Three Dimensional
Reconstruction of Human Lumbar
Spine from Bi-planar Radiographs

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a thesis submitted for the degree of
Doctor of Philosophy
at the University of Otago, Dunedin,
New Zealand.

31st, January 2017
And say: My Lord! Increase me in knowledge
Holy Quran Chapter 20 (Ta-Ha), verse 114.
I dedicate this thesis to my loving family: my mum Majida, my dad Abderazzak, my older brother Abdeslam, my older sister Salma, my younger brother Othmane, my nephew Adam and my niece Mia. My late Grandma.
Acknowledgements

All praise is due to Allah, the most gracious, the most merciful. I acknowledge my Creator Allah, all mighty God to put this destiny in my life with all the hardship and its outcome.

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Abstract

Three Dimensional Reconstruction of Human Lumbar Spine from Bi-planar Radiographs

This thesis investigates an accurate method for three dimensional (3D) reconstruction of the human spine from bi-planar radiographs with comparable results to CT scans or MRI. In this work, we generated a publicly available dataset which corresponds to the training data used. We subsequently solved the problem of correspondences using a landmark-free algorithm applied on the vertebrae. Finally, we developed a semi automatic method based on simulated radiographs for the reconstruction of the human lumbar spine in 3D from bi-planar radiographs. We validated the results in vitro on radiographs of dried vertebrae with models constructed from a laser-scanner, then in vivo on radiographs of living patients with models extracted from CT scans or MRI. The results show the feasibility of generating personalised models of patients from bi-planar radiographs.

The contributions of this thesis are:

- Evaluation of the methods for creating 3D models of vertebrae and estimation of the errors in comparison with ground truth data. These methods are applicable to other free-form shapes;
- Creation of landmark free ASMs of lumbar vertebrae;
- Definition and evaluation of a process for estimating the shape and position of lumbar spine from uncalibrated bi-planar radiographs.
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<td>A/P</td>
<td>Antero-Posterior</td>
</tr>
<tr>
<td>ASM</td>
<td>Active Shape Models</td>
</tr>
<tr>
<td>ANZACA</td>
<td>Australian &amp; New-Zealand Association of Clinical Anatomists</td>
</tr>
<tr>
<td>CT</td>
<td>Computerised Tomography</td>
</tr>
<tr>
<td>CMM</td>
<td>Coordinate Measuring Machine</td>
</tr>
<tr>
<td>DLT</td>
<td>Direct Linear Transformation</td>
</tr>
<tr>
<td>DXA</td>
<td>Dual-energy X-ray Absorptiometry</td>
</tr>
<tr>
<td>DWC</td>
<td>Dodd-Walls Centre For Photonic And Quantum Technologies</td>
</tr>
<tr>
<td>GPA</td>
<td>Generalised Procrustes Analysis</td>
</tr>
<tr>
<td>JC</td>
<td>Jon Cornwall</td>
</tr>
<tr>
<td>ICP</td>
<td>Iterative Closest Point</td>
</tr>
<tr>
<td>Lat</td>
<td>Latero-lateral</td>
</tr>
<tr>
<td>Lk</td>
<td>Lumbar Vertebra of level $k$. $k$ is from one to five inclusive</td>
</tr>
<tr>
<td>MRI</td>
<td>Magnetic Resonance Imaging</td>
</tr>
<tr>
<td>mm</td>
<td>Millimetre</td>
</tr>
<tr>
<td>µm</td>
<td>Micrometre</td>
</tr>
<tr>
<td>NHANES</td>
<td>National Health and Nutrition Evaluation Survey</td>
</tr>
<tr>
<td>NIH</td>
<td>National Institute of Health</td>
</tr>
<tr>
<td>NLM</td>
<td>National Library of Medicine</td>
</tr>
<tr>
<td>NSCP</td>
<td>Non Stereo Corresponding Points</td>
</tr>
<tr>
<td>PDM</td>
<td>Point Distribution Model</td>
</tr>
<tr>
<td>PET</td>
<td>Positron Emission Tomography</td>
</tr>
<tr>
<td>P/A</td>
<td>Postero-Anterior</td>
</tr>
<tr>
<td>PCA</td>
<td>Principal Components Analysis</td>
</tr>
<tr>
<td>RGB</td>
<td>Red Green Blue</td>
</tr>
<tr>
<td>SCP</td>
<td>Stereo Corresponding Points</td>
</tr>
<tr>
<td>SSM(s)</td>
<td>Statistical Shape model(s)</td>
</tr>
<tr>
<td>SSE</td>
<td>Sum of Squared of Errors</td>
</tr>
<tr>
<td>3D</td>
<td>Three Dimensional</td>
</tr>
<tr>
<td>2D</td>
<td>Two Dimensional</td>
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## Mathematical Notation

For quick reference, notations are defined here in alphabetical order. Otherwise, they are clearly defined when first introduced throughout the thesis.

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<thead>
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<td></td>
<td>Absolute value</td>
</tr>
<tr>
<td>arccos</td>
<td>Arccosine: angle between two vectors</td>
</tr>
<tr>
<td>$\bar{c}$</td>
<td>Centre of mass</td>
</tr>
<tr>
<td>$\circ$</td>
<td>Composition of transformations</td>
</tr>
<tr>
<td>$</td>
<td>$</td>
</tr>
<tr>
<td>$w_{ij}$</td>
<td>Conformal symmetric normalised weight of edge $(i, j)$</td>
</tr>
<tr>
<td>$C$</td>
<td>Covariance matrix of set of shapes</td>
</tr>
<tr>
<td>$\cot(\alpha)$</td>
<td>Cotangent of an angle $\alpha$</td>
</tr>
<tr>
<td>$\wedge$</td>
<td>Cross product of two vectors</td>
</tr>
<tr>
<td>$\cdot$</td>
<td>Dot product of two vectors</td>
</tr>
<tr>
<td>$||_F$</td>
<td>Frobenius norm</td>
</tr>
<tr>
<td>$\nabla$</td>
<td>Gradient</td>
</tr>
<tr>
<td>$H$</td>
<td>Hessian matrix of full quadratic patch</td>
</tr>
<tr>
<td>$S_j$</td>
<td>The $j^{th}$ shape in training data</td>
</tr>
<tr>
<td>$\mu$</td>
<td>Linear absorption coefficient</td>
</tr>
<tr>
<td>$||$</td>
<td>$l^2$-norm of a vector</td>
</tr>
<tr>
<td>$\bar{S}$</td>
<td>Mean shape of a set of shapes</td>
</tr>
<tr>
<td>$\Phi$</td>
<td>Normal basis of principal modes of variation</td>
</tr>
<tr>
<td>$</td>
<td>C</td>
</tr>
<tr>
<td>$P(A)$</td>
<td>Probability of event $A$ occurring</td>
</tr>
<tr>
<td>$P(A</td>
<td>B)$</td>
</tr>
<tr>
<td>$T$</td>
<td>Rigid transformation of a shape in 3D</td>
</tr>
<tr>
<td>$R_x$</td>
<td>Rotation around $x$ axis</td>
</tr>
<tr>
<td>$s_{cj}$</td>
<td>Scale of sample $Y_j$ after translation</td>
</tr>
<tr>
<td>$E_d$</td>
<td>Set of indices of neighbouring vertices</td>
</tr>
<tr>
<td>$(\phi, \delta)$</td>
<td>Spherical coordinates</td>
</tr>
<tr>
<td>$\sigma$</td>
<td>Standard Deviation</td>
</tr>
<tr>
<td>$t_x, t_y, t_z$</td>
<td>Translations along $x, y$ and $z$ axis respectively</td>
</tr>
<tr>
<td>$M^T$</td>
<td>Transpose of matrix $M$</td>
</tr>
<tr>
<td>$1_{n \times m}$</td>
<td>Unit matrix $\in \mathbb{R}^{n \times m}$ (ones everywhere)</td>
</tr>
<tr>
<td>$S^2$</td>
<td>Unit sphere in 3D space</td>
</tr>
<tr>
<td>Symbol</td>
<td>Description</td>
</tr>
<tr>
<td>--------</td>
<td>-------------</td>
</tr>
<tr>
<td>$b$</td>
<td>Weights associated to $\Phi$</td>
</tr>
<tr>
<td>$0_{n \times m}$</td>
<td>Zero matrix $\in \mathbb{R}^{n \times m}$ (zeros everywhere)</td>
</tr>
<tr>
<td>$\mathbb{R}^3$</td>
<td>3D real coordinate space</td>
</tr>
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<td>7.17</td>
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<td>7.18</td>
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<td>7.21</td>
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<td>7.22</td>
<td>Distribution of errors and heat map associated with the vertebra with second maximum Hausdorff distance.</td>
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<td>7.23</td>
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Figure 1: Figure showing an overview of the methods used in this thesis. The problem is the 3D reconstruction of lumbar spine from two radiographs (one lateral and one postero-anterior view). Firstly, we created a dataset of 3D models of vertebrae using a set of images/photographs of dried vertebrae. This dataset has been validated using arm scanner models and direct measurements on dried vertebrae using callipers. Then, we generated a statistical shape model of each group of lumbar vertebrae from the data set (group of L1, group of L2 etc), using the spherical demons algorithm which is based on spherical parameterisation. Finally, we fitted the statistical shape model on in vitro radiographs of dried vertebrae as isolated vertebrae with no soft tissues. The reconstruction has been validated against models of arm scanning and reconstruction from markers attached to dried vertebrae. We also fitted the statistical shape model to in vivo radiographs of patients with different abnormalities. The reconstruction has been validated against ground truth data. The reconstruction requires a rough manual initial alignment of the model with radiograph and delimitation of each vertebra by a bounding box defined by two opposite corners. To generate the statistical shape models, the models were roughly aligned manually to each other.
Chapter 1

Introduction

1.1 Thesis Problem Statement and Motivation

Clinicians often rely on accurate medical imaging as a diagnostic and treatment tool (Perdriolle and Vidal, 1987). This can be especially useful in instances where 3D analysis is required, such as for determining the nature or severity of spinal scoliosis (an abnormal lateral curvature of the spine), or clarifying whether bone or implant alignment is acceptable post-surgery. Two methods are currently available that allow accurate imaging of anatomical structures such as bone in three dimensions - Computed Tomography (CT) scans (see Figure 1.1) and Magnetic Resonance Imaging (MRI) (see Figure 1.2). However, these methods do have some limitations. CT scans cannot be acquired instantaneously and are high in potentially dangerous radiation (Levy et al., 1996), while MRI generally cannot be used when patients have received metal implants, although there are types of implants where applying MRI is possible. Additionally, it is quite scary, especially for young patients, as it is a long tube as shown in Figure 1.2, where the patient lies on their back. There is also a loud, almost unbearable banging noise as the scan is being done.
Figure 1.1: Image showing a CT Machine. The scan consists of a high number of radiographs taken in different direction and slices with different depth are reconstructed.

Figure 1.2: Image showing a MRI Machine. The image shows the tube and the bed which slides inside with the patient.
Consequently, post-implantation analysis is often undertaken using radiographs (see Figures 1.3 and 1.4) to determine the accuracy of implant placement, however this only allows clinicians two dimensional (2D) views of both bone and implant on which to base their clinical decisions. For diagnosis and treatment of scoliosis in children, orthopaedists need to track the development of the spine over many years. It is common practice for orthopedists to take bi-planar radiographs, almost always orthogonally - one Postero-Anterior (P/A) or Antero-Posterior (A/P) and one Latero-Lateral (Lat) - every six months to visualise the development of the spine without three dimensional (3D) information (Hodgson, 2010; Petit et al., 1998). The information from these two radiographs helps with the diagnosis of spine problems and orthopaedic afflictions such as scoliosis. Due to the limitations of CT scans and MRI mentioned previously, the ability to build an accurate 3D visualisation of the spine from uncalibrated bi-planar radiographs would be beneficial for both the orthopaedists and the patients.

Figure 1.3: Examples of Lat and P/A radiographs of an individual with scoliosis.

Figure 1.4: Examples of Lat and P/A radiographs of an individual with Implants. In this case it is not possible to perform an MRI scan.
There is therefore a need for accurate 3D models that can be generated quickly post-implantation to guide clinicians and assess implantation accuracy. The generation of a 3D model of bony structures from plane radiographs offers such a solution as images can be acquired quickly, with minimal radiation exposure to the patient, and potentially while the patient is still under anaesthesia. This would allow for timely, accurate analysis of any implantation or corrective intervention of bony deformity and the possibility for correction prior to patient removal from surgery. From an orthopaedist’s perspective, they would have a better diagnostic tool in general terms for spinal curves and also localised information for each vertebra. For the patients, the system would also be viable, as it would be less harmful in terms of exposure to x-rays, as well as more time and cost effective. Benefits from such technology are likely to include more accurate surgery, less corrective surgery, and as a result improvement of downstream economic and rehabilitation efficiencies.

Figure 1.5: Anatomy of the human spine. It contains 24 vertebrae divided into three main groups: Cervical, Thoracic and Lumbar.
A healthy spine is vital to our good health as it is central to sitting and lying comfortably, as well as our ability to move freely. It contains the spinal canal for the nerves which control other parts of the body. This is why its study and diagnosis is important and has been the subject of various studies for decades. The spine contains 24 vertebrae as shown in Figure 1.5. Figure 1.6 shows examples of individual vertebrae of the human spine viewed at different angles.

![Figure 1.6: Examples of individual vertebra viewed at different angles. A) showing a frontal view, B) a lateral view, C) the back view and D) an oblique view.](image)

The research in this work has focused on the lower spine which contains the lumbar vertebrae. Meeting the need for 3D reconstruction of human lumbar vertebrae from bi-planar radiographs to visualise and enable better diagnosis by orthopaedists is the motivation for this work. The final result to be achieved is a 3D visualisation of the lumbar spine as shown in Figure 1.7, also we are interested in the superimposition of the projection of the 3D model on the radiographs as shown in Figure 1.8.
Figure 1.7: Lat and P/A views of expected 3D output reconstruction from bi-planar radiographs. The colours here do not have a specific meaning except to highlight the 3D shape.

Figure 1.8: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs of a patient.
1.2 Benefits and Contributions

The benefit within the medical field for the patient is less exposure to radiation compared to CT scans, and as an alternative technique when MRI scans are not feasible because the patient has an implant as shown in Figure 1.4; it is also cheaper and less time consuming for the patient. The contributions of this thesis are:

- Evaluation of the methods for creating 3D models of vertebrae and estimation of the errors in comparison with ground truth data. These methods are applicable to other free-form shapes;
- Creation of landmark free Active Shape Models (ASMs) of lumbar vertebrae;
- Definition and evaluation of a process for estimating the shape and position of lumbar spine from uncalibrated bi-planar radiographs.

This project was suggested by a real need from the medical community (Hodgson, 2010).

1.3 Approach Justifications

3D reconstruction is a tedious process because it can be time consuming and/or costly. There are three different basic 3D modelling methods: range based process (such as laser scanners), image based algorithms and volumetric scanning.

The spine of living patients is not an easy object for 3D visualisation. This is because in the first instance it is \textit{in vivo}, there are soft tissues and fluid around the spine, the bone grows differently depending on where different forces of the body are applied to it and varies from patient to patient according to their different activities.

The problem of 3D reconstruction from bi-planar radiographs is an ill-posed problem as it accepts many solutions in 3D space. There is not enough information to do the reconstruction unless prior knowledge of the models is introduced. ASMs are a common method for encapsulating this prior knowledge and are used in this work.

There have been various solutions developed for the problem of 3D reconstruction from bi-planar radiographs with different accuracies, many of them use ASMs of vertebrae (more details are given in Chapter 2). The ASM algorithm captures different nonrigid shape variations and can be used to generate new shapes - usually by assuming the population varies according to a Gaussian distribution. ASMs are a landmark-based method. As far as we know no ASMs of the spine/vertebrae have been built without
the introduction of manually identified anatomical landmarks. The motivation of this work is to create an ASM of vertebrae that is landmark-free because it is challenging to accurately obtain these correspondences over a sample of shape models (Dalal et al., 2007) especially in 3D, and to generate them with precision.

The 3D ASM is based on 3D models, requiring 3D landmarks of the objects in study. Obtaining 3D models of the objects is a tedious process, and this is equally true for landmarking of the objects; it can be a long process, especially finding correspondences between objects with different sizes and rotations in space.

During this research, we built landmark-free ASMs of lumbar vertebrae and demonstrated their accuracy by application on bi-planar radiographs.

We assume that no patient-specific 3D models are available as this results in the most flexible system. Due to time constraints, this thesis will limit its focus to the lumbar spine, but the process is easily generalisable.

1.4 List of Publications

We presented a poster at Australian & New-Zealand Association of Clinical Anatomists (ANZACA) conference (2012) (see Appendix A). The poster summarises the Chapter 3 for building 2D ASM of L3 vertebra. We also published a paper (Bennani et al., 2016) in Data Science Journal. This publication is essentially Chapter 4 of this thesis. A 3D data set of lumbar vertebrae has also been published. This publication is a pillar for this research as it constitutes the training data used to train the Statistical Shape Models (SSMs) in Chapter 5. Consequently, it is the foundation for the ASMs used to reconstruct lumbar spine from bi-planar radiographs in 3D. Finally, we presented a poster at The Dodd-Walls Centre for Photonic and Quantum Technologies (DWC) symposium (2016) (see Appendix B). The poster summarises the work done in Chapter 6 for validating the method of 3D reconstruction from bi-planar reconstruction of dried vertebrae. The poster was awarded the second best poster at the conference.
1.5 Plan of the Thesis

The rest of this thesis is structured as follows. Chapter 2 describes medical imaging techniques, the anatomy of spine and a general literature review on 3D reconstruction from bi-planar radiographs. Chapter 3 presents an overview of ASMs and a 2D application to illustrate how they work. Chapter 4 describes the method used to create 3D models of individual vertebrae and the data set used. In Chapter 5, landmark free registration of 3D models is discussed. Chapter 6 is an application of these models to the medical field, by reconstructing 3D models of dried lumbar vertebrae from \textit{in vitro} radiographs; this chapter also addresses validation of the 3D reconstruction. Chapter 7 is another application of these models to the medical field, by 3D reconstruction of lumbar vertebrae on patients’ \textit{in vivo} radiographs and this chapter addresses validation of the 3D reconstruction of vertebrae by comparing it to a CT scan or MRI of the same individuals.

Finally, Chapter 8 discusses the materials and methods used, summarises the results, and suggests possible improvements and future work on the same topic.

A glossary has been added at the end of this thesis to provide definition for some terms that may not be clear to a general reader.
Chapter 2

Literature Review

2.1 Overview

This thesis is motivated by the need of the medical community for 3D reconstruction of the human spine from bi-planar radiographs for the analysis of pathological deformations. The information gathered will be useful either locally per vertebra or globally for the whole or partial reconstruction of the spine. In this Chapter, we present some background on medical imaging and the spine followed by a literature review on 3D reconstruction from bi-planar radiographs.

2.2 Medical Imaging

Medical imaging covers a set of techniques which help to visualise the internal structures of the human body to assist medical scientists. All the techniques are based on a common principle which is the measurement of tissue in response to an exposure to a physical phenomenon - a radiation source in the case of radiographs. The most common medical imaging techniques (Cho, 1993; Moore et al., 2013) are:

- Conventional radiography (plain films);
- Computerized Tomography (CT);
- Ultrasonography (sonography);
- Magnetic Resonance Imaging (MRI);
- Nuclear medicine imaging: Scintigraphy, Positron Emission Tomography (PET scan).

In the case of this study, the interest is focused on radiographs only as there is a need in this area, and potential to enhance current diagnostic tools used by orthopaedists. The
MRI and CT scans are used only as a validation process by comparing the bi-planar reconstruction to models extracted from MRI or CT scans.

### 2.3 The Spine

The spine (see Figure 1.5) comprises the sequence of short bones or vertebrae (see Figure 2.1) from the first, the atlas located just under the skull, to the coccyx. The average length of the adult spine is 70 to 75 cm. It protects the spinal cord and the spinal nerves, supports the weight of the body and is a partly rigid and partly flexible axis for the body as well as a pivot for the head. It also has a central role in posture and locomotion. Deformation of the spine can thus have very significant consequences, anatomically and functionally, and can also be painful for the patient.

![Figure 2.1: A description of components of a vertebra.](image)

In an adult, the spine is composed of 24 vertebrae (see Figure 1.5), and they can be divided as follows:

- 7 cervical vertebrae, forming the neck frame;
- 12 thoracic vertebrae, to which the rib cage is connected;
- 5 lumbar vertebrae, behind the stomach, from the top to bottom they are identified with the prefix “L” followed by the number one to five.

There are also four coccygeal vertebrae, welded and forming the sacrum and the coccyx.
The different types of vertebrae all have a specific shape, recognisable on radiographs. The articulations between the vertebrae allow the spine to be flexible. Intervertebral discs are located between two vertebrae in these articulations. Genetic and environmental factors bring variations in the vertebral shape.

Four main curvatures can be defined: cervical and lumbar curvatures are posteriorly concave (towards the front of the body) whereas thoracic and sacral curvatures are anteriorly concave (towards the back of the body) (see Figure 1.5). Abnormal curvatures are detected when the patient is standing in a normalised reference anatomical position (usually in a standing position where the head, the back and the legs are in a straight line) and measurements are done. Abnormalities have to be measured using two incidences: antero-posterior (or postero-anterior) and latero-lateral. For some deformations, only one incidence is sufficient, but for some, both of them are required. These deformations can be congenital anomalies that are revealed during the development of the patient, or a pathological process. Common examples of deformations are kyphosis, lordosis scoliosis or kyphoscoliosis (Moore et al., 2013).

2.4 3D Reconstruction From Radiographs

3D reconstruction from bi-planar radiographs is an ill-posed problem as there are many solutions in 3D space. It is an inverse problem as the data that generated the radiographs, is to be reconstructed. In the literature, there is no well known classification of the methods of 3D reconstruction from bi-planar radiographs. Benameur (2004) classified his literature review on this subject in three parts - reconstruction without a priori knowledge, reconstruction with geometrical a priori knowledge and reconstruction with statistical a priori knowledge. Other classifications could be used such as the level of the automation of the process (automatic/semi automatic/manual). Also, they could be classified according to the objects to be reconstructed (femur/vertebrae/cage ribs/pelvis/limb etc) or the applications it is being used for. Markelj et al. (2012) classified the methods for 3D/2D registration into extrinsic, intrinsic and calibrated-based. In this work, we divide our literature review into four different sections:

- Data Collection and Representation;
- Model to Model Correspondence;
- Model to Input Data Correspondence;
• Validation Process.

This choice is driven by how the research community extract/represent data from radiographs, how they solve the problem of correspondence (if not already solved) and how to fit the 3D data to radiographs. The final factor is how the validation of any method is conducted.

2.4.1 Data Collection and Representation

For 3D reconstruction, there is a need to find the geometrical transformation between the 3D coordinates of the object in study and the 2D points visible on the image, this is known as calibration. All information about the scene is known: the coordinates of the projection planes, the camera/source positions and parameters. In the literature, there are two types of radiograph machines: standard and EOS (EOS Imaging, Paris, France). EOS radiographs are already self-calibrated by the machine (Aubert et al., 2016) and they are low in irradiation (Baudoin et al., 2008). This provides self calibrated radiographs which makes the reconstruction easier as there are fewer parameters to estimate. They are also more accurate for 3D reconstruction as the machine takes simultaneously postero-anterior and lateral radiographs from head to feet (Kalifa et al., 1998; Dubousset et al., 2005). EOS radiographs have been mostly used in the last decade for example by (Aubert et al., 2016; Baudoin et al., 2008; Chaibi et al., 2012; Humbert et al., 2009; Lebailly et al., 2012; Le Bras et al., 2003; Mitton et al., 2006; Pomero et al., 2004; Quijano et al., 2013). EOS radiographs, even though they have advantages, are still not widespread as most literature uses standard radiographs. There is much historical data that has not been taken using the EOS imaging system, this leads to the desire for 3D reconstruction from bi-planar radiographs. The EOS imaging system is not of interest here as it is not widely spread as mentioned before and our data collected locally and used in this work, is not using this system.

The methods that do not use self calibrated radiographs need to use a calibration process that calculates the 3D/2D transformation. For example, Cheriet et al. (1999) and Dansereau and Stokes (1988) used a calibration object on the patient while taking the radiographs. This is not ideal or comfortable for the patient (sometimes the object is the size of the rib cage (Dansereau and Stokes, 1988)) and this method of reconstruction not useful for data where no calibration object has been used.

There are different methods for 3D reconstruction from conventional bi-planar radiographs. Some of them are point-based methods and others are contour-based meth-
ods. In point-based methods, there are Stereo Corresponding Points (SCP) and Non Stereo Corresponding Points (NSCP). SCP methods rely on identification of landmarks (definition in Section 2.4.2) on two (or more) radiographs. These points correspond and represent the same anatomical point on the bone structure. NSCP are points that are visible only in one radiograph, therefore not corresponding.

SCP based methods are probably the first methods used for 3D reconstruction from multi view radiographs. SCP methods rely on an expert to identify landmark points on radiographs then apply Direct Linear Transformation (DLT) (Abdel-Aaziz and Karara, 1971) to retrieve the 3D location of the points. SCPs correspond by definition which makes them landmarks. Several works (Pearcy, 1985; Stokes et al., 1981; Dansereau et al., 1990; André et al., 1994) used SCP methods then DLT to reconstruct 3D bone structures from radiographs. SCP methods require by definition at least 6 landmarks but Pearcy (1985), Stokes et al. (1981), Dansereau et al. (1990), and André et al. (1994) used from 6 to 9 SCP per vertebra. These methods did not generate a detailed geometry of the object to be reconstructed (Kadoury et al., 2009). Moreover, SCP and NSCP based methods also have some limitations as they rely on manual anatomical landmarks that are subject to errors (André et al., 1994). SCP/NSCP methods are time consuming and the reproducibility is not easily achieved by the same expert nor by different people (Kadoury et al., 2009). Some researchers even used more points (SCP/NSCP) (Mitton et al., 2000; Mitulescu et al., 2001) to get better results. As the shape reconstruction problem is under-constrained, all methods for solving it have to bring in prior information and are data-driven methods. Otherwise, the results would be not detailed and not enough information gathered for visualisation.

Aubin et al. (1997) introduced a non-deformable model of the spine scanned by digitisation with the Coordinate Measuring Machine (CMM) of 10 identification landmarks put on each vertebra. They used also SCP and DLT for 3D reconstruction. The model was used for validation to compare with the 3D reconstruction. A priori knowledge based on a generic object deformable under constraints was used by Mitton et al. (2000) and Mitulescu et al. (2001). These methods do not have a global a priori knowledge about the object to be reconstructed (Kadoury et al., 2009). Some methods (Chaibi et al., 2012; Humbert et al., 2009; Baudoin et al., 2008; Pomero et al., 2004) used parameterised models with certain number of parameters. These methods are weak as the model does not represent completely the shape of the object to reconstruct and the result is not always realistic (Kadoury et al., 2009). Zheng et al. (2011) used a SSM constructed from CT-segmentation-based binary volumes. They combined
the vertebrae levels to construct a unique SSM for all vertebrae. Parent et al. (2002) used a 3D digitizer of landmarks using a stylus and identified approximately 190 landmarks for dried lumbar vertebrae. It is quite a large data set of over 1000 thoracic and lumbar vertebrae. The same data set has been used to construct a SSM in (Bennameur et al., 2003, 2005). This database has been collected with a pointer accurate to +/- 0.2 mm (Bennameur et al., 2003).

Clogenson et al. (2015) used CT scans to get their data (92 in total) to construct an SSM of the C2 vertebra. They used manual segmentation on each slice and a Gaussian kernel for smoothing to generate the 3D models. Seven manual landmarks were subsequently used to register the surfaces and build a SSM of the C2 vertebra. This method relies on manual landmarking which is subject to error André et al. (1994).

There are limitations of using CT scans or MRI as both methods are costly relative to radiographs (Baka et al., 2011). CT scans also involve an unacceptable amount of radiation exposure (Brenner and Elliston, 2004) but this is not true for in vitro data.

Using statistical shape analysis which contains statistical a priori knowledge is an important tool for understanding and interpreting the anatomical structures from medical images (Dryden and Mardia, 1998). Model-based approaches have the ability to represent objects robustly and accurately (Turk and Pentland, 1991). Since the introduction of SSMs by Cootes et al. (1993), they have become increasingly common and popular among the research community in medical imaging. The a priori knowledge that we are interested in resides in SSMs of vertebrae which should be built first and in ASMs to fit to bi-planar radiographs. ASMs (Cootes et al., 1992; Cootes and Taylor, 1992; Cootes et al., 1995) have been used widely in the literature especially for 3D reconstruction of human anatomical structures (non rigid 3D/2D registration of the knee: (Cootes et al., 2000; Fleute and Lavallée, 1999, 1998), heart left ventricle: (Cootes et al., 1993), lungs: (Sun et al., 2012), vertebrae: (Smyth et al., 1997; Lorenz and Krahnstöver, 2000), segmentation of anatomical structures from 2D images: (Cootes et al., 1993; Hill et al., 1992; Zamora et al., 2003; Hill et al., 1994) etc). Moreover, a detailed presentation of ASMs and their use is given in Chapter 3.

In summary, the methods that are based on SCP, NSCP, contours have limitations as they are subject to errors, need in general a well trained technician, struggle to reproduce the same results due to difficulties in the repeatability of identifying the landmarks/points and do not use all the information from the radiographs. The methods that use generic models or parametric models do not give enough details and geometry of the object. This study is further motivated by the demand for SSMs in the
medical community (Sarkalkan et al., 2014). As presented by Sarkalkan et al. (2014),
statistical models are in limited supply for research and also commercial use. Manual
landmarking is becoming impractical and unpopular within the research community
as it is time consuming (it can take two hours to segment the vertebra but once the
model is built it could be used for segmentation (Clogenson et al., 2015)) and error
prone (André et al., 1994; Sarkalkan et al., 2014; Zheng et al., 2011). However, SSMs
depend highly on the training set used. To capture sufficient variation about the object,
the training data should be large enough to generalise well.

The ASMs based methods use training data where the models should be aligned
initially. The problem of alignment is based on the problem of correspondence between
models which should be solved as discussed next Section.

2.4.2 Model to Model Correspondence

Correspondence means that the point which represents a specific localisation in a sam-
ple is the same throughout the training data set. As seen in previous Section landmarking
is a tedious process, in the literature mostly Generalised Procrustes Analysis
(GPA) (Gower, 1975; Goodall, 1991) is used to find the best Euclidean similarity trans-
formations to register the models when the problem of correspondences is solved. Re-
construction of 3D ASMs is based on a correspondence problem. If the correspondences
are already set, the calculation of the SSM is well defined through Point Distribution
Model (PDM) and finding the principal components is straightforward as detailed in
Chapter 3. If the correspondences are not defined the problem is much harder. Model
to model correspondence can be subdivided into two subsections - alignment of mod-
els in the training set or comparison between 3D models reconstructed from bi-planar
radiographs to those constructed from CT scans or MRI. The principle is the same to
find the best transformation between two models, and the same idea could be used in a
number of samples in the training data. Also, it can be divided into rigid and non rigid
correspondence. In rigid correspondence only Euclidean transformations are allowed,
for non rigid correspondence the points could be moved on the surface to have a better
fit between the models.

To define the correspondences between shapes, the concept of landmarks is intro-
duced. A landmark is a corresponding point that matches between different shapes of
a population (Dryden and Mardia, 1998). Dryden and Mardia (1998) also divided the
landmarks into sub classes:

- Anatomical landmarks: are all landmarks identified by anatomist experts special-
ising in the field to annotate shapes either in 2D or 3D. They are corresponding biologically in the population;

- Mathematical landmarks: are all landmarks defined with a mathematical geometrical property on an object such as curvature, distance to centre of the object, extremum etc;

- Semi Landmarks (Pseudo landmarks): landmarks built on the object between other landmarks, often uniformly spaced.

Another grouping has been discussed by Dryden and Mardia (1998), Type I, Type II and Type III landmarks. This is not discussed here but later in Chapter 3.

When the problem of correspondences is not solved, the first important method is probably the Iterative Closest Point (ICP) algorithm which was developed by Besl and McKay (1992) and applied widely later on. The ICP algorithm searches iteratively to optimise the closest distance between two shapes. The closest distance is defined as the sum of the minimum distance between vertices under translation and rotation. The main drawbacks of this method are: the closest point in the shape is not always the corresponding point, it uses only rigid transformation (rotation, translation and scale), and depends highly on the initialisation.

Aubin et al. (1997) used 21 landmarks reconstructed in 3D that fit to a generic model using least squares. This was used for validation by comparing the 3D reconstruction with the measurement done on 3D models reconstructed from a certain number of landmarks. The model is not realistic as it uses few landmarks (21).

McCane (2013) introduced in 2D a non-rigid optimisation correspondence by parameterisation of the curves with normalised arc-length. The idea is to find a non-decreasing partition which maps the parameterisations. One of the drawbacks is that the method does not capture any occlusions or missing biological parts in a sample.

Zheng et al. (2011) used a Point Distribution Model (PDM) as a representation for the SSM. The PDM was constructed using Demons Algorithm, as implemented by MedINRIA (Thirion, 1998). A drawback of the Demons algorithm is that the transformation generated is not diffeomorphic (Vercauteren et al., 2009) which is needed especially in anatomy to be able to get unique correspondences. Each model is described by 5000 landmarks from which they generated the PDM. It is similar to our study but instead of using CT scans we used dried vertebrae scanned with an image-based method. Additionally, we used Spherical Demons Algorithm (SDA) (Yeo et al., 2008, 2010) where the mapping between models is diffeomorphic.

Lorenz and Krahnstöver (2000) defined a “coating scheme” to be able to solve
the problem of corresponding landmarks. This method is time consuming and not automatic.

Styner et al. (2006) used spherical harmonics to find the correspondences between brains’ morphometry and constructed the PDM. The disadvantage of this method is the selection of a template which brings some bias in the SSM as stated by Styner et al. (2006). This method requires a spherical topology, as in our case, but we used the SDA (Yeo et al., 2008, 2010) as presented in Chapter 5, which registers the training data to a mean shape (see Section 5.3.4).

Spherical demons (Yeo et al., 2008, 2010) has been introduced and applied on the brain using geometrical information of inflated cortical surfaces as a middle shape between the original shape and the spherical parameterisation. We show in this thesis the use of SDA (Yeo et al., 2008, 2010) applied to vertebrae. A detailed description is given in Chapter 5. A strength of SDA is the fact it is landmark free. It requires only an initial transformation for alignment of the spheres. SDA is faster (Yeo et al., 2008, 2010) than FreeSurfer (Fischl et al., 1999).

In summary, there are few landmark free methods for finding correspondences between models. We were interested in those which are bijective (one to one mapping) as a point representing the same geometrical information through all the training data. SDA is a good example as it is diffeomorphic and faster than FreeSurfer. SDA has not been applied yet on vertebrae and we validate its use on vertebrae in this thesis. We show this application in Chapter 5. In our case, we chose to generate a SSM for each level of lumbar vertebra. Once the SSMs have been built, then comes the phase of fitting to radiographs, which means we have a model to input data correspondence.

2.4.3 Model to Input Data Correspondence

A detailed review has been published by Markelj et al. (2012) on 3D/2D registration methods. Here we cite only the methods that are somehow similar to our work as we show in Chapters 6 and 7, where the problem is formulated as an optimisation problem of a cost function. Zheng et al. (2011) used a hybrid method between models to input correspondence and model to model correspondence. They used a semi automatic method to extract the image contours. Then, they found pairs of 2D points in the image between the apparent contour of the projected model and the image contour. Finally, using ray casting from the source to the 2D pairs, they solved iteratively an optimisation function that matched pairs in 3D. The optimisation was a sequential optimisation on shape and pose parameters. The results of this method depend highly on segmentation.
of the contours and the nearest neighbour might not be the corresponding point. The set of predefined anatomical landmarks used for the method are time consuming, user dependent and error prone (André et al., 1994).

Benameur et al. (2003, 2005) carry out simultaneous optimisation on pose and shape parameters of the model. The fitting function of the ASM was a two term energy function: a likelihood term measured on edge potential field done with segmentation on bi-planar radiographs and an a priori term measured on the SSM. The optimisation problem was solved with a gradient descent algorithm. One major limitation is that the method depends highly on the segmentation results of the contour. One of the strengths however, is that the fitting function contains an a priori energy term to measure the likelihood of the shape generated while optimising, but this could be a drawback for pathologies that are far away from the mean shape, which means their likelihood is small. In this research, we suppose that all the generated models have the same likelihood as presented in Section 3.4.

Fleute (2001) used a sequential registration of 3D models to bi-planar images. The first registration is ICP then the second one is non rigid with Levenberg Marquardt. The registration depends on the segmented contour on the images. As with Benameur et al. (2003, 2005), the results depend on the segmentation.

Digitally Reconstructed Radiographs (DRRs) generated from CT scans have been used to register 3D CT volume to corresponding radiographs. DRR based methods have been used by Zheng et al. (2006); Khamene et al. (2006). The idea is similar to our method, but in our case the simulated radiograph is generated from a 3D model not from CT scans.

Once the 3D reconstruction process is achieved, comes the process of validation of any method.

2.4.4 Validation process

In this thesis, we followed a well established method for validation similar to the work of Aubin et al. (1997) who used in vitro data on dried cadavers and compared them with manual measurements to compare the 3D models of reconstructed and dried vertebrae. Several papers (Benameur et al., 2003; Petit et al., 1998; Benameur et al., 2005; Zheng et al., 2011) used CT scans to compare bi-planar reconstruction with CT models. Zheng et al. (2011) used CT scans for testing data which has been already introduced in the training data for the SSM which makes the method weaker as the trained model already contains the variation of the test. Kadoury et al. (2009) used MRI models to validate
the 3D reconstruction. Manual measurements are subject to different errors: user, tools used and there is no possibility to make them *in vivo* unless they are made on models reconstructed from CT scans or MRI. In Chapter 4, we used manual measurements combined with model comparisons to those generated by an arm scanner. More details are given in Chapter 4. We compared (see Chapter 6) 3D reconstruction of *in vitro* dried vertebrae from bi-planar radiographs to reconstruction from embedded markers and to models reconstructed by arm scanning. We used CT scans or MRI, which are considered as the gold standard for acquiring 3D volumetric data *in vivo*, to validate the 3D bi-planar reconstruction (see Chapter 7) similar to several papers (Kadoury *et al.*, 2009; Benameur *et al.*, 2003; Petit *et al.*, 1998; Benameur *et al.*, 2005; Zheng *et al.*, 2011) cited here in this section.

### 2.5 Conclusion

We discussed in this Chapter the importance of ASMs and their interest and use by research community in 3D reconstruction from bi-planar radiographs. ASMs bring *a priori* knowledge. We argued the importance of automation of landmarks through the training data. And finally, we emphasised the importance of 3D reconstruction without segmentation and without manual landmarking of radiographs.
Chapter 3

Active Shape Models

3.1 Overview

In this Chapter, we give an overview of Active Shape Models (ASMs) by defining them in 3D space as they will be used later on in this thesis. We explain the general system of how they work and illustrate them in 2D as it is easier to work in 2D rather than 3D space.

3.2 Introduction

ASMs were introduced by Cootes et al. (1992); Cootes and Taylor (1992); Cootes et al. (1995) in 1992 and have been widely used on different objects. ASM construction follows the same principles regardless of the object of study. It is based on corresponding landmarks, alignment, generation of mean shape and finally, finding the principal modes of variation. These elements allow for the generation of new shapes according to a distribution function (usually Gaussian), and the model can therefore be used to fit to unseen data via optimisation of a matching function. ASMs have since been used in many different applications especially in the medical field (non rigid 3D/2D registration of the knee: (Cootes et al., 2000; Fleute and Lavallée, 1999, 1998), heart left ventricle: (Cootes et al., 1993), lungs: (Sun et al., 2012), vertebrae: (Smyth et al., 1997; Lorenz and Krahnstöver, 2000), segmentation of anatomical structures from 2D images: (Cootes et al., 1993; Hill et al., 1992; Zamora et al., 2003; Hill et al., 1994) etc).
3.3 Definition

In this section, we suppose we work in a 3D space, and we have \( n \) samples in our data set. The method is generalisable to any number of dimensions. ASMs are based on landmarks. A landmark is a particular point that contains some specific biological, anatomical, or geometrical information that is invariant through all samples of a training data set. Landmarks are often given semantic labels (names). Two landmarks in two samples with the same name are meant to specify the same anatomical point - in other words, they correspond. Landmarks are classified (Dryden and Mardia, 1998) into three different types:

- **Type I**: clear definition of points that can be biological, or anatomical or histological. They appear clearly on different samples of training set;
- **Type II**: a landmark defined by the local properties of the shape as minimum or maximum curvature or distance from centre;
- **Type III**: landmarks that are extremal points on the shape.

Type II and Type III landmarks are typically introduced to enrich the representation. Ideally only Type I landmarks would be used, but there are usually not enough of them to be able to meaningfully generate new shapes. Because of their definition, Type II and Type III landmarks are often poorly localised (Dryden and Mardia, 1998). After defining \( p \) corresponding landmarks between the \( n \) samples of the data set, Cootes et al. (1992); Cootes and Taylor (1992); Cootes et al. (1995) state that every sample in the population, denoted as \( Y \), is defined by a set of corresponding \( p \) control points or landmarks. In 3D, each sample is represented with \( p \) landmarks where

\[
\begin{pmatrix}
  x_i \\
  y_i \\
  z_i
\end{pmatrix} \in \mathbb{R}^{3 \times 1} \tag{3.1}
\]

in Cartesian coordinates would represent the \( i^{th} \) landmark. Consequently, the \( j^{th} \) sample is represented as follows:

\[
Y_j = \begin{pmatrix}
  x_{j,1} & x_{j,2} & \cdots & x_{j,i} & \cdots & x_{j,p} \\
  y_{j,1} & y_{j,2} & \cdots & y_{j,i} & \cdots & y_{j,p} \\
  z_{j,1} & z_{j,2} & \cdots & z_{j,i} & \cdots & z_{j,p}
\end{pmatrix} \in \mathbb{R}^{3 \times p} \tag{3.2}
\]

where column \( i \) represents the coordinates of the \( i^{th} \) landmark in the sample \( Y_j \). According to Kendall (1977), “shape is all the geometrical information that remains
when location, scale and rotational effects are filtered out from an object”. In other words as we are working in 3D, a shape is a set of 3D points that are invariant to rigid transformations (scale, translation, rotation and reflection). Consequently for each sample of the training data, we will filter out the scale, the translation and the rotation. To filter out translation, each sample is translated so that its centre of mass is at the origin as follows in Equation 3.4:

\[
\bar{c}_j = \frac{1}{p} \begin{pmatrix}
\sum_{k=1}^{p} (x_{j,k}) \\
\sum_{k=1}^{p} (y_{j,k}) \\
\sum_{k=1}^{p} (z_{j,k})
\end{pmatrix} \in \mathbb{R}^{3\times1}
\] (3.3)

where \(\bar{c}_j\) represents the centre of mass of sample \(Y_j\). We can now define:

\[
Y_{t_j} = Y_j - [(\bar{c}_j)_{x,p}] \in \mathbb{R}^{3\times p}
\] (3.4)

where \(Y_{t_j}\) represents the sample translated to the origin of coordinate system and \([(\bar{c}_j)_{x,p}]\) is the matrix constructed by \(p\) vector columns all equal to the vector \(\bar{c}_j\).

To filter out scale, each sample translated to origin of coordinate system, is normalised to have a unit norm by applying the transformation in Equation 3.5 defined as follows.

\[
S_j = \frac{1}{s_{c_j}} Y_{t_j}
\] (3.5)

where \(S_j\) represents sample \(j\) after translation and scaling.

We define the scaling factor \(s_{c_j}\) after translation of the sample as follows:

\[
s_{c_j} = \sqrt{\frac{1}{p} \sum_{k=1}^{p} (x_k^2 + y_k^2 + z_k^2)} \in \mathbb{R}
\] (3.6)

To filter out rotation, Generalised Procrustes Analysis (GPA) (Gower, 1975; Goodall, 1991) is applied as described in Algorithm 3.1. GPA seeks the best rotation, translation and scale from a shape to a reference shape. In our case, the reference shape at each iteration as described in Algorithm 3.1 is the mean shape of the set of shapes. So at each iteration, each shape is rotated as the square of the Frobenius norm between mean shape and current shape is minimized.

If we have \(n\) samples in data set, each one of them defined as in Equation 3.5, the
data matrix $D$ would be defined as below:

$$D = (\text{vec}(S_1) \ldots \ldots \text{vec}(S_n)) = \begin{pmatrix} x_{1,1} & \vdots & x_{n,1} \\ y_{1,1} & \vdots & y_{n,1} \\ z_{1,1} & \vdots & z_{n,1} \\ \vdots & \vdots & \vdots \\ x_{1,p} & \vdots & x_{n,p} \\ y_{1,p} & \vdots & y_{n,p} \\ z_{1,p} & \vdots & z_{n,p} \end{pmatrix} \in \mathbb{R}^{3p \times n}$$  \hspace{1cm} (3.7)

where column $i$ represents vectorisation of the $i^{th}$ shape and $\text{vec}$ is a function, $\text{vec} : \mathbb{R}^{a \times b} \rightarrow \mathbb{R}^{ab \times 1}$ defined by:

$$\text{vec}(M) = [m_1^T | m_2^T | \cdots | m_p^T]^T$$  \hspace{1cm} (3.8)

where $m_i$ is the $i^{th}$ column of the matrix $M$ in Equation 3.8. $|$ is used here to denote the concatenation of the vectors in the same line. We define also the inverse function of $\text{vec}$ as $\text{vec}^{-1}$ so: $\text{vec}^{-1}(\text{vec}(M)) = M \in \mathbb{R}^{a \times b}$ and $\text{vec}(\text{vec}^{-1}(m)) = m \in \mathbb{R}^{ab \times 1}$. In general as we are working in 3D space with shapes, $a$ will be $p$, the number of landmarks, and $b$ is 3 as a 3D space.

We apply GPA to align the samples (Equation 3.7) as shown in Algorithm 3.1. For Algorithm 3.1, we define $T : \mathbb{R}^{7} \times \mathbb{R}^{3 \times p} \rightarrow \mathbb{R}^{3 \times p}$ as a rigid transformation of any 3D shape $S$ as follows:

$$T(s, \theta_x, \theta_y, \theta_z, t_x, t_y, t_z, S) = sR_x(\theta_x)R_y(\theta_y)R_z(\theta_z)T_r(t_x, t_y, t_z)\begin{bmatrix} S \\ 1_{1 \times p} \end{bmatrix}$$  \hspace{1cm} (3.9)

where $s$ represents the scale, $t_x, t_y, t_z$ represent the translation along $x, y$ and $z$ axis respectively and $\theta_x, \theta_y, \theta_z$ lead to three rotation matrices around the three axis of the coordinate system and translation matrix $T_r$. The translation matrix $T_r$ in each direction of the coordinate system and the three rotation matrices $R_x(\theta_x), R_y(\theta_y), and R_z(\theta_z)$ are defined as follows:

$$T_r(t_x, t_y, t_z) = \begin{pmatrix} 1 & 0 & 0 & t_x \\ 0 & 1 & 0 & t_y \\ 0 & 0 & 1 & t_z \\ 0 & 0 & 0 & 1 \end{pmatrix}$$  \hspace{1cm} (3.10)
Algorithm 3.1: Alignment of Shapes using Generalised Procrustes Analysis.

**Input:** \( p \): number of landmarks representing the shape; \( n \): number of shapes in training set; \( D \): as defined in Equation 3.7.

**Output:** \( D \): matrix representing shapes alignment.

1. Calculate mean shape defined as
   \[
   \bar{s} = \frac{1}{n}(\sum_{j=1}^{n}(x_{j,1}), \sum_{j=1}^{n}(y_{j,1}), \sum_{j=1}^{n}(z_{j,1}), \cdots, \sum_{j=1}^{n}(x_{j,p}), \sum_{j=1}^{n}(y_{j,p}), \sum_{j=1}^{n}(z_{j,p}))^T \in \mathbb{R}^{3\times p} \times 1
   \]  
   (3.11)

2. repeat
3. Translate and scale \( \bar{s} \) as defined in Equations 3.4 and 3.5 respectively
4. for each shape \( \text{vec}(S_i) \in D \) do
5.   Align \( \text{vec}(S_i) \) to mean shape \( \bar{s} \): find best translation, scale and rotation which minimises sum of squared errors (SSE)
   \[
   \begin{align*}
   \left( s_{\text{min}}, \theta_{x_{\text{min}}}, \theta_{y_{\text{min}}}, \theta_{z_{\text{min}}}, t_{x_{\text{min}}}, t_{y_{\text{min}}}, t_{z_{\text{min}}} \right) &= \arg \min_{s, \theta_x, \theta_y, \theta_z, t_x, t_y, t_z} \text{SSE} \\
   \text{SSE} &= ||T(s, \theta_x, \theta_y, \theta_z, t_x, t_y, t_z, S_i) - \text{vec}^{-1}(\bar{s})||_F^2
   \end{align*}
   \]  
   (3.12)
   where: \( T \) defined in Equation 3.9. \( ||M||_F \) represents the Frobenius norm of \( M \), \( ||M||_F^2 = \sum_{i=1}^{q} \sum_{j=1}^{r} (a_{i,j})^2 \) with \( M \in \mathbb{R}^{q\times r} 
6. Update in \( D \): \( \text{vec}(S_i) = \text{vec}(T(s_{\text{min}}, \theta_{x_{\text{min}}}, \theta_{y_{\text{min}}}, \theta_{z_{\text{min}}}, t_{x_{\text{min}}}, t_{y_{\text{min}}}, t_{z_{\text{min}}}, S_i)) \)
7. end for
8. Recompute \( \bar{s} \).
9. until Convergence or maximum iterations exceeded
10. Return
\[ R_x(\theta_x) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos(\theta_x) & -\sin(\theta_x) & 0 \\ 0 & \sin(\theta_x) & \cos(\theta_x) & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \quad (3.13) \]

\[ R_y(\theta_y) = \begin{bmatrix} \cos(\theta_y) & 0 & \sin(\theta_y) & 0 \\ 0 & 1 & 0 & 0 \\ -\sin(\theta_y) & 0 & \cos(\theta_y) & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \quad (3.14) \]

\[ R_z(\theta_z) = \begin{bmatrix} \cos(\theta_z) & -\sin(\theta_z) & 0 & 0 \\ \sin(\theta_z) & \cos(\theta_z) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \quad (3.15) \]

Cootes et al. (Cootes et al., 1992; Cootes and Taylor, 1992; Cootes et al., 1995) proposed that most of the shape variation can be captured under the hypothesis that the data is normally distributed, with a mean shape \( \bar{S} \) of the shapes in training data and the \( 3p \times 3p \) covariance matrix \( C \). Once the shapes are aligned using Procrustes Analysis (as presented in Algorithm 3.1) to the same coordinate system, the mean shape \( \bar{S} \) is defined as follows:

\[ \bar{S} = \frac{1}{n} \text{vec}^{-1}\left( \sum_{i=1}^{n} \text{vec}(S_i) \right) \in \mathbb{R}^{p \times 3} \quad (3.16) \]

Equation 3.16 is a matrix representation of the vector \( \bar{s} \) in Equation 3.11, and the covariance matrix as follows:

\[ C = \frac{1}{n} \sum_{i=1}^{n} (S_i - \bar{S})(S_i - \bar{S})^T \quad (3.17) \]

The random independent variable \( D \) is defined by a mean \( \bar{S} \) and a covariance matrix \( C \). Then we apply Principal Components Analysis (PCA) to derive the principal modes of variations from the eigenvectors of the covariance matrix \( C \). The associated eigenvalues of these eigenvectors represent the percentage of variance introduced by each mode. The main variations are obtained by keeping the \( q \) largest of the eigenvalues to reduce dimensionality from \( n \) to \( q \) supposing \( n \leq p \). The value of \( q \) depends on how
much variability we want to capture in the sample data. Typically, we will keep the $q$ largest eigenvalues where the sum is higher than a predefined threshold. Once the $q$ main eigenvectors are defined, a new shape can be generated by choosing a vector $b = (b_1, \ldots, b_q) \in \mathbb{R}^n$ which represents the importance given to the associated eigenvector. The weights $b_i$ are usually limited to $|b_i| \leq 3\sqrt{\lambda_i}$\(^1\) to be able to generate acceptable shapes within the Gaussian distribution. $\lambda_i$ and $\sqrt{\lambda_i}$ represent respectively the variance and the Standard Deviation ($\sigma$) associated with the eigenvector $i$ ($\sigma = \sqrt{\lambda_i}$). The new shape is defined as follows:

$$S = \Phi b + \bar{S}$$

(3.18)

where $\Phi$ represents the normal basis of $q$ principal modes of variation constructed by columns from eigenvectors of the covariance matrix $C$, and $b$ are the associated weights. Each principal mode is associated with an eigenvector of the covariance matrix, if we concatenate the first $q$ eigenvectors associated with the first highest $q$ eigenvalues, we have the normal basis, consequently the matrix $\Phi$.

### 3.4 Explanation

Once the mean shape and the principal modes of variation are defined (this defines the Statistical Shape Model as a statistical description of the data), new shapes can be generated to fit new unseen data (the SSM combined with the fitting function constitute the ASM). If this new data is landmarked, there are correspondences set between the SSM and the new data. If there are no correspondences, the problem is harder, and we will see examples of this case in Chapters 6 and 7. A model is defined in 3D space: by pose parameters (rotation, scale and translation) and shape parameters as defined by the vector $b$ in Equation 3.18.

$$M = T(s, \theta_x, \theta_y, \theta_z, t_x, t_y, t_z, \Phi b + \bar{S})$$

(3.19)

where $T$ has been defined previously in Equation 3.9. If we set the problem of fitting the model to new data $N_d$ as a Bayesian problem, we have:

$$P(M|N_d) = \frac{P(N_d|M)P(M)}{P(N_d)}$$

(3.20)

\(^{1}\sqrt{\lambda_i}\) is well defined as the eigenvalues are real positives as $C$ is symmetrical ($C^T = C$)
where $P(event)$ is the probability of “event” occurring. Optimising the left hand side of Equation 3.20 is equivalent to optimising the likelihood of having the new data $N_d$ knowing the model $M$ given that all $N_d$ and $M$ are equally likely, if they are not equally likely, we consider that the data is given, therefore $P(N_d) = 1$. If all $M$ are equally likely then $P(M)$ can be ignored and that leaves us with $P(M|N_d) \sim P(N_d|M)$. So, we would choose a fitting function which would maximise this likelihood ($P(N_d|M)$) when generating new models to fit the new data.

Consequently, fitting is finding the model that best matches the new data $N_d$, which means finding the pose parameters (rotation, scale and translation) and the shape parameters defined by vector $b$ in Equation 3.18.

If the new data $N_d$ is landmarked, we would minimise the following SSE between the model and new data:

$$\min_{s, \theta_x, \theta_y, \theta_z, t_x, t_y, t_z, b} \text{SSE} = \|M - (N_d)\|^2_F$$

(3.21)

If the new data is not landmarked, it means no correspondences are defined with the SSM. Therefore, Equation 3.21 can’t be used unless correspondences are defined, or a different fitting function is defined. This problem is addressed in Chapters 6 and 7 as an example of fitting 3D SSM to two radiographs.

### 3.5 Illustrative Example: 2D ASM of L3 Vertebra

The purpose of this section, as an illustrative example of 2D ASMs, is to produce a computer model that fits the 2D shape of a normal L3 vertebral body from plain radiographs. The choice of this vertebra was arbitrary, and the same principle could be adapted to different objects. The data set used in this part was acquired from the second National Health and Nutrition Examination Survey (NHANES II) which is run by the Lister Hill National Center of Biomedical Communications at the National Library of Medicine (NLM) at the National Institute of Health (NIH)\(^2\) which contains approximately 17,000 digitised radiographs, with cervical and lumbar radiographs. For this study, fifty-nine normal adult lateral lumbar spine radiographs were chosen from this data set as the L3 vertebra contour was more visible to the human eye. They were marked up using 24 investigator-nominated points by co-investigator Dr Jon Cornwall (JC), a physiotherapist with a PhD in clinical anatomy and a research stream in spinal

morphology, to produce raw data. MatLab software (Mathworks, Natick, MA) was used to create an ASM (this accounts for population shape variance) from that data. An ASM was trained and generated as follows:

- Every sample $S_i$ of the $n=59$ x-rays (examples at Figure 3.1) was represented as a vector $x$ in a 48 dimensional space ($2D \times 24$ points) (see Figure 3.2);

\begin{figure}[h]
\centering
\includegraphics[width=0.8\textwidth]{image1.png}
\caption{Examples of training set radiographs used in this Chapter.}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=0.8\textwidth]{image2.png}
\caption{Marking of the radiographs in 2D. The radiographs were annotated using 24 points, the corresponding colours show the correspondence between landmarks through the data provided by JC.}
\end{figure}
So the sample $S_i = (x_1, \cdots, x_{24}, y_1, \cdots, y_{24})^T$;

- The 59 samples (before alignment Figure 3.3) were aligned (Figure 3.4) using GPA as presented in Algorithm 3.1;

**Figure 3.3:** Distribution of shapes before alignment with different scale and rotation.

**Figure 3.4:** Distribution of shapes after alignment and mean shape shown in black circles.
Then we calculated the mean shape $\bar{S}$ and the covariance matrix $C$; Figures 3.5, 3.6, 3.7 and 3.8 show the impact on the shape of the first four eigenvectors with their variations between -3 SD and +3 SD and the direction of how each landmark is distributed. As the first eigenvector is associated with highest eigenvalue, the impact is higher and so on for all following eigenvectors.

**Figure 3.5:** Variance and direction explained by the first component on the whole training data.

**Figure 3.6:** Variance and direction explained by the second component on the whole training data.
Figure 3.7: Variance and direction explained by the third component on the whole training data.

Figure 3.8: Variance and direction explained by the fourth component on the whole training data.
We generated random new shapes as a sum of mean shape and weighted eigenvectors as shown in Figure 3.9.

![Figure 3.9: Examples of generating new shapes with random weights distributed normally between -3SD and +3SD.](image)

3.6 Testing 2D SSM of L3 Vertebra

In Section 3.3, we demonstrated how we created an SSM of L3 vertebra. In this section, we will demonstrate how to fit the SSM to new data as presented in section 3.4. Twenty additional radiographs were used to evaluate the system and see if the ASM of L3 vertebrae is good enough to be able to fit to new data. The twenty additional radiographs were marked up by JC, and they were registered by the ASM model: the SSM generated is fitted following Equation 3.21 as this data is landmarked. We minimised the SSE between the generated model and the L3 marked vertebra under the rigid transformation (rotation, scale and translation) and non-rigid transformation (shape parameters). Five medical doctors were shown lateral lumbar radiographs with both marked-up points and the resulting contour of L3 produced by the shape model; they assessed contour accuracy for the purposes of medical diagnostics and spinal modeling using a Likert scale (very inaccurate, inaccurate, average accuracy, accurate,
very accurate). Figure 3.10 shows images shown to the medical doctors. The green contour shows the interpolation by cubic spline of the data picked up by JC. The red contours show the resulting interpolation with a cubic spline of ASM fitted to the data.

![Figure 3.10: The images shown to the five doctors.](image)
The number of eigenvectors was limited to explain 95% of the variance in the data which was explained by 20 eigenvectors. The model was deemed accurate or very accurate for 60% of the contours (mean 3.8 / 5); Fleiss Kappa score was 0.2 (see Table 3.1) which means that the medical doctors agree slightly. From Table 3.1, there is only one row, I18, with three point disagreement and only five out of eighteen with two point disagreement. In two thirds of cases, all five doctors chose within one point on a five-point scale which shows that the doctors mostly agreed.

<table>
<thead>
<tr>
<th>Images</th>
<th>MD1</th>
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<th>MD4</th>
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Table 3.1: Results of the survey with the five doctors. 5 represents extremely accurate, 3 average accuracy and 1 extremely inaccurate. The model was deemed accurate or very accurate for 60% of the contours (mean 3.8 / 5); Fleiss Kappa score was 0.2. (MD: Medical Doctor)
**Interpretation of Results of ASM of L3 Vertebra**

Current accuracy levels suggest refinement of the model is required, however these results indicate the process has potential including uses such as determining anatomical variation or assessing the effectiveness of spinal surgical interventions.

The L3 vertebra ASM model could be used to segment radiographs as has been used in (Behiels et al., 1999; Kulkarni, 2008; Cootes et al., 1993). The model was a starting point to get the contour on real radiographs and segment them. However, we have not used 2D ASMs any further in this research. This work has been published at ANZACA 2012 as a poster (see Appendix A).

### 3.7 Conclusion

The diagram in Figure 3.11 shows a summary of construction of ASMs. The three most important steps in generating ASM models are firstly finding data, either images for 2D data, or 3D models for 3D data. Secondly finding the corresponding points in the training data set. The third important step is the fitting of the model into the new unseen data which might not contain any extra user information. The purpose is to find the new shape which best fits the data. In this Chapter, we explained the theoretical background behind ASMs and gave an illustrative and easily understood example of ASMs. The rest of this thesis will show these processes on 3D data and their application to fit new data which is not landmarked.
Figure 3.11: Diagram summarising active shape models steps. The first step is to get data that we want to use. Then, we set the correspondences between different samples to generate a PDM. We align them to remove any translation, scale and rotation to keep only shape information. After that, we average the data to extract the mean shape and we apply PCA to extract the principal modes of variation. Once extracted, we can generate a new shape by linear combination of mean shape and weighted principal modes of variation. This gives a generated sample from the SSM. The new shapes generated are registered to new data by optimising a cost function. The search is defined as finding the best rigid and non-rigid transformations that minimise the error function defined.
Chapter 4

Three Dimensional (3D) Lumbar Vertebrae Data Set

4.1 Overview

As presented in Chapter 3, to build 3D ASMs of lumbar vertebrae, we need 3D models. The goal of this chapter is to present the methods used to build a lumbar vertebrae data set and its accuracy. The data set has been published by Bennani et al. (2016). Models from 86 lumbar vertebrae were constructed using an inexpensive method involving image capture by digital camera and reconstruction of 3D models via an image-based technique. The reconstruction method was validated using a laser-based arm scanner and measurements derived from real vertebrae using electronic callipers. Results show a mean relative error of 5.2% between image-based models and real vertebrae, a mean relative error of 4.7% between image-based and arm scanning models and 95% of vertices’ errors are less than 3.5 millimetres with a median of 1.1 millimetres. The accuracy of the method indicates that the generated models could be useful for biomechanical modelling, 3D visualisation of the spine or creation of SSMs of lumbar vertebrae.

4.2 Introduction

3D modelling of real objects has applications such as visualisation, measurement or statistical analysis of populations. The use of 3D models in medical science is useful for achieving accurate diagnoses, creating biomechanical models, developing educational resources, or assisting in improving intervention efficacy. Such models are particularly important for health science research into common conditions such as lumbar spine
pathologies, which have a lifetime prevalence of 60-70% in industrialised countries (Kaplan et al., 2013) and impart a huge social and financial burden on society (Mounce, 2002). Despite the prevalence of spinal pathologies there is a lack of freely available 3D datasets of individual vertebrae of the human spine, and in particular of the lumbar spine. Most available data sets are commercial\(^1\) \(^2\), of dubious origin and accuracy, or contain data from a single individual; this means that existing datasets are not easily accessed, are not readily able to be utilised, and may not be valid. The existing “SpineWeb”\(^3\) platform provides several medical Computed Tomography (CT) scans and Magnetic Resonance Imaging (MRI) of the human spine with reference manual segmentation which is subject to error (André et al., 1994). However, this data set does not provide surface data directly as we do in this chapter.

3D data sets can be constructed via three main methodologies: volumetric scanning, active scanning (such as laser or sonar), or passive / image-based reconstruction. While volumetric scanning (such as that acquired through CT and MRI) can generate 3D images for the purpose of biomechanical modelling or statistical analyses, there are limitations to the use of this technology in that both methods are costly and require skilled technicians to operate. In addition, CT potentially involves an unacceptable radiation exposure to participants (Brenner and Elliston, 2004) whereas MRI is generally safer but often cannot be used when patients have implants or metallic fragments in their bodies (Shellock and Titterington, 2014).

Acquiring 3D images from active scanners such as laser, structured light scanners or sonar scanners also has limitations. These scanners send a signal into the environment and measure the effect the environment has on the signal; they can produce very accurate 3D reconstructions but they can be expensive depending on the accuracy required. Kusnoto and Evans (2002) show that a Minolta Vivid700 3D surface laser scanner achieves an accuracy of 1.9 millimetres for face surface scanning and less than one millimetre for molar scanning, however accuracy of this level is only gained from expensive scanners (e.g. 93000 Euros for a Z35 scanner with an accuracy of ±18 ~ 148 µm (Slizewski and Semal, 2009)).

Passive scanning typically requires reconstructing 3D objects from multiple images of the object. The only equipment required is a digital camera, a computer, and the relevant software. Therefore, this option is very inexpensive, very flexible and easy to use. The method is usually known as structure-from-motion or multi-view

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\(^1\)http://www.turbosquid.com/3d-model/anatomy/spine  
\(^2\)http://www.3dcadbrowser.com/3dmodels.aspx?collection=anatomy  
\(^3\)http://spineweb.digitalimaginggroup.ca/
stereo (Hartley and Zisserman, 2003), and it works by finding corresponding points among images. In the case of known camera positions and imaging geometry (“camera calibration”: internal parameters and external parameters of the camera) (Fraser, 2013; Gruen and Huang, 2013; Remondino and Fraser, 2006), the distance of the points from the cameras can be directly reconstructed up to a scale which has unavoidable ambiguity from image-based reconstruction. If camera positions and geometry are unknown, then they too must be estimated, but this is possible and common for such data (Seitz et al., 2006).

Although such techniques have been used in other applications such as archaeology (Doneus et al., 2011; Plets et al., 2012; Verhoeven, 2011; Kersten and Lindstaedt, 2012) and reconstructing human crania (Katz and Friess, 2014), there are relatively few studies reporting the results of such techniques in human bone models. Furthermore, there are no studies examining whether it is possible to produce a validated model of complex shapes such as that of a human vertebra.

The lack of accurate 3D data for spinal modelling, and the cost and potential difficulty associated with generating such data, is problematic. Parent et al. (2002) used a 3D digitiser of landmarks using a stylus and identified approximately 190 landmarks for lumbar vertebrae, however this did not produce a 3D reconstruction of the vertebra. They demonstrated that the process is accurate, but it has not yet been validated with another method.

The goal of this work is to evaluate and validate an inexpensive method of 3D reconstruction of vertebrae and to establish a freely available surface data set of the same.

4.3 Materials and Methods

4.3.1 Ground-Truth Data Acquisition

To validate image-based reconstruction, we make use of physical measurements and laser-based range reconstruction of ten vertebrae in the data set. This subsection outlines those methods and the data set itself.

Human Skeletal Material

Human lumbar vertebrae used for the purposes of generating the 3D models were accessed through the W. D. Trotter Anatomy Museum at the Department of Anatomy,
Otago School of Medical Sciences, University of Otago, New Zealand. All human material was utilised in accordance with local ethical guidelines and the New Zealand Human Tissue Act (2008). A total of 86 lumbar vertebrae, selected from each of the five lumbar vertebral levels, were utilised for this study. Lumbar vertebrae are typically numbered 1 to 5 from the most superior to inferior, and are denoted as originating from the lumbar region by the prefix L. Lumbar vertebrae used in this study were: 21 from L1, 13 from L2, 19 from L3, 20 from L4, and 13 from L5. Exclusion criteria for this study included gross anatomical abnormality as determined by an experienced anatomist (JC). Vertebrae were from modern Indian donors of both sexes and were from individuals of skeletal maturity (over 25 years of age, as determined by closure of epiphyses).

Figure 4.1: Distances measured on real vertebrae and 3D models. The figure shows a single real L4 lumbar vertebra mounted on Blu-tack with the five distances that were manually measured indicated by solid lines. A) Distance between most lateral points of the two transverse processes; B) Height of the vertebral body; C) Width of the vertebral body; D) Anterior-posterior length of vertebral body; E) Anterior-posterior distance between anterior edge of the vertebral body and the posterior tip of spinous process. For anatomical terms please refer to Figure 2.1

Manual Measurements of Vertebrae

Electronic callipers (with an error of +/- 0.01 millimetres) were used to measure five different physical parameters on ten real vertebrae (Figure 4.1) chosen randomly from the 86 vertebrae available. These parameters were chosen to provide a variety of points
that included the main physical properties of a single vertebra. The different physical parameters measured are described in Figure 4.1.

Arm Scanning

Arm scanning models were acquired using a Faro Platinum (Metris, Leuven, Belgium) scanning arm, equipped with a “Model Maker” Z70 scanning head with a range of 10 centimeters. It takes an experienced technician approximately 90 minutes to acquire a 3D model of a single vertebra with the arm scanner. The “Model Maker” Z70 is advertised as having an accuracy of 0.05 millimetres for a flat plane measurement of $2\sigma$-95% and 0.075 millimetres for $3\sigma$-99.5%$^4$. A “Model Maker” Z70 scanner was rented and used to scan ten vertebrae at a total cost of NZD$400 (average cost of NZD$40 per vertebra scanned). The ten scanned vertebrae are the same ten vertebrae chosen in Section 4.3.1.

Validation of Arm Scanning Models

To verify the accuracy of the arm scanning, we measured on constructed models the same distances that were measured on real vertebrae. Measurements on the models were made with the MeshLab$^5$ software. We compared these measurements of real vertebrae and constructed models by calculating the absolute error and the relative error. If we denote the distance on real vertebrae as $d_r$ and the distance on reconstructed model as $d_m$, the absolute error is defined as:

$$AE = |d_r - d_m|$$

(4.1)

Where $|.|$ is the absolute value. The relative error is defined as:

$$RE = \frac{2|d_r - d_m|}{(d_r + d_m)}$$

(4.2)

4.3.2 Generation of 3D Models

Constructing 3D models via images requires four steps: generating digital images of the vertebra, pre-processing of the images, constructing the 3D models, and post-processing of the 3D models.


$^5$http://meshlab.sourceforge.net
Figure 4.2: Eight different positions of the camera. The first row shows the camera raised by 10 cm from the horizon. The second row is at the horizon. The vertebra was mounted in four different positions. Images presented are examples of those used for reconstruction.

Image Generation

A Canon EOS 650D (Canon Inc., Tokyo, Japan) equipped with an EF 20 millimetre 1:2.8 ultrasonic lens was used to capture images with a resolution of 5184 × 3456. Each individual vertebra was mounted on a turntable using Blu-Tack\(^6\); images were captured from a distance of 40 centimetres. The turntable was rotated approximately 10° between each photograph to get 30-40 images for a single 360° rotation. Approximate, rather than precise, rotations were used because PhotoScan is able to handle such uncertainty and it makes image acquisition easier for the practitioner. Each vertebra was mounted in four different positions, and the camera was positioned at two different heights (horizontal and 10 centimetres above the horizontal) to acquire a higher degree of overlapping between images. This resulted in eight possible camera/vertebra configurations as shown in Figure 4.2 and 30-40 images for each configuration, resulting in 240-320 images per vertebra. Acquiring 280 images took approximately 15 minutes. A plain background was used to allow easy separation of the vertebrae from the background. Originally a white background was used, however during the later stages of image acquisition this was swapped for a black background to match the colour of the turntable. Figure 4.3 shows one position of a single vertebra with the camera positioned 10 centimetres above the horizon with a white background (left image) and with the camera at the horizon with a black background (right image). Images were taken with

\(^6\)http://www.blutack.com
autofocus off, ISO set to 400, f-stop set to 8.0 and exposure time at 1/30s. No special illumination conditions were set and the room was illuminated both by artificial light (fluorescent tubes) and natural light (from nearby windows).

![Figure 4.3](image)

*Figure 4.3:* Photograph showing the set up for image acquisition. Here, a single vertebra is mounted on the turntable with Blu-tack, and the camera set up at 10cm above the horizon on the left image and at the horizon with black background on right image.

**Image Pre-Processing**

Once the photographic images were acquired for every vertebra, some unwanted parts in the reconstruction were visible such as the turntable or the Blu-tack. In order to remove these parts in the reconstruction, we automatically segmented the images using K-means clustering (Kanungo *et al.*, 2002) (Algorithm 4.1).

**Algorithm 4.1: K-Means Clustering.**

<table>
<thead>
<tr>
<th>Input:</th>
<th>$K$: number of centroids; $\mu_1, \ldots, \mu_k \in \mathbb{R}^3$: centroids initialisation (RGB colours).</th>
</tr>
</thead>
<tbody>
<tr>
<td>Output:</td>
<td>$K$ clusters $C_1, \ldots, C_k$ containing pixels.</td>
</tr>
<tr>
<td>1:</td>
<td>repeat</td>
</tr>
<tr>
<td>2:</td>
<td>for each pixel $p_i \in$ image $I$ do</td>
</tr>
<tr>
<td>3:</td>
<td>set $p_i \in {C_j \mid j = \arg \min_h |p_i - \mu_h|^2}$</td>
</tr>
<tr>
<td>4:</td>
<td>end for</td>
</tr>
<tr>
<td>5:</td>
<td>for each class $C_i$ do</td>
</tr>
<tr>
<td>6:</td>
<td>set $\mu_i = \frac{\sum_{p_i \in C_i} p_i}{</td>
</tr>
<tr>
<td>7:</td>
<td>end for</td>
</tr>
<tr>
<td>8:</td>
<td>until Convergence or maximum iterations exceeded</td>
</tr>
<tr>
<td>9:</td>
<td>Return</td>
</tr>
</tbody>
</table>

The background was either white or black. In the case of a white background, we have three different colours: vertebrae colour, white background and black turntable.
in which case $K$ is equal to 3. In the case of a black background, $K$ is equal to 2. The colour of background did not have any impact on the quality of the reconstruction as long as good segmentation was obtained.

The segmentation processing was run until the result was acceptable according to qualitative visualisation (i.e. good segmentation as opposed to poor segmentation Figure 4.4). K-means initialises centroids randomly and therefore different runs of the algorithm can produce different results. The processing time for one image takes from 10 to 40 seconds depending on the centroid initialisation, number of centroids, size of the images, and also the time for the user to evaluate if the segmentation is good enough. For more details see (Kanungo et al., 2002).

![Figure 4.4: Pre-processed image showing examples of segmentation quality from the same single L3 vertebra. A) Poor segmentation; B) Good segmentation.](image)

3D Construction of Vertebrae Models

The 3D construction was performed using an image-based algorithm. An educational licence was acquired to use Agisoft PhotoScan software\(^7\) on a Dell PowerEdge R815 with 64 cores and 512GB RAM (Dell Corp., Austin, TX). The operating system was CentOS\(^8\) 6.2 (64-bit Linux). It can also run on a standard desktop, but the performance depends highly on the specifications of the machine used. The software takes as input all available segmented images and produces a 3D model in the form of a triangle-based surface mesh and a 3D point cloud. Camera calibration is done automatically by PhotoScan using well established methods as presented in Section 4.2 in passive scanning. Initial intrinsic parameters are obtained from image EXIF data and are

\(^7\)http://www.agisoft.com
\(^8\)http://www.centos.org
then optimised along with extrinsic parameters\(^9\). It took approximately five hours of computer time to produce a single model from images of an individual vertebra; once the computer modelling was initiated, no supervision of the process was required. In Agisoft PhotoScan, users can choose between three different accuracies: high, medium, and low. Pair pre-selection can be either disabled or generic, which means looking for pairs of images that overlap then matching them; this function can be used to help reduce processing time\(^10\). In this instance, high accuracy was used and pre-selection disabled but if the reconstruction failed, we changed the parameters for pre-selection and lowered the accuracy of reconstruction.

3D Models Post-Processing

Once the 3D models were constructed, a post-processing step was used to remove spurious model parts as on occasion the Blu-tack was reconstructed as part of the model. This was performed in MeshLab by removing visible vertices that obviously did not belong to the vertebra, while simultaneously visually verifying that the digital reconstruction of the vertebra was consistent with the physical specimen.

PhotoScan sometimes generated disconnected triangles and vertices that did not belong to the surface, duplicated vertices that might generate edges with zero length, and surfaces with zero area. Furthermore, the topology of the object is not necessarily respected in the reconstructed model. The filling tool of MeshLab was used to generate closed object models. Duplicated vertices, zero length edges and zero area triangles were removed from the model programmatically. The vertebral foramen, the hole on the posterior aspect of the vertebra that usually contains the spinal cord, was not considered for this reconstruction because the focus was on reconstructing the complex, external bony shape of the vertebrae in the first instance.

4.3.3 3D Reconstruction Validation

The image-based reconstruction was validated by directly comparing the models from the arm scanning and real vertebrae after alignment. The image-based method does not respect the original scale so alignment is required. The models were roughly aligned manually, and then the Iterative Closest Point algorithm (ICP) (Besl and McKay, 1992) (Algorithm 4.2) was used to more precisely align the image-based models to the

\(^9\)http://downloads.agisoft.ru/pdf/photoscan-pro_0_8_5_en.pdf

\(^{10}\)personal communication with Agisoft (September 30, 2013)
arm scanning models, thus fixing the scale of the image-based models. Then manual measurements of the five distances as presented in Section 4.3.1 were performed.

**Algorithm 4.2: Iterative Closest Point Algorithm.**

**Input:** $S_f$: First sample supposed to be fixed; $S_m$: Second sample supposed to move towards $S_f$; Define initial transformation of $S_m$.

**Output:** $S_m$ transformed under rigid parameters.

1: repeat
2:  $\forall p \in S_m \mid x = \arg\min_{y \in S_f} ||p - y||$
3:  $S_m = T(S_m) \mid T = \arg\min_{r \in \mathbb{R}^3 \rightarrow \mathbb{R}^3} \sum_{p \in S_m} ||r(p) - x||$
4: until Convergence or maximum iterations exceeded
5: Return

### 4.4 Results

#### 4.4.1 Arm Scanning Models

**Manual Measurements**

The measurements taken from real vertebrae are presented in Table 4.1. The distance between most lateral points of the two transverse processes was between 53.3 and 90.7 millimetres, while the width of the vertebral body ranged between 20.9 and 27.2 millimetres. The height of the vertebral body ranged between 41.4 and 57.3 millimetres, and the anterior-posterior length of vertebral body was between 28.6 and 40.3 millimetres. Finally, the anterior-posterior distance between the anterior edge of the vertebral body and the posterior tip of the spinous process was between 65.8 and 96.2 millimetres.
### Arm Scanning Validation

<table>
<thead>
<tr>
<th>Vertebra Number</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Arm Scanning</strong></td>
<td><strong>A</strong></td>
<td>56.0</td>
<td>81.6</td>
<td>90.4</td>
<td>65.2</td>
<td>69.6</td>
<td>63.2</td>
<td>79.0</td>
<td>73.2</td>
<td>53.5</td>
</tr>
<tr>
<td><strong>Models (mm)</strong></td>
<td><strong>B</strong></td>
<td>26.6</td>
<td>25.3</td>
<td>27.5</td>
<td>22.1</td>
<td>22.3</td>
<td>20.4</td>
<td>23.6</td>
<td>22.5</td>
<td>24.6</td>
</tr>
<tr>
<td><strong>C</strong></td>
<td>51.1</td>
<td>53.3</td>
<td>57.6</td>
<td>40.7</td>
<td>43.8</td>
<td>47.2</td>
<td>42.7</td>
<td>43.5</td>
<td>45.3</td>
<td>48.2</td>
</tr>
<tr>
<td><strong>D</strong></td>
<td>38.6</td>
<td>38.7</td>
<td>37.0</td>
<td>28.1</td>
<td>28.5</td>
<td>30.7</td>
<td>31.1</td>
<td>33.5</td>
<td>33.8</td>
<td>33.2</td>
</tr>
<tr>
<td><strong>E</strong></td>
<td>89.9</td>
<td>94.5</td>
<td>81.8</td>
<td>65.9</td>
<td>69.9</td>
<td>68.0</td>
<td>71.6</td>
<td>69.2</td>
<td>72.6</td>
<td>66.9</td>
</tr>
<tr>
<td><strong>Real</strong></td>
<td><strong>A</strong></td>
<td>55.7</td>
<td>81.8</td>
<td>90.7</td>
<td>66.0</td>
<td>70.1</td>
<td>64.3</td>
<td>79.1</td>
<td>74.1</td>
<td>53.3</td>
</tr>
<tr>
<td><strong>Models (mm)</strong></td>
<td><strong>B</strong></td>
<td>27.2</td>
<td>26.1</td>
<td>27.0</td>
<td>23.2</td>
<td>22.0</td>
<td>20.9</td>
<td>24.1</td>
<td>22.5</td>
<td>24.8</td>
</tr>
<tr>
<td><strong>C</strong></td>
<td>51.9</td>
<td>54.4</td>
<td>57.3</td>
<td>41.4</td>
<td>43.5</td>
<td>47.6</td>
<td>42.4</td>
<td>43.8</td>
<td>45.6</td>
<td>48.2</td>
</tr>
<tr>
<td><strong>D</strong></td>
<td>40.3</td>
<td>39.3</td>
<td>36.9</td>
<td>28.7</td>
<td>28.6</td>
<td>31.1</td>
<td>31.6</td>
<td>33.0</td>
<td>34.0</td>
<td>33.3</td>
</tr>
<tr>
<td><strong>E</strong></td>
<td>91.5</td>
<td>96.2</td>
<td>83.1</td>
<td>65.8</td>
<td>69.4</td>
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<td>69.9</td>
<td>75.2</td>
<td>66.5</td>
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<tr>
<td><strong>Absolute</strong></td>
<td><strong>A</strong></td>
<td>0.3</td>
<td>0.2</td>
<td>0.3</td>
<td>0.8</td>
<td>0.5</td>
<td>1.1</td>
<td>0.1</td>
<td>0.9</td>
<td>0.2</td>
</tr>
<tr>
<td><strong>Error (mm)</strong></td>
<td><strong>B</strong></td>
<td>0.6</td>
<td>0.8</td>
<td>0.5</td>
<td>1.1</td>
<td>0.3</td>
<td>0.5</td>
<td>0.5</td>
<td>0.0</td>
<td>0.2</td>
</tr>
<tr>
<td><strong>C</strong></td>
<td>0.8</td>
<td>1.1</td>
<td>0.3</td>
<td>0.7</td>
<td>0.3</td>
<td>0.4</td>
<td>0.3</td>
<td>0.3</td>
<td>0.3</td>
<td>0.0</td>
</tr>
<tr>
<td><strong>D</strong></td>
<td>1.7</td>
<td>0.6</td>
<td>0.1</td>
<td>0.6</td>
<td>0.1</td>
<td>0.4</td>
<td>0.5</td>
<td>0.5</td>
<td>0.2</td>
<td>0.1</td>
</tr>
<tr>
<td><strong>E</strong></td>
<td>1.6</td>
<td>1.7</td>
<td>1.3</td>
<td>0.1</td>
<td>0.5</td>
<td>0.1</td>
<td>0.2</td>
<td>0.7</td>
<td>2.6</td>
<td>0.4</td>
</tr>
<tr>
<td><strong>Relative</strong></td>
<td><strong>A</strong></td>
<td>0.5</td>
<td>0.2</td>
<td>0.3</td>
<td>1.2</td>
<td>0.7</td>
<td>1.7</td>
<td>0.1</td>
<td>1.2</td>
<td>0.3</td>
</tr>
<tr>
<td><strong>Error (%)</strong></td>
<td><strong>B</strong></td>
<td>2.2</td>
<td>3.1</td>
<td>1.8</td>
<td>4.8</td>
<td>1.3</td>
<td>2.4</td>
<td>2.0</td>
<td>0.0</td>
<td>0.8</td>
</tr>
<tr>
<td><strong>C</strong></td>
<td>1.5</td>
<td>2.0</td>
<td>0.5</td>
<td>1.7</td>
<td>0.6</td>
<td>0.8</td>
<td>0.7</td>
<td>0.6</td>
<td>0.6</td>
<td>0.0</td>
</tr>
<tr>
<td><strong>D</strong></td>
<td>4.3</td>
<td>1.5</td>
<td>0.2</td>
<td>2.1</td>
<td>0.3</td>
<td>1.2</td>
<td>1.5</td>
<td>1.5</td>
<td>0.5</td>
<td>0.3</td>
</tr>
<tr>
<td><strong>E</strong></td>
<td>1.7</td>
<td>1.7</td>
<td>1.5</td>
<td>0.1</td>
<td>0.7</td>
<td>0.1</td>
<td>0.2</td>
<td>1.0</td>
<td>3.5</td>
<td>0.5</td>
</tr>
</tbody>
</table>

Table 4.1: Data on the five different measurements of each sampled vertebra. Differences between the measurements on the real vertebrae using the callipers with an error of +/- 0.01 millimetres, and the models constructed with arm scanning. Model measurements were made using MeshLab’s measurement tool. The absolute error in millimetres and the percentage of relative error are given. 1-10) Numbers indicate individual vertebrae. A) Distance between most lateral points of the two transverse processes; B) Height of the vertebral body; C) Width of the vertebral body; D) Anterior-posterior length of vertebral body; E) Anterior-posterior distance between the anterior edge of the vertebral body and the posterior tip of spinous process.
**Arm Scanning Models**

Arm scanning models are shown in Figure 4.5. The presented models are not whole and complete; some parts are missing, especially around the region incorporating the spinal canal. The manual measurements of the arm scanning models were repeated five times for each physical parameter measured to minimise the human error using the measurement tool of Meshlab. The distances are presented in Table 4.1.

*Figure 4.5: Different views of the vertebrae constructed by arm scanner.*
Figure 4.6: Histogram of relative errors of different comparisons. The first histogram looks better as it is compacted to the left and higher count. This was to be the case as arm scanning models are better 3D reconstruction than image-based models.
4.4.2 Validation of Arm Scanning Models

The differences between the distances measured on real vertebrae (manually measured with electronic callipers) and arm scanning models are shown in Table 4.1. The maximum difference between the real vertebrae and the models constructed by arm scanning is 4.8 per cent (mean 1.1%, standard deviation 1.0%). The first histogram of Figure 4.6 shows the histogram of relative errors between arm scanning models and real vertebrae. A Bland-Altman analysis (Bland and Altman, 1986) indicates that the 95% confidence interval for the arm scanning models versus real vertebrae using calliper measurements is between -0.9 and 1.7 millimetres.

4.4.3 3D Reconstruction Data

Photographic Images

Figure 4.2 shows examples of the image dataset of the same vertebra from different angles. The first row shows the camera raised by 10 cm from the horizon. The second row is at the horizon. The vertebra was mounted in four different positions. Images presented are examples of those used for reconstruction.

3D Models Visualisation

In this section we present 10 out of 86 vertebrae of this data set (see Figure 4.7). Vertebrae are presented from different angles to have a better view of the data set. These 10 vertebrae match those constructed with arm scanning. As can be seen in Figure 4.7 there are some models containing the spinal canal and others not. Across the whole data set, 29 models contain the canal and 57 models do not. For our study the reconstruction of the spinal canal has been ignored.
4.4.4 Validation of 3D Reconstruction Data

Image-based models were compared with the real vertebrae and the models generated by the arm-scanner. The difference of relative errors and absolute errors between real vertebrae and the image-based models are shown in Table 4.2. As performed previously for validating the arm scanning models, a similar comparison was performed between image-based models and real vertebrae. The maximum relative error indicated is 19.1% with a mean relative error of 5.2% and a standard deviation of 4.2%. The second
histogram of Figure 4.6 shows the histogram of the relative errors shown in Table 4.2. A Bland-Altman analysis (Bland and Altman, 1986) indicates that 95% confidence interval for the image-based models versus real vertebrae using calliper measurements is -4.4 to +/- 5.4 millimetres.

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Table 4.2: The differences in the five distances between the image-based models and the real vertebrae. Entries marked * indicate that the data was not constructed so could not be compared. 1-10) Numbers indicate individual vertebrae. A) Distance between most lateral points of the two transverse processes; B) Height of the vertebral body; C) Width of the vertebral body; D) Anterior-posterior length of vertebral body; E) Anterior-posterior distance between anterior edge of the vertebral body and the posterior tip of spinous process.

The differences between the distances measured on arm scanning models and image-based models are shown in Table 4.3. The maximum relative error was 17.3%, the mean error is 4.7% and the standard deviation 4.1%. The third histogram of Figure 4.6 shows the histogram of errors between image-based models and arm scanning models. A Bland-Altman analysis (Bland and Altman, 1986) indicates that 95% confidence interval for the image-based models versus arm scanning models is -4.8 to 5 millimetres.
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Table 4.3: The differences in the five distances between the image-based models and the arm scanning models. Entries marked * indicate that the data was not constructed so could not be compared. 1-10) Numbers indicate individual vertebrae. A) Distance between most lateral points of the two transverse processes; B) Height of the vertebral body; C) Width of the vertebral body; D) Anterior-posterior length of vertebral body; E) Anterior-posterior distance between anterior edge of the vertebral body and the posterior tip of spinous process.
The distribution of errors for all vertices when comparing the arm scanning models and image-based models is shown in Figure 4.8. Statistical analysis indicates that 95% of vertices’ errors are less than 3.5 millimetres with a median of 1.1.

Data in Figure 4.8 indicates that the worst matching vertebra has 90% of vertices less than four millimetres, 75% less than three millimetres, and 57% less than two millimetres. Figure 4.9 shows heat maps of errors for four example vertebrae.

**Figure 4.8:** Distribution of the errors between the arm scanning and image-based models of the ten vertebrae, after post-processing. The x-axis represents the distance in millimeters and the y-axis represents the percentage of the vertices of the vertebra having that error or smaller. 57% and 90% of vertices are less than two and four mm error respectively for the worst case among the 10 chosen vertebrae.

The image-based method sometimes constructs extra details that are not required, such as the Blu-tack. If there are visible, superfluous items on the images, these parts are removed during post processing. To get a closed manifold after removing these parts, the models were filled with extra faces to close the mesh. The algorithm does not always fit the shapes smoothly; this is demonstrated in the irregularity of the images of vertebrae 4 and 9 in Figure 4.7. We can see the models generated by arm scanning look less smooth compared to those generated by the image-based method because PhotoScan uses smooth surfaces by default, whereas the arm scanning models are not smoothed. Arm scanning models could be smoothed (e.g. as Poisson surfaces (Kazhdan et al., 2006)), but since it makes little difference to model accuracy, this was not done.
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**Figure 4.9:** Heat map of the errors of the two best vertebrae shown in Figure 4.8 and the two worst. The numbers shown represent millimetres and the colours represent the scale. The vertebrae numbering corresponds to the legend in Figure 4.8.
4.5 Discussion

This study has examined an inexpensive method of providing a 3D reconstruction of a complex anatomical shape. Results indicate success in regards to providing a 3D reconstruction of human vertebrae with 95% of vertices’ errors less than 3.5 millimetres with a median of 1.1 millimetres.

Single human vertebrae are commonly available around the world (Le Bras et al., 2003; Varol et al., 2006) however they have been mostly used for physical measurements (e.g. population parameters) and not for 3D reconstruction. If accessed and processed using 3D modelling, these models could generate larger data sets of lumbar vertebrae that could be used for shape modelling and analysis. 3D model data sets of bony structures are an essential component in understanding the variation of body shape in the human population. Making such databases publicly available helps to advance the state-of-the-art in various medical and anatomical fields. The process of using callipers to measure real bone shape has been widely used especially in quantitative morphometric studies (Hurxthal, 1968; Zamora et al., 2003; Gour et al., 2011; Varol et al., 2006; Kanani et al., 2012) and is considered the standard method for vertebrae measurements. However, using callipers is insufficient for constructing 3D models of bone shape, and such models are desirable for automatic and semi-automatic interpretation of medical images.

This study used between 240 and 320 images of every individual vertebra for constructing each model. We have not investigated whether this number is optimal. Generally, we need a large number of views to cover the whole object to be able to model the object completely, however this takes a longer amount of time because of the photography and image analysis process using the software. The closer the camera is positioned to the object, the more detail, precision and accuracy can be obtained in regards to the quality of image acquired. Furthermore, increasing the f-stop from that used in this study (8.0) may also facilitate an improvement in image analysis.

The high number of views used in this study was needed because vertebrae are complex shapes; fewer images might be appropriate but we have not investigated this systematically. In this respect, it was determined that a high number of images was required to assist this process. Katz and Friess (2014) used 65-85 views in a similar process to construct models of human crania, indicating that for some anatomical shapes far fewer images could be used to produce 3D models of acceptable quality. The main advantage of image-based approaches is cost, at the expense of some accuracy.
The models produced were accurate enough visually, with, in the worst case, 90% of reconstructed points being within 4 millimetres of arm scanning models. Given the likely variability in spinal morphology across the population, small reconstruction errors are of little importance if the goal is to build a statistical model of vertebra variability, such as an ASM (Cootes et al., 1995). A further advantage is that the equipment required is very portable and is able to be easily applied in the field and in challenging environments such as underwater. Image-based methods do not appear to require significantly more human time than active scanner methods, although they do require more computer time. Neither method works for internal structures in vivo, for which CT, MRI and ultra-sound are currently the most common approaches.

Other low-cost 3D reconstruction tools have been developed such as KinectFusion (Newcombe et al., 2011; Izadi et al., 2011) based on Microsoft’s Kinect sensor. KinectFusion reconstructs 3D models in real time, and is ideal for medium sized objects or scenes. For smaller objects, however, the resolution is limited to 1-2 millimetres per voxel. Meister et al. (2012) independently evaluated KinectFusion and found that it was suitable when ten millimetre resolution in world coordinates were sufficient (75% of surface points were within ten millimetres of ground truth). Our results show that for the worst scanned vertebra 75% of the surface points were within four millimetres of the ground truth.

We also initially experimented with the Kinect 1 as a tool for 3D reconstruction, but found the resolution of disparity image was too low (640 × 480 pixels) for our purposes. These drawbacks make the models much less dense which is confirmed by Khoshelham and Elberink (2012). However, KinectFusion could still be useful for many applications, especially given its speed and ease of use.

Limitations
The method used in this study does have several limitations. It is less accurate than active scanning methods which are preferred if high accuracy is needed. In particular, highly concave object parts, or holes, are often poorly reconstructed - such as the vertebral foramen which was poorly reconstructed in this study. Furthermore, the scale of reconstructed models is arbitrary and if a metric reconstruction is needed, then at least one physical measurement of the object is required. Also, the use of horizontal and vertical calibrated scale bars around the object could guarantee better geometric quality of the modelled objects, since the scale bars can be measured precisely in the high resolution images. The structure from motion technique used by PhotoScan also
has limitations as it can fail to find the right sequential bundle in a large set of images (Remondino et al., 2012), which happens in some cases in our reconstruction. We found that setting PhotoScan to construct lower resolution models solved this problem. Additionally, manual editing of the resulting models is often needed to remove gross errors.

Finally, the data set generated is certainly non representative to the general population because of the homogeneity of the models used. The vertebrae are all from the same spinal region and included none with pathology. Anatomically, they are representative of “normal” vertebrae, but may not represent the general population, with different ethnicity and origins. However, the method could be used to generate more representative data with little cost if access to appropriate specimens was available.

4.6 Conclusion

This study has illustrated a cost effective method for constructing a 3D model of a complicated anatomical shape such as the human vertebrae and has shown that such a method, while not as accurate as active scanning approaches, is accurate enough for several applications including visualisation and for constructing statistical shape models. Although these methods have been used on similar problems previously (notably human crania), they have not been applied to such a large collection of complex anatomical shapes. Both the images and the reconstructed dataset are provided for future use of the research community. The models are in the following repository "3D Lumbar Vertebrae Data Set"\footnote{http://dx.doi.org/10.6084/m9.figshare.3493643}, and the images are provided upon request as the size is about 1Gb per vertebra. The source code of segmentation and post processing is also available. As far as we are aware, no such public repository for human vertebrae currently exists. Additional investigations are required across different user groups to further validate the generated data and determine its usefulness across applications.
Chapter 5

3D Statistical Shape Models of Lumbar Vertebrae

5.1 Overview

The purpose of this chapter is to create SSMs of lumbar vertebrae in a 3D space using the data set generated in Chapter 4. To generate SSMs of lumbar vertebrae, we need to set the corresponding points between models of lumbar vertebrae. Getting the correspondences is a complex problem due to the nonrigid transformation of the shapes. Even for anatomists, landmarking vertebrae is a tedious task and potentially contains a large error margin, especially in 3D space because it is hard to visualise and select the right vertex on a 2D screen. We investigate here the application of the Spherical Demons Algorithm (SDA) (Yeo et al., 2008, 2010) to obtain these correspondences as a landmark free algorithm. SDA requires the models to be parameterised on spheres, which should be initially roughly aligned. Therefore we need a bijective map between the triangular mesh and a sphere. We use the method of Athanasiadis and Fudos (2011) to produce the map because it is parallelisable and can be used for large meshes. Briefly, the method iteratively morphs the shape to a sphere by maintaining local distances as best it can. For the initial alignment, we used Iterative Closest Point (ICP). The ICP algorithm is presented first, then we present the spherical parameterisation algorithm. Finally the spherical demons algorithm is applied and SSMs of each vertebrae are generated.
5.2 Introduction

Active Shape Models, as introduced by Cootes et al. (1992); Cootes and Taylor (1992); Cootes et al. (1995), almost always use landmarks to capture the variation of shape in a population. However, this can lead to difficulties in defining and localising landmarks; issues which can create high user workloads and significant errors if the landmarks are poorly localised. In anatomical structures there are very few true landmarks and these are typically characterised by intersections of different structures. Hence, for complicated shapes, practitioners often revert to “almost” landmarks that are defined geometrically to give enough data to capture shape variation. Unfortunately most such landmarks are poorly defined and poorly localised, leading to a source of potential error. One alternative to using landmarks is to use smooth mapping functions directly between shapes. An example using mappings on 2D shapes is given by McCane (2013). For 3D shapes the situation is more complicated (Figure 5.1), but we report here on using spherical demons (Yeo et al., 2008, 2010) for building and matching SSMs of lumbar vertebra.

Figure 5.1: Having two 3D vertebrae in 3D space, there are difficulties to select the corresponding points between the two models. They may have different number of vertices, some parts missing, different scales and different abnormalities etc.

As finding correspondences between 3D models is hard, we represent each vertebra by a sphere (there is a bijective mapping between the spheres and the vertebrae) then we align the spheres using SDA. We can then retrieve the corresponding points on 3D vertebrae.
Figure 5.2: Having two 3D vertebrae in 3D space, we represent each vertebra on a sphere as it is topologically a sphere. We define a bijective mapping between the sphere and the vertebrae. Then we align the spheres using mean curvature as geometric information and using SDA. Once the spheres are aligned, there is a bijective mapping between the spheres, with which we can retrieve the corresponding points between the vertebrae.

5.3 Material and Methods

5.3.1 Definition of Models

The models constructed in Section 4.3.2 are defined as a triangular mesh as follows:

- \( n \) 3D points/vertices - each vertex is defined by 3D coordinates \((x, y, z) \in \mathbb{R}^3\) in Cartesian coordinate system;
- In a triangular mesh containing \( p \) triangles, each edge is defined by two indices of the connected vertices. Each triangle is represented by three indices of the vertices that belong to that particular triangle.

This definition of the 3D models will be used in this research when referring to vertices, faces/triangles or edges. Figure 5.3 shows a small mesh where the black disc, red
triangles, and blue pentagrams represent vertices. The green segments are edges which form triangular faces.

Figure 5.3: The figure shows a triangular mesh (green lines), with some vertices represented as disc, triangles and pentagrams. We consider the vertex coloured black shaped as a disc, the red triangle vertices are considered as a 1-ring neighbourhood. The red triangle vertices and blue pentagram vertices are considered the 2-ring neighbourhood of the black disc vertex.

5.3.2 Initial Alignment With ICP

Besl and McKay (1992) developed the ICP algorithm which gives a rough alignment between shapes as presented in Algorithm 4.1. It is a rough alignment because it depends on the initial transformation, the solution is a local minima of the minimisation problem and the closest point as defined in ICP is not always the corresponding point.

In this section, ICP has been initialised manually with six landmarks on the vertebrae before processing. These landmarks help to find the initial transformation needed for ICP. User interaction is needed for SSMs generation only at this stage of the process.

Figure 5.4 shows these 6 black landmarks manually identified on the 3D models. They are numbered from one to six to be corresponding across the models. Four points would be enough but we added two other points to this number to get better
initialisation.

\begin{figure}[h]
\centering
\includegraphics[width=0.8\textwidth]{figure5.4}
\caption{The images show six landmarks numbered one to six and drawn in black colour. They are the landmarks used for the ICP initialisation. They were numbered so they are corresponding through all the models utilised.}
\end{figure}

\subsection{Spherical Parameterisation Algorithm}

The models are defined as presented in Section 5.3.1. Our assumptions are that the vertebrae models are closed manifolds and genus zero (topology of a sphere), and the origin of the coordinate system is at the centre of each vertebra. The vertebral foramen has been ignored as not all of the models constructed contain the vertebral foramen. Inclusion of the vertebral foramen would require a mapping between the model and a torus. This could be the subject of future research. Therefore, we used only 56 vertebrae out of 86 vertebrae generated in Chapter 4. Also, to visualise the vertebral foramen the surgeon will not take P/A and Lat radiographs as they do not contain enough information but normally use an oblique view (generally 45° from A/P view) (Simpson et al., 2009).

The goal of spherical parameterisation is to find a bijective mapping between the model defined as above and a sphere. Hence, in our case we chose to model the vertebrae surface on a sphere to be able to apply Spherical Demons (Yeo et al., 2008, 2010) as presented in the next section. The invertibility of the mapping guarantees no flipping or overlapping of the triangles of the mesh. As a consequence, there are unique correspondences between the models to be registered.

Therefore the purpose is to find a bijective function $f : \mathbb{R}^3 \leftrightarrow S^2$ defined as follows:

\begin{equation}
  f(x, y, z) = (\phi, \delta)
\end{equation}
where $\phi$ and $\delta$ represent the spherical coordinates: the polar and latitude angles respectively. $S^2$ is the unit sphere (the radius is considered as unit = 1) in 3D space. In this part, we followed Athanasiadis and Fudos (2011) because their method is parallelisable and could be used for large meshes. They used the definition of Gotsman et al. (2003) which says: “If each vertex position is expressed as some combination of the positions of its neighbours projected on the sphere (Equation 5.2), then the formed spherical triangulation is valid”. The neighbours of a vertex are defined as the vertices which are connected to a vertex by an edge in the triangular mesh in 3D space (Figure 5.3).

The equation of each vertex as a convex combination of each neighbour is as follows:

$$
\begin{align*}
\mathbf{v}_i = & \frac{\sum_{j \in N_i} \lambda_{ij} \mathbf{v}_j}{\| \sum_{j \in N_i} \lambda_{ij} \mathbf{v}_j \|} \\
\sum_{j \in N_i} \lambda_{ij} = & 1 \\
\lambda_{ij} = & \lambda_{ji} \\
\lambda_{ij} > & 0
\end{align*}
$$

(5.2)

with $\lambda_{ij}$ representing the symmetric weights $\lambda_{ij}$ and $N_i$ is the set of neighbours of the vertex $\mathbf{v}_i = (x_i, y_i, z_i) \in \mathbb{R}^3$.

The energy function is defined as follows:

$$
E(\mathbf{v}_1, \ldots, \mathbf{v}_n) = \frac{1}{2} \sum_{(i,j) \in E_d} \lambda_{ij} \| \mathbf{v}_i - \mathbf{v}_j \|^2
$$

(5.3)

where $E$ represents the energy to be optimised, $E_d$ is the set of indices of neighbouring vertices which means the set of indices of vertices that have an edge between them. In the final parameterization, we use weights $\lambda_{ij}$ as defined in Equation 5.2. And the energy function defined in Equation 5.3 will be at its minimum. Consequently the existence of $\lambda_{ij}$ guarantees that the spherical parameterization is valid.

The algorithm seeks to minimise the energy defined in Equation 5.3 using an iterative quadratic solver that could be parallelisable. The iterative procedure is presented in Algorithm 5.1. $w_{ij}$ represent the constant weights chosen which depend only on the initial mesh given. In our case, we chose normalised conformal symmetric weights.
(minimize the angular distortion). We used Equation 5.4 of (Dong et al., 2006).

\[ w_{ij} = \frac{\cot \alpha_{ij} + \cot \beta_{ij}}{\sum_{j/i,j \in E_d}(\cot \alpha_{ij} + \cot \beta_{ij})} \] (5.4)

where \( \alpha_{ij} \) and \( \beta_{ij} \) represent the angles opposite to the edge \((i, j)\) defined by vertices \(i\) and \(j\). In our experiments, we constrain \( \alpha_{ij} \) and \( \beta_{ij} \) to lie in the range between 5\(^\circ\) and 85\(^\circ\). If the angle is greater than 85\(^\circ\) then the angle is 85\(^\circ\) and if lower than 5\(^\circ\) the angle is given the value 5\(^\circ\). With this constraint on the angles, we guarantee positive weights \( w_{ij} \). Athanasiadis and Fudos (2011) experiments show that they could parameterise up to 367K triangles on the sphere in less than 23 seconds. In our context, we have meshes about 100K or fewer triangles. As a result the time required for parameterisation is reduced. The time of execution has not been calculated as parameterisation is a one step process, needed at this stage only and not repeated.

Algorithm 5.1: Iterative Procedure for Spherical Parameterisation.

**Input:** \( n \): represents number of vertices \( p_i = (x_i, y_i, z_i) \); \( w_{ij} \) represent the weight chosen which depends on original mesh; \( E_d \) edges of the mesh.

**Output:** \( n \) vertices spread on unit sphere.

1. repeat
2. for \( i=0 \) until \( n \) do
3. \( R = \sum w_{ij}Q_j \) For all neighbors \( Q_j \) of \( P_i \)
4. \( \lambda = P_i^T R - 1 \)
5. \( P_i = R - \lambda P_i \)
6. end for
7. until Convergence
8. Return

Convergence occurs when all vertices are on the unit sphere.
Results

Figure 5.5 shows one example of spherical parameterisation. The vertices lie on a unit sphere. There is a mapping between the vertebra and the sphere. Over all training data, 56 in total, each vertebra has a mapping onto the sphere after applying the spherical parameterisation. In general, it takes less than ten seconds to process a mesh depending how many resources on the GPU are used, which is not of interest in this research.

5.3.4 Spherical Demons Algorithm

Algorithm

The spherical demons algorithm matches a function defined on a sphere non-rigidly to a function defined on another sphere. The matching function requires appropriate geometric information of the object of interest to be used. The idea of spherical demons is as follows:

1. Choose any geometrical information: Gaussian curvature, mean curvature, or distance to the centre of origin of coordinate system;
2. Register the spheres that map the original models of vertebrae;
3. Spheres contain correspondences according to spherical coordinate system.

Mostly the mean curvature or Gaussian curvature is used. They are functions of minimum and maximum curvature which we will define in the next section. In what follows, we choose to use the mean curvature as the geometrical information at the vertices of vertebrae. We did not use the Gaussian curvature as it is a product of minimal and maximum curvature, and if one of them is zero then the Gaussian curvature would be zero. The minimum and the maximum curvature are the eigenvalues of the Hessian matrix of a fitting patch (detailed below) to the vertex and its neighbouring vertices. We used the full quadric patch as presented in (McIvor and Valkenburg, 1997) for noisy data and used 2-ring neighbours. The 2-ring neighbours of a vertex are defined as the neighbours, and the neighbours of the neighbours of a vertex as shown in Figure 5.3. Meyer et al. (2003) affirm that one ring neighbour is sufficient for non-noisy data but in our case the models are somewhat noisy as presented in Chapter 4, so we used 2-ring neighbours. We fitted a full quadric patch in the sense of least squares to the
neighbourhood of a vertex by:

\[ z = f(x, y) = ax^2 + by^2 + cxy + dx + ey + f \]  \hspace{1cm} (5.5)

For fitting, we calculated the normal vector \( n \) at each triangular face. If we suppose a face \( f_i \) is defined by three vertices \( v_1, v_2 \) and \( v_3 \). We defined the two edges, \( e_1 \) and \( e_2 \), as follows:

\[ e_1 = \frac{v_1 - v_2}{||v_1 - v_2||_F} \]  \hspace{1cm} (5.6)

\[ e_2 = \frac{v_1 - v_3}{||v_1 - v_2||_F} \]  \hspace{1cm} (5.7)

We define also the angle, used later, of the face \( f_i \) at the vertex \( v_1 \) by:

\[ \alpha = \arccos(e_1 \cdot e_2) \]  \hspace{1cm} (5.8)
The normal of the face is defined as:

\[ n = \frac{e_1 \wedge e_2}{||e_1 \wedge e_2||_F} \]  

(5.9)

To calculate the normal of a vertex \( v_i \), we supposed the vertex belongs to \( p \) faces associated with \( n_i \) normals with \( \alpha_i \) as angles at the vertex. The normal \( n_{vi} \) at \( v_i \) is computed as follows:

\[ n_{vi} = \sum_{i=1}^{p} \alpha_i n_i \]  

(5.10)

To describe the data locally at each vertex with a 2-ring neighbourhood, we rotate the data so the normal at the vertex is \([0, 0, 1]\) so the data (2-ring neighbourhood) can be described in \(XY\) plane instead of \(XYZ\) space. In case there is folding for 2-ring neighbourhood under the 1-ring neighbourhood (see Figure 5.6), we could represent the data just by 1-ring neighbourhood then do the fitting. In this thesis, we found the best fit from least squares with the 2-ring neighbourhood. The \(x\) and \(y\) coordinates are the local coordinates, as the vertex \( v_i \) is at the origin and the \(XY\) plane is defined by two orthogonal vectors which are orthogonal to the new normal \([0, 0, 1]\).

**Figure 5.6:** The figure shows a triangular mesh (green lines), with some vertices represented as disc, triangles and pentagrams. We illustrate the folding generated on the lower right side after projection of vertices from 3D space to 2D plane. The folding was generated as some intersecting edges are not on predefined vertices. This is in contrast to Figure 5.3 where there was no folding.
The Hessian of the full quadric patch (Equation 5.5) is as follows:

\[
H = \begin{bmatrix}
2a & c \\
2c & 2b
\end{bmatrix}
\]  
(5.11)

where \(a, b, c, d, e, f \in \mathbb{R}\), and \((x, y, z)\) are the coordinates of the neighbourhood of a vertex. From Equation 5.11 we extract the eigenvalues that we denote as \(\lambda_1\) (the highest) and \(\lambda_2\) (the lowest) which represent respectively the maximum and the minimum curvature at that vertex \(v_i\).

The Gaussian and mean curvatures \((gc, mc)\) are defined as follows:

\[
 gc = \lambda_1 \times \lambda_2 
\]  
(5.12)

\[
 mc = \frac{(\lambda_1 + \lambda_2)}{2} 
\]  
(5.13)

After calculating the mean curvature, we applied the spherical demons algorithm (Yeo et al., 2008, 2010) to register the spheres representing the 3D models of vertebrae. It is an extension of the demons algorithm from Euclidean space to spherical space. The spherical demons algorithm attempts to register models defined as spheres by a non rigid transformation of a sphere to a fixed sphere to be as “close” as possible. The problem is constrained as there are no folding of the faces or cross over of vertices between faces. With these constraints, they ensure that it is diffeomorphic so there is a bijective mapping between the two spheres (one to one mapping). In this section and subsequent sections we will define some initial notations:

- **\(F\)**: fixed sphere;
- **\(M\)**: sphere to be moved/transformed to be closer to \(F\);
- **\(\Upsilon\) and \(\Gamma\)**: two transformations from a sphere to a sphere. \(\Gamma\) is the resulting transformation we are looking for and \(\Upsilon\) is the intermediate hidden transformation for smoothing and it is assumed close enough to \(\Gamma\) at each iteration;
- **\(\Sigma\)** is in general a diagonal matrix which models the variability of a feature at a particular vertex.

Yeo et al. (2010) worked with the modified Demons objective function (Vercauteren et al., 2009; Cachier et al., 2003). The optimization is defined as follows:
\[(\Upsilon_{\text{min}}, \Gamma_{\text{min}}) = \arg \min_{\Upsilon, \Gamma} \|\Sigma^{-1}(F - M \circ \Gamma)\|_2^2 + \frac{1}{\sigma_t^2} \text{Dist}(\Upsilon, \Gamma) + \frac{1}{\sigma_t^2} \text{Reg}(\Upsilon)\]  

(5.14)

where \(\sigma_t\) and \(\sigma_x\) represent a tradeoff of second and third term of the cost function and \(\circ\) is the function composition \(((g \circ f)(x) = g(f(x)))\).

The first term of Equation 5.14 represents the similarity between the two spheres (fixed and moving). The second term is a distance between the hidden smoothing and the transformation we are seeking. The hidden smoothing should be as close as possible to the final transformation. Finally, the third term is a regularisation term of the hidden transformation. With the formulation of Equation 5.14, the authors suggested a two step sequential optimisation, the first step optimises the first two terms and the second step the last two terms of Equation 5.14. \(\Gamma\) transformation is defined as a composition of the hidden smoothing \(\Upsilon\) and \(u\) \((\Gamma = \Upsilon \circ u)\). \(u\) is a diffeomorphism defined from \(\mathbb{R}^3\) to \(\mathbb{R}^3\) parameterised by a function \(v\) which is a mapping from tangent vector space to \(\mathbb{R}^3\).

\[u = \exp(v)\]  

(5.15)

Equation 5.15 guarantees that the image points with mapping \(u\) be on the sphere. The second term of Equation 5.14 has been defined as the geodesic distance between \(\Upsilon\) and \(\Gamma\). The third term, the regularisation term, is defined as \(\|\nabla(\Upsilon - Id)\|_2^2\) (\(Id\) is the identity function), which means it penalises the gradient magnitude of \(\Upsilon - Id\).

**Experiments**

The authors of SDA provided the code used for their experiments. With all necessary routines, we adapted the code for our testing. We generated two meshes by subdivision of an icosahedron of 20 faces and 12 vertices. The subdivision at each iteration of each face is by a factor of 4 and the vertices are reprojected onto the sphere. The first mesh contains 10242 vertices and 20480 faces after 5 subdivisions. The second mesh contains 40962 vertices and 81920 faces after 6 subdivisions. This choice was made because the second mesh represents roughly the same number of vertices as in the training data. We run SDA on a multi scale registration using interpolation on the first mesh then the second mesh as defined above. For each step we used 20 iterations for the optimisation, and performed 3 registrations at each scale. The detailed method is presented in Algorithm 5.2. The initial transformation we used was the identity for
because the training data was already roughly registered using ICP algorithm.

**Algorithm 5.2:** SDA Applied on Vertebrae Spherical Parameterisations.

**Input:** $n$ spheres in training set, each vertex on sphere defined by mean curvature.

**Output:** $n$ spheres where the vertices have been displaced and vertices with the same spherical coordinates correspond.

1. **for** each level on the multi scale registration (two levels here) **do**
2. Get the level of registration on each sphere
3. **for** 1 to 3 (number of registrations) **do**
4. Interpolate the geometrical entity (mean curvature in this case) on the level
5. Calculate mean surface: average and variance of the spherical mapping of the geometrical entity (mean curvature in this case)
6. **for** each sphere represented by the scale level in training data **do**
7. Rigid registration by rotations of the variable current sphere to the mean surface
8. Optimisation of first two terms of Equation 5.14 (20 iterations, $F$ is the mean surface, $M$ is the current sphere)
9. Optimisation of last two terms of Equation 5.14 (20 iterations, $F$ is the mean surface, $M$ is the current sphere)
10. Interpolate the displacements on the original sphere
11. **end for**
12. **end for**
13. **end for**
14. Return

**Results**

The result of SDA is another sphere where the vertices have been moved on the sphere without any flipping of the faces or cross over of the faces. Figure 5.7 shows an example of displacement of the vertices on the sphere. All the points on the sphere having the same polar coordinates are corresponding.
Figure 5.7: The figure shows the displacement generated by SDA on the sphere of different vertices with different directions and different norm. The main result is that the vertices are still on the sphere and the points with same spherical coordinates are corresponding throughout the training data because there is no flipping and no overlapping.
5.3.5 3D Statistical Shape Models

Construction of SSMs

Once Spherical Demons are applied and the bijective mapping between spheres is found, the spherical parameterisations are aligned. As a consequence, the vertices with the same spherical coordinates correspond through all training data. We used the mesh with 10242 vertices (Section 5.3.4) on the sphere to represent each vertebra. As the spheres are aligned, these 10242 vertices correspond through the training data. We map these 10242 points back to the vertebrae models’ coordinate system (the inverse of spherical parameterisation). The 10242 vertices on each vertebra constitute the new training data with corresponding points through all shapes of vertebrae coordinate system. Then, we applied SSMs as presented in Chapter 3 to the coordinates of the 10242 vertices on vertebrae coordinate system. A detailed explanation is given in Appendix D, and summarised in Algorithm 5.3.

Algorithm 5.3: SSM after SDA.

Input: $n$ shapes in training set (each vertebra is represented with associated spherical parameterisation); $p$: number of vertices distributed on sphere (here 10242 which we denote by $S_d$); $D$ empty matrix of size $(3p \times n)$ representing the training data.

Output: Mean shape of training data; principal components in vertebra model coordinate system.

1: for each vertebra $\in$ training data do
2: for each vertex $v_i = (\alpha, \beta) \in S_d$ do
3: Find face $f_i$ to which $v_i$ belongs to in spherical parameterisation associated with current vertebra
4: Find Barycentric coordinates $(w_a, w_b, w_c)$ of $v_i$ in $f_i$ (Equation C.1)
5: Find the point $q_i$ in face $f_i$ in vertebra mesh using $(w_a, w_b, w_c)$
6: Add point $q_i$ to column in $D$ associated with current vertebra
7: end for
8: end for
9: $D$: as defined in equation 3.7 representing the vertebrae with $p$ 3D points.
10: Apply Algorithm 3.1
11: Calculate mean shape (Equation 3.16)
12: Calculate the covariance matrix (Equation 3.17)
13: Apply PCA.
14: Return
Results

Table 5.1 shows the total modes captured to cover 95% of the variation in the data in the Eigen analysis of active shape model of different lumbar vertebrae and total of models used for each lumbar.

<table>
<thead>
<tr>
<th>Vertebra</th>
<th>Number of Modes</th>
<th>Total of models used</th>
</tr>
</thead>
<tbody>
<tr>
<td>L1</td>
<td>11</td>
<td>16</td>
</tr>
<tr>
<td>L2</td>
<td>5</td>
<td>9</td>
</tr>
<tr>
<td>L3</td>
<td>10</td>
<td>14</td>
</tr>
<tr>
<td>L4</td>
<td>9</td>
<td>13</td>
</tr>
<tr>
<td>L5</td>
<td>3</td>
<td>4</td>
</tr>
</tbody>
</table>

Table 5.1: Results of number of modes needed to cover 95% of the variation in the data in the Eigen analysis of active shape model of different lumbar vertebrae and total of models used for each lumbar.

Table 5.2 shows the different eigenvalues associated with different eigenvectors for each lumbar vertebra. The values are times $10^{-3}$.

<table>
<thead>
<tr>
<th>L1</th>
<th>L2</th>
<th>L3</th>
<th>L4</th>
<th>L5</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.2157</td>
<td>3.3531</td>
<td>3.1911</td>
<td>3.1851</td>
<td>2.8099</td>
</tr>
<tr>
<td>1.9053</td>
<td>2.5344</td>
<td>1.6192</td>
<td>1.7971</td>
<td>2.3221</td>
</tr>
<tr>
<td>1.2883</td>
<td>1.4373</td>
<td>1.3855</td>
<td>0.9748</td>
<td></td>
</tr>
<tr>
<td>0.8028</td>
<td>1.1634</td>
<td>0.9288</td>
<td>0.8283</td>
<td></td>
</tr>
<tr>
<td>0.6486</td>
<td>0.7200</td>
<td>0.6757</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.5616</td>
<td>0.6714</td>
<td>0.5359</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.4017</td>
<td>0.5580</td>
<td>0.4533</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.3563</td>
<td>0.4766</td>
<td>0.4130</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.3108</td>
<td>0.4024</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.2919</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 5.2: Different eigenvalues obtained from Eigen analysis of different lumbar vertebrae. The values are times $10^{-3}$. The absolute values of the eigenvalues are not important but the relative values are important to compare each eigenvector variance in the data.
5.4 Results

In this section, we will present the SSM of each lumbar vertebra in this study. We will present the different mean shapes and a few of the main directions of variation of each level of lumbar vertebrae. Figure 5.8 presents two views chosen of the mean shapes generated in Section 5.3.5.

Figures 5.9, 5.10, 5.11, 5.12 and 5.13 show the impact of the first eigenvector on the mean shape compared to the second eigenvector on each of the five lumbar vertebrae. The arrows are shown in blue and red and they are in different orientations but the same direction. We can see that for the first eigenvector the arrows are larger which is explained by the fact that the related eigenvalue of the first component is higher than the eigenvalue of the second eigenvector. The arrow sizes have been chosen to represent \(-3\sigma\) and \(+3\sigma\).

Figures 5.14, 5.15, 5.16, 5.17 and 5.18 show the effect on the first eigenvector related to each of the lumbar vertebrae. The effect is visible on different parts of the vertebra. As it is hard to show a 3D model on a 2D plane, the effect shown is only in the view utilised, however, the eigenvector has an impact on whole vertebra. We have a large number of eigenvectors for each vertebra as shown in Table 5.1. So, it would be impossible to present all of them here. As each eigenvector is related to an eigenvalue and as the eigenvalues are decreasing, consequently, the impact of the first eigenvector is higher than the second one and so on till the last one which has the lowest effect because it is related to the lowest used eigenvalue which represents a low variance in the data.

Figure 5.19 shows a graphical user interface with sliders to see the impact of the eigenvector on the vertebrae. Here we represented just two eigenvectors, but the process is easily generalisable on all eigenvectors for a particular SSM of a vertebra.
<table>
<thead>
<tr>
<th>Vertebra</th>
<th>View 1</th>
<th>View 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>L1</td>
<td><img src="image1" alt="Image" /></td>
<td><img src="image2" alt="Image" /></td>
</tr>
<tr>
<td>L2</td>
<td><img src="image3" alt="Image" /></td>
<td><img src="image4" alt="Image" /></td>
</tr>
<tr>
<td>L3</td>
<td><img src="image5" alt="Image" /></td>
<td><img src="image6" alt="Image" /></td>
</tr>
<tr>
<td>L4</td>
<td><img src="image7" alt="Image" /></td>
<td><img src="image8" alt="Image" /></td>
</tr>
<tr>
<td>L5</td>
<td><img src="image9" alt="Image" /></td>
<td><img src="image10" alt="Image" /></td>
</tr>
</tbody>
</table>

Figure 5.8: Different views of the mean shapes of all levels of lumbar vertebrae in this thesis.
Figure 5.9: Comparison of first variance of eigenvector and second one for $L1$ vertebra SSM. The blue arrows show the $-3\sigma$ and red arrows the $+3\sigma$. 
Figure 5.10: Comparison of first variance of eigenvector and second one for $L2$ vertebra SSM. The blue arrows show the $-3\sigma$ and red arrows the $+3\sigma$. 
Figure 5.11: Comparison of first variance of eigenvector and second one for $L3$ vertebra SSM. The blue arrows show the $-3\sigma$ and red arrows the $+3\sigma$. 
Figure 5.12: Comparison of first variance of eigenvector and second one for $L4$ vertebra SSM. The blue arrows show the $-3\sigma$ and red arrows the $+3\sigma$. 
Figure 5.13: Comparison of first variance of eigenvector and second one for L5 vertebra SSM. The blue arrows show the -3σ and red arrows the +3σ.
Figure 5.14: Variations effect of the first eigenvector of L1 vertebra. The distribution of weight of the statistical shape model is between -3 of first $\sigma$ and +3 of first $\sigma$ with a step of .25 down the page. The shape in the centre is the mean shape of L1 vertebra. The shapes are on the same scale to be able to better visualise the effect. We choose a random view for visualisation but actually the effect is on all the vertebra not just on this view.
Figure 5.15: Variations effect of the first eigenvector of L2 vertebra. The distribution of weight of the statistical shape model is between -3 of first $\sigma$ and +3 of first $\sigma$ with a step of .25 down the page. The shape in the centre is the mean shape of L2 vertebra. The shapes are on the same scale to be able to better visualise the effect. We choose a random view for visualisation but actually the effect is on all the vertebra not just on this view.
Figure 5.16: Variations effect of the first eigenvector of L3 vertebra. The distribution of weight of the statistical shape model is between -3 of first $\sigma$ and +3 of first $\sigma$ with a step of .25 down the page. The shape in the centre is the mean shape of L3 vertebra. The shapes are on the same scale to be able to better visualise the effect. We choose a random view for visualisation but actually the effect is on all the vertebra not just on this view.
Figure 5.17: Variations effect of the first eigenvector of L4 vertebra. The distribution of weight of the statistical shape model is between -3 of first $\sigma$ and +3 of first $\sigma$ with a step of .25 down the page. The shape in the centre is the mean shape of L4 vertebra. The shapes are on the same scale to be able to better visualise the effect. We choose a random view for visualisation but actually the effect is on all the vertebra not just on this view.
Figure 5.18: Variations effect of the first eigenvector of L5 vertebra. The distribution of weight of the statistical shape model is between -3 of first $\sigma$ and +3 of first $\sigma$ with a step of .25 down the page. The shape in the centre is the mean shape of L5 vertebra. The shapes are on the same scale to be able to better visualise the effect. We choose a random view for visualisation but actually the effect is on all the vertebra not just on this view.
Figure 5.19: For a better visualisation of the impact of the eigenvectors, we developed a graphical User Interface (GUI) with sliders to be able to see the impact of the eigenvectors on the vertebrae. They can be set to see the unique impact of each eigenvector or together at the same time. The sliders go from -3 to +3 which is the interval allowed to the weight of standard deviation to have a reasonable shape. The figure shows 4 different views to be able to visualise the impact on different parts of a vertebra. Here, the sliders were at a random location, the vertebra chosen is L1 and we represented just the first two eigenvectors.
5.5 Discussion

In this section we discuss firstly the anatomical implications of the variations from $-3\sigma$ to $+3\sigma$ of the first two eigenvectors of each lumbar level. The anatomical terms have been presented in Figure 2.1. The videos of these implications are available online\(^1\) for visualisation for all the eigenvectors.

- **The impact of the first eigenvector on $L1$**
  The spinous process grows smaller till it reaches the mean shape then increases again. The vertebral body became bigger. The vertebra grew larger pedicles. The upper articular process is pushed higher of the vertebra and the lower articular process is lower. At the beginning the lower articular processes are uneven between the right and left side and at the end they almost even. The general shape of the vertebra becomes curved at the point between the vertebral body and the posterior vertebral arch;

- **The impact of the second eigenvector on $L1$**
  The vertebra becomes smaller in general as the posterior vertebral arch almost disappears, which is probably rare as a deformation. But this comes from variation in the dried vertebrae data set reconstructed due to some vertebrae being damaged. The vertebral body becomes smaller and slightly curved;

- **The impact of the first eigenvector on $L2$**
  The spinous process becomes bigger and lower. The vertebra gains bigger pedicles. The vertebral body becomes wider and smaller in length and slightly curved inside toward the posterior vertebral arch. The lower articular processes almost disappears or joins to the spinous process;

- **The impact of the second eigenvector on $L2$**
  The vertebral body becomes bigger and larger. The posterior vertebral arch almost disappears with all the components. Some deformations appear on the vertebra. The vertebra becomes more and more unsymmetrical and slightly curved on the side;

- **The impact of the first eigenvector on $L3$**
  The spinous process becomes smaller and is pushed lower. More deformities are shown on the vertebral body and also the posterior vertebral arch. The vertebral body is flatter and larger in length. The pedicles become less visible on the vertebra;

\(^1\)https://figshare.com/s/2467c7d85ea9517cde5
• The impact of the second eigenvector on \(L3\)
  The vertebral body becomes smaller but wider. The upper articular processes
  are more visible on the vertebra. The pedicles grow larger and more visible. The
  vertebra becomes somehow inflated;

• The impact of the first eigenvector on \(L4\)
  The vertebral body is slightly curved on the top and the bottom. All components
  of the posterior vertebral arch get smaller till the mean shape then bigger and
  somehow inflated evenly. The vertebral foramen gets almost visible but of course
  still a surface covering it. The surface is curved inside between the vertebral body
  and the posterior vertebral arch;

• The impact of the second eigenvector on \(L4\)
  The pedicles disappear slightly between the beginning and the end. The lower
  articular process becomes more visible. The vertebral body grows shorter but
  wider. The same for the posterior vertebral arch;

• The impact of the first eigenvector on \(L5\)
  The vertebral body becomes curved from the top and bottom. The posterior
  vertebral arch becomes more inflated but smaller when close to the mean shape.
  The upper articular process is bigger and the lower articular process smaller. The
  spinous process become shorter but wider. The vertebral foramen becomes some-
  how more visible as the surface grows more curved inside the vertebra from top
  and bottom;

• The impact of the second eigenvector on \(L5\)
  The vertebra becomes somehow longer as the spinous process gets longer. The
  vertebral body grows bigger larger on top and bottom and less wide on the sides.
  The lower articular process becomes more visible with the pedicles and also the
  upper articular processes.

A general comment could be made on the vertebrae. It seems that the variations are
more concentrated/captured on the posterior vertebral arch than the body. This may
be because the vertebral body contains more points than the posterior vertebral arch
which means the alignment can generate more variations for the posterior vertebral
arch than the vertebral body.

We have demonstrated an application of spherical demons on vertebrae to be able
to calculate the statistical shape models of lumbar vertebrae. The results show that it
is possible to do so, and the process is generalisable to different closed manifold objects.
The method needs user input for the initial alignment given to ICP algorithm, then
the whole process is automated.

Getting data for calculating statistical shape models, could be expensive and hard to validate, time consuming and subject to error, in comparison with our data collection, we did not use CT scans or MRI to generate 3D models for the SSM. We used a set of photographs for each of the dried vertebrae, and used an image-based method to be able to generate the 3D models as presented in Chapter 4. We did not use any segmentation as mentioned previously as it is time consuming and is subject to errors (André et al., 1994). The method is inexpensive and easy to use and could be applied on different objects.

Our results have some limitations such as:

- The dataset used has a limited size. The largest number of vertebrae per level is 16;
- The vertebral foramen has been ignored in our assumptions to be able to consider the vertebra as a closed manifold genus zero (topology of a sphere) and apply spherical parameterisation and spherical demons algorithm. In reality, the vertebra do contain the vertebral foramen, which is the hole that contains the spinal cord, in that case we suggest the parameterisation should be on a torus and then find the correspondences to generate SSMs;
- The variance captured by the eigenvectors is limited as the vertebrae are considered “normal” vertebrae. Another study would be to consider vertebrae with abnormalities recognised by medical doctors;
- Corresponding landmarks have been found using spherical demons, there are other methods such as FreeSurfer. This has not been applied here as Yeo et al. (2008, 2010) claim that spherical demons algorithm is faster than FreeSurfer. It would be better to do a comparison in time and results;
- The authors of spherical demons tested simultaneously with three geometrical features, a limitation of this work is the fact we worked with one. As a future work, we suggest testing with multiple geometrical information as a combination of mean curvature with Gaussian curvature and distance of each vertex to the centre of vertebra;
5.6 Conclusion

This chapter has illustrated the possibility to capture the principal components through a data set of vertebrae. Even though the number of vertebrae is small we could see the impact of these variations on the general population. We have constructed the SSMs in 3D of vertebrae. In the next two chapters we will show two applications of the SSMs with fitting functions to have active shape models working on bi-planar radiographs.
Chapter 6

3D Reconstruction of Dried Vertebrae from Bi-planar Radiographs

6.1 Overview

In this chapter, we validate the SSMs presented in Chapter 5. We reconstruct the 3D position and shape of dried vertebrae from bi-planar radiographs and validate them using five metal markers attached to dried vertebrae and the models reconstructed using an arm scanner as seen in Section 4.3.1.

6.2 Introduction

We are developing a method for 3D reconstruction of lumbar vertebrae from uncalibrated bi-planar radiographs. The idea is to use an ASM (Cootes et al., 1992; Cootes and Taylor, 1992; Cootes et al., 1995) and optimise an appropriate cost function to achieve the best match. We report on preliminary work where radiographs of a single dried vertebrae are imaged in vitro.

Such a study as far as we know has not been conducted with radiographs of dried vertebrae with embedded markers and 3D models reconstructed with an arm scanner although similar studies exist. In vitro, Baudoin et al. (2008) used 5 femurs and compared them to CT scans data. Fleute (2001) used L2 vertebra. For example for in vivo data, Clogenson et al. (2015) used CT scans to get their data (92 in total); they used manual segmentation on each slice and seven manual landmarks were used to
register the surfaces and build a SSM of the C2 vertebra. Zheng et al. (2011) also used CT scans of lumbar vertebrae to extract 3D models by a segmentation-based method. Parent et al. (2002) used a 3D digitizer to identify approximately 190 landmarks from dried lumbar and thoracic vertebrae resulting in a database of over 1000 examples. The same data set has also been used for 3D reconstruction in other studies (Benameur et al., 2003, 2005).

These methods are time consuming as it can take two hours (Clogenson et al., 2015) to segment each vertebra but once the ASM is built it can be used for segmentation. They often rely on manual anatomical landmarks that are subject to errors (André et al., 1994). Therefore the SSMs are subject to many errors, are time consuming to create and depend highly on the training set used. Since vertebrae are complicated shapes, many landmarks are needed to adequately capture the shape variation, further exacerbating time requirements and sources of error. In this chapter, we propose a method to generate SSMs of lumbar vertebrae without landmarks and show preliminary 3D reconstruction results on dried lumbar vertebrae from radiographs. The method is mostly automatic and requires very coarse segmentation only (rough bounding boxes of vertebrae).

The originality of this work resides in definition and evaluation of a process for estimating the shape and position of dried lumbar vertebrae from uncalibrated bi-planar radiographs.

6.3 Material and Methods

In this section, we detail the problem of 3D reconstruction from bi-planar radiographs of dried vertebrae. The solution is stated as a solution of an optimisation problem. The cost function is detailed below and a summary of the ASM steps in this thesis is presented.
Figure 6.1: Figure showing the setup of the sponges and the vertebra. The vertebra is placed between the sponges and was rotated manually to produce lateral and anterior-posterior radiographs.

6.3.1 Problem Statement and Representation

The problem is to calculate the translation, rotation and 3D shape of vertebrae from uncalibrated Lat and P/A radiographs as stated in Section 1.1. Figures 6.1 and 6.2 show the setup of the problem. The source (green point) is restricted to lie in a plane one meter away from the imaging plane and inside the rectangle defined by the orthogonal projection of the image corners onto that plane. This is based on the actual experiment when the radiographs of dried vertebrae were taken. We represent our problem as an optimisation problem of the different parameters which are:
1. Fifteen parameters for rigid transformations (denoted with vector \( r_p \)):
   (a) 3D position and orientation of the vertebra in each view (6 parameters per view);
   (b) 2D position of the x-ray source common to the two views;
   (c) Scale factor common to the two views. This factor is to scale the vertebra to a normalised size to fit the model;

2. Parameters for nonrigid transformations: captured by a SSM as described in Chapter 5. We denote these parameters with vector \( r_s \).

**Figure 6.2:** Figure showing the position of the source (green dot inside of the camera) according to the x-ray plane, and the vertebra position between the source and the x-ray plane as in the real world. The source of the x-ray lies in the plane parallel to the x-ray plane at 1 meter distance. The source position is constrained to a rectangle defined by the projection of the image corners.

The objective function (Equation 6.1) is the sum of squared differences between real radiograph images and simulated images (simulated radiographs) based on current parameter estimates for both views jointly.

\[
(r_{p_{\text{min}}}, r_{s_{\text{min}}}) = \arg \min_{r_p, r_s} \| I_l - X_l \|_F^2 + \| I_f - X_f \|_F^2
\]

(6.1)

where \( I \) represents the simulated radiographs as presented later in this Chapter in Section 6.3.4 and \( X \) dried vertebrae radiographs. The subscripting \( l \) and \( f \) for lateral and posterior views respectively.

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We used Matlab 2016 `fmincon` function to solve this optimisation problem using an interior-point algorithm (Byrd et al., 1999). We initialise the x-ray source at the centre of the rectangle of the projected corners on the source plane, and the vertebra with a rough rotation so it matches the direction of projection. The vertebra has been translated so its gravity centre matches the centre of the image on the image plane. The scale has been initialised manually. The weights of the modes of the active shape model are initially set to 0 and constrained to lie within 3 standard deviations of the mean.

The reconstruction process occurs in two stages. In the first stage, the model is fitted rigidly and the scale and active shape model parameters are fitted jointly on both views without specifying a common co-ordinate system. Then in the second stage, Procrustes analysis is used to align the models produced from each view and fix the relative orientation and world coordinate system between the two views.

### 6.3.2 Active Shape Models

The process for building an ASM using spherical demons involves three overall steps:

1. Clean/preprocess the data as presented in Chapter 4;
2. Build the SSM using spherical demons as the registration method as in Chapter 5;
3. Search for best pose and shape parameters to fit the models to dried vertebrae radiographs presented in this Chapter.

### 6.3.3 Bi-planar Radiographs of Dried Vertebrae

In anatomy, bi-planar radiograph imaging is the process of taking two different radiographs with different orientations (almost always orthogonal). For spinal imaging, one is in the sagittal plane and the other one the frontal plane (see Figures 1.3 and 1.4).

The vertebrae used in this study were those presented in Section 4.3.1. Radiographs of twenty dried vertebrae were acquired through Otago Radiology at Mercy Hospital in Dunedin, New Zealand.

The source of the x-ray machine and the image plane were fixed between lateral and anterior-posterior view and only the vertebra was rotated as shown in Figures 6.1 and 6.2. The vertebrae were stabilised using pieces of synthetic sponge. The radiograph
images were manually preprocessed before use to delete parts where the sponges were visible.

### 6.3.4 Simulated Radiograph Generation.

In this section, we present how an x-ray machine works and how it generates a radiograph image. The purpose of this section is to explain how to simulate radiographs of 3D models. X-rays are a type of radiation that have a wavelength between 10 to $10^{-3}$ nm and energy proportional to its frequency as all radiation Waseda et al. (2011). The x-ray photons are produced in a vacuum between an anode and a cathode. Once the photons are generated they penetrate a substance with initial intensity $i_0$. The rays go through an object/body and there are sensors on a plane behind the object to detect the received intensity. On each sensor, the intensity $i$ after absorption through a distance $d$ is given by (Waseda et al., 2011):

$$ i = i_0 \exp(-\mu d) $$

where $\mu$ is linear absorption coefficient which is a function of the wavelength, the absorbing material and has a unit inverse of distance. In general, if we have a combination of materials that the x-rays go through, the Equation 6.2 can be rewritten as follows:

$$ i = i_0 \exp(-\sum \mu_i d_i) $$

where $\sum \mu_i d_i$ represent the sum of absorption over the material components present in front of the x-rays source.

We consider a detector behind the object having sensors distributed as a grid of size $(m \times n)$. As each sensor received the intensity at that point, the result of the grid is an $m \times n$ image, denoted $I$. The image generated depends on the original intensity $i_0$, the density of the body passed through and also the wavelength. In x-ray images, the parts of the body that have thicker and higher density look brighter because Equation 6.2 is reversed. So, we reverse the equation black to white and white to black as it appears on a radiograph by subtracting the original intensity. We denote $D = [d_{ij}] \in \mathbb{R}^{m \times n}$ the matrix representing the distance $d$ traversed in the object in the direction of the source to each pixel/sensor on the detector. So Equation 6.2 becomes:

$$ I = i_0 \mathbb{1}_{m \times n} - i_0 \exp(-\mu D) $$

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where \( m \) and \( n \) represents the size of the grid and \( \mathbf{1}_{m \times n} \) represents the unit matrix (ones everywhere) with \( m \) lines and \( n \) columns and \( \exp(\mathbf{D}) = [\exp(d_{ij})] \in \mathbb{R}^{m \times n} \). As \( i_0 \) is a constant we ignore it because it depends on the initial parameters (x-ray machine). Once they are defined they are fixed and not changed during the process. To account for machine’s \( i_0 \) which scales the x-ray differently from one machine to another, we normalise the image \( I \) to 0 - 1 as presented in Equation 6.6.

\[
I = \frac{I - i_{\min}}{i_{\max} - i_{\min}}
\]

where \( i_{\min} \) and \( i_{\max} \) represent the minimum and the maximum intensities of the image \( I \) before normalisation.

The final equation of the image on the detector:

\[
I = \mathbf{1}_{m \times n} - \exp(-\mu \mathbf{D})
\]

We assume no loss outside of the object. In our experiments, Figure 6.3 shows the impact of coefficient of absorption \( \mu \) on simulated radiographs, we used \( \mu = 0.1 \) to have a better contrast of bone to compare to dried vertebrae radiographs. The choice for \( \mu \) is purely experimental. Additionally, we used the normalisation as presented in Equation 6.6.

We simulated this process on the 3D models making several simplifying assumptions. The most notable of these is that bone is of uniform density (\( \mu \) constant), and therefore the radiograph can be simulated by measuring the distance an x-ray travels through the vertebrae. The models are represented by a triangular mesh. To generate a simulated radiograph we simulate a source and a plane as shown in Figure 6.2 and the vertebra between them.
<table>
<thead>
<tr>
<th>Lateral View</th>
<th>Anterior View</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1" alt="Image" /></td>
<td><img src="image2" alt="Image" /></td>
</tr>
<tr>
<td><img src="image3" alt="Image" /></td>
<td><img src="image4" alt="Image" /></td>
</tr>
<tr>
<td><img src="image5" alt="Image" /></td>
<td><img src="image6" alt="Image" /></td>
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<tr>
<td><img src="image7" alt="Image" /></td>
<td><img src="image8" alt="Image" /></td>
</tr>
<tr>
<td><img src="image9" alt="Image" /></td>
<td><img src="image10" alt="Image" /></td>
</tr>
</tbody>
</table>

**Figure 6.3:** Impact of the density coefficient on the simulated radiographs. From the first row to the last row we used the following values: 0.01, 0.1, 0.4, 0.6, 1 and 5. For higher $\mu$ the image becomes black and white which is supposed to happen as if the density is higher the absorption is higher then the loss is almost complete in the body x-rayed.
To make the process of generating simulated radiographs somewhat efficient, we used the following procedure. All vertices of the model are projected onto the image plane by tracing a ray from the source through the vertex. Each face is represented on the plane by a triangle. The plane is subdivided into pixels according to the resolution of the radiographs as shown in Figure 6.4. For each pixel in the image, the 3D points of all triangles projecting to that pixel are computed. The 3D distances to the image plane are sorted and the total bone distance is computed by taking the distance between each pair of 3D points. In most cases there will be only two 3D points, but in complicated regions there can be 4 or very rarely 6. If we have odd numbers of points, practically, the intersection is on a vertex or the ray is contained in a plane of a face. We shift this particular ray by an epsilon and we work with the new ray. Working with floating points makes these cases rare. The total bone distance for each pixel is then used to compute the x-ray image on the detector via Equation 6.7. Algorithm 6.1 shows the process of generating simulated radiographs. Figures 6.5 and 6.6 show examples of a lateral and anterior-posterior simulated radiograph respectively.
**Figure 6.5:** Example of simulated radiograph of the Lat view of an L3 vertebra.

**Figure 6.6:** Example of simulated radiograph of the P/A view of an L3 vertebra.
Algorithm 6.1: Simulated Radiograph Generation

**Input:** $V$: set of $n$ vertices in 3D; $F$: set of $p$ triangles/faces. Each triangle is represented as three indices into $V$; $P$: image projection plane; $s$: position of the source in 3D.

**Output:** $I$: matrix representing simulated radiograph on $P$.

1: for each face $f_i \in F$ do
2: Generate the three lines through the three vertices of $f_i$ and source $s$
3: Calculate intersection of each line with plane $P$
4: Scan image plane line by line and find the intersections with the projected edges
5: Select pixels inside of the projected face $f_i$
6: for each pixel $p_i \in f_i$ do
7: Generate the line $p_i s$ through the pixel $p_i$ and source $s$
8: Find intersection $j$ between $f_i$ and the line through $p_i$ and $s$
9: Find Euclidean distance between $s$ and the intersection $j$
10: Add the distance to the buffer associated with pixel $p_i$
11: end for
12: end for
13: for each pixel $p_i \in P$ do
14: Sort $p_i$’s buffer from minimum to maximum value.
15: Calculate difference of distances of odd spaces. (The rays are in and out into the model)
16: Sum up the buffer of pixel $p_i$. We denote the sum by $d_i$
17: Apply Equation 6.7: $I_i = 1 - \exp(-\mu d_i)$
18: end for
19: Normalise image $I$ between 0 - 1
20: Return

Convergence occurs when all faces, vertices and pixels have been processed.

### 6.4 Validation and Results

Simulated radiographs defined in Section 6.3.4 are used to optimise the location and shape parameters of the models. Results are compared against ground truth which is estimated using physically attached markers as described in Section 6.4.1. To validate our algorithm, we divided the validation part into two steps, the first for the rigid parameters and the second for the SSM.
6.4.1 Embedded Markers

To validate the results of the algorithm proposed, we attached five 2mm diameter steel balls to 20 vertebrae and acquired Lat and P/A radiographs. Figure 6.7 shows a lateral radiograph with attached markers on a vertebrae and on the ruler. The same positions were manually located on the corresponding arm scanning 3D models to validate the 3D position of the vertebra in the space. We also attached 13 markers to a plastic ruler at a one centimetre spacing to give absolute scaling at the depth of the vertebrae. The markers were segmented on the radiographs with a two-stage circular Hough transform (Yuen et al., 1990; Davies, 2004). Atherton and Kerbyson (1999) phase coding method was also tested and it gives similar results. The markers on the ruler allowed us to estimate the absolute size of a pixel and hence reconstruct the 3D world to scale.

![Figure 6.7: Lateral radiograph of dried vertebrae from L3 level with steel balls segmentation.](image)

6.4.2 Rigid Validation

The purpose of the rigid validation is to validate the simulated radiograph generation in ideal conditions. For this we use radiographs of a particular vertebra and its corresponding 3D model as acquired by the arm scanner as seen in Section 4.3.1. We use an extra ten vertebrae compared to Section 4.3.1 where we used only ten vertebrae, so a total of 20 vertebrae. Optimisation was performed by minimising the sum of squares of differences between the simulated radiographs and the radiographs of dried vertebrae over the parameters of a rigid transformation as presented in Equation 6.8.

\[
(r_{p_{\text{min}}}) = \arg \min_{r_p} \| I_l - X_l \|_F^2 + \| I_f - X_f \|_F^2
\]

(6.8)
where $I$ represents the simulated radiographs as presented in Section 6.3.4 and $X$ dried vertebrae radiographs. The subscripting $l$ and $f$ for lateral and posterior views respectively.

These results were then compared to parameters estimated using the attached markers. The marker parameters (as presented in Equation 6.9) were computed by minimizing the distance between the detected markers in the radiographs and the projection of the estimated marker positions on the models using a quasi-Newton algorithm with BFGS update (Broyden, 1970) via Matlab’s fminunc.

$$(r_{p_{\text{min}}}) = \arg \min_{r_p} ||P_l - C_l||_F^2 + ||P_f - C_f||_F^2 \tag{6.9}$$

where $P$ represents the projections on the image plane of the estimated marker positions on the models and $C$ the detected markers (Section 6.4.1) in the radiographs. The subscripting $l$ and $f$ are for lateral and posterior views respectively.

Once the parameters are estimated for both optimisations, we re-project the markers from both optimisations into the lateral and the anterior-posterior views. The sum of distances (Euclidean distance) between these projections and the marker centres are compared. The distance is presented in Equation 6.10 as follows:

$$d(P, C) = \sum_{i=1}^{5} (||P_{l_i} - C_{l_i}||_F + ||P_{f_i} - C_{f_i}||_F) \tag{6.10}$$

where $P$ represents the projections of markers from either optimisation and $C$ the detected markers (Section 6.4.1) in the radiographs. The subscripting $l$ and $f$ for lateral and posterior views respectively, and $i$ represents the $i^{th}$ marker. We apply this Equation 6.10 once on marker-based optimisation and once on simulated radiograph optimisation which gives the distances $A$ and $B$ as presented in Table 6.1.

Figure 6.8 shows these different projections for one particular case. Table 6.1 shows these results in tabular form. Simulated radiograph optimisation has approximately twice the error compared to marker-based optimisation. Nevertheless, with an average error per vertebra and per marker of 2.3 mm, the visual result of the superimposition of the simulated radiograph with the dried vertebra radiograph is good enough to produce reasonable 3D pose reconstructions.
Figure 6.8: Figure showing the projections of the markers of different optimisations. The blue dots are the projections of the markers using simulated radiographs. The green dots are the projections of the markers after the markers based optimisation. And the red ones are the centre of steel balls. We cannot see some red dots because the green dots are on top of them.

<table>
<thead>
<tr>
<th>Vertebra</th>
<th>A(mm)</th>
<th>B(mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>V1</td>
<td>16.4</td>
<td>23.7</td>
</tr>
<tr>
<td>V2</td>
<td>12.4</td>
<td>22.2</td>
</tr>
<tr>
<td>V3</td>
<td>10.5</td>
<td>21.5</td>
</tr>
<tr>
<td>V4</td>
<td>11.2</td>
<td>25.2</td>
</tr>
<tr>
<td>V5</td>
<td>9.3</td>
<td>22.9</td>
</tr>
<tr>
<td>V6</td>
<td>11.3</td>
<td>21.3</td>
</tr>
<tr>
<td>V7</td>
<td>12.6</td>
<td>27.1</td>
</tr>
<tr>
<td>V8</td>
<td>10.7</td>
<td>26.6</td>
</tr>
<tr>
<td>V9</td>
<td>9.3</td>
<td>22.2</td>
</tr>
<tr>
<td>V10</td>
<td>10.2</td>
<td>27.7</td>
</tr>
<tr>
<td>V11</td>
<td>12.7</td>
<td>20.7</td>
</tr>
<tr>
<td>V12</td>
<td>13.5</td>
<td>20.5</td>
</tr>
<tr>
<td>V13</td>
<td>12.0</td>
<td>30.2</td>
</tr>
<tr>
<td>V14</td>
<td>13.6</td>
<td>18.3</td>
</tr>
<tr>
<td>V15</td>
<td>14.6</td>
<td>28.0</td>
</tr>
<tr>
<td>V16</td>
<td>12.5</td>
<td>17.5</td>
</tr>
<tr>
<td>V17</td>
<td>12.9</td>
<td>18.2</td>
</tr>
<tr>
<td>V18</td>
<td>24.8</td>
<td>37.5</td>
</tr>
<tr>
<td>V19</td>
<td>8.5</td>
<td>12.4</td>
</tr>
<tr>
<td>V20</td>
<td>11.4</td>
<td>18.0</td>
</tr>
</tbody>
</table>

Table 6.1: Comparison between the errors of the projections of the markers and the optimisation with simulated radiographs. Distance A shows the reprojection error of marker-based optimisation (ground truth). Distance B shows the reprojection error of simulated radiograph optimisation of arm scanning models. The mean error per vertebra for A measure is 12.5 mm and for B measure is 23.0 mm. The mean error per vertebra over one marker for A measure is 1.2 mm and for B measure is 2.3 mm.
6.4.3 Nonrigid Validation

To validate the SSMs, the resulting 3D model reconstruction by ASMs is compared to the 3D models generated by arm scanning and the error is shown as a heat-map where the color of the heat map represents the distance from the 3D resulting model estimate to the arm scanning estimate. The distances were estimated using ICP as per Section 4.3.3.

<table>
<thead>
<tr>
<th>Vertebra</th>
<th>Mean Error</th>
<th>Maximum</th>
<th>Minimum</th>
<th>(\sigma)</th>
</tr>
</thead>
<tbody>
<tr>
<td>V1</td>
<td>1.4</td>
<td>7.0</td>
<td>0.0</td>
<td>1.1</td>
</tr>
<tr>
<td>V2</td>
<td>1.5</td>
<td>8.7</td>
<td>0.0</td>
<td>1.2</td>
</tr>
<tr>
<td>V3</td>
<td>1.9</td>
<td>7.1</td>
<td>0.1</td>
<td>1.0</td>
</tr>
<tr>
<td>V4</td>
<td>2.5</td>
<td>9.8</td>
<td>0.1</td>
<td>1.3</td>
</tr>
<tr>
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<td>1.5</td>
<td>7.6</td>
<td>0.1</td>
<td>0.9</td>
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<tr>
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<td>7.2</td>
<td>0.0</td>
<td>1.1</td>
</tr>
<tr>
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<td>1.4</td>
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Table 6.2: Errors between ASM and arm scanning models. Measurements in millimetres.

We compare the results of ASM with 20 arm scanning models. Table 6.2 shows the comparison between arm scanning models and the 3D construction models by simulated radiograph optimisation. Figure 6.9 shows the distribution of errors over the twenty vertebrae in comparison between the registered models to radiographs of dried...
vertebrae and the arm scanning models.

**Figure 6.9:** Figure showing the distribution of errors between the 3D reconstruction from registering the ASM to dried vertebrae radiographs and arm scanning models. The distribution shows that over 91.2% of vertices for the worst case vertebra have less than five millimetres error, and 69.5% have less than three millimetres error.

Figure 6.10 shows examples of heat maps of the difference between the constructed models and the arm scanning models.

The maximum error is less than 16 millimeters with a mean error over all models less than 2.5 millimetres. As can be seen from Figure 6.10, the errors are concentrated around the edges of the model, indicating that the model has failed to capture some high frequency components of the data which is to be expected. The Figures also show that the main body of the vertebra has been quite accurately captured.

Figure 6.11 shows superposition of the dried vertebrae radiographs with the simulated radiographs. We can see that the superposition has missed in few places around the edges. Figure 6.12 shows the 3D scene of the vertebra relative to the image planes and position of the sources considered as cameras.
<table>
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<th>Lateral View</th>
<th>Superior View</th>
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<td><img src="image17" alt="Heat map" /></td>
<td><img src="image18" alt="Heat map" /></td>
</tr>
</tbody>
</table>

**Figure 6.10:** Heat maps of the errors between the arm scanning models and the ASM. The values represented are in millimetres.
Figure 6.11: Superposition of simulated and *in vitro* radiographs. We can see that the superposition has missed in few places around the edges where pixels are whiter.

6.5 Conclusion

We have demonstrated that it is possible to 3D reconstruct dried vertebrae from bi-planar radiographs. The method requires us to solve an optimisation problem. This has several limitations. It does depend on the initialisation given by the user. The solution might be local minima not a global minima. If we wanted to generate a global minima we could use simulated annealing or generate different samples at different positions and do several optimisations. The results look promising with 91.2% of vertices with an error less than five millimetres. We have demonstrated the plausibility of constructing a 3D model of a vertebra from bi-planar radiographs in the ideal case of very clean radiographs with little noise or signals from other tissues whose projection blur the projection of bones. The next step is to apply the method to “real” radiographs *in vivo.*
Figure 6.12: 3D scene of vertebra reconstructed from bi-planar radiographs. The second and third images show a zoom in at different angles.
Chapter 7

3D Reconstruction of In Vivo Human Lumbar Spine from Bi-planar Radiographs

7.1 Overview

The reconstruction of lumbar vertebrae from bi-planar radiographs can be accomplished using ASMs. In this chapter, we present a method for 3D reconstruction of in vivo human lumbar vertebrae from bi-planar radiographs. We used non calibrated radiographs to reconstruct the 3D vertebrae and a priori information stored in an active shape model. The active shape model was constructed based on spherical demons algorithm which was introduced in Chapter 5. We constructed the 3D models of the lumbar spine from bi-planar radiographs then we compared them to either CT scans or MRI models of the same individuals taken at worst case one and half years apart. A method similar to that described in Chapter 6 is used, but applied simultaneously to five lumbar vertebrae rather than just one.

7.2 Materials and Methods

In this section, we detail the problem of 3D reconstruction from in vivo bi-planar radiographs of patients with different abnormalities. The solution is stated as a solution of an optimisation problem using ASMs. The cost function is detailed below. We present the data collected from patients with some background information about them.
7.2.1 ASM and Optimisation

In this section we used the SSMs defined in Chapter 5. As in Chapter 6, the simulated radiographs are generated the same way (Section 6.3.4) and the optimisation problem is defined similarly as Equation 6.1 with slight changes as shown next. For each vertebra $L_k$ of lumbar spine, we define a bounding box $B_k$ by two corners around the vertebrae on lateral and anterior-posterior views. Matrix $B_k$ contains the coordinates $(x, y)$ of the left top and right down corners. We have ten (two views and five vertebrae) bounding boxes in this representation as shown in Figure 7.9. The new fitting function defined in this chapter is as follows:

$$\{ (r_{pmin}, r_{smin}, s_{min}, r_{lpmin}) = \arg \min_{r_p, r_s, s, r_{lp}} SSE \}$$

$$\begin{align*}
SSE &= \sum_{k} (||I_{lin} - X_{lin}||_F^2 + ||I_{fin} - X_{fin}||_F^2 + |I_{lout}| + |I_{fout}|)
\end{align*}$$

(7.1)

where $I$ and $X$ represent respectively the simulated radiographs and patient radiograph. The subscripting $l$ and $f$ represent respectively Lat and P/A views. Subscripting $in$ and $out$ represent the pixels inside and outside respectively of each bounding box $B_k$. $\mid \cdot \mid$ represents the cardinality of a set. $r_{pmin}$ parameters for rigid transformations for all five (unless radiographs show fewer vertebrae) vertebrae combined. Five vertebrae, 7 parameters for each, a total of 35 parameters for this problem. $r_{smin}$ represents shape parameters for all the vertebrae. Again, we use fewer parameters if the radiographs contain fewer vertebrae. $s_{min}$ is a vector representing the source position in 3D space. $r_{lpmin}$ is a vector representing the three rotations and translations between the P/A and Lat views, which are set to be orthogonal at initialisation. $|I_{lout}|$, $|I_{fout}|$ represent the number of pixels outside of the bounding box on the Lat image and the P/A image. The terms $I_{fout}$ and $I_{lout}$ are there to penalise pixels outside of the bounding boxes as they do not belong to the vertebrae which are delimited by the bounding boxes. But, if the projection is completely inside of the bounding box, the terms $I_{fout}$ and $I_{lout}$ are 0, and so have no effect.

7.2.2 Data Acquisition and Validation Process

In Chapter 6, we used radiographs of dried vertebrae. This chapter, and research, utilises data collected from Otago Radiology, Dunedin, New Zealand. The Ethics
Committee approval to collect data and the associated conditions are presented in Appendix F and is in accordance with New Zealand legislation. The data acquisition consisted of MRI or CT scans, and radiographs corresponding to the same patient. In the worst case the interval between radiograph and MRI/CT scans is a year and a half. The images came from healthy patients or are pathological pictures. In some pictures the whole spine is represented and in the others only some vertebrae, mainly lumbars which we are interested in. The radiographs were taken for lumbar diagnostics.

To test the 3D reconstruction from bi-planar radiographs, it was necessary to utilise radiographs of patients and their corresponding MRI or CT scans. Table 7.1 summarises the data collected from patients visiting Otago Radiology with information identifying the differing genders and ages of the patients and dates of data collection. We can see that the data is spread in age and gender. We do not have any diagnosis or information about the different abnormalities that might appear on the spine.

The images obtained from Otago Radiology were processed to do the 3D reconstruction then compared to the 3D reconstruction with the original MRI or CT scan. We used ICP (initialised as in Section 5.3.2) to compare the models produced by the bi-planar reconstruction process and models extracted from MRI or CT scans.

### 7.3 3D Reconstruction from MRI and CT Scans

We extracted the lumbar spine from the MRI and CT scans and compared them to the reconstruction done by our method in Section 7.4. The validation process has been used before in the literature where mostly CT scans are compared to the 3D reconstruction (Livyatan et al., 2003; Nikkhade-Dehkori et al., 1996; Benameur et al., 2003).

#### 7.3.1 3D Reconstruction from MRI

**MRI Alignment**

Each slice of MRI is a Digital Imaging and Communications in Medicine (DICOM) file in either plane: axial/transverse, sagittal or coronal as defined in Figure 7.1.
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</tbody>
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Table 7.1: Information about data utilised to validate our 3D models. (Do: Date of)
Much of the material presented in this section is sourced from Section C7.6.2.1.1 from (NEMA, 2011)$^1$. The purpose is to find the transformation that maps the voxel in DICOM file to the patient coordinate system for each slice. This transformation is an affine transformation represented by matrix \( A \) in the following. For each slice we define the DICOM affine formula \( A \) as follows:

\[
\begin{bmatrix}
    p_x \\
    p_y \\
    p_z \\
    1
\end{bmatrix} = \begin{bmatrix} r \\ c \\ 0 \\ 1 \end{bmatrix} A
\]

(7.2)

where :

- \( r \): Row index in the image plane/slice. The first row index is zero;
- \( c \): Column index in the image plane/slice. The first column index is zero;
- \( P = (p_x, p_y, p_z) \): The coordinates of the voxel \( P \) at position \((c, r)\) in the slice’s

image plane in units of mm;

- \( A \) represents the 3D affine transformation from the image plane to 3D coordinate system of the world.

Matrix \( A \) is defined (NEMA, 2011) as follows:

\[
A = \begin{bmatrix}
j_4 \Delta r & j_1 \Delta c & \Delta s n_1 & t_1 \\
 j_5 \Delta r & j_2 \Delta c & \Delta s n_2 & t_2 \\
 j_6 \Delta r & j_3 \Delta c & \Delta s n_3 & t_3 \\
 0 & 0 & 0 & 1 \\
\end{bmatrix}
\] (7.3)

where \( j_i \) are elements of the matrix \( B \) Image Orientation (code = (0020,0037) in DICOM file), which specifies the direction cosines of the first row and the first column with respect to the patient.

\[
B = \begin{bmatrix}j_1 & j_4 \\
 j_2 & j_5 \\
 j_3 & j_6 \end{bmatrix}
\] (7.4)

where:

- \( \Delta c \): first value of vector Column Pixel Spacing (code=(0028,0030) in DICOM file) in mm;
- \( \Delta r \): second value of Row Pixel Spacing (code=(0028,0030) in DICOM file) in mm;
- \( \Delta s \): spacing between slices (code = (0018,0088) in DICOM file) in mm;
- \( n = (n_1, n_2, n_3) = b_1 \land b_2 \) with \( b_i \) column \( i \) of \( B \);
- \( T = (t_1, t_2, t_3) \): ImagePositionPatient (code=(0020,0032) in DICOM file).

Equation 7.2 becomes with all definitions above as follows:

\[
\begin{bmatrix}p_x \\
p_y \\
p_z \\
1 \end{bmatrix} = \begin{bmatrix}
j_4 \Delta r & j_1 \Delta c & \Delta s n_1 & t_1 \\
 j_5 \Delta r & j_2 \Delta c & \Delta s n_2 & t_2 \\
 j_6 \Delta r & j_3 \Delta c & \Delta s n_3 & t_3 \\
 0 & 0 & 0 & 1 \\
\end{bmatrix} \begin{bmatrix}r \\
 c \\
 0 \\
1 \end{bmatrix}
\] (7.5)

After alignment to the same coordinate system of the slices, we have a result as shown in Figure 7.2.

**MRI Slices Pre-processing**

The slices have been pre-processed (see Figure 7.3) before the optimisation presented
Figure 7.2: Figure showing the alignments of slices. Here, we have slices in sagittal and axial planes.

in the next Section. The pre-processing consists of a Gaussian smoothing of the MRI with a $\sigma$ of 4 pixels ($\sigma = 4$). The Gaussian smoothing is as follows at each pixel of the image slice we apply:

$$ G(x, y) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{x^2 + y^2}{2\sigma^2}\right) $$  \hspace{1cm} (7.6)

Then, we apply a gradient function with central differences on the slices as follows:

$$ I(x, y) = \sqrt{\left(\frac{\partial I}{\partial x}\right)^2 + \left(\frac{\partial I}{\partial y}\right)^2} $$  \hspace{1cm} (7.7)
where $\frac{\partial I}{\partial x}$ and $\frac{\partial I}{\partial y}$ are defined as follows:

$$\frac{\partial I}{\partial x} = \frac{(I_g(x + 1) - I_g(x - 1))}{2} \quad (7.8)$$

$$\frac{\partial I}{\partial y} = \frac{(I_g(y + 1) - I_g(y - 1))}{2} \quad (7.9)$$

where $I_g$ is the image after Gaussian smoothing has been applied. This pre-processing has been used because it gave better results visually at the reconstruction and because the edges of the vertebrae were more visible on the images.

Figure 7.3: Lat and P/A slices from MRI with corresponding resulting images after pre-processing.
Optimisation Problem

To fit the ASM to the MRI slices, we optimise a problem with rigid (Euclidean similarity transformations) and nonrigid parameters. We used the SSMs to reconstruct the shape of the vertebrae with the MRI providing the cost function defined in Section 7.3.1.

Initialisation of the Optimisation Problem

We define a rectangular bounding box around each vertebrae we want to 3D reconstruct by two 2D points diagonally opposed. This has been done manually for each vertebra on each patient on one slice. It has been done in the sagittal middle slice where the vertebra contour is most likely to be visible. We do a manual transformation of the mean shape to align it with the planes in the coordinate system of the slices. Then, we translate the mean shape as its centre of gravity matches the centre of the bounding box (average of the corners). We apply the same transformation as the mean shape to the matrix $\Phi$ (Equation 3.18) of the eigenvectors of the vertebrae so both (mean shape and $\Phi$) are in the same coordinate system. This initialisation gives a rough alignment. A quick check and manual corrections are applied from time to time to make the model fit to the bounding box.

Cost Function

The model (as defined in Equation 3.18), being a triangular mesh (Section 5.3.1) intersects all or some slices (sagittal and/or axial depending on data), we calculate these intersections over all the triangles with each slice and take the negative sum of the gradients along the intersection curve. A mathematical representation is as follows:

$$\begin{align*}
\left( r_{p_{\text{min}}}, r_{s_{\text{min}}}, s_{\text{min}}, r_{l_{p_{\text{min}}}} \right) &= \arg \min_{r_{p}, r_{s}, s, r_{l_{p}}} SSE \\
SSE &= -\left( \sum_{k} M \cap S_{Ax_{k}} + \sum_{k} M \cap S_{Sag_{k}} \right)
\end{align*}$$

(7.10)

where $n$ and $p$ represent number of slices respectively in the sagittal plane and the axial plane.

The solution of the problem of intersection of a triangle with a slice is presented in Appendix E.
The Optimisation Process

The optimisation has been done using Matlab 2016 fmincon function. The rigid transformations are bounded here to speed up the process and also to prevent implausible results. The translation is allowed up to ten pixels and the rotation up to $\pi/12$ ($15^\circ$) in each rotation axis. The nonrigid parameters have been bounded by $3\sigma$. Figure 7.4 presents some individual intersections of one vertebrae with some successive slices in both sagittal and axial planes. An example of 3D reconstruction from MRI slices is presented in Figure 7.5 and the intersection of the slices with the 3D spine model is shown in Figure 7.6.

Figure 7.4: Intersection of one vertebra with some successive slices in the sagittal and axial plane.
Figure 7.5: Lat and A/P view of the 3D reconstruction from MRI slices.
Figure 7.6: Intersection of the slices in the axial plane (top image) and the sagittal plane (lower image) with the 3D lumbar spine reconstructed from MRI.
7.3.2 3D Reconstruction from CT Scans

InVesalius 3

There is already software using CT scans to extract bone structures. We used InVesalius 3 to extract the 3D models that come as a structure of 3D point clouds: 3D vertices in the 3D space, and the triangular faces connecting the vertices. InVesalius 3 is open source software for 3D reconstruction from CT and MRI. We did not use it for MRI as it did not give good results on our dataset. It has been developed by Centro de Tecnologia (CTI) da Informação Renato Archer\(^2\), in Brazil. The models produced by InVesalius 3 require some user post-processing. This has been done using Meshlab software to extract each vertebra separately and to clean the data. We present examples of the 3D reconstruction from CT scans for two different patients. Figure 7.7 represents visually a better reconstruction but still some post processing is required to separate the vertebrae. Figure 7.8 shows one of the patients where the CT scans were not taken for the whole lumbar spine.

Figure 7.7: 3D reconstruction from CT scans using InVesalius. The left image shows a Lat view, and the right image an A/P view. This reconstruction needed post processing as the data is noisy and we also separated each vertebra to compare.

\(^2\)http://www.cti.gov.br/
Figure 7.8: 3D reconstruction from CT scans using InVesalius. The top image shows a Lat view, and the lower image an A/P view. This reconstruction needed post processing as the data is noisy. In real data, the five lumbar vertebrae are not always taken.
7.4 3D Reconstruction from Bi-planar Radiographs

7.4.1 Data and Pre-processing

The radiographs used here correspond to the same patient as either the MRI or the CT-scans. The radiographs are supposed to be roughly orthogonal and one is latero-lateral and one is antero-posterior. The radiographs have been smoothed by a mean filter with a width of five pixels. This filter has been applied three times on the radiographs. This was an experimental choice.

7.4.2 Initialisation of The Optimisation

We define a rectangular bounding box around each vertebrae we want to 3D reconstruct by two 2D points diagonally opposed (Figure 7.9). This has been done manually for each one of the vertebrae for each patient on each radiograph. We do a manual transformation of the mean shape to align it with the planes in the coordinate system of the radiographs. Then, we translate the mean shape so the projection (simulated radiograph) fits the bounding box. We apply the same transformation as the mean shape to the matrix $\Phi$ (Equation 3.18) of the eigenvectors of the statistical modes so both (mean shape and $\Phi$) are in the same coordinate system. This initialisation gives a rough alignment. A quick check and manual corrections are applied from time to time to make the model fit to the bounding box.

7.4.3 Optimisation

The optimisation function used for the radiographs has been defined in Section 7.2.1. Here, we work with five lumbar vertebrae and one source, one plane of projection, the relationship between the P/A and Lat view and finally the parameters of shape. For each vertebra, we have three rotations and three translations in the 3D space and one scale, which means seven degree of freedom per vertebra. A total of 35 parameters for the 5 lumbar vertebrae. We have three parameters for the source, three rotations and three translations as relationship between the two planes of projection. So a total of 44 parameters for pose. For shape parameters, as defined in Table 5.1, we have 38 shape parameters for all lumbar vertebrae. The optimisation couldn’t be divided into two different optimisation (one for pose and one for shape parameters) because the parameters are correlated, and generating simulated radiographs gives overlapping between the vertebrae as shown in Figure 7.9. The parameters have been constrained
into intervals: two cm for translation and 15° for rotation to ensure convergence of the optimisation as they are compact intervals. To optimise this problem, we used Matlab 2016 \texttt{fmincon} function, with a step of 0.1mm for translations and 0.5° for rotations. Figure 7.10 shows a comparison of a simulated radiograph result with an \textit{in vivo} radiograph of a patient. The radiographs are much more noisy than simulated radiographs due to the simplicity of the model used to generate simulated radiographs. The \textit{in vivo} radiographs contain information about soft tissues and different organs which are not modelled in this thesis. In case of modelling different parts of the human body for simulated radiographs, we would be using the general Equation 6.3.

![Figure 7.9: Lat and P/A views of simulated radiographs of whole lumbar spine with the bounding boxes associated to each vertebra.](image)

### 7.4.4 Results

The final result achieved is a 3D visualisation of the lumbar spine as shown in Figure 7.11, also we are interested in the superimposition of the projection of the 3D model on the radiographs as shown in Figure 7.11 because there is a possibility to see if the projection of the 3D model is superposed with the actual radiograph of the patient. Figures 7.12, 7.13, 7.14, 7.15 and 7.16 show 3D reconstruction of a patient from radio-
Figure 7.10: Lat and P/A radiographs and simulated radiographs. Figure showing a comparison of a simulated radiograph result with an *in vivo* radiograph of a patient.
graphs. Figures 7.17 and 7.18 represent patients who had implants with the associated
reconstructions with the method proposed in this thesis. Some images (as in Figure
7.15) are not the same dimensions because the data provided was not.

Figure 7.11: Lat and P/A superimposition of the projection of the model on the Lat
and P/A radiographs, and Lat and A/P 3D reconstruction of a patient.
Figure 7.12: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient.
Figure 7.13: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient.
Figure 7.14: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient.
Figure 7.15: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient.
Figure 7.16: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient.
Figure 7.17: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient. The patient had implants in two different vertebrae.
Figure 7.18: Lat and P/A superimposition of the projection of the model on the Lat and P/A radiographs, and Lat and A/P 3D reconstruction of a patient. The patient had implants throughout the spine.
7.5 Results

In this section, we compare the models generated from MRI or CT scans to those generated from bi-planar radiographs. The models are first aligned using ICP then Hausdorff Distances (Aspert et al., 2002) are calculated and shown in Appendix G. Over all patients and all vertebrae we have a mean Hausdorff distance of 10.3 millimetres and a standard deviation of 3.7. Figure 7.19 shows the histogram of Hausdorff distances.

![Histogram of Hausdorff distances](image)

**Figure 7.19:** Histogram of Hausdorff distance of all patients and all vertebrae.

Figures 7.20 and 7.21 show the two vertebrae with the lowest Hausdorff distance and histogram of distances between ground truth reconstruction and bi-planar reconstruction. Figures 7.22 and 7.23 show the two vertebrae with the maximum Hausdorff distance and histogram of distances between ground truth reconstruction and bi-planar reconstruction.
Figure 7.20: Distribution of errors (both ground truth and bi-planar reconstruction) and heat map associated with the vertebra with lowest Hausdorff distance.
Figure 7.21: Distribution of errors (both ground truth and bi-planar reconstruction) and heat map associated with the vertebra with second lowest Hausdorff distance.
Figure 7.22: Distribution of errors (both ground truth and bi-planar reconstruction) and heat map associated with the vertebra with second maximum Hausdorff distance.
Figure 7.23: Distribution of errors (both ground truth and bi-planar reconstruction) and heat map associated with the vertebra with maximum Hausdorff distance.
7.6 Discussion

In this Chapter, we used radiographs of in vivo human lumbar vertebrae. We have shown the possibility of 3D reconstruction of human lumbar vertebrae from uncalibrated bi-planar radiographs.

The method requires solving an optimisation problem which has many limitations: the solution might be a local minima which may not represent the desired result. To overcome this, in general, we incorporated a step for the optimisation for each parameter. The initialisation of the user has an impact on the optimisation, which means if the optimisation does not converge to a desired solution, the user can use another initialisation. The method is limited as in the simulated radiographs we did not model the soft tissues that are present around the bones. As in this work, Benameur et al. (Benameur et al., 2003, 2005) used a simultaneous optimisation on shape and pose parameters as opposed to (Zheng et al., 2011) who used a sequential optimisation.

Although the method could reconstruct different levels or a number of selected of vertebrae, it has some limitations. It depends highly on the training data from which the SSMs have been trained. It also depends on the user interaction and how it is initialised. In this work we did not have complete information about the scene or the source intensity.

A reconstruction of a patient with implants can be seen in Figure 7.18. The Lat superposition view shows relatively good results especially for lumbars L3, L4, L5. We can see there is less precision for L1 and L2. For the P/A view, we have bad results as the radiograph is actually not a P/A, but rather between Lat and P/A views. For the patient with implants Figure 7.17, the results show better precision especially on Lat view where it is easier to see the boundaries of vertebrae. For other patients, the general problem faced is the reconstruction for spinous process, which was not constructed in most cases. This could be explained by a non uniform scaling factor which could be introduced in future work to the optimisation by integrating three different scales in the three directions of the 3D space. The optimisation fails to find the boundary of the vertebrae especially if it is occluded by soft tissues.

Additionally, in the P/A view, we remark that the transverse processes have not been constructed fully due to the fact that the training data was not good enough as the dried vertebrae used were degraded. Most of errors either visually or numerically are centred on L5 and L2. This could be explained by the fact that the SSM of these two vertebrae contain fewer modes of variations as shown in Table 5.1 due to the fact
that fewer models have been used to train the SSM. L5 has higher mean error (see Appendix G) than other vertebrae because even for an expert it is hard to see the boundary of the vertebra on radiographs as the hips occlude it especially on Lat view.

A commonly used method is making a comparison with Hausdorff distance. Unfortunately, this measure does not give enough information about the distribution of the errors. The comparison with ground truth data has a major limitation as the ground truth data and the radiographs do not have a common known coordinate system. If it was the case, there would be no need to apply ICP but a straight measure of error. The validation of the 3D reconstruction is made against MRI and CT-scan reconstructions which is considered as ground truth data. The methods of reconstruction of MRI and CT scans have not been validated in this thesis which is a limitation. They have been assessed visually but no quantitative measure has been made. There was no data available where the MRI and CT scans could be compared as the patients had either a CT or MRI scan.

Finally, the results from the superposition of the simulated radiographs and patient radiographs show there is a potential of this method for 3D reconstruction. Visually, we can see that some components have been reconstructed and others still failed to localise the boundary of the vertebra such as L2. Modelling the simulated radiographs with a unique coefficient of absorption is an important limitation to this work. The coefficient can be optimised for each patient and for each vertebra in a future work. As stated previously, the soft tissues have not been modelled. A numerical perspective with Hausdorff distances shows that the errors are large. Most of these errors are located at the extremities of vertebrae.

### 7.7 Conclusion

We have demonstrated a new method for 3D reconstruction from bi-planar uncalibrated radiographs. The method uses a priori knowledge through an active shape model, and an optimisation of a fitting function comparing simulated radiographs to radiographs of in vivo structures. The method depends on the initialisation of the user and the initial parameters of the different variables.
Chapter 8

Conclusion

8.1 Contributions

We have examined the problem of 3D reconstruction of lumbar spine from bi-planar radiographs. The only input to this process were bi-planar radiographs and some a priori information represented by active shape models of lumbar vertebrae. The method required user input to get bounding boxes around the vertebrae on both views and a manual rough alignment of the vertebrae to fit the bounding boxes. The main purpose of this research is to be able to visualise the lumbar spine in 3D from just bi-planar radiographs with minimal input of an expert and without segmenting the contours of vertebrae in radiographs. We proposed a framework for creating 3D models of vertebrae and for using those models to reconstruct the location and shape of lumbar vertebrae from bi-planar radiographs. We have contributed to research in this area in different ways. We have:

• Created a 3D surface data set of 86 human dried lumbar vertebrae from a set of images (280 on average per vertebra). The data set has been made public in the following repository “3D Lumbar Vertebrae Data Set”\(^1\);

• Defined a landmark-free framework to create statistical shape models from this data set which is automatic except the initial transformation before spherical parameterisation using ICP. The results show that is possible to generate statistical shape models of vertebrae and can be extended to any object that is topologically a sphere;

\(^1\)http://dx.doi.org/10.6084/m9.figshare.3493643
• Fitted the active shape models to radiographs of dried vertebrae. The method used a matching function between simulated radiographs and radiographs of dried vertebrae. This process was a validation of simulated radiographs in perfect conditions as the radiographs of dried vertebrae do not contain any other information except bone, no soft tissues, which is not true for radiographs of \textit{in vivo} structures. The method was set as an optimisation problem of a fitting function that compares the simulated radiographs of the 3D model in 3D space with radiographs of dried vertebrae;

• Applied the method to \textit{in vivo} vertebrae, the results have been validated against CT scans or MRI data as volumetric data is considered the most accurate method to extract 3D information \textit{in vivo}. The solution, presented in Chapter 7, is the solution of an optimisation problem of a fitting function that compares the radiographs of patients to simulated radiographs of five lumbar vertebrae.

The method can be applied to any shape, especially bone shapes for three dimensional reconstruction from bi-planar radiographs.

8.2 Limitations and Future Work

There are many ways to make this work better and for further research in this area. Some of the points would be refinement of the actual work, some of them would be generalisation of different ideas and greater scope. The different limitations/future work are presented in the sequence of how they have been introduced in the chapters of this thesis:

• In Chapter 3, ASMs were introduced using PCA. Fletcher \textit{et al.} (2004) used Principal Geodesic Analysis (PGA) for the study of non-linear shapes. In this work, we used PCA (SVD in Chapter 5) over PGA for simplicity of the method and using a technique well understood over another. As a future work, we can look at the PGA to study the SSMs of vertebrae;

• To construct the 3D vertebrae data set in Chapter 4, we used on average 280 images per vertebra which are a large number of images and time consuming to capture. To speed up this process, the impact of fewer images on 3D reconstruction of the models could be investigated in the future;
• The data set generated in Chapter 4 contained only 86 vertebrae which has some limitations as it is not large, so the data does not use a wide range of variations. The data is considered to come from “normal” spines (no back pain). We can extend the data set of vertebrae by making more models and include different abnormalities of vertebrae to be able to represent larger variations within the population and between populations. The dried vertebrae were also not in perfect condition;

• There is no comparison between the PhotoScan models and other image-based models results. A quantitative study could be made for this purpose.

• The vertebrae used for the ASM are only closed simple manifolds and genus zero. The future work could look at adapting the algorithm to non-spherical manifolds. We did not consider at all the vertebral foramen. It is not really a limitation here as the vertebral foramen will be looked at in a different angle radiograph from those used here (P/A and Lat), but it is interesting to find automatically the correspondence between vertebrae that are topologically a torus instead of a sphere;

• Generating a SSM can be done with different data sets that represent each population. The populations could be normal vertebrae versus abnormal ones. We can analyse in a future work the differences of ASM between different abnormalities, different vertebrae and different populations as (Zheng et al., 2011) who constructed ASM based on broken vertebrae and full vertebrae;

• The 3D SSMs have not been validated according to model compactness, generalisation and specificity as developed by Styner et al. (2003);

• This research did not include a SSM for the whole spine as one. This could be done in a future work. Then, we could fit the whole spine SSM to visualise in 3D the human spine from radiographs. This work would need a data set representing different spine of patients where landmarks are set either automatically or manually. It will be interesting to see the variations of the relationships between the vertebrae within the spine;

• We did not analyse the correlation between the SSM of different lumbar vertebrae to see if some variations of a vertebra are included in another one;
• While generating the simulated radiographs, the assumption of constant coefficient of absorption through the whole vertebra is made which is not true as the density of bone is different in parts of vertebrae. In different modelling, we could include this information;

• As the radiographers define energies for different part and for different views of radiographs, the simulated radiographs generated are a simplified model of the radiographs of any object. This can be improved by analysing the factor of absorption as well as the energy on the images according to the intensity of the source of x-rays. For this thesis we did not have this information as it was not collected while gathering the data;

• The initial alignment with radiographs is done roughly and manual corrections were applied. In future work, this could be automated;

• The results have been compared against ground truth data, but not from an orthopedists point of view. It will be interesting to get the opinion of orthopaedic surgeons on the usefulness of these results. This could guide the next stages to improve the models;

• This research presents a semi automatic method that could be in future work developed to an automatic method by removing the bounding box.

• The method is limited by two manual identifications from the user. The first one, while aligning the training set, was done using six landmarks manually identified on the vertebrae to ease ICP algorithm. Automatic registration could be applied by (Gelfand et al., 2005; Ayyagari et al., 2005). The second one was the alignment of the models projection on the radiographs with the radiographs. There are methods to find bone structures on radiographs automatically using ASM in 2D. We cite a couple (Roberts et al., 2006; Zheng et al., 2004) that can be incorporated in to this work in the future.

• In this work we have presented a proof-of-concept that in vitro structures are able to be reconstructed using only bi-planar radiographs of the patients utilising landmark-free ASMs. While the analysis is useful in such a case, there was not a specific target error to achieve as such. A validation between models from MRI/CT scans with those generated here is one way of validation as we considered MRI/CT as ground truth data. However, we did not validate the
accuracy of models reconstructed from MRI/CT scans. To generate the accuracy of the reconstruction, we used Hausdorff distances, there are other distances like root mean squares. The correspondences used for the Hausdorff distances were the nearest neighbour on the face. We could have found the correspondences between MRI/CT scans models and 3D reconstruction models using spherical demons algorithm and then calculated the Hausdorff distances. It is hard to interpret any accuracy found as it was easy to visualise the results. We did use the landmark-free algorithm, to avoid any errors occurring with manual identification of landmarks.

8.3 Final thoughts

The process for reconstructing lumbar spine in 3D from bi-planar radiographs described in this thesis has yielded promising experiments and results. The method could be generalisable to include thoracic and cervical vertebrae or any other bone. This proof-of-concept would benefit from more direct input from medical doctors in terms of evaluating the usefulness of this method for diagnosis through visualisation or even measurements for pre and post surgery. A validation process is an important step for any method that will potentially be used for diagnosis of medical conditions in human beings. Our hope is that this work, or part of it will be able to be validated by medical community and used for diagnosis purposes in the future.


Doneus, M., Verhoeven, G., Fera, M., Briese, C., Kucera, M., and Neubauer, W. (2011). From deposit to point cloud - a study of low-cost computer vision approaches for the straightforward documentation of archaeological excavations. *Geoinformatics FCE CTU*, 6, 81–88.


Fleute, M. (2001). Shape reconstruction for computer assisted surgery based on non-rigid registration of statistical models with intra-operative point data and X-ray images. *These de l’Université Joseph Fourier, Grenoble I*. 152


dica, 56*(212), 1–45.

tion. *Orthopedics, 10*(6), 909–915.


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Appendix A

Poster for ANZACA

The poster presented in this Appendix has been presented at ANZACA 2012.
Background

Spinal pathologies are prevalent in society and computer-generated information frequently utilised in radiological imaging. However, computer-based models that provide predictive information on spinal shape are not readily available. A preliminary model was previously built to demonstrate proof-of-concept for the development of 3D images from two plain X-rays (figure 1). This current project was undertaken to provide a more advanced model that would more accurately define the contours of individual vertebrae. Such a tool could model the spine and assist spinal diagnosis and treatment.

Method

Fifty-nine normal adult lateral lumbar spine radiographs were marked up using 24 investigator-nominated points (JC) to produce raw data (figure 2). MatLab software (Mathworks, Natick, MA) was used to create an active shape model (accounts for population shape variance) from that data (figure 3).

Twenty additional X-rays were used to evaluate the system. Five medical doctors were shown lateral lumbar X-rays with both marked-up points and resulting contour of L3 produced by the shape model (figure 4); they assessed contour accuracy for the ‘purposes of medical diagnostics and spinal modeling’ using a Likert scale (very inaccurate, inaccurate, average accuracy, accurate, very accurate).

Results

The model was constructed by aligning points from each of the radiographs and establishing the main variance in each direction (figure 3). The number of directions was limited to explain 95% of the variance in the data. The model was deemed accurate or very accurate for 60% of the contours (mean 3.8 / 5); Fleiss kappa score was 0.2.

Discussion

A computer model that can model a given contour of the L3 vertebrae was developed, however the accuracy of the current model in predicting the ‘correct’ anatomical outline was only moderate indicating further refinement is required. Potential applications could include aiding medical imaging, determining anatomical variation or assessing the effectiveness of spinal surgical interventions.

Conclusions

- A model was developed that can ‘predict’ the outline of a vertebral body
- Current accuracy levels are moderate
- Further refinement of the model is required
- The application has potential for spinal modeling
Appendix B

Poster for DWC

The poster presented in this Appendix has been presented at the symposium of The Dodd-Walls Centre For Photonic And Quantum Technologies (DWC) in July 2016, Queenstown - New Zealand. The poster was selected as the second best poster at the conference. It summarises the work that has been done in Chapter 6.
**Problem Statement**

Can we reconstruct the 3D bone structure in vivo from just two x-rays?

(a) Antero-Posterior x-ray of human spine  
(b) Latero-Lateral x-ray of human spine

- The reconstruction is an ill-posed problem
- Use of prior knowledge through 3D models of human vertebrae
- Vertebrae are difficult and complicated, but mostly smooth shapes
- Calculate the 3D variations of the data set and directions of variations
- Generate new models to fit to new data
- Find the best fit to new data x-rays

---

**Statistical Shape Models**

Using well known methods of morphological studies we could extract different variations and directions:

- In 3D, each vertebra represented with n landmarks \((x_i, y_i, z_i) \in \mathbb{R}^3\) in cartesian coordinates
- \(x = (x_1, y_1, z_1, ..., x_n, y_n, z_n)^T \in \mathbb{R}^{3n}\)
- Using N shapes, mean shape \(\hat{x}\) is defined as follows:
  \[
  \hat{x} = \frac{1}{N} \sum_{i=1}^{N} x_i 
  \]
  \(\text{(1)}\)
- and the covariance matrix as follows:
  \[
  C = \frac{1}{N} \sum_{i=1}^{N} (x_i - \hat{x})(x_i - \hat{x})^T
  \]
  \(\text{(2)}\)
- PCA on C covariance matrix
- new shape \(= \phi b + \hat{x}\) where: \(\phi\) represents the orthogonal basis of principal modes and \(b\) are the associated weights taken in general between \(-3\)SD and \(+3\)SD

- (a) Mean shape of L3 vertebra
- (b) Shape generated by mean -2SD of first principal component
- (c) Shape generated by mean +2SD of first principal component
- (d) Shape generated by mean +2SD of second principal component
- (e) Shape generated by mean +2SD of second principal component

---

**Fitting Prior Knowledge To New X-Rays**

To find the best model and location which fits best to the new x-rays we use gradient descent methods.
- Start at mean shape
- Generate pseudo x-ray
- Do a comparison with real x-ray (using a defined error metric)
- Descend along shape and relative position of x-rays planes.

(a) Antero-Posterior pseudo x-ray of human vertebra  
(b) Latero-Lateral pseudo x-ray of human vertebra

---

**3D Models Of Human Vertebrae**

How to extract 3D point clouds from images of real world?

- Use 87 models accessed through the W. D. Trotter Anatomy Museum at the Department of Anatomy, Otago School of Medical Sciences, University of Otago, New Zealand.
- Take on average 280 images around the vertebrae
- Segment the images to remove the non-vertebra parts in images
- Use an image-based technique to reconstruct 3D models (3D point clouds of vertebrae)

(a) Anterior View  
(b) Lateral View  
(c) Lateral View  
(d) Superior View

- (a) Anterior View
- (b) Lateral View
- (c) Lateral View
- (d) Superior View

---

**Conclusions, Open Problems, etc.**

- Compare results to those provided by a CT scan or/and MRI
- Construct statistical shape model for the whole spine
- Model the soft tissues to have better pseudo x-rays

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**DWC 2016, June 27 - July 1, Queenstown, New Zealand**
Appendix C

Definition of Barycentric Coordinates

Suppose we have a triangle ABC, for any point P inside the triangle or on the edges of the triangle, the coordinates of point P are defined as a weighted sum of the vertices (Tutte, 1963).

\[ P = w_a A + w_b B + w_c C \]  \hspace{1cm} (C.1)

where \( w_a, w_b \) and \( w_c \) are the weights corresponding respectively to Vertices A, B and C. To make these these weights unique, we add two constraints as follows:

\[
\begin{align*}
    w_c + w_b + w_a &= 1 \\
    \forall i \in \{a, b, c\} \quad w_i &\geq 0
\end{align*}
\]  \hspace{1cm} (C.2)
Appendix D

3D SSMs of Vertebrae

To generate the SSM, we used $S_d$ containing 10242 vertices on the sphere and 20480 triangular face. Each vertex is defined on the sphere by polar coordinates. For each vertex $v_i$ from the 10242 vertices, we get the polar coordinates of that vertex $(\alpha, \beta) \in \mathbb{R}^2$. On each spherical parameterisation, we find the point $p_i$ on the sphere that is defined by the polar coordinates $(\alpha, \beta) \in \mathbb{R}^2$. If the point $p_i \in f_i$ ($f_i$ is the face in the spherical parameterisation mesh that contains the point $p_i$). We find the barycentric coordinates $(w_a, w_b, w_c)$ of the point $p_i$ in $f_i$ according to Equation C.1 in Appendix C. The face $f_i$ on the spherical parameterisation corresponds to the face $f_i$ on the 3D vertebra, as we have correspondences between the faces of the 3D model and the spherical parameterization. We calculate the point $q_i$ using the barycentric coordinates of $p_i$ in $f_i$ in the sphere and the vertices of $f_i$ in the 3D vertebra using Equation C.1. We iterate the process for all of vertices in $S_d$, as a result we have selected 10242 vertices on the 3D vertebrae that are corresponding through all the training data. The SSM is computed as seen in Chapter 3. The alignment is done as shown in Algorithm 3.1. Once the models are aligned, we calculate the mean shape (Equation 3.16), then we apply principal components to the covariance matrix (Equation 3.17) of the data and we extract the first eigenvectors that generate more than 95% of the variance within the data as presented in Chapter 3 in Section 3.3. Applying PCA on huge data like this one (as every shape is represented in 3*10242D space), with only at the most 16 shapes in the training data in our case, is really slow and requires a lot of memory. SVD decomposition is a better method to overcome this computation as it finds at most the $r$ eigenvalues where $r$ is the rank of the matrix representing the data. SVD finds the eigenvectors and eigenvalues of the covariance matrix without the need to compute the covariance matrix.
Appendix E

Intersection of Triangular Face with a Slice

The problem is the intersection of a triangular face $f_i$ with a rectangular slice $S_i$. A rectangular slice lie on a plane. We calculate the equation of the plane:

$$S_i : ax + by + cz + d = 0 \quad (E.1)$$

by getting three point $p_1$, $p_2$ and $p_3$ not aligned. The easy way is to get the points is to take them at position $(0, 0)$, $(0, d - 1)$ an $(n - 1, 0)$ as a slice is represented as an image where $n$ and $d$ represent here respectively the height and width of the image. We calculate the normal. The normal $n$ is the cross product of $p_2 - p_1$ and $p_3 - p_1$:

$$n = (p_2 - p_1) \wedge (p_3 - p_1) \quad (E.2)$$

Then, we normalised $n$ as follows:

$$n = \frac{n}{\|n\|_F} \quad (E.3)$$

The normal defines the values $(a, b, c)$ of Equation E.1.

The value $d$ is: $-\, \text{dot product of } P_2 \text{ with the normal } n$.

$$d = -P_2 \cdot n \quad (E.4)$$

Once the values $(a, b, c, d)$ defined, Equation E.1 is well defined.

We calculated the signed distances (Equation E.5) of the vertices of the face $f_i$ to
the slice $S_i$. The signed distance of vertex $v_i$ to the plane defined by a normal $n$ and a value $d$ is: sum of the dot product of the vertex by the normal and the value $d$

$$SignedDistance(v_i) = v_i \cdot n + d$$  

(E.5)

If all distances are null, it means the triangular is in the plane we never faced this case as we work with large floating points, if it did happen we would have just subdivided the face surface so the points distances are smaller than pixel spacing. If two distances are null means the edge is part of the plane, we subdivide the edge with the pixel spacing of the corresponding slice which is defined in the DICOM file (code=(0028,0030)), we subdivide the edge as the distance between points is under the pixel spacing. This subdivision of the edge defines the points of intersection. If one distance is null, means just that vertex is on the slice, which is the intersection. If all distances are not null, the intersection is defined if at least one vertex has a positive or negative distance and two other have negative or positive distances respectively. The intersection is the segment between the points defined as the intersection of the edges that cross the slices. Again we subdivide the edge as the distance between points is under the pixel spacing.

We define the intersection of a segment and a plane. The segment extremities do not lie on the plane and they are in different sides of the plane. Let’s assume a segment defined by two points $p_A$ and $p_B$ and a plane defined with a normal $n$ and a value $d$. The point $p_M$ of intersection:

$$p_M = p_A + \left( -\frac{SignedDistance(p_A)}{SignedDistance(p_B) - SignedDistance(p_A)} \right) \cdot (p_B - p_A)$$  

(E.6)

In general if the model faces are small enough the distance of the edge which intersects the slice is smaller than the pixel spacing so we don’t need to subdivide.

The interpolation is done by interpolating the gradient image on the intersection. To speed up the interpolation we project the 3D space, to 2D space of the slice by defining two orthogonal vectors defined by the previous points $p_1$, $p_2$ and $p_3$ used to define the plane Equation E.1. Project the intersections to this new basis and then interpolate using a Triangulation-based cubic interpolation (Yang, 1986; Watson, 2013) where the values of the pixels are the intensities of the gradients.
Appendix F

Ethics
HUMAN ETHICS APPLICATION: CATEGORY A

1. University of Otago staff member responsible for project:
   A/P Brendan McCane, Computer Science Department
   Dr Jon Cornwall, Anatomy Department

2. Department:
   Computer Science

3. Contact details of staff member responsible:
   Email: mccane@cs.otago.ac.nz
   Phone: +64 3 479 8588

4. Title of project:
   Building a Three-Dimensional (3D) Computer Model of the Adult Human Spine

5. Indicate type of project and names of other investigators and students:

<table>
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<th>Staff Research</th>
<th>Names</th>
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<tbody>
<tr>
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</tr>
<tr>
<td></td>
<td>Jon Cornwall</td>
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<table>
<thead>
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<td>Hamza BENNANI</td>
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   Level of Study (e.g. PhD, Masters, Hons)
   PhD

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<th>External Research/ Collaboration</th>
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</tr>
<tr>
<td>Names</td>
</tr>
<tr>
<td>Dr Grant Meikle</td>
</tr>
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</table>

   Institute/Company
   Radiologist and Chairman, Otago Radiology
6. **Is this a repeated class teaching activity?**
   No

7. **Fast-Track procedure**
   Do you request fast-track consideration? (See ‘Filling Out Your Human Ethics Application’)
   No

8. **When will recruitment and data collection commence?**
   During June, 2013

   **When will data collection be completed?**
   It will be completed by 31st December, 2013

9. **Funding of project.**
   Is the project to be funded by an external grant?
   No

   If commercial use will be made of the data, will potential participants be made aware of this before they agree to participate? If not, please explain:
   No commercial use

10. **Brief description in lay terms of the purpose of the project** (approx. 75 words):
    The purpose of this study is to build a 3D computer model of the adult human spine by utilizing ‘real’ patient data. The gathered data (X-rays, MRIs and CT scans of patients) will be used to build and test the 3D model.

11. **Aim of project, including the research questions the project is intended to answer:**
    The aim of the project is to create a diagnostic and pedagogic tool in the form of a 3D spine modelling program. Research question: Is it possible to build an accurate 3D computer generated model of the adult human spine from bi-planar X-rays? The data gathered will be used to build a prior model and also to test the computational techniques that are developed.
12. **Researcher or instructor experience and qualifications in this research area:**

Brendan McCane is a staff member of the Department of Computer Science at Otago University. He has worked on previous projects involving medical imaging that lead to several scientific outputs such as:

Brendan McCane, Shape Variation in Outline Shapes (2013), *Systematic Biology* 62(1), 134-146

Brendan McCane, Martin R. Kean, Integration of Parts in the Facial Skeleton And Cervical Vertebrae, *American journal of orthodontics and dentofacial orthopedics* 139(1), e13-e30


B. McCane, T. King, J.H. Abbott, Calculating the 2D motion of lumbar vertebrae using splines, *Journal of Biomechanics* 39(14), 2703-2708

J H Abbott, Julie M Fritz, Brendan McCane, Barry Shultz, Peter Herbison, Brett Lyons, Georgia Stefanko, Richard M Walsh (2006), Lumbar segmental mobility disorders: Comparison of two methods of defining abnormal displacement kinematics in a cohort of patients with non-specific mechanical low back pain, *BMC Musculoskeletal Disorders* 7(45)

Dr Jon Cornwall, from the Department of Anatomy, is a qualified physiotherapist and anatomist whose research encompasses spinal morphology.
13. Participants

13(a) Population from which participants are drawn:

Patients visiting Otago Radiology from June 2013 to 31st of December 2013 for radiological investigation involving their spine.

13(b) Specify inclusion and exclusion criteria:

Inclusion: Individual adults over 25 years old, male and female, having radiological investigation of their spine, who give their consent to be part of the study. We will anonymously use their X-rays, CT scans or MRI as data for developing the computer modelling programme.

Exclusion: Extreme pathologies, children and teenagers
The extreme pathologies are excluded because they can narrow the study and bias the model towards outliers, thereby making the model too specific.
Children and teenagers (up to 25 years old) are excluded because their musculoskeletal system is not mature until the age of 25 years and their data may bias the model and render it invalid for the purposes of modelling an adult spine.

13(c) Estimated number of participants:

500

13(d) Age range of participants:

From 25 to 50 years old

13(e) Method of recruitment:

Systematic invitation to all individuals at the radiology clinic who meet the inclusion criteria until the appropriate sample size is reached.

13(f) Please specify any payment or reward to be offered:

Nil
14. Methods and Procedures:

Each patient will be invited to join the study by a staff member at the reception of Otago Radiology. Individuals will be given an information sheet if they indicate that they are interested in participating. The patient will be able to ask the staff member any questions they need to make an informed decision to join the study. A consent form will be signed for the patient’s data to be included in the study.

The data (radiological images) will be collected as image files (e.g. jpeg) and transported to the Computer Science Department using password-protected hardware. The data will be anonymised. The images will be analysed in Hamza Bennani’s computer. Data will be stored on password-protected computers in the Computer Science Department with the password known only to the principal investigators. Original data will be kept for at least 5 years and possibly indefinitely.

15. Compliance with The Privacy Act 1993 and the Health Information Privacy Code 1994 imposes strict requirements concerning the collection, use and disclosure of personal information. These questions allow the Committee to assess compliance.

15(a) Are you collecting and storing personal information directly from the individual concerned that could identify the individual?

The personal data (medical images) will be anonymous and it will not be possible to use them to identify the patient.

15(b) Are you collecting information about individuals from another source? Please explain:

No

15(c) Collecting Personal Information:

- Will you be collecting personal information?
  
  Yes, in the form of individuals age, sex, and spinal images

- Will you be informing participants of the purpose for which you are collecting the information and the uses you propose to make of it?
  
  Yes

- Will you be informing participants who will receive the information?
  
  Yes
Application Form for ethical consideration of research and teaching proposals involving human participants

- Will you inform participants of the consequences, if any, of not supplying the information?
  Yes

- Will you inform the participants of their rights of access to and correction of personal information?
  Yes

Where the answer is YES, please make sure the information is available in the Information Sheet for Participants.

15(d) Please outline your data storage and security procedures.

The data will be collected on an external hard drive, secured with a password known only by the principal investigators. A secured backup copy will be made on the Computer Science Department server. The data will not be shared on the internet or on the University of Otago or Computer Science Department network.

15(e) Who will have access to personal information, under what conditions, and subject to what safeguards?

Hamza Bennani and Brendan McCane will have full access and will be the only persons to know the password. Jon Cornwall will have access when visiting the computer science department. Access will be given by one of the previously cited persons.

Will participants have access to the information they have provided?

Data will be able to be accessed on behalf of the individual if requested. They will have normal access to these data from the radiology department as per the rights of any individual not participating in the study.

15(f) Do you intend to publish any personal information they have provided?

Yes

If YES, please specify in what form you intend to do this?

Publication of the results may include examples of images that are gathered along with age and sex matched to images. It is highly unlikely individuals would be identifiable from the publication of the images and the individuals age and sex.
15(g) Do you propose to collect demographic information to describe your sample? For example: gender, age, ethnicity, education level, etc.

Yes

15 (h) Have you, or do you propose to undertake Māori consultation? Please choose one of the options below, and delete the options that do not apply:

YES We have ALREADY undertaken consultation.

16. Does the research or teaching project involve any form of deception?

NO

17. Please disclose and discuss any potential problems: (For example: medical/legal problems, issues with disclosure, conflict of interest, etc)

18. Applicant's Signature: .................................................................

[Principal Applicant: as specified in Question 1]

Date: ............................

19. Departmental approval: I have read this application and believe it to be scientifically and ethically sound. I approve the research design. The Research proposed in this application is compatible with the University of Otago policies and I give my consent for the application to be forwarded to the University of Otago Human Ethics Committee with my recommendation that it be approved.

Signature of *Head of Department: ..........................................................

Name of Signatory (please print): ..........................................................

Date: .............................................................

[Reference Number 13/070]
[27 March 2013]
3D Modelling of the Spine
INFORMATION SHEET FOR PARTICIPANTS

Thank you for showing an interest in this project. Please read this information sheet carefully before deciding whether or not to participate. If you decide to participate we thank you. If you decide not to take part there will be no disadvantage to you and we thank you for considering our request.

What is the Aim of the Project?

The aim of this project is to construct a 3-dimensional computer model of the human spine. This model could be used by medical professionals for generating new images of the spine, and potentially could assist in visualizing the spine with less radiation for patients than current imaging protocols.

What Type of Participants are being sought?

We are looking for volunteers between 25 and 50 years old, male and female, who present for spinal radiology investigations (X-ray, CT, MRI). We would like to use the radiology images of your spine to help us build a computer model.

What will Participants be Asked to Do?

Should you agree to take part in this project, you will be asked to sign a consent form indicating that you allow us to use your spinal radiology images. We also need to record your age and sex for the research project.

What Data or Information will be Collected and What Use will be Made of it?

The data collected (images of the spine with matching age and sex) will be used to build the computer model. The information gathered will also be used in scientific publications. Although some of the images may be used within this publication, it is highly unlikely that anyone could identify you by looking at these images.

The data will be securely stored and available only to the research team. It will be retained for at least 5 years and probably more in a secure manner. This data could be an invaluable resource for other projects of this type. Therefore, we are also asking participants to use their data on future projects under the same conditions as this project.
If you would like to access the personal information you have provided for this study you can contact either of the principal investigators listed below.

**Can Participants Change their Mind and Withdraw from the Project?**

You may withdraw from participation in the project at any time and without any disadvantage to yourself of any kind.

**What if Participants have any Questions?**

If you have any questions about our project, either now or in the future, please feel free to contact either:

A/Prof Brendan McCane  
Department of Computer Science  
Telephone Number: +64 3 479 8588  
Email Address: mccane@cs.otago.ac.nz

Or

Mr Hamza Bennani  
Department of Computer Science  
Email Address: hamza@cs.otago.ac.nz

This study has been approved by the University of Otago Human Ethics Committee. If you have any concerns about the ethical conduct of the research you may contact the Committee through the Human Ethics Committee Administrator (ph 03 479 8256). Any issues you raise will be treated in confidence and investigated and you will be informed of the outcome.
3D Modelling of the Spine

CONSENT FORM FOR PARTICIPANTS

I have read the Information Sheet concerning this project and understand what it is about. All my questions have been answered to my satisfaction. I understand that I am free to request further information at any stage.

I know that:

1. My participation in the project is entirely voluntary;

2. I am free to withdraw from the project at any time without any disadvantage;

3. Raw data on which the results of the project depend (X-rays, CT scans, or MRI scans with matching age and sex) will be retained in secure storage for at least five years;

4. No risk related to the study has been identified;

5. There is no remuneration or compensation for my participation in the study;

6. The results of the project may be published and will be available in the University of Otago Library (Dunedin, New Zealand) but the anonymity of the patients will be preserved;

7. I, as the participant,

   a) agree to my data (X-rays, CT scans, MRI scans, with matching age and sex) being used anonymously in this and future projects and publications; OR

   b) agree to my data (X-rays, CT scans, MRI scans, with matching age and sex) being used anonymously in this project and related publications only.

I agree to take part in this project.

............................................................................. ........................................
(Signature of participant) (Date)

.............................................................................
(Name of participant)

This study has been approved by the University of Otago Human Ethics Committee. If you have any concerns about the ethical conduct of the research you may contact the Committee through the Human Ethics Committee Administrator (ph 03 479 8256). Any issues you raise will be treated in confidence and investigated and you will be informed of the outcome.
Appendix G

Results Per Patient Per Vertebra
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<th>L4</th>
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| Mean per Vertebra | 10.1 | 10.1 | 10.4 | 9.5 | 11.4 |

**Table G.1:** Results between 3D reconstruction from bi-planar radiographs and ground truth (MRI or CT scans). The distances represent the Hausdorff distance. The table is per patient per vertebra. The mean and the standard deviations are per patient and per vertebra. The distances are in millimetres. The mean of all values is 10.3 mm, and the standard deviation is 3.7.
Glossary

**Antero-Posterior (A/P):** the name given to the position of the body relative to the sensor while taking the radiographs. The chest is facing the x-ray source and the back facing the sensor.  

**Bi-planar:** the process of taking two plane images.  

**Diffeomorphism:** is an isomorphism in which both surfaces are 'smooth' and representable by differentiable functions.  

**Fleiss Kappa score:** a statistical measure for reliability of agreement between participants of a survey.  

**Frobenius norm:** also called Euclidean norm, defined as the square root of the sum of the absolute squares of the elements.  

**In Vitro:** the process of taking images out of living organisms.  

**In Vivo:** the process of taking images within living organisms.  

**Landmark:** a corresponding point that matches between different shapes of a population.  

**Latero-Lateral (Lat):** the name given to the position of the body relative to the sensor while taking the radiographs. The left or side of the body facing the sensor while the other side facing the x-ray source.  

**Point Distribution Model (PDM):** a statistical model to represent the mean geometry and some modes of variation within the training data. All the points of the PDM correspond through the data set.
**Postero-Anterior (P/A):** the name given to the position of the body relative to the sensor while taking the radiographs. The chest is facing the sensor and the back facing to x-ray source.

**Radiograph:** the image resulting from the x-rays hitting a sensor, as a photograph is the result of hitting the light on a sensor of camera, it is generally called x-ray.

**Scoliosis:** back deformation where the vertebral column is bended sideways.

**Uncalibrated:** when there is lack of information about how the data has been generated. In this thesis, there is no information about the position of the source, sensor plane and body to take the images.