystems over reducing them to genetic information places this example squarely on the non-anthropocentric continuum.

The problem with the gene soup example is that it professes to appeal to instrumental value but it does it on classically non-anthropocentric territory. It is not clear that a genetic ark contains little useful information. It is still a genetic record of every single extant species which necessarily includes all undiscovered species and its preservation requires less space than typical wildlife preserves. However it is appealing to think that genes are more informative when they are instantiated in flourishing, interacting biological organisms. This is a non-anthropocentric intuition and it isn’t overwritten by the presence of instrumental value. It is possible for a biological element to be intrinsically valuable and instrumentally informative. Santana’s argument that gene soup is less informative than a comparable functioning ecosystem is an appeal to non-anthropocentric value. It is just an appeal to non-anthropocentric value which is obscured behind an instrumental façade.
Based on the textual evidence I have presented in this subsection I conclude that eliminativists are appealing to non-anthropocentric value and that their argument for eliminating biodiversity should also be understood as non-anthropocentric value compass eliminativism. This conclusion further complicates the value compass argument as I have also argued that it should be understood as appealing to instrumental and intrinsic value. So to avoid equivocation, eliminativists need to distinguish between three types of biological value with numerous sub types when they appeal to biological value in their examples. The addition of non-anthropocentric value to the possible interpretations strengthens the case for equivocation. If Santana were to argue that intrinsic value compass eliminativism incorrectly represents his view then my case that his examples appeal to non-anthropocentric value still implies equivocation in the value compass argument for biodiversity eliminativism. I have now presented evidence that eliminativists’ value examples are appealing to instrumental, intrinsic, and elements of deep ecology. In the next section I will argue that since eliminativists need their examples to motivate the value compass argument and since those examples appeal to multiple types of biological value, that the ‘value’ in value compass eliminativism needs to be understood as pluralistic biological value.

7.6 Why the ‘Value’ in the Value Compass Case is Pluralistic
In this section I will argue that the eliminativists’ appeals to biological value require a pluralistic conception of biological value. Pluralist theories take multiple contenders for a concept and treat them all as correct. Instrumental, intrinsic, and non-anthropocentric value are all important dimensions of biological value so pluralistic biological value recognises all of these dimensions as correctly describing some element of biological value. I present textual evidence of the author’s appeals to these differing dimensions to argue that the value compass case uses pluralistic biological value as the standard for biodiversity. I appeal to my conclusions from early sections to argue that eliminativists are appealing to pluralistic biological value. Since Santana understands intrinsic features with an instrumental lens I present a detailed argument that his standard for biodiversity must be pluralistic rather than just instrumental value. I discuss his tacit appeals to intrinsic value and argue that because he defines ecological value as an aggregate of values ecological value must include multiple dimensions.

Pluralist systems take multiple distinct concepts and treat them all as correct (Hull 1997, 358). Biodiversity is treated as such a concept by certain realists. It has a strong species core with multiple dimensions of: phylogeny, trait diversity, genetic diversity, functionality, and others. To be a pluralist about biological value is to treat different theories of value such as instrumental and intrinsic as multiple dimensions of biological value. Each captures important elements of biological value but no individual theory correctly describes biological value by itself. Pluralism leads to conflict in operationalisability. The intrinsic value of the snail darter may require it to be saved even if it does not possess enough instrumental value to be worth conserving. But pluralism allows conservationists to consider multiple distinct value systems before making a decision.
The eliminativist conception of value is pluralist because the examples which eliminativists use appeal to different types of biological value. So if the examples are to be persuasive then eliminativists must presume that the type of value correctly describes an important dimension of the environment. In this chapter I have presented textual evidence to argue that the examples which Santana, Angermeier, and Karr present are relying on intuitions about instrumental value, intrinsic value, and varying degrees of non-anthropocentric value. The case for Angermeier and Karr’s conception of value is straightforward. They acknowledge instrumental value but also appeal to intrinsic non-anthropocentric value with their preference for naturalness. Naturalness is a key factor in biological and ecological integrity which they argue should replace biodiversity as a goal of conservation.

To be effective, conservationists will need to openly profess their values and persuade others that natural biotic diversity contributes significantly to the quality of human lives. (Angermeier 2000, 379)

The capability of supporting and maintaining a balanced, integrated, adaptive community of organisms having a species composition, diversity, and functional organization comparable to that of natural habitat of the region. (Karr and Dudley 1981, 56)

Whereas diversity is a collective property of system elements, integrity is a synthetic property of the system. Unlike diversity, which can be expressed simply as the number of kinds of items, integrity refers to conditions under little or no influence from human actions; a biota with high integrity reflects natural evolutionary and biogeographical processes (Angermeier and Karr 1994, 692).

Therefore the type of value which Angermeier and Karr use to motivate premise three of the value compass argument is pluralistic. They point out the importance of non-anthropocentric and intrinsic elements whilst also appealing to the instrumental value of the environment. They argue that ecosystems which are closer to their natural state will contribute significantly to human lives.

The case for Santana’s pluralism is more complex than that of Angermeier and Karr’s because Santana prefers non-intrinsic analyses of value. In his 2017 article he is sceptical of intrinsic value and presumes its existence for the sake of argument (Santana 2017, 89). However he does clearly state that “Ecological value comprises at least these: economic, aesthetic, cultural, and existence values” (Santana 2017, 89). Economic, aesthetic, and cultural value are all examples of instrumental anthropocentric values. They are valuable to agents from a human centric approach to the world. Existence value is typically an intrinsic form of value but Santana explicitly defines it as the satisfaction we derive from knowing that an object is persisting (Santana 2017, 88). So this particular account of existence value is also both anthropocentric and instrumental. Despite this, I contend that Santana’s concept of ecological value is actually pluralistic. Santana’s appeals to value are presented as instrumental but whether they are compelling is dependent on a variety of intrinsic and non-anthropocentric intuitions.

I offer two reasons to think that Santana’s concept of ecological value is pluralistic. The first is the textual evidence I presented in the intrinsic and non-anthropocentric sections. Santana may be suspicious of intrinsic value but he is appealing to our intrinsic
intuitions with his examples. A preference for nature in its natural state or presuming that a genetic ark has less value than a functioning ecosystem containing the same information is a tacit appeal to non-anthropocentric systems of intrinsic value. The second reason is that Santana also states that the ecological value which he believes biodiversity fails to track is “the aggregate of values we place in the environment” (Santana 2017, 86). The use of ‘we’ suggests anthropocentrism but the use of ‘place’ is ambiguous. It could refer to a human construction or an act of inference such as ‘based on the thermal imaging I place the nest over there’. A true aggregate of values includes intrinsic and anthropocentric values and it is only anthropocentric in the sense that the values are identified by humans. So ecological value includes the weak intrinsic value of (Hargrove 1992), the instrumental value of (Kaufmann 1980), and the non-anthropocentric rejection of the instrumental-intrinsic distinction by (Paterson 2006). Therefore Santana’s concept of ecological value is also pluralistic. Instrumental, intrinsic, and non-anthropocentric are all values that authors place in the environment so if ecological value is the aggregate of values we place in the environment then it includes those three and many of their sub types.

**Biodiversity** eliminativists use a variety of examples to advance their thesis that **biodiversity** is not suitable for the goals of conservation. These examples are presented with the implicit claim that they are examples of biological value. They represent organisms or biological phenomena that we ought to preserve. I have argued throughout this chapter that they are valuable in different ways. Since eliminativists believe that these are compelling examples of biological value which biodiversity fails to protect and they are appealing to different systems of value then the kind of value which eliminativists are concerned about is pluralistic. They believe that biological value refers to multiple distinct elements captured by different theories. Ecosystems are valuable for human use but they also possess a value intrinsic to themselves and it might be best to approach it in a non-anthropocentric way where possible. Thus the value compass argument for **biodiversity** eliminativism relies on pluralistic biological value. Eliminativists are arguing that biodiversity fails to preserve the instrumental, intrinsic, and non-anthropocentric value of the environment so we ought to use a different target for conservation; one which better approximates pluralistic biological value. In the next two sections I will discuss problems with using pluralistic biological value as the standard for conservation surrogates. I begin with eliminativist equivocations of ‘value’.

### 7.7 Eliminativist Equivocations of 'value'

In this section I will argue that **biodiversity** eliminativists are not being careful enough with their appeals to biological value and so are equivocating in the value compass case for **biodiversity’s** elimination. Angermeier and Karr use a concept of integrity which equivocates the health of an ecosystem with its natural state. They identify dimensions of ecosystem health as the priority of conservation but then appeal to examples of ecosystems in a natural state. Santana explicitly argues for instrumental value but tacitly appeals to intrinsic and non-anthropocentric instances of biological value. So his concept of ecological value equivocates instrumental value with pluralist biological value.
### 7.7.1 Biological Integrity as Pluralist biological value

Angermeier and Karr’s integrity concept equivocates in their value compass case because they present biological integrity as a concept of health but appeal to a lack of naturalness to criticise biodiversity.

This incomplete view fails to recognize that elimination of extensive areas of old growth forest, dramatic declines in hundreds of genetically distinct salmonid stocks in the Pacific Northwest, and the loss of chemically distinct populations from different portions of a species range represent significant losses of biodiversity, regardless of whether any species become extinct. (Angermeier and Karr 1994, 692)

The inadequacy of current conceptions of biodiversity recently was made clear to me in several independent discussions with natural resource managers and scientists, where I asserted that introductions of exotic species into the wild diminish rather than enhance biodiversity. (Angermeier 1994, 660)

So Angermeier and Karr’s value compass argument for biodiversity eliminativism takes the following form.

**The Value Compass Case for Biodiversity Eliminativism**

1) Conservation ought to preserve the valuable elements of the environment.
2) Biological integrity reliably tracks biological value.
3) Biodiversity does not correlate well with biological value or biological integrity.
4) Therefore: The goal of conservation ought to be biological integrity rather than biodiversity.

Biological integrity is presented as a health concept. In *Biological Integrity versus Biological Diversity as Policy Directives* Angermeier and Karr (1994, 692) offer the following table to break biological integrity down into its components.

<table>
<thead>
<tr>
<th>Hierarchy</th>
<th>Elements</th>
<th>Processes</th>
<th>Indicators</th>
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<tr>
<td>Taxonomic</td>
<td>Species</td>
<td>Range expansion or contraction</td>
<td>Range size</td>
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<td>Extinction</td>
<td>Number of populations</td>
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<td>Evolution</td>
<td>Isolating mechanisms</td>
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<td>Genetic</td>
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<td>Mutation</td>
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<td>Recombination</td>
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<td>Selection</td>
<td>Inbreeding or outbreeding depression</td>
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<td>Ecological</td>
<td>Population</td>
<td>Abundance fluctuation</td>
<td>Age or size structure</td>
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</table>
Colonization or extinction | Dispersal behaviour
---|---
Evolution | Gene flow
Assemblage | Competitive exclusion | Number of Species
Predation or parasitism | Species evenness
Energy flow | Number of trophic links
Nutrient Cycling | Element redundancy
Landscape | Disturbance | Fragmentation
Succession | Number of communities
Soil formation | Persistence

Table 7.1: Components of Biological Integrity

So biological integrity should be understood as a measure of how well the biological processes of an ecosystem are functioning. This is an analysis of health. If species richness is steady but nutrient cycling is failing then integrity is reduced.

But in their examples which criticise biodiversity, Angermeier and Karr both appeal to the naturalness of an ecosystem multiple times.

Biological Integrity — The capability of supporting and maintaining a balanced, integrated, adaptive community of organisms having a species composition and functional organisation comparable to that of natural habitat of the region. (Karr 1990, 285)

When a river is damned, integrity is reduced, resulting in declines of populations adapted to the natural hydrological regime.

Such a change may be interpreted as either a gain or loss in diversity, but integrity is clearly reduced because of the shift away from native conditions.

Artificial elements reduce integrity through widely documented effects on native elements and processes and should be excluded from evaluations of biodiversity. (Angermeier and Karr 1994, 693–94)

Thus, ecological integrity reflects the completeness of evolved elements and processes over a broad range of organizational levels and spatiotemporal scales (Angermeier 1994, 601).

The capability of supporting and maintaining a balanced, integrated, adaptive community of organisms having a species composition, diversity, and functional organization comparable to that of natural habitat of the region. (Karr and Dudley 1981, 56)

So Angermeier and Karr’s version of the value compass case equivocates in the following way.
The Value Compass Case for Biodiversity Eliminativism

1) Conservation ought to preserve the valuable elements of the environment.
2) Biological integrity (understood as ecosystem health) reliably tracks biological value.
3) Biodiversity does not correlate well with biological value or biological integrity
   (understood as ecosystem naturalness).
4) Therefore: The goal of conservation ought to be biological integrity rather than biodiversity.

The argument equivocates the different meanings of ‘biological integrity’. Health and naturalness are distinct properties. Health is just as difficult to measure as biodiversity but naturalness is a deeply contentious concept. Human beings are a part of the ecosystem which conservation aims to protect (Takacs 1996, 42). Our preference for unspoilt naturalness is a recent development which often overlooks the indigenous people who were shifted off that land. The equivocation here is problematic because it argues that conservation should protect the health of an ecosystem by keeping things human free in a natural state. Arguing that health is a better goal for conservation than biodiversity is difficult enough without substituting ‘health’ for ‘naturalness’. Naturalness is a more contentious concept than health which is itself less contentious than biodiversity.

To complicate matters further Angermeier and Karr both appeal to instrumental value in their arguments as well.

Only in the presence of a functioning biological system are other resources (for example, energy, minerals) useful to man. (Karr and Dudley 1981, 56)

The total worth of biodiversity to society comprises a broad array of values, including aesthetic, ecological, and utilitarian values. Some of that value is inherently dependent on the variety of biotic systems. (Angermeier 1994, 601)

To be effective, conservationists will need to openly profess their values and persuade others that natural biotic diversity contributes significantly to the quality of human lives. (Angermeier 2000, 379)

These are appeals to anthropocentric instrumental value because they appeal to ways in which the environment provides a means to human ends. So the examples they use to motivate premise three of the value compass argument appeal to health and naturalness which are intrinsic and non-anthropocentric but they also appeal to instrumental value and anthropocentric values. There is an equivocation of biological value because Angermeier and Karr are treating distinct conceptions of biological value as the same concept.

7.7.2 Santana's instrumentalism as pluralist biological value
Santana equivocates in his value compass case for biodiversity’s elimination because he presents instrumental value as the goal of conservation but appeals to intrinsic and non-anthropocentric value in his motivating examples. Santana initially uses instrumental value as the goal for conservation. He is explicitly sceptical of intrinsic value and defines
ecological value instrumentally (Santana 2017, 89). “Ecological value comprises at least these economic, aesthetic, cultural, and existence values.” (Santana 2017, 89). Whilst value for existing is typically an intrinsic type of value, Santana defines it instrumentally as “the satisfaction derived merely from knowing that an object persists in its desired form” (Santana 2017, 88). So rather than value for existing, existence value is how much we enjoy knowing that something exists which is a clear example of means to an end. Santana argues that we should reject biodiversity because it does not track ecological value well.

The principle role played by biodiversity in conservation biology is as a comparative measure of value. Biodiversity does not fulfil that role well, in part because it is not straightforwardly measureable quantity. Moreover, it does not fulfil that role well because it does not closely track ecological value, the aggregate of values we place in the environment. (Santana 2017, 86)

So Santana’s value compass argument takes the following form.

The Value Compass Case for Biodiversity Eliminativism
1) Conservation ought to preserve ecological value.
2) Therefore: The goal of conservation ought to reliably track ecological value.
3) Biodiversity does not reliably track ecological value.
4) Therefore: Biodiversity ought not to be a conservation goal.

Santana has defined ecological value instrumentally. Even his appeals to naturalness are worded as the value people derive from a natural ecosystem.

Additionally it seems to be the case that many people value keeping ecosystems as close as possible to the state of nature. But a richness scale suggests that we can improve a system by deviating from the state of nature and importing species by, say, adding a fish to a lake. (Santana 2014, 769)

Whilst Santana sets the goal for conservation as instrumental value, his motivating examples appeal to multiple types of value. Consider his appeal to gene soup to reject genetic diversity as a candidate for the meaning ‘biodiversity’.

Genetic diversity, however, is nearly a non-starter. A “gene soup” containing a random sample of genetic material from a given place would furnish little in the way of useful information for several reasons. (Santana 2014, 771)

In this example Santana prefers functioning ecosystems over genetic soup because it is more informative. So his motivation is instrumental. But, provided that it is a genetic ark rather than a bowl of D.N.A., gene soup is as instrumentally valuable as a functioning ecosystem containing the same genetic information. It contains a genetic record of every extant species and we can study that record in a single place. It is also possible that Santana is appealing to existence value. Some agents prefer wild ecosystems to botanic gardens but for every agent who values genes in the wild there is an agent who values genetic soup. Santana defines existence value in terms of how much we enjoy a biological
element’s existence and there are many reasons to enjoy the existence of gene soup. A container of every biological gene makes for a fascinating station at a museum.

Gene soup cannot rely solely on instrumental value for its persuasiveness because there is as much instrumental value in gene soup as there is in a functioning ecosystem. This is because instrumental value is the value of a means to an end so there are as many instrumental values as there are preferences in sentient agents. This is also because a complete genetic ark provides immediate access to the genetic information of all species. For gene soup to be a persuasive example it must appeal to intrinsic value in the sense of a non-extrinsic property or some other non-anthropocentric value. Santana sets instrumental value as the target for conservation but appeals to non-anthropocentric value. So, his value compass argument for biodiversity eliminativism equivocates in the following way.

The Value Compass Case for Biodiversity Eliminativism
1) Conservation ought to preserve ecological value (instrumental value).
2) Therefore: The goal of conservation ought to reliably track ecological value (instrumental value).
3) Biodiversity does not reliably track ecological value (non-anthropocentric value).
4) Therefore: Biodiversity ought not to be a conservation goal.

This equivocation is echoed in his concern for biodiversity cold spots. “The trend in conservation biology of prioritising biodiversity “hot spots” distracts from attending to biodiversity “cold spots”.” (Santana 2014, 770–71). Instrumental value ought to decrease as species richness and functionality do. A concern for biodiversity cold spots is a non-anthropocentric one which attempts to treat various biological organisms as equal rather than give undue weight to species rich ecosystems. Biodiversity cold spots such as deserts are still as valuable as biodiversity hotspots and deserve conservation’s attention (Durant et al. 2014, 114).

Santana’s value compass case for elimination equivocates because it presents itself as concern about how well biodiversity tracks instrumental value but the motivating examples appeal to instrumental value, intrinsic value, and non-anthropocentric value. Santana sets instrumental value as the goal of a conservation surrogate but criticises biodiversity for failing to approximate multiple distinct types of biological value. Treating distinct types of biological value under a single category is a mistake. However restricting value compass eliminativism to a specific dimension of biological value such as economic instrumentalism is not a palatable option for eliminativists either because they would have to give up many of their motivating examples. The best option for biodiversity eliminativism is to understand the value compass case as focusing on pluralistic biological value. Then eliminativists can retain their examples as instances of biological value which biodiversity does not track well. Pluralistic value compass eliminativism is the best interpretation of eliminativist arguments but as I will argue in the next section it comes with its own problems.
7.8 Conclusion

In this chapter I have introduced the value compass case for biodiversity’s elimination and sought to identify the type of value which eliminativists are appealing to. Identifying the type of value is important because while eliminativists argue that biodiversity is a poor surrogate for biological value but there are multiple distinct types of biological value and eliminativists do not identify which type of value biodiversity is a poor surrogate for. Treating all types of biological value as the same risks equivocation in the value compass argument so in this chapter I used textual evidence to identify the types of biological value that eliminativists appeal to in their examples and argue that the value compass argument for biodiversity eliminativism is far more problematic when care is taken to distinguish types of biological value.

I began by discussing different types of biological value and arguing that Santana, Angermeier, and Karr appeal to them in their examples of biodiversity correlating poorly with biological value. I explained instrumental value as a means to an end and highlighted different types of instrumental value such as: economic, aesthetic, and cultural. I explained intrinsic value as its own end but also drew attention to three different uses of intrinsic: non-instrumental, non-extrinsic property, and value independent of an agent’s beliefs. I introduced non-anthropocentric value as an alternative to intrinsic value. I argued that whilst intrinsic value and non-anthropocentric value are often treated interchangeably they are distinct. There is a continuum of anthropocentricity along which instrumental and intrinsic sit in overlapping positions. I used textual evidence to argue that Santana, Angermeier, and Karr appeal to all three types of value in their examples which are used to motivate premise two of the value compass case. Angermeier and Karr’s appeals focus on non-anthropocentricity and intrinsic value but they also appeal to instrumental value. Santana identifies ecological value as instrumental but his examples do appeal to intrinsic and non-anthropocentric types of value. I noted that identifying these examples as appealing to both intrinsic and non-anthropocentric value is important. If eliminativists are opposed to their work being analysed in terms of intrinsic value then they still have to argue that their motivating examples are not appealing to non-anthropocentric value.

Using this textual evidence I concluded that the value compass case was focused on pluralistic biological value. Eliminativists are in fact arguing that a good conservation surrogate should approximate multiple types of biological value. I then argued that eliminativists are equivocating in their arguments. Angermeier and Karr criticise biodiversity for failing to prioritise integrity and the naturalness of an ecosystem but they use examples which highlight a loss of instrumental value. Santana criticises biodiversity for correlating poorly with instrumental value but uses examples which highlight losses of intrinsic and non-anthropocentric value. In the next chapter I will argue that the pluralistic value compass case for biodiversity’s elimination is unsuccessful.
8 The Value Compass Case for Eliminating *Biodiversity* is Unsuccessful

8.1 Introduction

In this chapter I will argue that the value compass case for eliminating *biodiversity* fails. This chapter’s conclusion relies on the material from chapter seven. In chapter seven I sought to identify the kind of biological value which eliminativists were appealing to in their arguments. I identified several equivocations in the eliminativists’ use of ‘value’ and argued that the best way to understand their arguments was as an appeal to pluralistic ecological value. Eliminativists argue that the priority for conservation ought to reliably track our common intuitions about biological value. The assumption in the eliminativists’ argument that biodiversity ought to be a value compass is an important one. Not just because it is the standard which is used to justify eliminating *biodiversity* but also because it motivates the conceptual and empirical cases for elimination. A common thread in the conceptual and empirical case for eliminating *biodiversity* was the eliminativists’ appeals to biological value. Demonstrating that the value compass case is unsuccessful also highlights further flaws in the conceptual and empirical cases.

I begin in section 8.2 by re-introducing the value compass case for eliminating *biodiversity*. Biodiversity ought to track pluralistic ecological value but it often does not. In section 8.3 I discuss problems with using a value compass as the standard which a conservation goal must meet. I argue that pluralistic ecological value is a punishing standard, that eliminativists have not told us why biodiversity ought to be a reliable value compass, and that the value compass case for elimination is self-eliminating. In section 8.4 I argue that even if biodiversity is not a reliable value compass then there are still good reasons to retain *biodiversity* as a conservation goal. Biodiversity is a better conservation priority than the alternatives and it tracks reductions of biological value even if it does not reliably maximise value. In section 8.5 I identify an equivocation in the value compass case and argue that the same equivocation occurs in both the conceptual case and the empirical case for *biodiversity*’s elimination. I conclude that the value compass case fails and that because the conceptual and empirical cases for elimination also fail, we have good reasons to use biodiversity as a goal for conservation.

8.2 The Value Compass Case for Eliminating *Biodiversity*

In this section I will outline and motivate the value compass case for eliminating *biodiversity*. The value compass case for elimination argues that conservation should not use biodiversity as a goal because it does not track pluralistic biological value well. Actions such as the extermination of smallpox, lower biodiversity but promote biological value (Santana 2014, 769). This is due in part to the complex relationship between what is valuable for the environment and what is valuable in the environment for human beings now. Conservation does not prioritise the survival of smallpox because it poses a significant threat to the well-being of human beings. Similarly, the relationship between biodiversity and biological value is also a complex one. Whilst the preservation of
biodiversity is a goal for conservation, in practice conservationists also dedicate many resources to eradicating elements of biodiversity. The control or eradication of pest species is a high priority for conservation because it protects biological value.

The value compass argument is an amalgamation of the arguments for biodiversity’s elimination presented by Santana, Angermeier, and Karr. All three authors present motivating examples for biodiversity’s elimination, in which preserving biodiversity would not protect biological value. In chapter seven I discussed these examples at length. I argued that whilst they all appeal to biological value, they all appeal to different types of biological value. I concluded that biodiversity eliminativists use pluralistic biological value as the standard for a conservation goal. They expect the goal of conservation to track the many different types of biological value which are borne by the environment. Adjusted for the conclusion of chapter seven, the value compass case for biodiversity eliminativism can be formalised in the following way:

**The Value Compass Case for Biodiversity Eliminativism**

1) Conservation ought to preserve pluralistic biological value.
2) The goal of conservation ought to reliably track pluralistic biological value.
3) *Biodiversity* is the goal of conservation.
4) *Biodiversity* does not reliably track pluralistic biological value.
5) If the goal of conservation does not reliably track biological value then it ought to be eliminated.
6) Therefore: *Biodiversity* ought to be eliminated as the goal of conservation.

The value compass case is my construction of the author’s arguments so its premises require justification. Premise three is not contentious although it has rightly been pointed out that biodiversity can be understood as one important goal for conservation rather than the only important goal for conservation (Burch-Brown and Archer 2017, 988). However given that ‘biodiversity’ appears as a priority in a number of international treaties of conservation, it is fair to treat it as a high priority even if conservation has other goals as well (Maclaurin 2017, 57). The examples in chapter seven justify premise four. All three authors have presented multiple examples of biodiversity failing to track pluralistic biological value. Certainly, biodiversity sometimes conflicts with our conservation intuitions. Faith, for example, contemplates preserving only one species of tuatara because further species do not maximise phylogenetic diversity.

Premise one that “conservation ought to preserve pluralistic biological value” is an assumption which Santana, Angermeier, and Karr rely on in their arguments. If one argues that the failure to track biological value is a good reason to eliminate biodiversity as a conservation goal then one is assuming that conservation ought to preserve biological value. To that end premise two is required; if conservation ought to preserve pluralistic biological value then whatever we set as the goal of conservation ought to reliably track pluralistic biological value. This is an assumption but it is a sensible one. Conservationists have limited resources and when we cannot preserve all elements, we ought to preserve the most valuable elements. Likewise, premise five that “if the goal of conservation does not reliably track biological value then it ought to be eliminated” is also a sensible assumption.
Goals are only effective when they track the objective which they are required to. For example, profit is an ineffective goal for medical research because treating disease can be expensive.

Lastly, the value compass case for biodiversity eliminativism does not consider the role of risk in conservation decision making. Risk is an important factor in decision making because what we ought to do is not only a function of what is valuable but also of risk based factors such as the probability of success and the danger of producing harm. Small pox was eradicated because it was dangerous to humans and conservationists often face difficult decisions with fund allocation. Restoring a critically endangered species is costly and difficult, whereas the same money could effectively protect an several endangered species. The value compass case does not consider these factors because it is a response to the eliminativist challenges against biodiversity and those eliminativists do not discuss risk at detail in their appeals to biological value. These chapters are a direct response to the eliminativist position and as such are a focused response to their arguments.

My strategy for the value compass case will be to accept the truth of premise four and three but challenge the truth of premises: one, two, and five. Biodiversity is the goal of conservation and I accept that it does not reliably track pluralistic biological value but I deny that it ought to. In section 8.3 I will identify several problems with using a pluralistic biological value compass as the minimum standard for a conservation goal. I will use these problems to argue that contra to premises one and two, pluralistic biological value is an inappropriate standard to measure the success of conservation goals. In section 8.4 I will argue that even if biodiversity is a poor value compass then, contra to premise five there are still good reasons to retain it as conservation goal. In section 8.5 I will argue that the value compass case for biodiversity’s elimination is faulty because it relies on conflating biological value with conservational normativity. I will argue that this mistake also motivates the conceptual and empirical cases. For these reasons I will conclude that the value compass case for biodiversity’s elimination is unsuccessful.

8.3 Problems with Setting Pluralistic Biological Value as the Goal
In this section I will outline several problems with using pluralistic biological value as the target for a conservation surrogate. The type of biological value which eliminativists are appealing to in the value compass case is pluralistic. Their motivating examples, however, appeal to specific dimensions of biological value such as aesthetic instrumental value or non-anthropocentric value. Aside from the equivocation risk there are further problems with setting pluralistic biological value as the standard that a conservation surrogate must achieve. In this section I will discuss three such problems. In section 8.3.1 I will argue that pluralistic biological value is too punishing a standard for a conservation goal. In section 8.3.2 I will argue that biodiversity eliminativists have not explained why conservation goals must achieve such a high standard. ‘All biological value’ is a difficult standard which few conservation surrogates could effectively track. It is not surprising that biodiversity struggles to track: instrumental, intrinsic, and non-anthropocentric elements of biological value. In section 8.3.3 I will argue that the concept of pluralistic biological value is vulnerable to the eliminativists’ own strategy. If general conceptions of
biodiversity ought to be eliminated because they are not operationalisable, then pluralistic biological value ought to be eliminated because it is less operationalisable than biodiversity.

8.3.1 Pluralistic Value is too punishing a minimum standard
In this subsection I will argue that using pluralistic biological value as a standard to judge the performance of a conservation goal is too punishing. This is because of two reasons: there is no consensus among value theorists as to which theory correctly describes biological value, and systems of pluralistic value make conflicting recommendations.

It is unfair to test a conservation goal as a value compass because there is no consensus among value theorists about what biological value is. The material I presented in chapter seven demonstrated that the current debate over the nature of biological value is still unsettled. Like the species problem and the biodiversity problem, there are many conflicting theories about which theory of biological value is correct. No individual theory provides a complete account of value so multiple theories are necessary to give an accurate account of the nature of value. When there is no consensus on the nature of biological value, conservation goals cannot be value compasses. We cannot test a conservation goal by how well it selects the most valuable biological elements because we cannot agree on which elements are the most valuable. Even if there were a value theorist consensus on the nature of biological value, a concept like biodiversity could never reflect everyone’s intuitions about which biological organisms are valuable. Santana’s example of the eradication of smallpox is a persuasive example because it aligns with our personal intuitions about biological value. It is not so much a clear example of an increase in biological value as an example of an organism which conservationists ought not to preserve for the benefit of human beings.

A pluralistic biological value compass test is also a punishing standard because pluralistic systems often make conflicting recommendations. The biological species concept and the morphological species concept disagree over whether hybrids are unique species. Utilitarians and deontologists disagree over whether it is right to kill one person to save five (Kagan 2011, 107). So, a pluralist moral system consisting of utilitarian and deontological dimensions would conflict over whether such an act is morally permissible. Pluralistic systems generate inconsistent recommendations because their multiple dimensions disagree over classification. Because biological value is a pluralistic system there will be problem spots for any conservation goal which is trying to function as a value compass. The eradication of smallpox to protect human beings appeals to instrumentalists but intrinsic value theorists will disagree that we are permitted to exterminate a species for human benefit. The preservation of ecosystems in their native conditions appeals to the deep ecology movement but not to authors such as Cronon who see problems with the wilderness concept (Cronon 1995).

These examples are the problem spots of a pluralistic system of biological value. They tell us little about the accuracy of a conservation goal and much more about how difficult it is to make sense of biological value. Because of the conflicting recommendations of pluralistic systems all conservation goals will struggle to reliably track biological value, so biodiversity should not be held accountable for struggling as a
value compass. In the next subsection I will argue that eliminativists have not explained why biodiversity ought to be a compass for pluralistic biological value.

8.3.2 Eliminativists have not explained why biodiversity ought to track pluralistic biological value

Biodiversity eliminativists have appealed to multiple types of biological value in their motivating examples but they have not explained why the standard for a conservation surrogate should be ‘all of biological value’. This is problematic for the eliminativist position because their motivating examples, whilst compelling, rely on that assumption. Angermeier and Karr are correct that we should be concerned about deforestation long before the individual species are about to go extinct (Angermeier and Karr 1994, 692). Santana is correct that adding more species to an ecosystem is not the same as returning it to its naturally evolved state (Santana 2014, 769). But neither have they explained why the acceptable threshold for a conservation surrogate is that it accurately approximates multiple systems of biological value. When a conservation surrogate is expected to correlate with multiple systems of biological value it will miss valuable organisms. A push to mitigate species loss may do nothing to protect the migration of the monarch butterfly. However it would protect countless other instances of valuable biology such as organisms which are instrumentally or intrinsically valuable.

If eliminativists want a conservation surrogate which successfully protects multiple systems of value then few surrogates will be up to the task and the eliminativist observation that ‘biodiversity fails to protect this’ will be less persuasive. If biodiversity were expected to protect a single dimension of biological value such as instrumental value then observations that it was failing at its task would be quite powerful. But in so far as eliminativists expect conservation surrogates to get all of biological value correct, their observations highlight the tensions of a pluralist system rather than a shortcoming of biodiversity. In fact, it is not clear that any conservation surrogate could accurately approximate pluralistic biological value. Pluralistic biological value has more internal conflict than biodiversity because multiple dimensions are determined by an agent’s personal interests. As I will argue in the next subsection, by Santana’s own standard for a conservation surrogate, pluralistic biological value is self-eliminating.

8.3.3 As a standard for elimination, pluralist biological value is self-eliminating

A serious problem for the value compass case is that, by Santana’s own standards, it is self-eliminating. Understanding biological value as a single clustered property with multiple loosely correlated dimensions is structurally no different to understanding biodiversity as a single clustered property with multiple loosely correlated dimensions. The central argument in Santana’s work is that the multiple dimensions of biodiversity do not correlate highly enough to warrant being treated as a single property (Santana 2014, 761). But as diverse as the multiple dimensions of biodiversity are, the multiple dimensions of biological value are more so. This leads pluralistic biological value to the same dilemma which Santana used against biodiversity. Biological value is the target for conservation and can either be pluralistic or specific. If biological value is pluralistic then is not
operationisable. If it is specific then it has counterexamples. In the case of biodiversity Santana offered examples to convince us that species, morphology, functionality, evolution, and genetic diversity cannot represent biodiversity. If you believed that biodiversity was genetic diversity then you would be satisfied with preserving a gene soup containing as many genes as possible. But you are not satisfied with gene soup so there is more to biodiversity than genetic diversity (Santana 2014, 771).

It is a convincing argument but mutatis mutandis arguments can be produced against biological value. If you believe that biological value was a matter of instrumental value then you would have no problem with whaling practices which did not threaten extinction. But you are not satisfied with whaling practices even if whaling brings instrumental value to some people so there must be more to biological value than instrumental value. Examples are easily replicable so if Santana contends that the first observation is sufficient to question the use of ‘biodiversity’, then the second observation is sufficient to question the use of biological value. Where Santana argues that we should eliminate biodiversity because it cannot be understood as species, genetics, or functionality, then we should eliminate biological value because it cannot be understood as instrumental, intrinsic, or non-anthropocentric value. Understanding biological value as pluralistic implies that value motivated eliminativism is relying on a vague cluster property (biological value) to exploit apparent conflicts with another vague cluster property (biodiversity). This is a self-undermining strategy because all vague cluster properties are susceptible to the pattern of arguments which Santana uses against biodiversity. Santana’s dilemma between specific dimensions with counterexamples and general but non-operationisable conceptions applies as well to biological value as it does to biodiversity. So, pluralistic value compass eliminativism is self-eliminating.

8.4 There are still good reasons to retain Biodiversity even if it is not an effective value compass

In this section I will argue that even if biodiversity is not an effective compass for pluralistic biological value, there are still good reasons to retain it as a goal for conservation. This conclusion will falsify premise five of the value compass case for biodiversity eliminativism which states “If the goal of conservation does not reliably track biological value then it ought to be eliminated”. Since the premise is a conditional statement, a counterexample is produced by assuming the truth of the antecedent and demonstrating the falsity of the consequent. Biodiversity is the goal of conservation so a counterexample requires an instance in which biodiversity does not reliably track biological value but ought to be retained as a goal for conservation. In this section I argue for two such instances. Firstly, I argue that biodiversity is a better conservation target than the alternatives. A conservation goal ought to be retained if it meets the needs of conservation better than its competing theories. Secondly, I argue that even if maximising biodiversity does not maximise biological value, it still tracks losses of biological value. A conservation goal ought to be retained if it monitors a loss of value. So biodiversity can be an important goal during decreases of biological value without being an important goal during increases of biological value.
8.4.1 Biodiversity is a Better Conservation Target than the alternatives

In this subsection I will argue that one reason to retain biodiversity as a target of conservation if it is not a reliable value compass is that it is still a better conservation target than its competitors. First I explain the philosophy of science behind this idea. Historically, science has been better served by favouring the best performing theory than rejecting imperfect theories. Then I outline several goals which the focus of conservation must meet. Next, I presume that biodiversity is not a reliable value compass but argue that it is better suited for the goals of conservation than the following competitors: biological integrity, biological value, and the specific dimensions of biodiversity. I conclude that even if it were an unreliable value compass, biodiversity should be retained as a goal of conservation because it is a better target than the alternatives.

There are good reasons to retain biodiversity as a conservation target even if it is not a reliable value compass because theories which perform better than their competitors are worth retaining. An important historical example of this is the continued use of naïve set theory despite its inconsistency. There is no clearer proof of the incorrectness of a theory than a demonstration that it generates an internal contradiction. Naïve set theory was demonstrably incorrect but it remained in used for approximately thirty years until it was replaced with Zermelo-Fraenkel set theory with the axiom of choice (Colyvan 2008, 24–25). Similar issues faced the infinitesimal calculus of Leibniz and Newton until a more suitable method was discovered (Brown and Priest 2004, 379). Scientific work continues with problematic theories because restricting the tool set to problem free theories leaves few tools to work with. Theory selection in scientific progress is less about which theory is not problematic and more about which theory is the least problematic.

All conservation goals will be somewhat problematic because effective conservation has several difficult requirements. Santana, Angermeier, and Karr correctly identify one such requirement that our conservation goal prioritise the most valuable biological elements for conservation. But, conservation has other requirements. The goal of conservation must also be: pragmatic, operationalisable, amenable to legislation, and balance benefits for the environment such as low habitat fragmentation with humans’ desires such as urban development. The goal must be pragmatic because we must be able to conserve it. It must be operationalisable because we need to measure and calculate for triage and reporting. It must be amenable to legislation so that we can set down clear policy and perhaps most difficult, it must balance the environment’s needs with human’s desires. Conservation ought to preserve organisms but for political purposes it also ought to keep human beings happy. Smallpox is not eligible for conservation because it poses a significant threat to human beings.

Biodiversity is a suitable conservation goal because even if it is not a reliable value compass it still meets the other conservation requirements very well. As a goal for conservation, biodiversity is pragmatic, operationalisable, amenable to legislation, and balances the environment’s needs with humans’ desires. It is pragmatic because it sets conservation the task of preserving the greatest biological diversity with limited resources. It is also operationalisable. In chapters four to six of this thesis I showed how it can be measured and calculated. It is amenable to legislation because its specific dimensions can be used to set targets and monitor progress in policy and there is general agreement on
what those dimensions are. It also strikes a balance between the needs of the environment and the desires of human beings. It can explain why humans care about certain unique species such as the tuatara but also explain why we need to preserve all the pieces of the environment which make the survival of the tuatara possible. Biodiversity is the top performer when it is compared with its modern competitors. In the following comparisons I presume that biodiversity is not a reliable value compass. However, I argue that biodiversity ought to be retained as a conservation goal because it is better at conservations requirements than the following competitors: biological integrity, biological value, and the specific dimensions of biodiversity.

Biodiversity is a more suitable goal for conservation than biological integrity because whilst biological integrity is an operationalisable goal, it is not pragmatic, amenable to legislation, and does not balance the environment’s needs with humans’ desires. In section 7.7.1 I argued that as a concept, biological integrity encapsulates both ecosystem health and native conditions, which according to Angermeier and Karr, represents an ecosystem that has evolved with minimal interference. It is operationalisable because Angermeier and Karr provide us with a large number of specific dimensions to measure and argue that we should evaluate an ecosystem’s health by comparing it to other similar ecosystems (Angermeier and Karr 1994, 692). It is not a pragmatic goal because achieving ecosystem health and native conditions, as Angermeier and Karr conceive of them, requires removing human beings. This is also not a pragmatic condition for conservation because of climate change (Takacs 1996, 56). We cannot return any ecosystem to how it was 100 years ago. It is not amenable to legislation because of the problems with native and wilderness concepts (Cronon 1995). It also does not balance humans’ desires with the environment’s needs. Instead, it ejects human beings for the sake of the environment.

Biodiversity is a more suitable goal for conservation than biological value because whilst biological value would balance the environment’s needs with human’s desires, it is not pragmatic, operationalisable, or amenable to legislation. As a goal for conservation, biological value would balance human desires with the environment’s needs because pluralistic biological value balances instrumental value with non-anthropocentric value. It is not a pragmatic goal because we cannot only preserve the valuable organisms. Biological organisms with instrumental value for human beings tend to be either key stone species, phylogenetically unique, members of the charismatic megafauna, or directly related to ecosystem services. Conservation requires that we preserve more than the valuable organisms.

Organisms are a part of an interactive ecosystem and they require that ecosystem to flourish. It is not practical to only preserve the valuable organisms and ecosystems because there are numerous species which are not key stone species, phylogenetically unique, members of the charismatic megafauna, or directly related to ecosystem services. Those species make up ecosystems which are essential to the flourishing of the valuable organisms. It is not pragmatic to only preserve the tuatara and not the myriad of species which make up the ecosystem that the tuatara needs. Nor will the valuable organisms provide umbrella protection to other species. Selecting places for conservation based on
the presence of the charismatic megafauna has been shown to be less effective than selecting places at random (Sarkar 2005, 173).

One response to this problem is to argue that the less valuable species are instrumentally valuable to the tuatara. This response leads to a lengthy regress of instrumental values for the sake of supporting other instrumental values. Tuataras are instrumental valuable because humans enjoy them. Spiders are instrumentally valuable because Tuatara’s eat them. Flies are instrumentally valuable for spiders and excrement is instrumentally valuable for flies. This response still implies that biological value is not a pragmatic goal because extending out instrumental value along a regress makes almost all organisms instrumentally valuable and we cannot preserve every organism any more than we can only preserve the valuable organisms. As a goal of conservation biological value is also not operationalisable or amenable to legislation. It is an intangible property without a consensus on how to measure or calculate it. To make the issue more complex, some intrinsic theories of value seem to assign infinite value to certain organisms (Santana 2017, 89).

Biodiversity is a more suitable goal for conservation than its specific dimensions because whilst the specific dimensions of biodiversity are pragmatic goals for conservation, they are partially operationalisable, partially amenable to legislation, and do not balance the environment’s needs with human’s desires well. The specific dimensions of biodiversity are pragmatic goals because we can set a clear target of maximising species richness or protecting local phylogenetic diversity. However, they are only partially operationalisable and amenable to legislation. In chapter six I argued that there was not a suitable replacement for biodiversity because only a small number of dimensions are operationalisable and Santana has already argued that those do not track biological value well. Without operationalisability we cannot put targets or monitoring into policy so the specific dimensions of biodiversity are not amenable to legislation. They also do not balance the environment’s needs with human’s desires well. In chapter two I argued that as a concept biodiversity reduces misdirection because it forces people to engage with the multidimensional nature of the environment. Engaging with specific dimensions imperils the environment for the sake of human beings. Buckets of beetles are a wonderful source of species richness but we should conserve more than just beetles.

In this subsection I argued that one good reason to retain biodiversity as the goal of conservation is that even if it is not a reliable value compass, it still outperforms its competitors at the other demands of conservation. I motivated this argument with some brief history of science and outlined four additional requirements for a conservation goal. Conservation goals must be: pragmatic, operationalisable, amenable to legislation, and balance the environment’s needs with humans’ desires. I argued that biodiversity meets these goals well compared with its competitors: biological integrity, biological value, and the specific dimensions of biodiversity. In all three cases I argued that biodiversity is a better goal for conservation because even if it did not track biological value well, it still satisfies more of conservations’ requirements than its competitors. In the next subsection I will argue that there is another reason to retain biodiversity as a conservation goal if it is not an effective value compass. Biodiversity still tracks losses of biological value.
8.4.2 Biodiversity Tracks Reductions of Biological Value

In this subsection I will assume that biodiversity is not a reliable value compass but argue that we ought to retain it as a goal for conservation because it is still a useful surrogate for reductions in biological value. That is, maximising biodiversity will not always maximise biological value but mitigating biodiversity loss will mitigate loss of biological value. I argue that biodiversity is therefore a useful goal because global biodiversity is rapidly diminishing (Sepowski 2017, 26).

Santana, Angermeier, Karr all argue that biodiversity does not predict biological value well but they are focusing on ways in which maximising aspects of biodiversity does not maximise biological value. Simply increasing the species richness, phylogenetic diversity, or phenotypic diversity of an ecosystem does not always increase its biological value because theories of value are diverse. Introducing new species can endanger current species and some people value ecosystems in a native state (Santana 2014, 769; Angermeier 1994, 600). The eliminativist point is correct, maximising biodiversity does not maximise biological value. For example, the value of homeowners’ gardens is decreased when weeds become rampant. However, conservationists can have biodiversity as a goal without wishing to maximise it (Burch-Brown and Archer 2017, 988). Even if maximising biodiversity does not maximise biological value, mitigating biodiversity loss will mitigate the loss of biological value. We cannot significantly reduce the species richness, phylogenetic diversity, or phenetic diversity of an ecosystem without also decreasing its biological value.

The suitability of biodiversity as a goal for conservation depends on whether conservation is focused on preserving or increasing biodiversity. Bearing in mind that I am only assuming that biodiversity does not reliably track biological value for this section, biodiversity is a more suitable goal for preservation than restoration. Conserving biodiversity requires cataloguing what still exists and protecting as much of it as possible. Increasing biodiversity in instances such as the predator free islands of New Zealand requires protecting certain species and eradicating the local population of others. Biodiversity is therefore a very important goal for conservation because practically all conservation performs critical triage (Maclaurin and Sterelny 2008, 178). The planet is in a sixth major extinction event (Sepowski 2017, 35). Around 90% of species are still undocumented so many of these will go extinct without being discovered (Mora et al. 2011, 2). The once worst case scenario for climate change of two degree increase is now our best case scenario (IPCC 2014, 10). By 2025 we expect two thirds of the world to face freshwater scarcity because of the depletion of ancient aquifers of water and by 2050 we expect there to be more plastic than fish in the oceans (Sarkar 2012, 158; Ellen MacArthur Foundation 2016, 7). We are also haemorrhaging biological value because biodiversity loss is creating an ecosystem services debt (Isbell et al. 2015, 119). Biodiversity is an important goal for conservation because it monitors biodiversity loss and by proxy, the reduction in biological value.

Biodiversity is an effective tool for tracking a loss of value even if maximising biodiversity will not maximise biological value. In ‘Mammal diversity will take millions of years to recover from the current biodiversity crisis’ Davis, Faurby, and Svenning (2018) apply a phylogenetic analysis to modern rates of extinction. They find that
extinction rates in mammals are disproportionately high compared to the number of species which have gone extinct (Davis, Faurby, and Svenning 2018, 11262). The dominance of human populations makes us a competitive force with the survival of other mammals with the net effect that we have heavily pruned the mammalian branch of the tree of life. They conclude that if our current rate of mammalian extinctions continues for 50 years then it would take five to seven million years to recover the mammalian phylogenetic diversity which has been lost (Davis, Faurby, and Svenning 2018, 11265). The work here does not presume that biodiversity is the only indicator of biological value, but it does use one important dimension of biodiversity to track a loss of biological value caused by the sixth extinction event. There is more to biological value than phylogenetic diversity so maximising feature diversity will not maximise biological value. However, this phylogenetic analysis tracks the loss of biological value by emphasizing how many of the extinctions are borne by a major branch of the tree of life.

In this section I assumed that biodiversity does not reliably track biological value to argue that premise five of the value compass case for elimination is false. Premise five claims that “if the goal of conservation does not reliably track biological value then it ought to be eliminated” so I assumed the antecedent and argued that even if biodiversity was a poor value compass, there are two good reasons to retain it as a goal for conservation. In section 8.4.1 I argued that problematic theories are retained if they outperform their competitors. I then argued that as a goal for conservation, biodiversity meets the diverse requirements better than biological integrity, biological value, and the specific dimensions of biodiversity. In section 8.4.2 I argued that biodiversity is a useful tool for tracking the loss of biological value even if it is not a useful tool for maximising biological value. If biodiversity does not track biological value well then it is better suited for preservation rather than restoration. These arguments imply that premise five of the value compass case for elimination is false. It is not the case that conservation goals ought to be eliminated if they fail to reliably track biological value. In the next section I will argue that the value compass case is faulty because it conflates biological value with conservation normativity.

8.5 The value compass case is unsuccessful because it conflates biological value with normativity

In this section I will argue that the value compass case for elimination is unsuccessful because it conflates biological value with normativity. That is, eliminativists treat biological value as predictive tracker for ‘what conservationists ought to do’ which I will call ‘conservation normativity’. I will argue that these two features come apart in important ways. Whilst limited resources imply that we ought to preserve the most valuable biological elements, ‘conservation oughts’ are generated for many reasons other than value. This conclusion will strengthen the position of biodiversity as a goal for conservation because it is a guide to conservation normativity beyond its ability to act as a compass for pluralistic biological value. In section 8.5.1 I argue that biological value is a poor guide to conservation normativity before arguing in section 8.5.2 that the value compass case overlooks this distinction. In section 8.5.3 I argue that this conflation is also
present in both the conceptual case and the empirical case for *biodiversity* eliminativism. I conclude that the value compass case for *biodiversity’s* elimination is unsuccessful.

### 8.5.1 The value compass case overlooks the distinction between value and normativity.

In this subsection I will argue that the value compass case for *biodiversity’s* elimination conflates biological value with conservation normativity. One reason for this argument’s persuasiveness is that it analyses biodiversity in terms of its relationship with biological value but criticises it in terms of its relationship with conservation normativity. To motivate the conflation, I begin by discussing the intuition that value tracks normativity; the value of an act or an object has a close relationship with what we ought to do. I then argue that biological value does not track conservation normativity well. I outline examples of valuable biological organisms which ought not to be preserved and conservation oughts which are not the product of biological value. I use these examples to argue that the value compass case is conflating biological value with conservation normativity.

In the literature conservation normativity and biological value are often discussed interchangeably. In chapter seven I discussed several appeals to biological value by biodiversity eliminativists. They presume that the role of a conservation goal is to recommend the most valuable biological elements for conservation. Part III of *The Routledge Handbook of Philosophy of Biodiversity* (2017) is titled ‘Why protect biodiversity?’ It contains five chapters by McShane, Callicott, Heinzerling, Odenbaugh, and Minteer, all of which are on the relationship between biodiversity and biological value.

Other authors also approach the analysis of biological value with a similar goal. Biological value is a guide to what we ought to conserve.

Here I argue that wild nature has intrinsic value, which gives rise to obligations both to preserve it and to restore it. (Elliot 1992, 138)

Resource economists have long been aware of the significance of the opportunity to delay an irreversible investment decision. In the 1970s Arrow and Fisher (1974) introduced the term ‘quasi-option value’ to represent the additional value obtained when the option to delay was fully integrated into the decision process. (Forsyth 2000, 413)

It is only the evolution of a universal environmental system that could save the environmental movement from gradual extinction. (Balasubramaniam 1994, 1329)

Unity, communality, ethicality, and equality are the values that are constructed as the basis for acceptable environmental actions, and are partly written and expressed openly, and partly present as hidden meanings in the texts. (Onkila 2009, 295)

Conservation requires decision making, and here intrinsic value falls short. (Maguire and Justus 2008, 192)
Many reasons for conservation have little to do with biodiversity as we have defined it. Forests may be valued as homes to particularly charismatic or culturally important plants and animals, or as a source of key natural resources. (Burch-Brown and Archer 2017, 988)

Elliot justifies conservation by appealing to intrinsic value and Forsyth considers the impacts of delaying environmental action on options value. Balasubramaniam argues that a universal value system is needed for conservation to survive whilst Onkila identifies four values as the justification for conservation. Maguire and Justus criticise intrinsic value for failing to guide conservation normativity, and Burch-Brown and Archer note that conservation is a product of what human beings value in the environment. We presume that biological value is a reliable guide to conservation normativity because the justification is intuitive. Conservation has limited resources so the decisions require triage (Maclaurin and Sterelny 2008, 178). It cannot preserve everything so it should prioritise the most valuable organisms. The argument is persuasive but I will argue that biological value and conservation normativity come apart in important ways.

Biological value does not reliably track conservation normativity because they are functions on significantly different sets. Biological value is the function of a pluralistic set of conflicting valuations: the instrumental value which the environment provides humans, the non-anthropocentric value of unique species, and the intrinsic value of sentient species. The value of an organism or an ecosystem is a function of the different dimensions of value. Conservation normativity is the function of multiple diverse goals: environmental needs, option value, biological value, biodiversity, triage constraints, and human interests. What conservationists ought to do is a function of conflicting goals and biological value only represents one of those goals. So the oughts’ of conservation and biological value come apart in important ways.

There are examples of biological value which conservation ought not to preserve because there are many different types of biological value. Many species which pose a threat to the health of human beings such as smallpox or house mould are not priorities for conservation. Both bear some form of non-anthropocentric value or instrumental value for people who wish to study them. Imported species which become pests are like-wise a low priority for conservation. Rabbits, weasels, stoats, and gorse add phylogenetic diversity, species richness, and bear non-anthropocentric value. They also increase instrumental value for non-human organisms because they thrive so well in their new ecosystems. The New Zealand ecosystem evolved as a reasonably safe environment for avian species so it contains a wealth of instrumental value for carnivorous land predators. Those land predators have a great deal of their interests met by New Zealand’s ecosystem. In extreme cases conservation cannot remove pest species because humans value them so highly. Cats and dogs are excellent at catching avian species but they are so instrumentally valuable to New Zealanders that conservation ought not to get rid of them. Lastly, the triage constraints of conservation mean that sometimes valuable species are passed over for conservation priority (Durant et al. 2014, 116). These are some of the possible reasons for conservationists not to preserve a valuable species. Biological value comes apart from conservation normativity.
There are also examples of conservation normativity without biological value. These are actions which conservationists ought to undertake that preserve no (or marginal amounts) of biological value. This occurs when we need to protect functioning ecosystems. Individual species of flora and insects are essential to maintaining nutrient cycling in the soil which in turn supports the life of the ecosystem. They aren’t highly valuable because they are often interchangeable. Ecosystems require a certain number of species of flora and insects performing crucial biological functions to support life, they rarely require specific species. This can be seen in recent work on the role of non-native organisms in local biodiversity. Philosophers of biology have begun to argue that the introduction of non-native species often enhances biodiversity (Schlæpfer, Pascal, and Davis 2011; Schlæpfer 2018). The exception is keystone species which are essential to the current state of an ecosystem but these are rare (Takacs 1996, 56). To use the well-worn analogy, conservation is about preventing the popping of rivets along an air plane wing (Ehrlich and Ehrlich 1981). A few rivets are not a problem but many rivets are a problem as we go further and further down a slippery slope. That is precisely the point; one rivet is not valuable but we still ought to protect rivets because we need to protect a functioning wing. Grazers require grass to eat but that doesn’t make a blade of grass valuable because grass is plentiful and interchangeable. However, if you plan to keep grazers then you ought to have grass.

Another important source of conservation normativity without biological value is collective action problems. A collective action problem occurs when the actions of a single agent have no negative outcomes, unless multiple other people are all performing the same action (Nefsky 2011, 364). The standard example from the literature is overgrazing on common fields (Hardin 1968, 1244). The utility increase of a herdsman adding one more sheep to the flock will not exhaust the common grazing area, unless all the other herdsman are reasoning the same way. Collective action problems also apply to: pollution, climate change, collapse of fisheries, and the depletion of ancient aquifers. Conservation requires that we emit less carbon and consume less water but not because small amounts of those resources are valuable. By definition, collective harm problems apply to harmless actions which are only harmful if multiple people are engaged in them (Kagan 2011, 108). One agent cannot consume enough water or fish in their entire lifetime to have a negative environmental impact. The negative environmental impact is a produce of multiple agents performing harmless tasks.

One more example of this will be useful. Imagine that Alice is faced with the decision to clear some trees to build a new house. The trees are young, not endangered and do not house unique species. Alice’s decision to clear some trees to build a house does not lower biological value but we still ought to be careful of clearing trees to build new houses because so many other people reason the same way. In fact work on island biogeography indicates that species richness drops as the islands which contain that richness get smaller and further away from the mainland (Macarthur and Wilson 1967, 22). Alice’s new house is part of multiple new developments which convert green areas to a series of isolated islands. Collectively, urban development’s decrease species richness by fragmenting habitats (Swenson and Franklin 2000, 723). Crucially, the conservational ought is generated by a collective action problem rather than a reduction of biological value.
Individually, no house reduces biological value. Collective action problems are an important example of the way that biological value and conservation normativity come apart because so much of conservation is a collective action problem.

One possible objection to my examples is that I have not taken full advantage of the available framework for biological value. If grazers need grass then it has instrumental value for them. If we ought to conserve water and fish then surely they must be valuable. This objection does not hold. Grass has negligible instrumental value to grazers because it is plentiful and interchangeable; grazers can access it easily and any grass will do. Using an object to some end does construe instrumental value but the amount of value is proportionate the accessibility and interchangeability of the resource. Tissues have little instrumental value to a healthy person, more value to a person with a running nose, and high value to a person with a running nose who is about to run out of tissues. Grass to grazers also bears little instrumental value because it is interchangeable. Goats, for example, will eat just about anything.

Secondly, conservation normativity cannot confer value on pain of circularity. If we preserve things because they are valuable and things are valuable because we preserve them then biological value cannot advise conservation decisions. Likewise we must be careful of ad hoc applications of value to justify conservation normativity. Declaring that Alice should not build her house because other people find existence value in the trees, addresses the thought experiment, but weakens the usefulness of biological value as a goal for conservation. These are examples of biological value coming apart from conservation normativity in important ways. In the next subsection I will outline how this distinction affects the value compass case for biodiversity’s elimination.

8.5.2 The value compass case conflates biological value with conservation normativity
In this subsection I will argue that the value compass case fails to distinguish biological value from conservation normativity. These two are conflated by the value compass case because it presumes that conservation goals ought to track biological value when they ought to track conservation normativity. Consider a version of the argument in which ‘biological value’ is replaced with ‘conservation normativity’.

The Value Compass Case for Biodiversity Eliminativism
1) Conservation ought to preserve [conservation normativity].
2) The goal of conservation ought to reliably track [conservation normativity].
3) Biodiversity is the goal of conservation.
4) Biodiversity does not reliably track [conservation normativity].
5) If the goal of conservation does not reliably track [conservation normativity] then it ought to be eliminated.
6) Therefore: Biodiversity ought to be eliminated as the goal of conservation.

With the exception of premise three, this substitution drastically changes the truth value of the premises. Premise one is now redundant because conservation ought to preserve what it ought to preserve. Premises two and five are now true because conservation goals should
be a prescriptive guide to action. Importantly, premise four is now false. In section 8.3 I argued that there are very good reasons why biodiversity cannot be a reliable value compass, however, biodiversity is an excellent guide to conservation normativity.

The value compass case is significantly weaker when it is focused on conservation normativity because premise four is now false. Biodiversity is an excellent guide to conservation normativity. What conservationists ought to do is a function on a complex and often conflicting set of goals. Environmental needs conflict with human interests. One of the causes of harmful algal blooms is overfishing (Jackson et al. 2001, 631). The ocean needs to be fished less but the billions of human beings also need a food. Option value theory argues that we should preserve as much diversity as possible as hedge bet against future interests but that conflicts with the interests of current human populations. Biological value identifies the most valuable organisms or ecosystems but it also comes apart from the goals of conservation in important ways. Conservation normativity is therefore a complicated function which needs a reliable guide.

Biodiversity is an excellent guide to conservation normativity because it strikes a middle ground between acts which benefit the environment and those which satisfy the desires of human beings. This makes biodiversity an excellent tool for conservation because whilst human beings benefit enormously from sustainable flourishing ecosystems, it can be difficult to explain why a human interest such as urban development is not as important as preventing steady habitat fragmentation. Biodiversity explains why we need to preserve the small biological elements of an ecosystem; it maintains high species richness and maximises diversity. It explains why human beings take such an interest in unique species such as the red kangaroo (Macropus rufus) or the velvet worm genus Peripatus; they are phylogenetically unique. It explains why organisms are better off in full ecosystems than in controlled enclosures; it increases functional diversity. It permits human beings to manipulate the environment; all species affect their environment but because we are such a successful species, we need to be careful about permanently damaging the environment. Biodiversity helps to preserve biological value and option value because it tracks losses of both. Biodiversity can advise triage decisions by prioritising species richness or phylogenetic uniqueness depending on whether the ecosystem is a biodiversity hot spot or has a phylogenetic diversity score disproportionately large to its species richness. It can also explain why we ought to care about more than the charismatic megafauna; preserving the megafauna requires preserving the biodiversity around it. Biodiversity is a successful conservation goal because it can balance so many other goals of conservation. For this reason, biodiversity is a reliable tracker of conservation normativity and the reinterpreted value compass case for its elimination is very weak.

In this subsection I argued that the value compass case for biodiversity’s elimination conflates biological value with conservation normativity. I outlined intuitions about correlations between the value of organisms and what conservation ought to conserve. Then I argued that biological value does not correlate highly with conservation normativity. I demonstrated that substituting ‘conservation normativity’ for ‘biological value’ in the value compass case for elimination significantly weakened the argument. Biodiversity is not a reliable compass for pluralistic value because no conservation goal is,
but it is an excellent guide to conservation normativity. In the next subsection I will argue that the conflation of value and normativity in the value compass case is also present in the conceptual and empirical cases for biodiversity’s elimination.

8.5.3 The conflation of value and normativity also drives the conceptual case and the empirical case for eliminativism

In this subsection I will argue that the conflation between biological value and conservation normativity which is present in the value compass case for elimination is also present in the conceptual and empirical cases. In the conceptual case, I argue that concerns about value which are used against specific dimensions of biodiversity and precision in the surrogacy chain are actually concerns about conservation normativity. In the empirical case, I argue that premise five of the empirical poor fit argument which attacks within-surrogate operationalisability is actually a concern about conservation normativity. Understanding these arguments as concerns about conservation normativity further weakens the conceptual and empirical case for biodiversity’s elimination.

In the conceptual case for biodiversity eliminativism Santana disqualifies several candidates for a meaning of ‘biodiversity’ based on value focused counterexamples.

“Nor does preserving richness reliably preserve biological value. Because richness is nothing more than a count of the number of species in an area, value on the richness scale increases with speciation and decreases with extinction but this misrepresents common values.” (Santana 2014, 769)

“But the relative abundance of species also fails to represent biological value well.” (Santana 2014, 770)

“Diversity, on this account, is important because it enables evolution, making genetic diversity a key component of biodiversity. This approach is present in many writings on biodiversity (e.g. Frankel and Soule 1981), but it requires the questionable assumption that evolution is in itself valuable.” (Santana 2014, 771)

“Nor does ecological diversity function as a reliable means to assess the biological value of an area.” (Santana 2014, 772)

“One final option considers the diversity of biological processes and services such as biogeochemical cycles. Biological processes are indubitably often valuable, but I fail to see how they can be directly incorporated into a concept of biological diversity.” (Santana 2014, 772)

Santana presents these as counterexamples. He argues that species richness can be high whilst biological value is low, that abundance tells us little about value, and that diversity can only track value if evolution is inherently valuable. He also argues that ecological diversity does not correlate with biological value, and that functional diversity is not operationalisable. But these counterexamples conflate biological value with conservation normativity. They look like criticisms of the relationship between biodiversity and biological value because Santana is arguing that even if it increases biodiversity, smallpox is not a valuable organism. However, these examples are actually criticisms of the
relationship between biodiversity and conservation normativity because they falsely suggest that preserving biodiversity would prescribe conserving smallpox.

Biodiversity cannot guide conservationists to preserve smallpox because the marginal increase in species richness, feature diversity, and functionality could never outweigh the impact on the other goals of conservation. Preserving smallpox restricts our option value because an important option for future generations is to live in a world without smallpox. In the same vein it decreases instrumental value because human beings hold the world in higher value when there are as few human threatening diseases as possible. One more species with some unique adaptations is not a justifiable reason for preservation when it poses such a risk to the flourishing of human beings. Understood as a critique of conservation normativity rather the biological value the extinction of smallpox is an unconvincing example because high biodiversity cannot justify its preservation.

Also in the conceptual case, Santana argued that including biodiversity in the surrogacy chain makes the conservation process more prone to error. A key assumption in this argument was that the role of a conservation goal was to track biological value. However, I have argued in this section that conservation normativity does not always correlate highly with biological value. Replacing biological value with conservation normativity gives the following surrogacy chain.

Estimator Surrogate → True Surrogate → Biodiversity → Conservation Normativity

This replacement weakens Santana’s argument because, as I argued in section 8.3, no conservation goal is a reliable guide to biological value and I argued in section 8.5 that biodiversity is an excellent guide to conservation normativity. Biodiversity is not a reliable guide to pluralistic biological value but it is very good at striking a balance between the needs of the environment and the desires of human beings. On this interpretation, including it in the surrogacy chain increases precision along the chain.

In the empirical case for biodiversity’s elimination, Santana criticised the operationalisability of the specific dimensions of biodiversity because they failed to accurately predict biological value. Premise five of the empirical poor fit argument states that “individual dimensions of biodiversity are either: not operationalisable, do not accurately track biodiversity, or do not accurately track biological value”. Understanding these as critiques of conservation normativity instead of biological value weakens the empirical poor fit argument further. Some specific dimensions of biodiversity do struggle as reliable value compasses because biodiversity is not always commensurable with pluralistic biological value. However, specific dimensions of biodiversity are useful guides to conservation normativity. It is just a matter of prioritising the right set of dimensions to the right context. New Zealand requires more attention to phylogenetic diversity than species richness because many of our species evolved without land predators. Biodiversity hot spots require a focus on species richness because 34 biodiversity hotspots in the world shelter at least 50% of vascular plant species and 42% of terrestrial vertebrates (Burch-Brown and Archer 2017, 992). The reason why a multidimensional tool like biodiversity is so useful for complicated situations is that the performance of its dimensions is context dependant.
In this subsection I argued that the conceptual and empirical case for elimination make the same conflation as the value compass case. At several stages, *biodiversity* eliminativists criticise biodiversity or its specific dimensions because it is not a reliable value compass. These arguments are discussed in terms of the relationship between biodiversity and biological value but they are actually critiques of the relationship between biodiversity and conservative normativity. The precision of the surrogate chain and the within-surrogate operationalisability of biodiversity’s dimensions are concerns about the ability of biodiversity to prescribe the actions of conservationists and not its ability to track biological value. This error further weakens both the conceptual and the empirical case because biodiversity tracks conservation normativity better than it tracks pluralistic biological value.

### 8.6 Conclusion

In this chapter I argued that the value compass case for *biodiversity* eliminativism is unsuccessful. In section 8.2 I reintroduced the value compass case for eliminating *biodiversity* with an edit based on the material from chapter seven. In that chapter I argued that the kind of biological value which they appeal to in their examples is a pluralistic system. The value compass case rests upon two major claims: that biodiversity is not a reliable value compass and that the conservation goals should be evaluated by how well they track pluralistic biological value. I challenged both of these claims. I accepted the truth of premises four and three. Biodiversity is the current goal of conservation and it is not reliable compass for pluralistic biological value. In section 8.3 I argued that premises one and two were false. Premise one assumed that conservation ought to preserve pluralistic biological value and to serve this purpose premise two stated that the goal of conservation ought to reliably track that value. I argued that these premises were false because there are a number of issues with setting the tracking of pluralistic biological value as the minimum standard for a conservation goal. I argued that it was too punishing a standard, that eliminativists have not explained why it should be the standard, and that the standard was so punishing that it was self-eliminating. Against premise five, I argued that a conservation goal which is not a reliable value compass could still be retained for other reasons. Assuming that it does not reliably track biological value, biodiversity is still the best available conservation goal and it is important because it tracks losses of biological value.

In section 8.6 I sought to identify an error in the value compass case to explain its persuasiveness. I argued that eliminativists treat biological value as a compass for conservation normativity; the valuable elements of biology are the ones which conservation ought to preserve. I argued that this was a mistake because conservation’s oughts’ are generated for diverse reasons. It is the case that given the resource constraints of conservation we ought to preserve the valuable biological elements but some should be preserved for different reasons even if they are not valuable. I then argued that this mistake occurs throughout the arguments for *biodiversity*’s elimination. The motivating examples and the reasoning in the conceptual, empirical, and value compass case for *biodiversity*’s elimination misunderstand the relationship between biodiversity and biological value. The
value compass case for biodiversity’s elimination is unsuccessful for this reason and because premises one, two, and five are false. Likewise, in chapter three I argued that the conceptual case for biodiversity’s elimination is unsuccessful and in chapter six I argued that the empirical case for biodiversity’s elimination is unsuccessful. Biodiversity is a good conceptual, empirical, and value tracking fit for its role in conservation biology.
9 Conclusion

9.1 Project Conclusions

Biodiversity is a good fit for its role in conservation biology. As a goal for conservation, the biodiversity concept has adapted over time to incorporate multiple distinct dimensions of biology. Eliminativists argue that the concept is now too bloated to be a useful goal for conservation. In this project I have collected the arguments of Santana, Angermeier, and Karr and categorised them as either a conceptual, empirical, or value compass case for biodiversity's elimination. I have argued that biodiversity survives the arguments for its elimination. It is a complicated multi-dimensional concept but like health and poverty, it is an important one which requires monitoring. It is difficult to operationalise, but using the surrogacy strategy and transforming data sets for cross comparison informs the decisions of conservation. It has a complicated relationship with biological value but it is an excellent guide to conservation normativity.

In the conceptual case for elimination Angermeier and Karr argued that biodiversity misleads conservation. Santana argued that ‘biodiversity’ has no clear meaning and unnecessarily complicates the surrogacy strategy. In response, I developed an homeostatic property cluster which avoided eliminativists’ criticisms. It allows for a general meaning of ‘biodiversity’ which is also informative and its multi-dimensional nature reduces misdirection in conservation. In the empirical case for elimination Santana argued that biodiversity is not operationalisable. In response, I defended the surrogacy strategy against the problems of incommensurability and multiple surrogates. I argued that the empirical case misrepresents the state of biodiversity measurement. I then outlined the methodological detail of five true surrogates for biodiversity. I used that detail to argue that the expanding multiplicity of biodiversity measures is overblown and that the empirical case for elimination is unsuccessful. By Santana’s own standards, the specific dimensions of biodiversity are not a suitable empirical replacement for biodiversity.

In the value compass case for elimination Santana, Angermeier, and Karr argued that biodiversity is a poor guide to conservation because it is a poor guide to biological value. In response I first discussed what type of biological value eliminativists are appealing to. In chapter seven I argued that eliminativists are appealing to a pluralistic system of biological value. This system includes disparate theories of biological value such as instrumental, intrinsic, and a range of non-anthropocentric views. I formally applied this standard to the value compass case for biodiversity’s elimination and in chapter eight I argued that it was unsuccessful for three reasons.

Firstly, there are problems with using pluralistic value as a minimum standard for a conservation goal. It is too punishing, eliminativists have not explained why biodiversity ought to track it, and it is a self-eliminating goal. Secondly, there are good reasons to retain biodiversity as a conservation goal even if it is not a reliable value compass. It is a better conservation goal than its competitors and biodiversity is still necessary for biological value. Thirdly, the value compass case for elimination conflates biological value with conservation normativity. These two concepts are distinct from one another but because eliminativists use biological value as a proxy for conservation normativity, they
overlook how successful biodiversity is as a direct guide to what we ought to preserve. This error is also present in the conceptual and empirical arguments of eliminativists. Since biodiversity survives all three cases for its elimination, we have excellent reasons to retain it as the goal of conservation.

9.2 Open Questions
In this section I will briefly discuss open directions for research suggested by this project. I will focus on three outstanding issues: the role of abundance in species diversity, operationalising functional diversity, and the relationship between biological value and conservation normativity.

9.2.1 Abundance and Diversity
Abundance has a complicated relationship with biodiversity. In chapters two and three I discussed the motivations for incorporating it as a dimension of biodiversity. Systems are more diverse when the groups within them have even representation. A board of directors is more diverse when it has equal representation of gender and race. An ecosystem is more biodiverse when the organisms within it are evenly represented (Maurer and McGill 2011, 56). In chapter five I discussed the problems with operationalising species diversity. Diversity is the combination of richness and evenness. Even representation of groups is captured by diversity measures but it is not the kind of abundance which is good for an ecosystem (Santana 2014, 770). Ecosystems require more food sources than organisms which consume them and dominant species are only a problem once their abundance has significant impact on the ecosystem.

One direction for research would be to make abundance a dimension of ecosystem health instead of a dimension of biodiversity. Biodiversity can focus on metrics of richness for species and phylogenetic diversity. Ecosystem health can focus on abundance counts for endangered species and to monitor sudden population drops. This shift would not impact the motivating reason for the preference of calculations of species diversity over species richness. At times, species richness can seem like a misleading measure because species may be close to extinction without affecting counts of species richness (Santana 2014, 769). This is a good objection but it is best understood as a concern about accuracy over time. Species richness is still informative because a species with a population of one is typically due for extinction. Species richness will drop but it will only do it once the species is extinct rather than doomed to extinction. In this sense, measures of richness are not misleading so much as lagging behind the state of an ecosystem. Moving abundance to health addresses this because abundance helps to detect how well an ecosystem is performing and whether it is in a steady decline. It also separates abundance from richness in an important way because it focuses on individual species and tasks us with considering what kind of evenness is beneficial for an ecosystem. The answer isn’t equal representation for all species but it is an interesting question.
9.2.2 A Future for Functional Diversity

Calculations of functional diversity are currently problematic for two reasons: they aren’t functional enough and they fall foul of the trait dilemma. The values don’t capture the high-level functional phenomena which are used to motivate the importance of functional diversity. The tiger moth can jam bat sonar (Corcoran, Barber, and Connor 2009, 327). However, including it an ecosystem will not raise the functional diversity value any more than a similar moth without sonar jamming functionality. This is because ‘functional trait’ is defined so generally that it is almost synonymous with phenotypic trait. Calculations of functional diversity cannot weight high-level functional phenomena because their conception of functional trait is too general. They also struggle to approximate the functional diversity of an ecosystem because of the trait dilemma. Shared functional traits are uninformative but informative functional traits are not widely shared.

A direction for research on functional diversity would be to re-evaluate how we approach the issue of measuring functional diversity. Interaction is an extrinsic property between multiple organisms but we have been calculating it in terms of the intrinsic properties of individual organisms. Intrinsic properties have been used as a proxy for functional diversity because all properties are also causes of effects. Height can be understood as a functional trait because it impacts the fitness of an organism. Because the fitness of an organism impacts the flourishing of other organism’s height is functional in the sense that, besides being an intrinsic property, it is a part of causal relation with other organisms. But, we could shift the focus towards conversions between intrinsic properties. Conversions are a common property of functions. In logic a function converts one value to another value. In philosophy of mind, functionalists argue that our mental states are the causal relationships between input, output, and other mental states (Mandik 2014, 109). Functional diversity could be analysed in terms of biological conversions. Research could focus on the level of nutrient cycling, the conversion rates of gases, daily consumption of prey, annual leaf fall, measures of species density. Matrices could be developed for common interactions such as the above. Organisms with high-level functional interactions such as the tiger moth could be prioritised as key stone functional organisms. Functional diversity is a fascinating dimension of biodiversity and it deserves our attention.

9.2.3 The Relationship between Biological Value and Biodiversity

The relationship between biodiversity and biological value is still unclear. Eliminativists use a number of examples in which biodiversity functions as a poor guide to biological value. I have argued in chapter eight that biodiversity should be understood as a guide to conservation normativity rather than to biological value. As a guide to pluralistic biological value, biodiversity is ineffective. This is however, a feature of the complexity of pluralistic biological value rather than a serious shortcoming of biodiversity. My arguments from chapter eight are not intended to suggest that biodiversity has no relationship with biological value. Rather, the relationship is unclear because there is little consensus about the nature of biological value and evidence is difficult to come across which does not rely heavily on personal intuition. This leaves open the question of what the relationship is between biodiversity and biological value and more importantly, how preserving biodiversity might preserve biological value.
One approach to this problem would be to focus on the relationship between biodiversity and specific theories of biological value. One issue with the value compass case for biodiversity’s elimination is that the eliminativists cast a very wide net over value theories. Because they appealed to multiple types of theory, it was implausible to expect a conservation goal to track them all. This does not imply that biodiversity cannot reliably track certain kinds of value such as instrumental value. Instrumental value is the value of means to an end so we can infer that organisms derive instrumental value from the biological elements which they rely on (Rolston 1992, 253). Then biodiversity would reliably track instrumental value because it requires interactions and a more diverse ecosystem has more interactions. There is already important work on the link between biodiversity and specific theories of biological value. Maclaurin and Sterelny argue that biodiversity protects our option value theory which is the value of having as many options with the environment as possible in the future (Maclaurin and Sterelny 2008, 154). More recently, Faith has continued to argue that there is a strong link between biodiversity and the availability of ecosystem services (Faith et al. 2017, 717). These are important results because more work is required on the subject of how well we can preserve biological value by preserving biodiversity.

9.3 Final Remarks
Criticism is essential to the empirical reputation of science. It makes theories stronger and explains when a theory should be eliminated. Biodiversity eliminativists have presented serious conceptual, empirical, and value tracking criticisms but biodiversity has weathered them. It is true that biodiversity has adapted multiple times to new empirical observations. It is also true that biodiversity has become a complex multi-dimensional concept with a variety of measurement strategies and a complicated relationship with biological value. But it is that inherent conceptual complexity and empirical flexibility which makes it such a successful guide to conservation normativity. Biodiversity is an excellent fit for its role because of the subject matter of the biological sciences. Biology is a science of continuous properties and vague boundaries. It is successful because it embraces complexity. We should expect a successful conservation goal to be just as complex.
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