

A Voronoi-based Distributed Genetic Algorithm

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ABSTRACT

The use of space for supporting evolution has been previously studied in the context of distributed Genetic Algorithms (DGA), where two standard approaches, island and grid based, are employed to define the population structure and connectivity relationships between individuals. The grid-based approach uses a fixed, regular grid to define the neighbourhood relations between individuals, resulting in Moore or Von Neumann relationships between population individuals. This short paper begins to address the question of the influence of non-fixed spatial relationships between individuals in a distributed genetic algorithm, where the sub-population of each population member is defined by the 1st order Voronoi neighbourhood of that individual. Initial results suggest that the irregular nature of the distribution produces an improved performance for the DGA, and that the Voronoi model of neighbours is appropriate for dynamic environments.

Keywords and phrases: Voronoi, distributed genetic algorithm, spatial subpopulation

1 INTRODUCTION

Evolutionary computation (EC) is a computational form of population-based search that uses the notion of fitness, selection and variation to search the defined problem space for near-optimal solutions. The two main concepts of EC are heritable variation and selection, which implies that over a period of generations or states those individuals that are currently performing well will be more likely to pass on portions of their representation to future individuals. Heritable variation in a population is a measure of the diversity of that population, resulting in potentially different behaviour (phenotype expression) between each population member and the environment. The heritable nature of variation occurs across generations, either through single parent to child mutation, or through combining different parent genetics to make a child; selection drives the system by allowing 'fitter' individuals to survive and pass on their genetic description. One important step during this process is the selection of parents. In a standard Genetic Algorithm (GA), selection of any parent occurs across the entire population, which has the unfortunate side effect of leading to premature convergence, especially when there are just a few individuals that dominate the fitness early in the evolution. Due to the expansion of distributed systems, and the observation that biological evolution is distributed in space and time, has led to the study of Distributed Genetic Algorithms (DGA). Since selection can only act on individuals that are localised in space and time (Hull 1980), there is interest in studying how subpopulations can be structured in space and what, if any, are the effects on the evolution due to this structuring.

The use of space in EC has been limited to one of two main approaches: spatial models for use in distributed computation; and explicit spatial positioning of individuals when studying co-evolution. The use of a Voronoi-based neighbourhood as a method for defining sub-populations, in the style of a fixed, irregular grid, has not been previously considered in detail. This paper will briefly explore a framework for using Voronoi neighbourhoods

with DGAs, and show some simple empirical results using some toy problems to illustrate the properties of the approach.

This paper is structured as follows: §2 gives the background to previous work and the motivation for the current study; §3 describes the basic Voronoi-based model of population and space used throughout this study; §4 describes the behaviour of the Voronoi approach for some simple pattern-based problems; and §5 discuss the implications of this work and presents conclusions and future work.

2 BACKGROUND AND MOTIVATION

The application of an explicit spatial model for selection and interaction has been previously applied in two main contexts. The use of space to constrain interactions in an artificial life context tend to use a representation of continuous space. The second context of using space involves frameworks for distributed computation of evolution. The two main models in distributed EC are cellular-based and island-based.

Cellular or fine-grained models of EC contain a single population that is distributed over a grid (Robertson 1987). The shape of the grid is often a two-dimensional torus, although other topologies have been explored (Schwehm 1992). Interactions between individuals are based on the neighbourhood defined by the grid. For example, with a square lattice each individual typically has four or eight nearest neighbours. The configuration of the space and the neighbourhood for each individual is fixed throughout the evolution.

Island models of EC take several sequential systems and execute them in parallel (Grefenstette 1981). Selection in this model is constrained by limiting parent selection to individuals that are within the same subpopulation, and migration between subpopulations is used to slow convergence. Other work has considered hybrid methods that incorporate island-based populations that are grids, and so on.

One of the few works that have explored the consequences of a Voronoi-based model for connectivity in evolution is based on a study of cellular automata (Flache & Hegselmann 2001). The authors considered the question as to the whether relaxing the regular neighbourhood structure of a grid for cellular dynamics models would have an influence on performance. Their results were tentative, however the use of an irregular neighbourhood did bring about properties of the system that had not been previously observed.

3 Voronoi-Based Genetic Algorithm

The Voronoi-Based Genetic Algorithm (VGA), uses the Voronoi-neighbourhood of each individual to define the subpopulation of that individual. In the same manner as a fixed grid, this subpopulation can then be used to select parents and therefore to produce the new offspring for a particular site. The Voronoi polygon surrounding any point (individual) is defined as the polygon that encloses the space (usually 2D Euclidean) that is nearer to the individual than to any other individual. The immediate Voronoi neighbours of any point can then be defined as those points who share a boundary with their Voronoi polygons. Figure 1 show the structure of a Voronoi neighbourhood for a simple collection of points, whereas Figures 2(a) and 2(b) show the Voronoi polygons for a regular grid and a random distribution of points within a unit square.

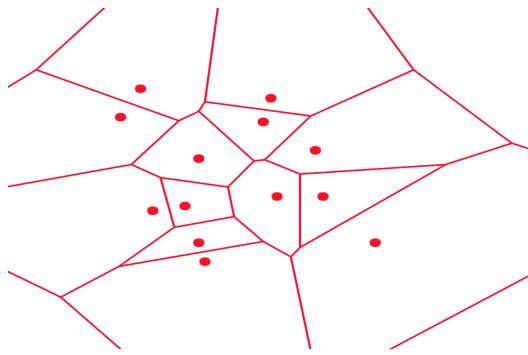


Figure 1: Voronoi Polygons for a set of points.

Two approaches will be considered with the Voronoi GA. The first will look at using the Voronoi neighbourhood to replace the standard grid neighbourhood in a standard fixed-grid GA. Hence new individuals will replace individuals at the same location, and therefore the neighbourhood will remain fixed during the evolution. The second approach will introduce a random placement within the Voronoi polygon of one parent when replacing individuals. Hence the neighbourhood relationships will vary during the evolution. Considering the fixed Voronoi grid approach, the following generational algorithm will be used:

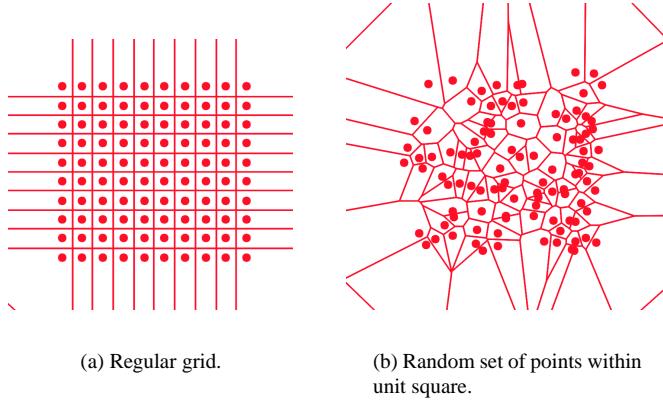


Figure 2: Voronoi Polygons for regular and random point distributions.

Parameter	Value
Population Size	100
Selection	2-Tournament Selection
Replacement	Generational
Generations	200
Crossover Prob.	80%
Crossover Type	Single-Point
Mutation Bit Prob.	1%
Bit Length	100
Bit Pattern	2

Table 1: Parameter Setup for Voronoi-Based Genetic Algorithm.

1. Create an initial population $P = \{p_1, p_2, \dots, p_N\}$ of N individuals over a 2-dimensional euclidean plane, bounded by $[x_{\min}, y_{\min}] \rightarrow [x_{\max}, y_{\max}]$.
2. **While Number Generations not complete Do**
 - (a) **For each individual** $p_i \in P$ **at location** $p_i(x, y)$
 - i. Construct the Voronoi-neighbourhood of individuals $V_i \in P$
 - ii. Select two individuals, p_j and p_k from V_i , using 2-tournament selection without replacement.
 - iii. Perform crossover and mutation with some probability to produce two new individuals p_j' and p_k' .
 - iv. Randomly select one of these individuals to replace p_i in the next generation
 - v. Place the new individual at location $p_i(x, y)$.

The above algorithm is extended to allow movement by setting the position of the new individual to be randomly placed within the Voronoi polygon V_i . Note that this means the Voronoi polygons must be rebuilt after each generation, and that the neighbourhood relationships between individuals will also generally change each generation.

4 EXPERIMENTAL SETUP AND RESULTS

The following experiment was run to determine whether altering the neighbourhood relationships using a Voronoi space would have an affect on the behaviour of the genetic algorithm. A series of runs were performed, where the point distribution of individuals commenced with a regular grid, and was gradually randomly disturbed from their initial positions. The parameters for these runs are shown in Table 1. Each point placement experiment was run 1000 times. The problem was to evolve a 100 bit string that had a repeating pattern 0011001100..... The comparison concerned whether the evolving system could discover the complete string pattern within 200 generations. A comparison of the total number of successful runs (maximum 1000) was used to compare the performance.

An example of the gradual change in distribution of the points (individuals) is shown in Figure 3. Here, the random amount that any point varies in the x and y direction from their original fixed position is gradually increased, where the parameter ρ is multiplied by a random number between [0.0-1.0]. This is randomly added or subtracted to the x value, and the process repeated for the y value. Note that once ρ reaches approximately 0.15 the point distribution is approaching the random distribution of points, as shown in Figure 2(b).

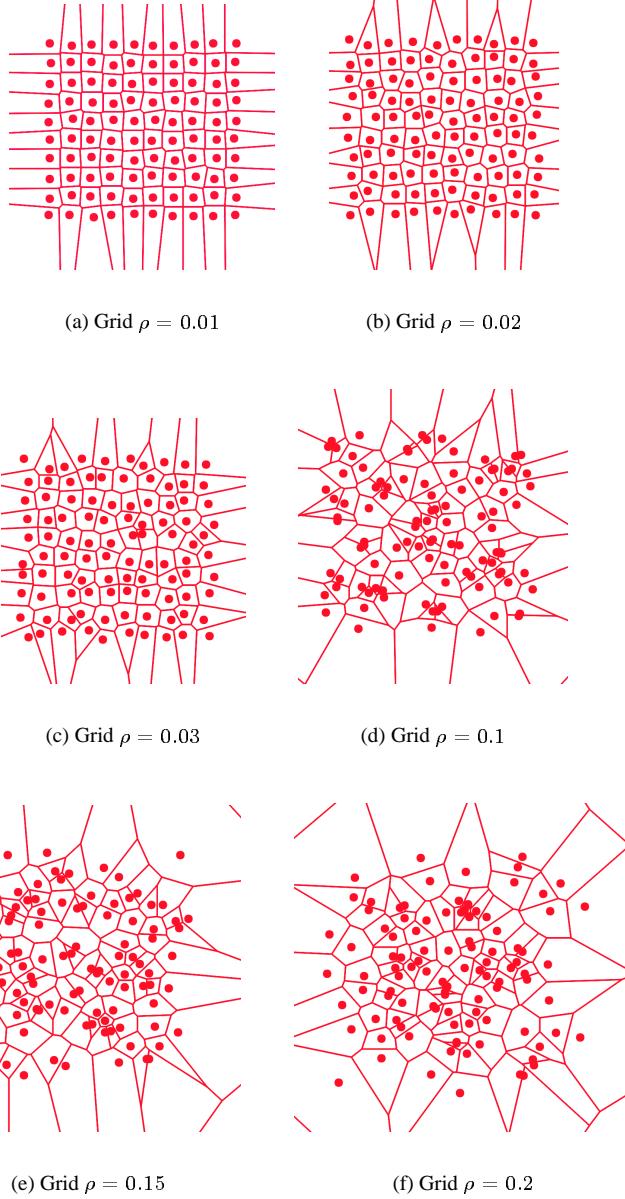
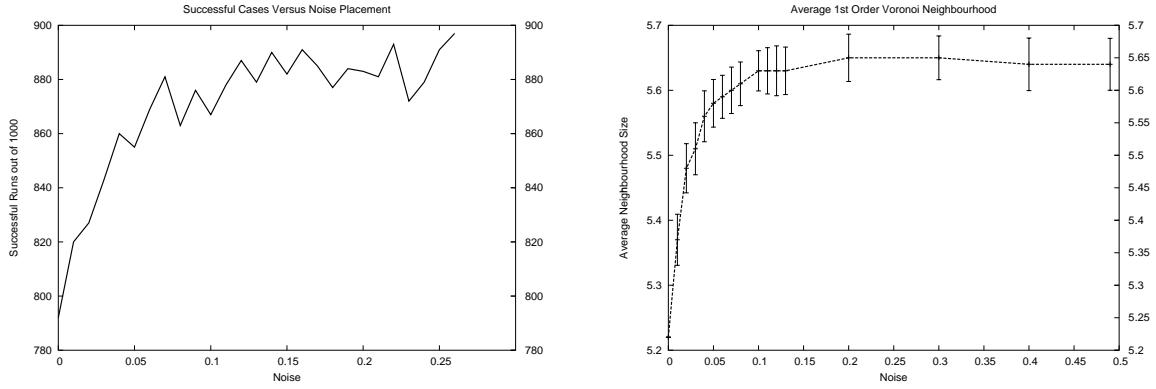


Figure 3: Voronoi Polygons for increasingly random point distributions.

Figure 4 shows the results for the 1000 runs of the population for a variety of values of ρ . Note that the performance of the VGA significantly improves until $\rho \approx 0.15$. This figure matches closely with the average increase in the number of neighbours, suggesting that there is a relationship between the increasing connectivity of the neighbourhood and the performance of the GA. To test this concept, the GA was run using a fixed grid, but where each individual had a Moore neighbourhood (8 neighbours). If the performance improvement is essentially due to the increasing connectivity then this should produce an improvement over the Voronoi neighbourhood. The results were that 923 runs were successful, hence implying that the larger connectivity of the grid was the cause of the performance improvement. This was further supported by producing a random connectivity matrix with approximately 30% of the individuals randomly connected to each other. Note that this also defined non-



(a) Number of successful runs for increasing ρ .

(b) Average neighbours for increasing ρ .

Figure 4: Resulting success for a variety of Voronoi neighbourhoods.

transitive relationships, since individual p_i may have p_k in its neighbourhood, but the opposite may not be true. Surprisingly with this setup the resulting evolution successfully found the solution on every run. Clearly the number of neighbours, and the relationship between the selection method and the fitness landscape (i.e. the problem) are fundamental to understanding the performance of a system.

A second set of experiments were also performed to determine whether placement of new individuals, based on the Voronoi neighbourhood of a random parent, would improve the performance of the VGA. The results showed that there was an improvement in terms of the number of evaluations to solve a 50 bit problem, when the fixed or random initial population was allowed to evolve with new individuals being placed when created. Note that the Voronoi neighbourhood was updated after each generation. The results were that for a fixed grid with no placement, the average number of generation was 37.4 ± 5 , a random grid with no placement, 36.2 ± 4.6 , and with a random or fixed grid that placed new individuals based on the Voronoi polygon of a random parent, 35.1 ± 4.5 . Although the improvement was slight, this showed some promise and demonstrated that changing the connectivity relationships between individuals during evolution may be a beneficial approach.

5 DISCUSSION AND CONCLUSION

The use of a Voronoi-based neighbourhood structure did not demonstrate an improvement against a standard grid with a Moore neighbourhood for the simple problem that was considered. However, the work demonstrates that different forms of connectivity have a great influence on GA performance, and this type of model can be used to explore these properties in more detail. Additionally, the concept of moving new individuals as they evolve, and therefore altering the neighbourhood structure of the population, seems to have merit in terms of a self-organising structure. Although the work here did not demonstrate whether these properties will lead to a more useful GA model, they have shown a framework for creating neighbourhood models, based on points, that do not rely on a distance metric to determine connectivity.

The use of Voronoi neighbourhoods for selecting subpopulations seems to have natural analogies with physical systems, and therefore is worthy of further study. Although this may not lead to more efficient structures for evolving all problems, a number of questions arise:

1. What are the types of problems most suitable for evolving with Voronoi neighbourhoods?
2. Do Voronoi neighbourhoods produce biologically plausible models of physical evolution?
3. Are non-transitive neighbourhood relationships useful, and how do they relate to current sub-population models?
4. How do different placement strategies for evolved individuals alter the sub-population structures based on Voronoi neighbourhoods, and what strategies are meaningful in an evolutionary context?

The use of Voronoi neighbourhoods for defining sub-populations for selection is a bridge between the fixed grid approaches and continuous representations that determine sub-population structures based on a distance metric. Further work in this field will no doubt add to our understanding of the relationship between evolving population dynamics and the pressure of selection.

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