Wind Farm Layout Optimization using Population Distributed Genetic Algorithms

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Problem Description

This master thesis is an investigation of how different genetic algorithm models perform when used to solve the wind farm layout optimization problem. It is investigated if population distributed genetic algorithms can obtain better results than traditional non-population distributed genetic algorithms.

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- Supervisor: Professor Keith Downing

Abstract

Wind turbine technology is a promising source of renewable energy. However, the potential of wind turbine technology can not be utilized unless the wind farm layout is efficient. The challenge with wind farm layout optimization is that finding the optimal layout in the huge search space of different layouts is hard, if not impossible, to do analytically. Genetic algorithm techniques have been applied in many fields to solve non-linear optimization problems, and has shown promising results when used on wind farm layout optimization. Even so, not much effort has been put into investigating whether different genetic algorithm models can improve the results.

In this project, it is investigated if population distributed genetic algorithms are able to solve the wind farm layout optimization problem better than traditional non-population distributed genetic algorithms. This project is a contribution to a wind farm layout optimization contest launched by the Genetic and Evolutionary Computation Conference (GECCO) 2016.

An advanced genetic algorithm containing four different genetic algorithm models was implemented for this project. One of the genetic algorithm models was a traditional genetic algorithm, and three were population distributed genetic algorithms. The program was connected to a wind farm simulator provided by GECCO 2016 so that the performance of the different genetic algorithm models could be investigated on realistic wind scenarios.

The results showed that the traditional non-population distributed genetic algorithm consistently obtained better results than the three population distributed genetic algorithms. While two of the population distributed algorithms showed promising results, the third seemed unfit for solving the wind farm layout optimization problem. It is concluded that when providing the different genetic algorithm models the same amount of computational resources, the population distributed genetic algorithms come in short.

Sammendrag

(This is a Norwegian translation of the abstract.)

Vindmølleteknologi er en lovende kilde til fornybar energi. Likevel kan ikke potensialet til vindmøllene utnyttes hvis ikke posisjoneringen av vindmøller i vindmølleparken er optimalisert. Utfordringen med vindmølleposisjonering er at løsningrommet - antall mulige vindmølleposisjoneringer - er enormt, og det er ekstremt vanskelig, om ikke umulig, å finne den optimale posisjoneringen analytisk. Genetiske algoritmer har vist seg å være svært nyttige når de har blitt brukt til å løse ikke-lineære optimaliseringproblemer, og de har vist lovende resultater brukt i vindmølleposisjonering. Det er likevel lite forskning på hvorvidt populasjonsdistribuerte genetiske algoritmer kan oppnå bedre resultater enn ikke-populasjonsdistribuerte algoritmer for vindmølleposisjonering.

I dette prosjektet har det blitt undersøkt om populasjonsdistribuerte genetiske algoritmer kan løse vindmølleposisjoneringsproblemet bedre enn den tradisjonelle genetiske algoritmen. Prosjektet er et bidrag til en konkurranse for vindmølleposisjonering lansert av konferansen GECCO (the Genetic and Evolutionary Computation Conference) 2016.

En avansert genetisk algoritme bestående av fire forskjellige modeller var implementert for dette prosjektet. En av de genetiske algoritmene var en tradisjonell genetisk algoritme, mens de tre andre var populasjonsdistribuerte genetiske algoritmer. Programmer ble koblet sammen med GECCO 2016's vindfarmsimulator slik at de forskjellige genetiske algoritmene kunne bli observert og sammenlignet på forskjellige vindsenarioer.

Resultatene viste at den tradisjonelle genetiske algoritmer konsekvent fant bedre vindmølleposisjoneringer enn de tre populasjonsdistribuerte modellene. To av de populasjonsdistribuerte algoritmene gav lovende resultater, mens den tredje viste seg å være uegnet til å finne tilfredstillende vindmølleposisjoner. Resultatene ledet til konklusjonen at populasjonsdistribuerte algoritmer ikke alltid klarer å levere like gode resultater som den tradisjonelle genetiske algoritmen når hver modell er tildelt de samme resursene.

Preface

This project is a master thesis written at the Department of Computer and Information Science, Norwegian University of Science and Technology.

I wish to thank my supervisor Professor Keith Downing at the Department of Computer and Information Science for his invaluable guidance and support throughout this project.

Contents

Chapter 1

Introduction

This thesis is a contribution to the third edition of the wind farm layout optimization contest launched by the Genetic and Evolutionary Computation Conference (GECCO) 2016. The contest involves optimizing the number of turbines and turbine positioning in a wind farm with goal of producing maximum power to minimum cost using genetic algorithms. The wind farm simulator is provided by GECCO 2016, hence, the focus of this thesis will be on improving the genetic algorithm that will be used to search for the optimal wind farm layout. This is accomplished by investigating the state of the art within wind farm layout optimization and genetic algorithms and experiment with variations of the genetic algorithm.

This chapter provides an introduction to this thesis. Section 1.1 contains the background and motivation. Section 1.2 introduces the goal and research questions that will be investigated. In section 1.3 a brief overview of the research method is given. Contributions is given in section 1.4, and an overview of the thesis structure is given in section 1.5.

1.1   Motivation and Background

Transitioning from non-renewable energy sources to renewable energy sources is one of the largest, if not the larges political challenge of today. Renewable energy is less polluting than non-renewable energy and should therefore be preferred. However, renewable energy sources make up only 21% of the world's energy sources as of 2011 [EIA, 2015]. Wind turbine technology is a

promising source of renewable energy. Advances in wind turbine technology have led to increased power production at lower cost. Despite these improvements, wind turbines still produce less energy than predicted because of the wake effect; reduction in wind speed caused by turbines placed in front of other turbines [Samorani, 2013]. For wind energy to become a bigger player in the world's energy sources, sophisticated methods for wind turbine placement in wind farms need to be developed so that each turbine produces as much energy as possible.

Wind turbine positioning is hard to optimize analytically. Fortunately, a wide variety of local search methods and bio-inspired methods have shown promising results, with genetic algorithms being the most popular method. As more advanced approaches to evaluate layouts has been developed, and more realistic constraints are introduced, more sophisticated genetic algorithms are required. To come up with more advanced genetic algorithms for solving the wind farm layout optimization problem, the annual Genetic and Evolutionary Computation Conference (GECCO) 2016, launched a competition where different contestants will provide their own implementation of a genetic algorithm [IRIT, 2015]. The goal of the competition is to bring more realistic problems to algorithm developers, and to create an open source library useful beyond the scope of the competition. Wind parameters and evaluation mechanisms are provided by GECCO 2016, therefore, the focus of this thesis will be on optimizing the genetic algorithm. Still, some knowledge of wind turbines, wind farms, and wind- and power models are crucial to understanding this thesis and will therefore be introduced in chapter 2.

Greedy heuristics, simulated annealing search, ant colony algorithms, particle swarm optimization and genetic algorithms have all been used in solving the wind farm layout optimization problem, and these will all be reviewed in chapter 3. Turbine positioning has been improved by genetic algorithms for more than 20 years, each approach bringing something new to the field such as a new type of genetic algorithm, a more realistic environment, or combinations of genetic algorithms and other approaches. A few researchers have solved the wind farm layout optimization problem by implementing a population distributed genetic algorithms called the Island model, and it has shown promising results. However, as far as the author knows, no attempt has been made in implementing any of the other existing population distributed models. This is the main motivation behind this thesis, and has inspired the

author to investigate the effect different population distributed algorithms can have on the wind farm layout optimization problem. Chapter 2 contains a review of the population distributed genetic algorithm investigated in this thesis.

1.2 Goal and Research Questions

This section states the goal statement and research questions that will be investigated in this thesis.

Goal statement

> *The project goal is to investigate the potential advantages of using population distributed genetic algorithms in optimizing wind farm layout, i.e. solving the wind farm layout optimization problem.* [Samorani, 2013]

The performance of population distributed genetic algorithms will be observed and compared to the performance of a simple genetic algorithm (non population distributed genetic algorithm) in order to answer the first research question. In addition, each of the population distributed genetic algorithms will be compared against the others with the goal of answering the second research question.

Research question 1

> *Can distributed genetic algorithms improve the quality of the solution to the wind farm layout optimization problem as compared to a simple genetic algorithm?*

Research question 2

> *Which distributed genetic algorithm works best for the wind farm layout optimization problem? What properties are essential for its success?*

Both research questions will be answered by testing the different distributed genetic algorithms in a wind farm simulator provided by GECCO 2016. The

genetic algorithms will be implemented from scratch in order to give the author control of the environment, as well as the possibility of adding functionality fast and easy. Each genetic algorithm will be tested on different wind scenarios which are also provided by the contest. Research question 1 will be answered by implementing 3 different types of population distributed genetic algorithms and compare their results with a simple genetic algorithm on different wind scenarios. Research question 2 will be tested the same way, and the results from each of the population distributed algorithms will be compared.

1.3   Research Method

In order to answer the research questions, a genetic algorithm was implemented for this thesis. Even though a simple genetic algorithm were provided by GECCO 2016 along with a wind farm evaluator and wind scenarios, the choice was made to implement the algorithm from scratch so that the population distributed genetic algorithms could be added easily, and so that more functionality could be added to the program.

To evaluate the different genetic algorithm models, 4 scenarios provided by GECCO 2016 were used. The scenarios provided contained wind parameters, terrain description, and wind turbine parameters. First, experiments were run to find parameter values for the genetic algorithm suitable for the wind farm layout optimization problem. Second the different genetic algorithms were run with those settings. The genetic algorithms were compared on four different wind scenarios and the results for each scenario is presented, along with overall performance on all scenarios for each genetic algorithm. Finally, the results from the different simulations were compared and analyzed in order to to answer the research questions.

1.4   Contributions

The contribution to the field of wind farm layout optimization provided by this thesis is a comparison of different population distributed genetic algorithms and their ability to solving the problem. As far as the author knows, no attempt has been made in comparing population distributed genetic algo-

rithms on the wind farm layout optimization problem, therefore this thesis can contribute with clearance as of which, if any, is the best choice for the given problem.

This thesis also contribute with an extensive survey of the state of the art within wind farm layout optimization and artificial intelligence approaches. The survey is provided in chapter 3 and can be useful beyond the scope of this thesis for everyone who wants to get an overview of research within the field of wind farm layout optimization using genetic algorithms.

1.5 Thesis Structure

The thesis is divided into six chapters. Chapter 2 contains an introduction to the wind farm layout optimization problem, a description of the simple genetic algorithm, and a description of each of the different population distributed genetic algorithms that will be implemented. Chapter 3 is a survey of the state of the art within wind farm layout optimization using genetic algorithms and other methods. The chapter also contains a discussion/conclusion of related work. Chapter 4 contains the methodology used to implement and test the genetic algorithms. In chapter 5 the results are presented and discussed, and finally, the research questions are answered and discussed in chapter 6.

Chapter 2

Background

This chapter contains the background for this thesis. In section 2.1 the wind farm layout optimization problem is defined, and challenges of wind farm construction are presented. The first part of section 2.2 gives an introduction to genetic algorithms, this sub-section can be skipped if the reader is already familiar with genetic algorithms. The second part of section 2.2 introduces the 3 population distributed genetic algorithms that will be investigated in this thesis.

2.1 Wind Farm Layout Optimization

This section aims to give the reader an understanding of the wind farm layout optimization problem. It is divided into two parts. Part one formally defines the wind farm layout optimization problem. Part two gives a brief introduction to wind farm construction with the goal of providing the reader with an understanding of its complexity and an introduction to the main challenges of wind farm layout design.

2.1.1 The Wind Farm Layout Optimization Problem

An overview of the wind farm layout optimization problem is presented by Samorani [2013]. Grouping of wind turbines in a wind farm decreases installation- and maintenance costs. However, positioning of wind turbines in a farm also introduces new challenges. The power produced by wind turbines is largely dependent on wind speed, therefore it is important that the

wind speed that hits each wind turbine is as large as possible. The main challenge for wind farms is that a wind turbine positioned in front of another will cause a wake of turbulence, meaning that the wind speed that hits the second wind turbine will be decreased. This effect is called *wake effect*, and will be explained in the following sub-section. Since the goal is to produce as much power as possible, it is very important to position the wind turbines so that the wake effect is minimized. Samorani [2013] stated the wind farm layout optimization problem like this "The wind farm layout optimization problem consists of finding the turbine positioning (wind farm layout) that maximizes the expected power production". In this thesis, the problem formulation will be extended to include both cost constraints and optimization of the number of wind turbines, not just their positions. A formal definition is given below

> *"The wind farm layout optimization problem consists of finding the number of turbines and turbine positioning (wind farm) that maximizes the expected power production while minimizing costs."*

A typical solution to the wind farm layout optimization problem is given in figure 2.1 [Grady et al., 2005]. The rectangular grid represents the wind farm. Black cells represents positions containing wind turbines, and white cells represents empty positions. The wind farm layout in the figure is the optimal layout for a simple wind scenario where the wind is blowing at one direction with constant speed. When the wind is blowing from different directions with variable wind speed the turbines will be more scattered around in the grid.

2.1.2 Challenges of wind farm construction

Samorani [2013] gives an overview of the main challenges of wind farm construction. First, a suitable site has to be found, meaning a site with good wind conditions. Wind power conditions are partitioned into 7 different wind power classes. With today's technology, sites with power class 4 or higher are considered suitable for hosting a wind farm. Even though the wind farm has the required wind conditions, it might not be suitable for hosting a wind farm because it might be far from the electronic grid, so that connecting it to it would be too costly, or it could require costly road work because current
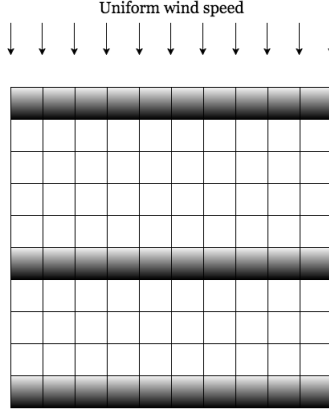
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Figure 2.1: Optimal layout for a simplified wind scenario [Grady et al., 2005]. This figure is provided as an example of a wind farm layout.

infrastructure is not able to handle the transportation trucks. Second, land owners has to be contacted and convinced that hosting a wind farm on their land is a good idea. Land owners usually gets a percentage of the wind farm profit. This phase of contract negotiation usually takes a few months. At the same time, wind distribution need to be measured as accurately as possible. This step is extremely important, since the layout of the farm is optimized based on the measured wind distribution. Getting enough data to capture the wind distribution can take a few months if wind conditions are stable all year long, but if the wind conditions vary extensively over the year this step can take a few years.

An equally important step is to decide on which turbines to buy for the wind farm. A trade-off exists between power and cost since larger wind turbines are usually more expensive than smaller turbines, but they generally also produce more power. Realistic estimation of maintenance cost is also crucial in deciding on turbine type. In Samorani [2013] the number of wind turbines are also decided in this step, but in this project, deciding the number of turbines is included in the wind farm layout optimization problem and will therefore be part of the next step.

Only after the site is found, wind turbine type is selected, and wind distribution is measured, can the layout optimization begin. Layout optimization

faces different challenges. At some locations, the terrain is a great challenge because it contains areas which are unsuitable for wind turbines. These areas has to be dealt with by the layout optimization algorithm so that turbines are only positioned in legal areas. There are also constraints on how close turbines can be positioned, according to Şişbot et al. [2010], the minimum spacing rule states that the minimum distance between turbines is 8D in prevailing wind direction, and 2D in cross wind direction, where D is the rotor diameter. Still, the greatest challenge of wind farm layout optimization is the wake effect. As mentioned above, the wake effect is the effect of reduced wind speed in the wake behind a wind turbine. Samorani explains the wake effect using the Jensen wake model [Jensen, 1983]. As will be apparent after chapter 3, most research in wind farm layout optimization use the Jensen model because it is quite accurate and simple. The Jensen model will be explained below in order to give a brief understanding of how the wake effect is calculated.
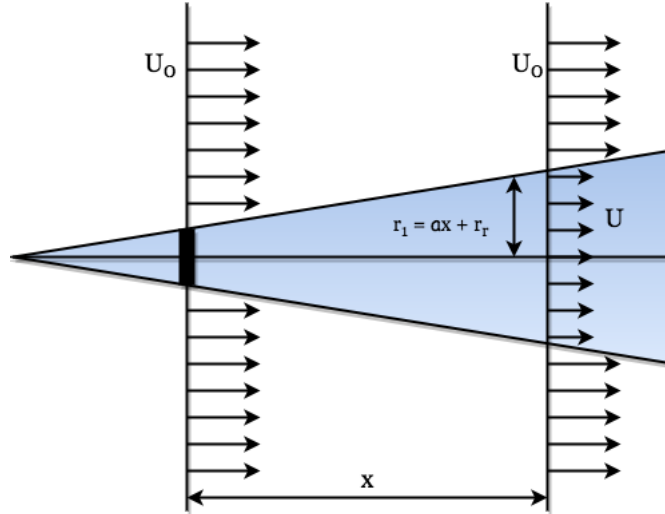
Figure 2.2: The wake effect [Samorani, 2013].

In figure 2.2 the small, black rectangle represents a wind turbine, and the blue area behind it illustrates the area that is affected by the turbulence created by the wind turbine. In the figure, the wind is blowing from left to right with uniform wind speed U_0. As the wind hits the wind turbine it creates a

wake of turbulence behind it so that the wind speed at distance x behind the wind turbine is $U < U_0$. The area behind the wind turbine that is affected by the wake at distance x has the radius $r_1 = \alpha x + r_r$ where r_r is the rotor radius and α is the entrainment constant, a constant that decides how fast the wake expands. For a detailed, mathematical explanation of the Jensen model and other wake models see references [Jensen, 1983] and [Liang and Fang, 2014].

In summary, construction of a wind farm is a complicated and time consuming process. Consecutive important decision have to be made before one can even begin the layout optimization. The layout optimization is dependent on turbine cost, terrain parameters, wind conditions and turbine positioning. Finding the optimal layout is a non-linear, complex problem that only sophisticated algorithms can solve.

2.2   Genetic Algorithms

This section provides the background needed to understand genetic algorithms. The first sub-section gives a step-by-step introduction to simple genetic algorithms invented by Holland [1992]. If not otherwise stated, this section is based on the books Holland [1992] and Goldberg [2005]. If the reader is familiar with genetic algorithms he or she can skip this sub-section. The second sub-section introduces the 3 population distributed genetic algorithms tested in this theses: The Island model, the Cellular model and the Pool model [Gong et al., 2015].

2.2.1   Simple Genetic Algorithms (SGAs)

Genetic algorithms are probabilistic search algorithms inspired by evolution. Figure 2.3 shows the five steps that constitute the genetic algorithm. The genetic algorithm operates on a population of individuals each representing a solution to the given problem. The first step is therefore to generate the initial population, which usually consists of randomly generated individuals. The second step of the genetic algorithm is evaluation. The child population is evaluated based on some predefined fitness function (objective function); a measure of the goodness of the solution. Note that the terms fitness function

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and objective function will be used interchangeably in this thesis. The third-and forth step, adult selection and parent selection respectively, is the process of deciding which individuals from the child population are allowed to grow up into adults. These are chosen to be parents for the next generation of individuals. These steps are naturally guided by the fitness of the individuals. The fifth and last step is called recombination. In this step, the genes of the parent population are recombined and altered in order to generate a new, hopefully improved, child population. After the new child population is generated the process starts again and continues until some predefined stop condition is reached.
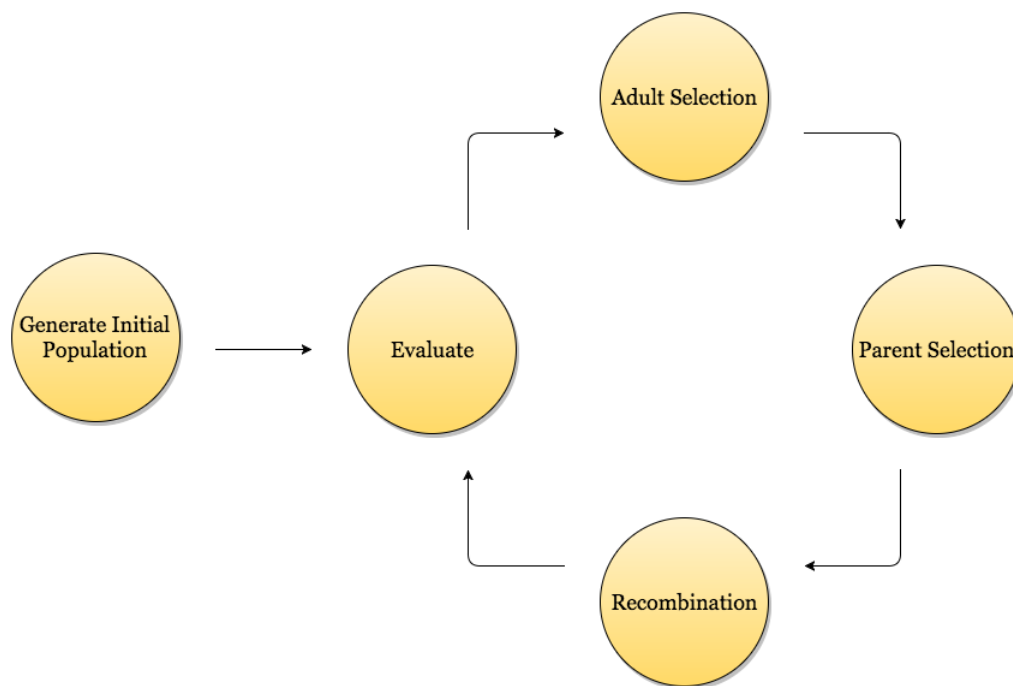
Figure 2.3: Overview of the five steps that constitute the genetic algorithm.

Inspired by survival of the fittest, the population evolves into a population of better solutions to the given problem. Two properties are crucial for the utilization and success of the genetic algorithm: (1) One have to know how to measure the fitness of the individuals (goodness of the solutions), and (2) one have to find a way to represent individuals so that genetic operations can be

performed on them. Examples of representation, fitness calculation, selection and genetic operations will be given below. Note that numerous different selection schemes and genetic operations exists and that the sub-sections below only provides one example of each in order to provide understanding of how a typical genetic algorithm works. How these steps are actually implemented in this thesis is explained in chapter 4. If the reader is familiar with simple genetic algorithms he or she can jump to sub-section 2.2.2.

Representation

In genetics, an organism's hereditary information is called its genotype, and its observable properties its phenotype. For example, the hereditary information in your genes (genotype) are responsible for your eye color (phenotype). The genetic search algorithm usually works on genotypes represented as bit strings. Goldberg [2005] explained this with a simple example. Let's say the objective function that we want to find the optimal solution for is x^2 for $x \in \{0, 31\}$. Then we can generate genotypes for the random solutions using bit strings of size 5, each representing a decimal value (phenotype) between 0 and 31. Figure 2.4 displays the genotype and phenotype for four randomly generated individuals. Here, the phenotypes are just the genotypes on decimal form, but in other problems the phenotype could be everything from eye color to a wind farm layout.

Genotype	Phenotype
0 1 0 1 1	11
1 0 0 1 0	18
0 0 1 1 0	6
0 0 1 0 1	5

Figure 2.4: Genotypes and phenotypes for 4 individuals where the phenotype is the decimal value of the genotype (binary number).

Selection

As mentioned above, selection is a two-step process: Adult selection and parent selection. Adult selection is the decision of choosing which children are allowed to grow up and enter the adult pool and thereby become potential parents for the next generation. The simplest form of adult selection is called *full generational replacement* and it consists of simply replacing the previous adult pool with the new child population. This adult selection scheme is one out of three adult selection mechanism implemented for this thesis. These will all be explained in detail in chapter 4.

Parent selection is the process of selecting which individuals from the adult population that will be the parents of the next child population. The simplest form of parent selection is to simply select the fittest individuals. Unfortunately, this selection strategy often leads to premature convergence of non-optimal solutions. It is important to prioritize exploration, at least in the beginning of the search, otherwise, parts of the search space that could have lead to the optimal solution are cut off too soon. To cope with this problem *controlled elitist selection* schemes are preferred. A very popular selection strategy is *tournament selection* [Razali and Geraghty, 2011]. In tournament selection, groups of n individuals are randomly drawn from the population and the fittest individual in the group is appointed the tournament winner, and is therefore selected. Figure 2.5 illustrates how tournament selection works. In the example, n is equal to 3, therefore the three individuals with fitness 9, 4 and 6 are randomly drawn from the population. Since in this thesis, the best individuals are those with lowest fitness, the individual with fitness 4 wins the tournament and is chosen for reproduction.

By varying the value of n you can control how much exploration your algorithm should do. If n is equal to the population size only the best individuals are selected, and if n is equal to 1 the search is completely random. This means that low values of n leads to more exploration of the search space, something that can potentially guide the population to find better solutions. Higher values of n on the other hand will often lead to fast convergence to sub-optimal solutions. These properties make it desirable to vary the value of n during the genetic search so that exploration is prioritized at the beginning of the search, while exploitation (making use of seemingly good solutions) is prioritized at the end. Tournament selection is one out of two parent se-
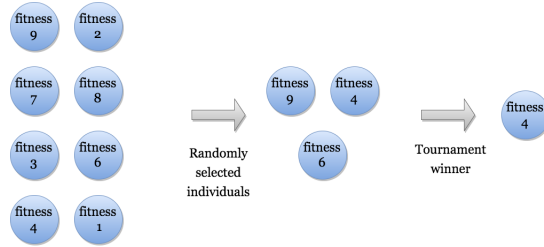
Figure 2.5: Tournament selection. A group of three individuals are randomly drawn from the pool of all individuals. The best individual in the group, the one with fitness 4, is selected for reproduction [Razali and Geraghty, 2011].

lection methods implemented in this thesis, these will also be explained in detail in chapter 4

Crossover

Crossover means combining genes of parent solutions to produce child solutions. One of the most common crossover schemes is called *uniform crossover*. For each gene of the child solution there is a 50% chance the gene will be inherited from the first parent and a 50% chance that the gene will be inherited from the second parent. Figure 2.6 shows how uniform crossover works. As can be seen, the first gene of child 1 is taken from parent 1, the second and third gene from parent 2, and the forth gene from parent 1 and so on. Uniform crossover is one out of three crossover methods implemented for this thesis.

Mutation

In biology, mutation is defined as a permanent alteration in the DNA sequence that makes up a gene. When the genetic algorithm works on genotypes of bit strings the process consists of simply flipping bits. Mutation is usually implemented by flipping some of the bits of the genotype as shown in figure 2.7.

Mutation is important because without mutation a population can evolve to a population of individuals where each genotype has the same value at a
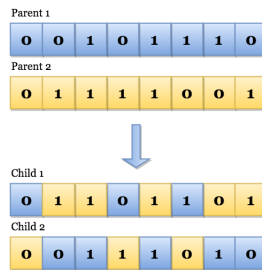
Figure 2.6: Uniform crossover. Two child genotypes are created by combining the genotypes of two parents. Each gene is drawn from one of the parents with equal probability.
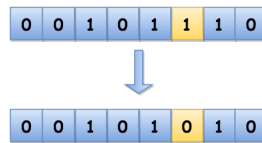

Figure 2.7: Mutation of a single bit. The bit in position 6 at the upper bit string has the value 1 before the mutation, while after mutation the value is flipped to 0.

given position. Since every individual has the same value in their genotype at the same position, reproduction will never be able to make a new individual that does not also have the same value at the same position. With mutation however, there is always a probability of the value being flipped. Mutation is therefore crucial for maintaining diversity in the population and keeping it from becoming sterile.

Even though mutation is important, the probability of mutation needs to be kept low. If the mutation rate is very high, the genotype of a new individual will almost be a random bit string. Remember that a new individual is made by recombination of two individuals with high fitness in the previous population. If mutation changes the new individual heavily, it will not inherit the good features of its parents and the whole point of evolutionary search will be gone.

2.2.2 Population Distributed Genetic Algorithms

One of the main challenges of simple genetic algorithms is keeping diversity in the population long enough so that the population does not converge to a sub-optimal solution. By distributing the population, the algorithm is able to explore different solution paths. This is usually an advantage, because the solutions that obtains the best fitness in the end is not always the solutions that seem best right away. This section introduces the 3 different population distributed algorithms that are investigated in this thesis. For an in-depth introduction to the models see [Gong et al., 2015].

The Island Model

In the Island model, the population is divided into sub populations that are distributed onto different Islands. By letting each population evolve separately, different islands can explore different solutions. Figure 2.8 displays a population divided into four sub-populations.
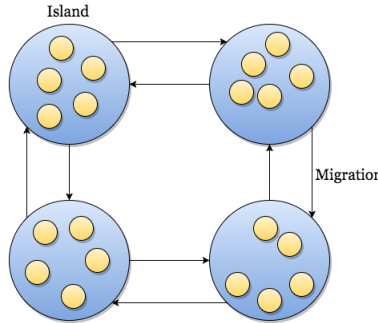
Figure 2.8: An Island model using a ring topology with four demes (Islands) of size five. [Gong et al., 2015]

According to Huang [2007], six parameters must be specified when using the Island model. First of all, one need to decide on the number of demes (Islands). Second, the deme size needs to be specified; the number of individuals on each island. In figure 2.8 the deme size is five, and four demes are used. Third, the topology must be specified; the allowed routes to migrate from one population to another. Numerous topologies can be used. In figure

2.8 the arrows represents legal migration routes. Since the topology forms a circle it is called a ring topology. The forth and fifth parameters listed by Huang are migration rate and migration interval, meaning the number of individuals that migrate from one population to another and the number of generations between each migration respectively. These parameters are very important since they largely affect the time the population gets to explore different solutions before the best solutions from some of the demes takes over the population. Sixth, the policy of deciding which individuals that migrate, and how to replace existing individuals with new migrants needs to be specified.

The parameters listed above must be given careful thought when implementing the Island model, but as Gong explains, they are not the only ones. If the Island model is implemented in parallel one also have to decide if the migration is synchronous or asynchronous. Synchronous migration means that all migration is performed at the same time; at a specific generation. Asynchronous migration on the other hand, can be performed whenever one of the parallel processes are ready. Additionally, it has to be decided if the Island model is homogeneous or heterogeneous. By a homogeneous Island model, Gong et al. means an Island model where each sub population use the same selection strategy, genetic operations and fitness function, while as an heterogeneous Island model can implement different settings for different Islands.

The Cellular Model

Figure 2.9 displays the Cellular model from Gong et al. [2015]. In the Cellular model the population is distributed in a grid of cells where each cell holds one individual. Each individual can only "see" the individuals of its neighborhood (as decided by the given neighborhood topology) and can only be compared with, and mate with individuals in its neighborhood.

The takeover time is defined as the time it takes for one individual to propagate through the whole population. The neighborhood topology largely affects the takeover time. In figure 2.9 the neighborhood topology is defined as only the individuals to the left, right, over and under the given individual. Since the topology includes a small number of individuals, the takeover time will be long, meaning that exploration is prioritized. If the topology consists
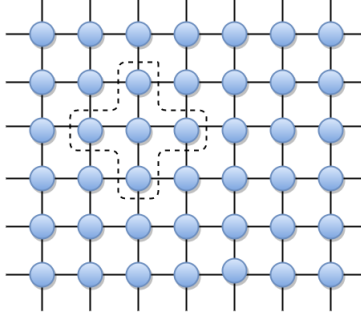
Figure 2.9: Cellular model where the neighborhood topology consist of the cells to the left, right, over and under the given cell [Gong et al., 2015].

of a larger number of cells the takeover time will, off course, be much shorter.

The Cellular model can also be implemented in parallel, ideally with one processor for each cell. As in the Island model, updating of the cells can be both synchronous and asynchronous.

Pool Model

Another population distributed model is called the Pool model. In this model the population is put in a shared global resource pool of n individuals, where it can be accessed by different workers (threads). The resource pool is partitioned into equal size partitions, and each of these partitions are assigned to exactly one worker. Each worker perform selection, child generation and evaluation independently by selecting individuals from the entire resource pool, but only updating the positions in the resource pool for which it is responsible for. This process is demonstrated in figure 2.10.

A worker w_1 is responsible for k positions in the pool. This is indicated by the coloring scheme in figure 2.10, where the worker and the positions it is responsible for has the same color. Each worker draws a population of individuals $i_1, i_2, ..., i_k$ from random positions in the pool and performs genetic operations and fitness calculations on them. Next, each new child individual is written back to the worker's associated positions $1, 2, ..., k$, given that its fitness is higher than the fitness of the individual currently occupying the position. The implementation details of this, and the other population dis-
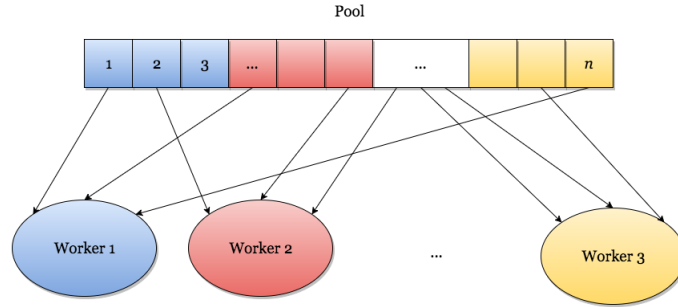
Figure 2.10: The pool model. Each worker has its own positions in the pool which it returns individuals to. The red processor is responsible for the red positions in the pool, and so on. Workers draw individuals from random positions in the pool, as indicated by the arrows, but can only write them back to its own positions, given that their fitness is higher than the fitness of the individual currently occupying the position [Gong et al., 2015].

tributed models, are presented in chapter 4.

2.3   Structured Literature Review

In order to get a deep understanding of genetic algorithms the books Holland [1992] and Goldberg [2005] was read. By reading the initial work of Holland, the inventor of the genetic algorithm, and the in depth explanation and analysis presented by Goldberg, the author got the proper understanding of genetic algorithms needed to write this thesis.

After an extensive literature search, the author was able to come up with the goal and research questions that will be investigated in this thesis. The literature search was performed in the following way: First, Google Scholar was used to search for articles with the search words *genetic algorithms* and *wind farm layout optimization*. A few of the first hits were read by the author. After reading these initial papers the author's understanding of the domain and domain vocabulary increased so new searches were made with the search words *genetic algorithm*, *evolutionary algorithm*, *genetic computation*, *wind farm layout optimization* and a few more. The resulting papers were col-

lected by the author and review based on the following metrics: (a) Number of citations, (b) similarity of the problem to the problem investigated in this thesis, (c) whether the article brings something new to the field, and (d) publishing date. Articles published in resent years were preferred, a long with a few initial papers because they laid the foundation for the field. The twelve articles summarized in table 3.3 were selected to give the reader an extensive understanding of wind farm layout optimization using genetic algorithms. Additionally, 4 articles about wind farm layout optimization using other artificial intelligence algorithms were chosen to be presented in order to give the reader a brief overview over other approaches that has been used in solving the given problem.

In summary, this chapter has introduced the wind farm layout optimization problem and the challenges that comes with wind farm construction. The simple genetic algorithm has been explained, and each of the 3 population distributed genetic algorithms have been introduced. The next chapter will give the reader an overview over the current research within wind farm layout optimization using genetic algorithms and a few other techniques.

Chapter 3

Related Work

Wind farm layout optimization has been studied extensively over the last 20 years and the goal of this section is to provide the reader with an overview of the research. This section is divided into three parts; Section 3.1 gives an extensive overview of wind farm layout optimization using genetic algorithms, since genetic algorithms are the main focus of this thesis. Section 3.2 gives a short review of other optimization approaches, and section 3.3 contains a summary/discussion of related work.

3.1 Wind Farm Layout Optimization using Genetic Algorithms

Mosetti et al. [1994] were the first to successfully demonstrate the utilization of the genetic algorithm in solving the wind farm layout optimization problem. Although their work was made for illustrative purposes only, it laid the foundation for a number of more extensive studies of wind farm layout optimization using genetic algorithms.

In order to properly model a wind farm one have to specify a wake model, a power curve and a cost function. To model the wind decay, Mosetti et al. used a wake model similar to the one developed by Jensen [1983]. Power generated by each turbine i was modeled as a cubic function of the wind speed u and site roughness z_0, and summed up to get the total power produced by the farm in one year as shown in equation 3.1. This power model is called the Betz power model [Albring, 1967]. Cost was modeled as a simple function of

the number of turbines N_t, assuming the cost/year of a single turbine is 1, and that a maximum cost reduction of $\frac{1}{3}$ can be obtained for each turbine if a large number of machines are installed, as shown in equation 3.2

$$Power_{total} = \sum_{i}^{N_t} z_0 u_i^3, \tag{3.1}$$

$$cost_{total} = N_t \left(\frac{2}{3} + \frac{1}{3} e^{-0.00174N_t^2} \right). \tag{3.2}$$

With the goal of producing a great amount of power at low cost, the objective function to be minimized was formulated as a combination of equation 3.1 and 3.2

$$Objective = \frac{1}{P_{total}} w_1 + \frac{cost_{total}}{P_{total}} w_2 \tag{3.3}$$

where w_1 and w_2 are weights. In the current study, w_1 was kept small so that the focus would be on lowest cost per energy produced.

Mosetti et al. divided the wind farm terrain into a 10×10 quadratic grid where a wind turbine could be installed in the middle of each cell. The optimization problem would then be to position the turbines in the cells in a way that maximize power production and minimize cost. With this representation, an individual of the genetic search could be represented as a binary string of length 100, where each index represents a cell in the grid, so that a value of 1 means that a wind turbine is installed in the corresponding cell, and a value of 0 means that there is no wind turbine in the corresponding cell. Figure 3.1 illustrates how an individual represents a wind farm for a wind farm partitioned into 100 cells. The genetic algorithm used was a simple, single-population genetic algorithm. The crossover operation was performed at random locations with probability $0.6 < P_c < 0.9$ and mutation was performed with probability $0.01 < P_m < 0.1$.

The model was tested using a single turbine type on three different wind scenarios: (a) Single wind direction, (b) multiple wind directions with constant intensity, and (c) multiple wind directions and intensities. For each scenario, the results were compared to random configurations of 50 turbines. One

| 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | .... | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 |

1
Wind Farm Genotype n
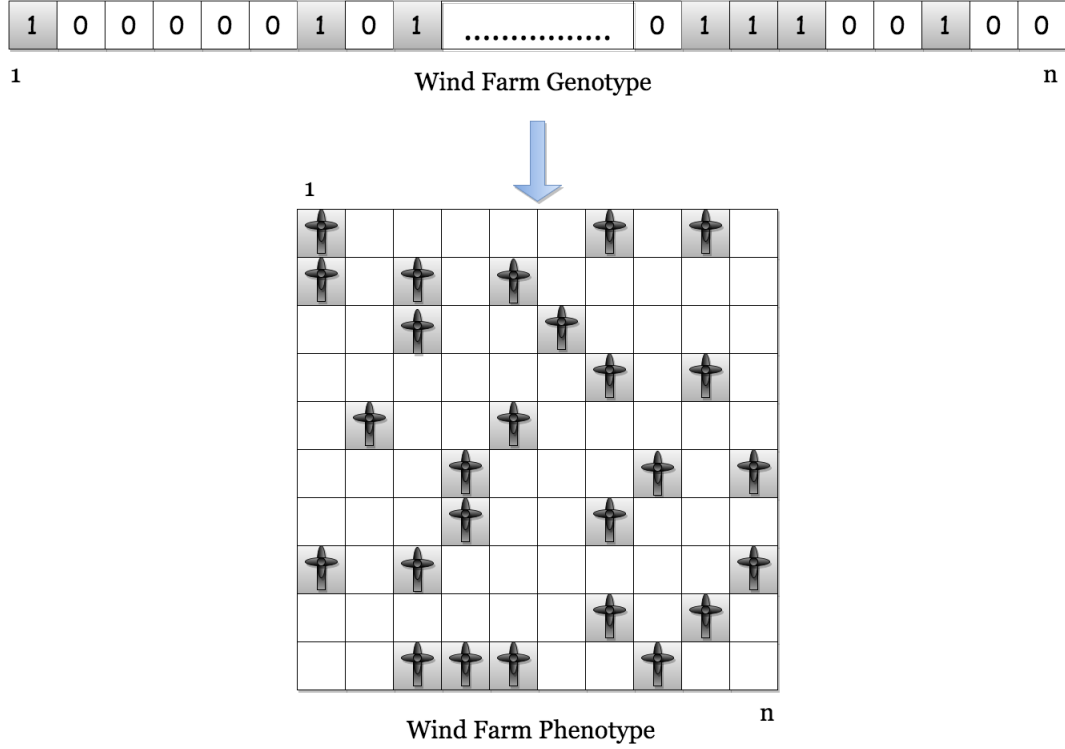
1

Wind Farm Phenotype n

Figure 3.1: An example of how the wind farm is represented in the genetic search from Mosetti et al. [1994]. An individual is represented as a bit-string of size 100, where each cell can either contain the value 1 or 0, representing a position containing a turbine and a position not containing a turbine, respectively.

of the metrics used to compare the models were efficiency which is defined as the amount of energy produced out of the energy that would have been produced without wake effect. In scenario (a), the efficiency of the random configuration was 0.50, while the efficiency of the optimized solution was 0.95. In (b), the efficiency was increased from 0.35 in the random configuration to 0.88 in the optimized configuration. And, in (c) the efficiency was increased from 0.34 to 0.84. For each scenario the number of wind turbines was decreased drastically in the optimized version. Table 3.1 summarizes the results obtained.

Table 3.1: Optimized configurations compared against random configurations for each of the three scenarios (a) single wind direction, (b) multiple wind directions with constant intensity and (c) multiple wind directions and intensities[Mosetti et al., 1994].

Scenario	Configuration	Efficiency	P_{tot}(kWyear)	cost/kWyear	Number of turbines
(a)	Random	0.50	13025	2.57×10^{-3}	50
	Optimized	0.95	12375	1.57×10^{-3}	25
(b)	Random	0.35	9117	3.68×10^{-3}	50
	Optimized	0.88	8711	1.84×10^{-3}	19
(c)	Random	0.34	4767	7.04×10^{-3}	50
	Optimized	0.84	3695	3.61×10^{-3}	15

As pointed out by Mosetti et al., different simplifying assumptions were made in the model such as the cost- and power model. The results were also only compared to randomly generated layouts. In order to find out if genetic algorithm are applicable to real-world problems they should be compared against layouts obtained by industry-accepted optimization methods. However, the purpose of this initial paper was to demonstrate the applicability of genetic algorithms on the wind farm layout optimization problem, and it has certainly laid the ground work for a number of studies performed over the last 20 years.

Grady et al. [2005] picked up where Mosetti et al. [1994] left of. They recognized that while the results of Mosetti et al. beats random configurations they were not close to beat configurations made by simple empirical placement schemes. In their study, they wanted to show that by implementing a population distributed genetic algorithm, the effectiveness of the algorithm could also be compared to optimal configurations. As Mosetti et al., they used the Jensen wake decay model, as well as the same cost- and power function, shown in equation 3.2 and 3.1 respectively. However, the objective function was changed into the following

$$Objective = \frac{cost}{P_{tot}}. \tag{3.4}$$

The same three scenarios as Mosetti et al. were considered. However, the number of individuals was increased from 200 to 600, and run for 3000 generations instead of 400. The population distributed model used was an Island model where the individuals were divided into 20 sub-populations. Sadly,

not many implementation details were shared. On the first scenario, Grady et al. recognized that with uniform wind distribution the optimal solution could be obtained empirically by optimizing one single row of the layout, and copy it to the rest. As opposed to Mosetti et al., the obtained results identical to the optimal solution. In scenarios (b) and (c) however, the optimal solutions could not be obtained empirically, and therefore the results are just compared against those of Mosetti et al. The results for each scenario is displayed in table 3.2. The first thing to notice is the difference in number of turbines. Grady et al. ends up with more turbines in each case, approximately doubling the number of turbines in scenario (b) and (c). The explanation behind this observation lies in the objective function. Objective function 3.3 prioritizes low cost and hence prioritizes a lower turbine count. For each scenario the fitness of Mosetti et al. is higher than the fitness obtained by Grady et al. With exception of the first scenario, the efficiency is also higher in Mosetti et al. These results make sense since fewer turbines leads to less wake effect and decreased efficiency. However, in each case, the total power production is largely increased in the current study, which also makes sense based on the turbine count.

In summary, Grady et al. were able to show that by implementing a population distributed genetic algorihtm optimal solution for scenario (a) can be obtained. They also showed that the power production obtained in Mosetti et al. could be increased by optimizing parameter values and using a more sophisticated implementation of the genetic algorithm. However, they make no attempt to compare their solutions for scenario (b) and (c) to solutions obtained using other optimization techniques. For a similar study where individuals are implemented as matrices in MATLAB see Emami and Noghreh [2010].

Zhao et al. [2006] presented a very interesting study, where the electrical system of an off shore wind farm on Burko Bank in Liverpool Bay was optimized using a genetic algorithm. Although this is a study of cable clustering design, with fixed wind turbine count and positions, it is very interesting because it is compared against actual results obtained by the Burbo project team. To get an understanding of the optimization problem four example clustering designs are presented in figure 3.2.

In their publication, Zhao et al. present an extensive study of different ge-

Table 3.2: A comparison of the results obtained by Mosetti et al. [1994] and Grady et al. [2005] for each of the three scenarios.

Scenario	Parameter	Mosetti et al.	Grady et al.
(a)	Fitness	0.0016197	0.0015436
	Total power (kW year)	12 352	14 310
	Efficiency (%)	91.645	92.015
	Number of turbines	26	30
(b)	Fitness	0.0017371	0.0015666
	Total power (kW year)	9244.7	17220
	Efficiency (%)	93.859	85.174
	Number of turbines	19	39
(c)	Fitness	0.00099405	0.00080314
	Total power (kW year)	13 460	32 038
	Efficiency (%)	94.62	86.619
	Number of turbines	15	39

Figure 3.2: Four example clustering designs [Zhao et al., 2006].

netic algorithm techniques to find out which technique leads to the best results on this type of optimization problem. Premature convergence is discovered as the main problem of the genetic algorithm and to deal with this, different techniques are presented such as a diversity check, and a crowding technique called restricted tournament selection. For implementation details

see reference Zhao et al. [2006]. Different genetic algorithm designs were tested, and the results showed that the final design obtained was equal to the design obtain by the Burbo project team! This shows that optimization using sophisticated genetic algorithms can find the same solution as current optimization techniques for optimization of electrical systems.

Huang [2007] presented a study showing that a population distributed genetic algorithm performs better than a simple genetic algorithm. Huang uses a more realistic objective function than the previous studies, taking into account the selling price of electric energy, as well as cost and energy production. The distributed genetic algorithm used is the Island model, with 600 individuals divided among 20 demes, with the ring-topology shown in figure 3.3.
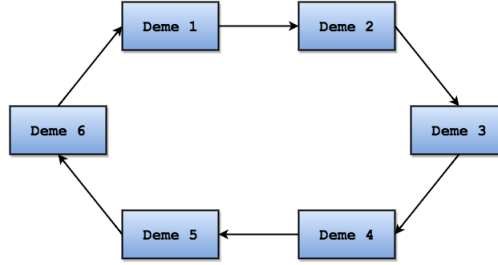

Figure 3.3: Ring topology example with 6 demes [Huang, 2007].

The simulation was run for 2500 generations with the migration strategy that 3.3% of the individuals with highest fitness was selected as migrants, to replace the individuals with lowest fitness in the new population every 20th generation. The distributed algorithm was tested using the same three scenarios as Mosetti et al. [1994] and Grady et al. [2005], and compared against a simple genetic algorithm. In case (a) the population distributed genetic algorithm was able to come up with the optimal solution (presented by Grady et al.), while as the simple genetic algorithm was not. For each of the three scenarios the population distributed algorithm ended up with higher fitness value, more power produced, lower CPU time and fewer generations. In case (a) the turbine count was equal for both algorithms, resulting in higher efficiency for the distributed algorithm. In scenario (b) and (c) the population distributed algorithm produced solutions with one additional turbine com-

pared to the simple algorithm, resulting in slightly lower efficiency.

All studies presented above have used binary encoding in their wind farm representation, but Mora et al. [2007] presented a study where the binary encoding was replaced by an integer encoding. In their approach, an individual was represented as a set of (x, y)-coordinates representing turbine positions. In addition to optimize turbine position, Mora et al. also wanted to optimize both turbine type and height. In order to do this, they represented the individuals by a matrix as shown in figure 3.4. The first row contained the x-coordinates of the turbines, the second row the y-coordinates, the third row turbine type and the forth row turbine height as shown in figure 3.4. Note that with this type of encoding, different individuals can have different lengths, depending on the number of turbines in each solution.

Figure 3.4: Representation of an individual of length k (layout with k turbines), where the first row represents x-coordinates of the turbines, the second row y-coordinates, the third row turbine type, and the forth row turbine height [Mora et al., 2007].

Five crossover methods, and a masked mutation method were presented for the new type of encoding, see Mora et al. [2007] for implementation details. To model the wind speed, the Weibull distribution was used, a more realistic wind speed model than the one used in the previous studies. The Weibull distribution will be explained in more detail in chapter 4, since it is also used in this thesis. Three different case studies were performed. The first one is a search for the optimal solution when the number of turbines are decided beforehand. The second is a search for the optimal positioning, type and height of turbines within a given budget. And the third one a search for the optimal solution with no such constraints. The results are only briefly

discussed. However, this paper marks the shift from binary- to integer encoding, and from simple wind models to the Weibull distribution.

Wan et al. [2009] criticized the simple power-, and wind distribution model presented by references Grady et al. [2005], Mosetti et al. [1994]. Rather, they used the Weibull distribution as Mora et al. [2007] to model the wind, and they introduced a novel power model

$$\int_{u_{in}}^{u_{out}} P(u)f(u)du, \tag{3.5}$$

where u_{in} is the cut-in wind speed of the turbine, and u_{out} is the cut-out wind speed of the turbine. $P(u)$ is the power output for the wind speed u and $f(u)$ is the probability density of the wind speed u. The genetic algorithm was similar to that of Grady et al., and results showed that the produced power increases.

One of the most complete studies of the wind farm layout optimization problem was done by Kusiak and Song [2010]. Their study is based on six assumptions, which according to the authors are realistic and industrial-accepted. The study assume a fixed, predetermined turbine count, small variations of surface roughness, turbines with equal power curves, wind speed following the Weibull distribution, that wind speed at different locations with same direction share the same Weibull distribution, and last, it assumes that any two turbines must be separated with at least four rotor diameters. A multi-objective function was used to calculate the fitness of the solutions. It consisted of one objective function to maximize expected energy produced, and one to minimize the constraint violations. Kusiak et al. critiques Mosetti et al. and Grady et al. for not basing their wind energy calculation on the power curve function and not thoroughly discussing wind direction. Their work include an extensive model of wind energy based on a discretization of the expected power production for each wind direction. Their algorithm was tested on real wind data, and compared against an upper bound on power production (power produced without wake effect), and their results show that less than 2% of power is lost due to wake effects when 6 turbines are positioned in the wind farm.

Assumptions such as cost models only dependent on the number of turbines are unrealistic, and needs to be refined in order to model the wind farm layout optimization problem in a realistic way. González et al. [2010] introduced a cost model based on the net present value, which takes into account wind speed, wind distribution, the number-, type-, rated power- and tower height of turbines, loss due to wake effects, auxiliary costs, road infrastructure, buildings, substation, electrical framework and financial aspects such as return on investment. For example, In order to more accurately model civil cost they present a greedy search which connects wind turbines to auxiliary roads or other turbines dependent on their position. Figure 3.5 shows how the greedy algorithm works. First, the distance between each turbine and every road is calculated. Since turbine A is closest to road 1, they are connected. Second, the distance between the remaining turbines and the roads and turbines already connected are compared, and turbine C is connected to road 2. At last, turbine B needs to be connected. Since it is closer to turbine A, than turbine C or any of the roads, it is connected to turbine A.

Other new features includes a local search used when the genetic algorithm cannot find a better individual, and a genetic algorithm that can manage forbidden areas and that gives penalties for turbines positioned in undesirable terrain. Individuals are represented the same way as in reference Mora et al. [2007] displayed in figure 3.4. Results are compared against Grady, and shows higher produced energy. The authors also include three case studies showing how their algorithm can handle restrictions such as roads crossing, forbidden zones, undesirable zones and maximum investment cost.

Şişbot et al. [2010] published a case study of wind turbine placement on a wind farm at the Island Gökçeada, at the north east of the Aegean Sea. A distributed genetic algorithm was used, but unlike Huang's, the individuals were evaluated based on multiple objective functions; one that measures the total cost (installation and operational), and one that measure total power production. Şişbot et al. argue that in an environment with changing demands, the use of a multi-objective function gives the decision-makers the opportunity to evaluate the different designs based on cost and power production separately, without ill-informed, randomly generated weights. The selection process used is a controlled, elitist process, meaning that not only the fittest, but also some individuals that can spread diversity to the population are selected for reproduction. The genetic algorithm returns a set of
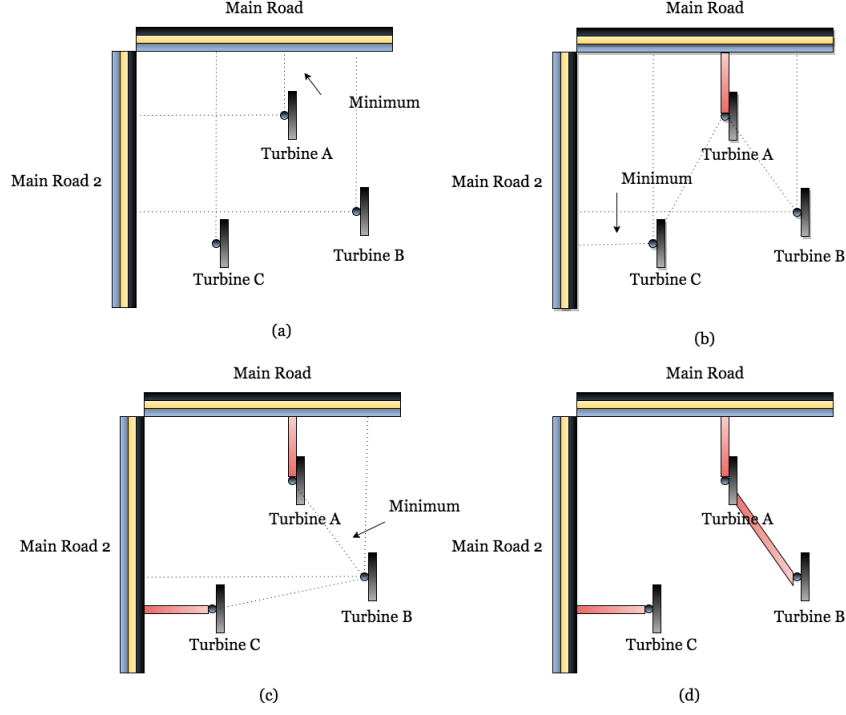
Figure 3.5: Greedy algorithm to estimate civil cost. [González et al., 2010].

Pareto optimal solutions; a set of solutions that are not dominated by any other solution in the set. Stated more formally, solution $\mathbf{y}$ is said to dominate solution $\mathbf{x}$ if

$$\forall i : f_i(\mathbf{x}) \leq f_i(\mathbf{y}) \; and \; \exists j : f_j(\mathbf{x}) < f_j(\mathbf{y}) \tag{3.6}$$

where f_i is the objective function [Murata et al., 2001]. Other interesting features of this study is the introduction of constraints on wind turbine positions and constraints on the cost, meaning that individuals with wind turbines outside the area of the island, and individuals with costs larger than the budget are removed from the population. Even though constraints on individuals are not in accordance with the nature genetic algorithms, they can be necessary when the algorithm is applied to a real problem. Another feature introduced in this paper is rectangular cells. The argument behind this decision is that the safe distance between wind turbines is dependent on the direction of the turbine. The minimum distance between turbines in

prevailing wind is 8D, while the minimum distance between turbines in the crosswind is 2D. Despite this attempt to make the wind scenario more realistic, it is critiqued because it operates with a constant wind direction and constant speed, using the average wind direction and speed measured at the Island [Samorani, 2013]. Results are not compared against previous studies, and the argument behind this decision is that it is difficult to compare a Pareto-optimal set of solutions to one of the previous solutions.

Another very interesting solution to the wind farm layout optimization problem was proposed by Saavedra-Morena et al. [2011]. Four novel improvements were included in their model. First, a shape model was introduced to model the terrain shape. By introducing this model, the simplification of a square grid was lost, and every terrain shape could be implemented. Second, an orography model was used to model the wind speed on different heights. Using this technique, the wind model is much more realistic because it takes into account that wind speed differs at different heights. Third, they introduce a new cost model, which takes into account installation cost, connection between turbines, road construction and net benefit from the produced energy. The fourth, and maybe most exiting improvement presented was that a greedy heuristic was used to decide the initial positioning of the turbines for some of the individuals. This improvement was requested by Mosetti et al. in 1994, but not included by anyone until now. The greedy heuristic works by placing turbines one by one in the position with maximal wind speed. First of all, the first turbine is positioned in the position wind maximum wind speed. Next, the wind speed is updated because of the reduction in wind speed caused by the wake effect of the first turbine. Third, the second turbine is positioned in the position with maximal wind speed. This process continues until N wind turbines have been placed. Clearly, the resulting layout is largely influenced by the positioning of the first turbine, and leads to a sub-optimal solution on its own. However, it is much better than a random solution, and as it turns out a good starting point for the genetic search. Results for 15 different orographys for the same terrain shape were provided, showing the objective function values obtained by the greedy heuristic, a simple genetic algorithm with random starting positions, and the seeded genetic algorithm (the genetic algorithm with starting positions found by the greedy heuristic). In each case, the genetic algorithm with random starting positions beats the results obtained by the greedy heuristic, but more importantly, in each case, the seeded genetic algorithm beats the results of the

simple genetic algorithm.

Both Mora et al. [2007] and González et al. [2010] used the genetic algorithm to optimize the height of the turbines, as well as other parameters by representing individuals as shown in figure 3.4. Another approach to optimize turbine height was presented by Chen et al. [2013]. They state that normally, the same turbine type can be bought with several different heights, and that it therefore makes sense to use different height turbines. To optimize turbine position and height, they used two nested genetic algorithms. The first was used to optimize turbine positioning, while the second was used to decide between two turbine heights. For each generation of the first genetic algorithm, the second one was run for 50 generations to optimized turbine height. Binary encoding was used for individual representation in both genetic searches as shown in figure 3.6. The first binary string represent turbine positioning in the environment, while the second binary string represents turbine height for each position that contains a turbine. Several case studies were performed in the paper, and results show that turbine layout with different turbine height, produce more energy than same-height turbines every time.

Gao et al. [2015] also implemented a population distributed genetic algorithm to solve the wind farm layout optimization problem. Unfortunately, the implementation details have not been published. Integer encoding was used to represent individuals, but unlike those presented earlier [González et al., 2010, Kusiak and Song, 2010, Mora et al., 2007, Saavedra-Morena et al., 2011], each individual had the same number of turbines. The algorithm was tested on the same three scenarios from Mosetti et al. and compared against other studies [González et al., 2010, Grady et al., 2005, Mosetti et al., 1994, Wan et al., 2009]. For the comparison to be valid they force their solutions to use the same number of turbines as obtained in the results of the previous studies. In each case their resulting layout is able to produce more energy, and has higher efficiency, however, it never achieves the highest fitness. In addition to this comparison, Gao et al. introduce an interesting hypothetical case study of wind turbine placement on an offshore farm located in the Hong Kong southeastern water. By using real wind data, collected over 20 years, they demonstrate that the distributed genetic algorithm can be applied to a real-world wind farm layout optimization problem. The resulting wind farm layout was estimated to be able to produce 9.1% of yearly electrical consumption in Hong Kong (2012).
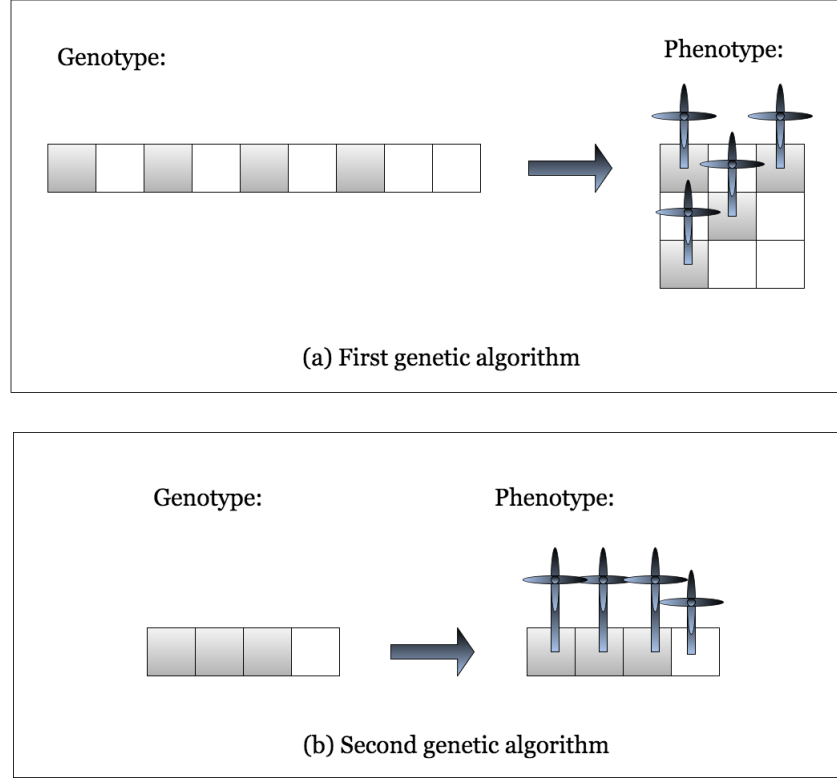
Figure 3.6: Genotype to phenotype translation from Chen et al. [2013]. (a) Binary string representing turbine positions, (b) binary string representing height of the given turbines positioned by the first genetic algorithm.

3.2 Wind Farm Layout Optimization Different Approaches

A greedy heuristic approach to the wind farm layout optimization problem was presented by Ozturk and Norman [2004]. The algorithm starts with an initial solution, where a number of wind turbines are positioned in the wind farm at random positions. Next, the greedy algorithm tries to improve the layout by performing either an add operation, a remove operation or a move operation. The add operation works by randomly position one new turbine in the terrain a number of times at different locations, and observe the change in the objective function value. The remove operation works by

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observing the change in objective function value when a turbine is removed, the process is repeated for all turbines. A move operation consist of moving each turbine 4 rotor diameters away from its current position in eight wind directions one at a time, and observe the change in the objective function value. The operation performed by the algorithm is the one that improves the objective function value the most. The greedy heuristic often converged to a local optimum, and the authors try to cope with this problem by performing randomly perturbations on a number of turbine positions if no improvements could be found using the add-, remove-, or move operation. Three approaches were investigated to find the initial position of the turbines; (1) randomly positioning, (2) packing the wind farm with as many turbines as possible, and (3) start with zero turbines. Preliminary testing showed that the second approach produced best results. The greedy algorithm was tested, and the results were compared to a feasible solution with the maximum number of turbines positioned, i.e. the initial layout before the algorithm was run. In 10 out of 12 case studies the algorithm improved the layout of the wind farm, with an average improvement of 4.3%.

Bilbao and Alba [2009] designed a simulated annealing algorithm to solve the wind farm layout optimization problem. The same wind parameters and representation as Grady et al. [2005] was used, and the algorithm was tested on the same three scenarios. The simulated annealing algorithm works as follows: First, an initial layout is obtained by randomly positioning a predefined number of turbines. Later, a random position that contains a turbine is chosen, and a new, randomly generated location is suggested. If the new position is better, the turbine is moved, but if the new position is not better, the turbine is moved with a given probability which is regulated by a decreasing temperature parameter, in order to prevent the algorithm from converging to a local optimum. In case (a) from [Grady et al., 2005] the simulated annealing algorithm was able to find the same optimal solution, and that by using only $\approx 4\%$ of the execution time of Grady et al., and only $\approx 1\%$ of the time spent evaluating the solution. In case (b) and (c) the simulated annealing algorithm was able to find solutions with better fitness, higher power production, higher efficiency, and significantly lower execution- and evaluation times, showing that simulation annealing might be a good technique to search for the optimal wind farm layout, and it should definitively be tested in a more realistic environment.

Eroğlu and Seçkiner [2012] proposed an ant colony algorithm for the wind farm layout optimization problem. The algorithm was inspired by the way ants search for food, and how ants guide each other to food sources by leaving a pheromone trail. The algorithm operates on a predetermined number of turbines, randomly positioned. The pheromone quantity of each turbine is decided by calculating the wake loss for the given turbine, resulting in a stronger pheromone trail for turbines with worse locations. Ants will follow the pheromone trail, therefore more ants will try to better the position of the worse turbines by moving them in random directions - the turbine is only moved if the new position is better than the current. Results are compared against [Kusiak and Song, 2010] and it is shown that the ant colony algorithm was able to position two more turbines, eight turbines in total, and that when the number of turbines was greater than two, the ant colony algorithm produced more power, experienced less wake loss and obtained higher efficiency.

Another technique to search for the best wind farm layout is swarm optimization, and Wan et al. [2012] demonstrates how a Gaussian particle swarm algorithm can solve the wind farm layout optimization problem. Swarm optimization, is an optimization technique inspired by fish schooling, insect swarms and bird flocking. The algorithm presented used an objective function that tries to maximize produced power, while minimizing constraint violations. The algorithm works as follows: First, N particles are placed in random (x, y)-positions. Second, the initial solution is evaluated and the results are saved. Third, the population best position z^g is saved, along with the current best position observed for each particle Z^p, which in the beginning will be the initial positions. An algorithm is presented, to decide which, out of two layouts, is the best. It works by first prioritizing layouts which violates less constraints, and second compare power produced by the two layouts. Forth, an updating scheme is run for a given number of iterations. It first checks if the local best position observed by that particle z^p is equal to the global best position z^g, and if so, uses an regeneration scheme that moves the particle to a random position. Otherwise, a new position is calculated for the particle based on the particles current position, its current best observed position and the global best observed position and two normalized random Gaussian numbers. If the new position is better than the previous one, the particle is moved. A differential evolution local scheme is also incorporated in each iteration to improve the algorithms local search ability. It basically

works by randomly picking three random particles as potential parents for a given particle, and combine these to generate an alternative new position, which is assign to the particle, if it is better than the current one. Results were compared against [Grady et al., 2005], and they showed that the power generated is higher using this algorithm. Their algorithm is also tested in a more realistic environment and compared against an empirical method as well as a simpler particle swarm algorithm. The results showed that the power generated was increased using the proposed algorithm.

3.3   Discussion Related Work

In order to summarize the different publications that use genetic algorithms to solve the wind farm layout optimization problem the wake-, wind-, power-, and cost model, along with the objective function, type of genetic algorithm, representation of individuals, and novelties presented in each publication is presented in table 3.3. Note that the table is simplified so that it fits on one page, but it still provides a good overview over the publications.

As can be seen in the table, each article utilized some variation of the Jensen model, developed by Jensen [1983], and later improved upon by Katic et al. [1986] and Frandsen et al. [2007], to model wind speed decay as a consequence of the wake effect. The same model will also be used in this thesis.

Even though not many improvements has been made to the wake model, the wind model has evolved a lot since Mosetti et al. [1994]. As presented earlier, the three wind scenarios developed by Mosetti et al.: (a) Single wind direction, uniform intensity, (b) multiple wind directions, uniform intensity, and (c) multiple wind directions and intensities, are not very realistic (these scenarios are represented as "simple scenarios" in table 3.3). The Weibull distribution, introduced by Mora et al. [2007], models the wind distribution much better, and has been adopted by everyone, except those who still wanted to compare their results against Mosetti et al. [1994] and Grady et al. [2005]. As mentioned before, the Weibull distribution will also be used to model wind distribution in this thesis, and will be described in more detail in chapter 4.

The majority of the publications presented used the power model presented by Mosetti et al. [1994], however, Kusiak and Song [2010] present a more realistic, linear power model, which also will be used in this thesis which also is explained in chapter 4.

The quality of the cost model has varied greatly in the different studies. The very unrealistic cost model that only takes turbine count into account has been adopted by many, as can be seen in table 3.3 represented as "simple". However, [Mora et al., 2007], [González et al., 2010], [Şişbot et al., 2010], [Saavedra-Morena et al., 2011], and [Chen et al., 2013] used more realist cost models, taking into account different parameters such as net present value, installation cost, maintenance work, civil work, interest rate and so on, these are represented as "complex" in the table. In the current thesis, a very complicated objective function is presented, one which takes into account turbine cost, substation cost, interest rate, operating costs, and turbine count as well as produced power. chapter 4 gives an detailed explanation of the objective function.

Other methods than the genetic algorithm also shows promising results in solving the wind farm layout optimization problem. Simulated annealing [Bilbao and Alba, 2009], ant-colony optimization [Eroğlu and Seçkiner, 2012] and swarm optimization [Wan et al., 2012] are popular algorithms within the artificial intelligence community, that should be optimized in order to solve the wind farm layout optimization problem. The greedy heuristic approach presented in [Ozturk and Norman, 2004] needs to be tested in a more realistic environment in order to find out if this method really could be used on turbine layout positioning.

In this thesis, the wake-, wind-, power-, and cost model, and objective function was provided by GECCO 2015, and therefore no attempt will be made in improving any of these. Since the simple genetic algorithm presented by Mosetti et al. [1994], different approaches has been tested in order to improve the results. Already in 2005, it was shown that by using a population distributed genetic algorithm [Grady et al., 2005], and change a few parameters, the results from Mosetti et al. [1994] could be improved. In Huang [2007] the focus was on showing how the Island model performed better than a simple genetic algorithms on solving the wind farm layout optimization problem, and his results show that the population distributed genetic algorithm is

never beaten by the simple genetic algorithm. Both Grady et al., and Huang et al., uses the Island model when implementing their population distributed genetic algorithms. Even though these results indicate that population distributed genetic algorithms works better, the results of Grady et al., is beaten by the simple genetic algorithm of González et al. [2010] when a local search is used together with the genetic algorithm. Also, in Saavedra-Morena et al. [2011] it is shown that a seeded simple genetic algorithm shows promising results, even though it is not compared against a population distributed genetic algorithm. Gao et al. [2015] also demonstrates how their population distributed genetic algorithm performs better than González et al. [2010], Grady et al. [2005], Mosetti et al. [1994], Wan et al. [2009], but sadly they do not share many implementation details. These results clearly show that population distributed genetic algorithms can be an effective optimization technique for the wind farm layout optimization problem, and they are the motivation behind the goal statement and research questions..

In summary, this chapter has given an overview over them most important research within the field of wind farm layout optimization and genetic algorithms. It has been shown that no effort have been put in testing other population distributed genetic algorithms than the Island model. Additionally, it has been shown that optimization methods other than genetic algorithms also can be used to optimized wind farm layout. The next chapter contains the implementation details of the genetic algorithm models implemented for this thesis.

Table 3.3: A simplified overview over the publications from section 3.1. In the column "Wind Model" the term "Simple scenarios" refer to the three wind scenarios developed by Mosetti et al. [1994]. The cost model and objective function columns are defined as "Simple" if it only takes into account the number of turbines. In the "GA" column, "SGA" stands for simple genetic algorithm, and "PDGA" stands for population distributed genetic algorithm.

Publication	Wake Model	Wind Model	Power Model	Cost Model	Objective	GA	Representation	Novelties
Mosetti et al. [1994]	Jensen [1983]	Simple scenarios	Betz [Albring, 1967]	Simple	Simple	SGA	Binary	Novel.
Grady et al. [2005]	Jensen [1983]	Simple scenarios	Betz [Albring, 1967]	Simple	Simple	PDGA	Binary	Population distributed.
Huang [2007]	Katic et al. [1986]	Simple scenarios	Betz [Albring, 1967]	Simple	Simple	PDGA	Binary	Compared DGA and SGA. Realistic objective.
Mora et al. [2007]	NA	Weibull distribution	NA	Complex	Complex	SGA	Integer	Weibull distribution, integer encoding.
Emami and Noghreh [2010]	Jensen [1983]	Simple scenarios	Betz [Albring, 1967]	Simple	Simple	SGA	Binary	Matrix representation of individuals.
Wan et al. [2009]	Jensen [1983]	Simple scenarios	Betz [Albring, 1967]	Simple	Simple	PDGA	Binary	New power function.
Kusiak and Song [2010]	Jensen [1983]	Weibull distribution	Linear	NA	Complex	SGA	Integer	Realistic environment.
González et al. [2010]	Frandsen et al. [2007]	Weibull	Betz [Albring, 1967]	Complex	Complex	SGA	Integer	Extensive cost model.
Şişbot et al. [2010]	Jensen [1983]	Simple scenarios	Betz [Albring, 1967]	Complex	Complex	PDGA	Binary	Multi-objective with pareto ranking.
Saavedra-Morena et al. [2011]	Frandsen et al. [2007]	Weibull distribution	Betz [Albring, 1967]	Complex	Complex	SGA	Integer	Seeded genetic algorithm.
Chen et al. [2013]	Jensen [1983]	Simple scenarios	Betz [Albring, 1967]	Complex	Simple	SGA	Binary	Nested genetic algorithms.
Gao et al. [2015]	Jensen [1983]	Real wind data	Betz [Albring, 1967]	Simple	Simple	PDGA	Integer	Hong Kong case study.

Chapter 4

Methodology

In this chapter, the simulator used to investigate the research questions is described. An overview of the system is presented in section 4.1. Section 4.2 includes implementation details, and design decisions made when implementing the genetic algorithm which is the foundation for all the population distributed genetic algorithms. Sections 4.4 contain implementation details of the population distributed genetic algorithms. The wind scenarios used to evaluate the different population distributed genetic algorithm are described in section 4.3, and the choice of implementing the genetic algorithm from scratch is defended in section 4.5.

4.1 System Architecture

The program is implemented in Java and the interactions between the different classes of the program are shown in figure 4.1. The GeneticAlgorithm class is extended by the three population distributed genetic algorithm classes: IslandModel, CellularModel and PoolModel. In addition, the GeneticAlgorithm class is also implemented as instances in all three population distributed algorithms. The main loop of the program is contained in the GeneticAlgorithm class. It uses instances of the classes WindScenario, WindFarmLayoutEvaluator, Population, AdultSelection, ParentSelection, Crossover and Mutation. AdultSelection and ParentSelection are interfaces that needs to be implemented if new methods are to be added to the program, and Crossover is an abstract class containing one method which every Crossover class must implement. Mutation is a class containing four
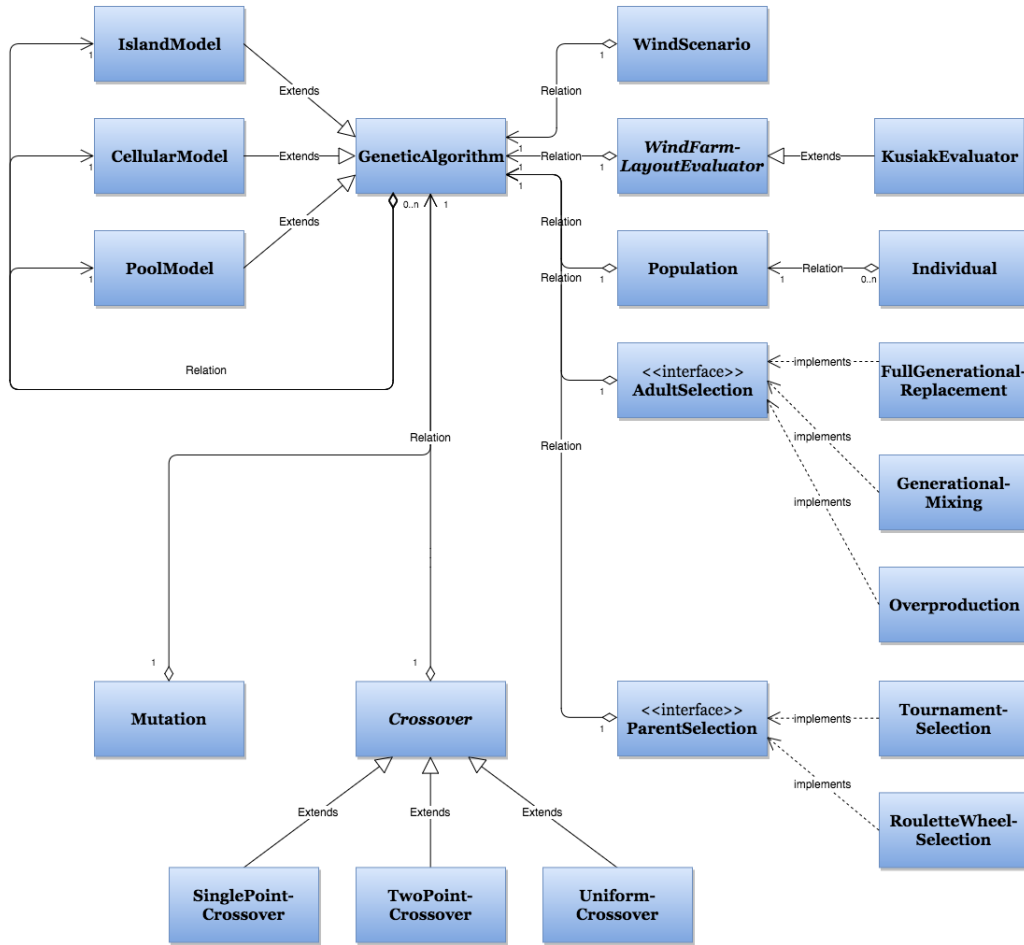
different mutation methods.

Figure 4.1: Class Diagram.

4.2 Genetic Algorithm Implementation Details

As mentioned in chapter 2, the genetic algorithm is a four step process: Adult selection, parent selection, recombination such as crossover and mutation, and fitness evaluation as shown in figure 4.2. Implementation details of each

step is described in the subsequent sub sections. In addition, the wind-, wake-, and power model used in evaluating the genetic algorithm are described in the following subsections since these are crucial to understanding the fitness function.
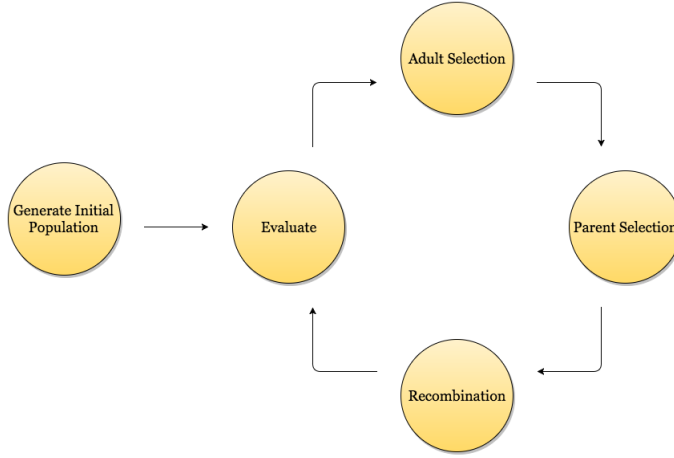
Figure 4.2: Genetic algorithm.

The simple genetic algorithm is implemented using the Master/Slave model. The Master/Slave model is the most common way of implementing a simple genetic algorithm. Evaluation of the different layouts in a population is by far the most time consuming step of the genetic algorithm. The Master/Slave model copes with this problem by distributing the evaluation to different slave processes, one for each core of the computer. By evaluation the population in parallel, the heaviest computational load is split between all the cores of the computer and the speed-up is proportional to the number of cores. The Master/Slave model is displayed in figure 4.3.

4.2.1 Representation

As in most of the studies presented in chapter 3, the individuals implemented for the genetic algorithm for this thesis are represented by binary strings. However, each position in the binary string can be directly mapped to a position in the terrain kept in an array called "grid". The purpose behind this design decision is that not all positions in the terrain, when dividing the
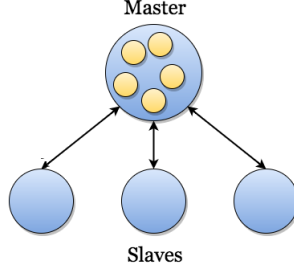
Figure 4.3: Master-slave model. The master process distributes the population to different slave processes, which calculate the fitness of each individual and return the results to the master process [Gong et al., 2015].

terrain into a squared grid, are legal turbine positions because of the existence of obstacles. By implementing individuals this way, the genetic operations can be performed on individuals without having to check for illegal positions since this is already taken care of as soon as the scenario is read from file. Also, this design decision makes sure that no space is wasted keeping illegal positions in the binary representation. Figure 4.4 shows how a given terrain is represented using a binary string and the grid-array. The grid to the left in the figure represents the terrain. Red cells represent illegal positions while grey cells represents legal positions. An individual and the grid array are presented to the right. Since there are only 9 legal positions in the terrain the individual has length 9. The grid-array contains the (x,y)-positions of each legal positions in the terrain. The given individual has the value 1 in positions 2, 4 and 8 respectively (zero indexed), meaning that wind turbines are positioned in the (x,y)-positions in positions 2, 4 and 8 in the grid-array, meaning position (1,2), (2,0) and (3,2) in the terrain. Wind parameters and obstacle positions are read into the program from the scenarios provided by GECCO 2016, these will be described later in this chapter.

4.2.2 Adult Selection

Adult selection is the process of selecting which individuals that are allowed to step into the adult pool and thereby become potential parents for the next generation of individuals. Three adult selection mechanisms were implemented in this thesis: Full generational replacement, generational mixing,
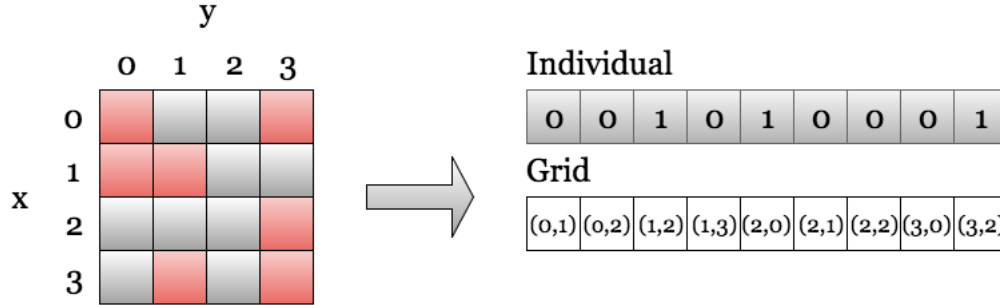
Figure 4.4: Individual representation. The grey squares represent legal turbine positions in the terrain, while the red represent illegal positions. Since there are only nine legal positions in this example, an individual is represented as a binary string of length 9. The grid array is shared between all the individuals and holds the (x, y)-coordinates for each legal position.

and overproduction. Each method was tested in order to decide which adult selection method was more suitable for solving the wind farm layout optimization problem.

Full generational replacement, the simplest adult selection mechanism, replaces the previous adult population with the newly generated child population. The second method, generational mixing, is illustrated in figure 4.5. As the name suggests, generational mixing mix the previous adult pool together with the new child pool and selects the best individuals from the mix to become the new adult population. As can be seen in the figure, the new adult pool consists of the best individuals from both the newly generated child pool and the previous adult pool. The two individuals with fitness 2 and 3 are selected from the child pool, and the two individuals with fitness 4 and 4 is selected from the previous adult pool. The new child population will therefore contain individuals with fitness 4, 2, 3 and 4, instead of fitness of 5, 6, 3 and 2, which would be the adult population if full generational replacement was used.

Overproduction, the third adult selection mechanism, is illustrated in figure 4.6. The newly generated child population consist of twice as many individuals as there are room for in the adult population. Therefore, the children
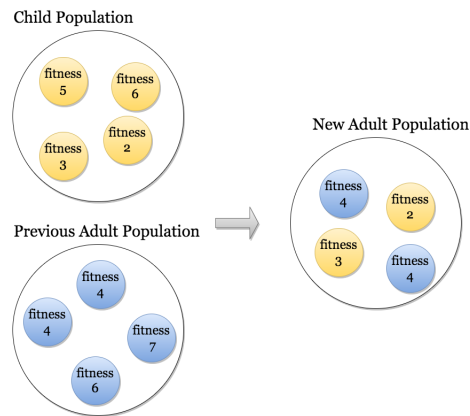
Figure 4.5: Generational mixing. The best individuals, from the pool consisting of individuals from the previous adult population and the new child population are selected as new the adult population.

have to compete against each other for the spots in the adult pool.
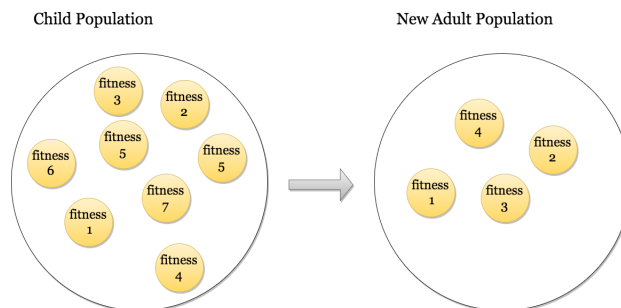

Figure 4.6: Overproduction. The newly generated child population consist of twice as many individuals as there are room for in the adult population. Therefore, only the fittest individuals from the large child population grow up into adults.

4.2.3 Parent Selection

Parent selection is the process of deciding which adults become parents for the next child generation. When choosing parent selection method there are a few concerns that needs to be addressed. First, it is important that parents with good genes, i.e. lower fitness, gets their genes transferred to the next generation. However, it is also important to keep diversity in the population so that one does not end up with a sub-optimal solution; a local maximum. Two parent selection methods are implemented for the genetic algorithm for this thesis: Tournament selection and roulette wheel selection.

In tournament selection, a given number of individuals are drawn randomly from the population. The number of individuals drawn is decided by the variable *tournament size*. These individuals compete in a tournament for one spot in the parent pool. The individual with best fitness is selected as a parent. These tournaments continue until the adult pool is full. Figure 4.7 shows how tournament selection works. As can be seen in the figure, three individuals are drawn randomly from the adult pool, meaning that the tournament size in this example is 3. The best individual, the individual with fitness 4 is the tournament winner and is allowed to enter the adult pool. In order to maintain diversity in the population there is a small probability that parents are selected randomly from the adult pool instead of with tournament selection. This probability is called *epsilon* and makes sure that a small percent of the parents that might not currently be best are not killed of right away. Different values of the *tournament size* variable needs to be tested in order to find the settings that allow the algorithm to explore different solutions, but that also prioritize the best solutions. In chapter 5, results obtained for different values of *tournament size* and *epsilon* are compared.

Roulette wheel selection assigns a probability of being chosen as parent to each individual proportional to its fitness. Individuals with better fitness will therefore have a higher probability of beings selected into the parent pool. Figure 4.8 shows how roulette wheel selection works. The roulette wheel on the left shows the probability for each of the four individuals being selected. Since $individual_4$ has the best fitness, it has a larger probability of being selected than the others.
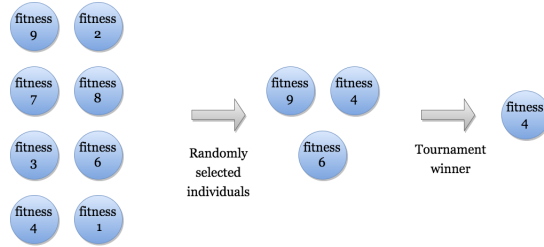
Figure 4.7: Tournament selection. Three individuals with fitness 9, 4 and 6 respectively, are selected randomly from the adult population. The individuals with best fitness, fitness 4, is the tournament winner and is selected into the parent pool.
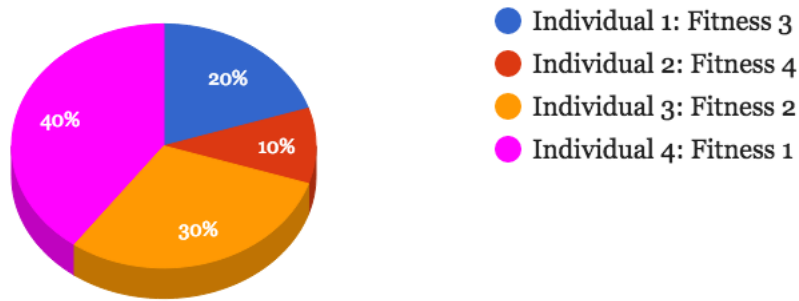

Figure 4.8: Roulette wheel selection. The roulette wheel is shown to the left, the four individuals to the right. Individual$_4$ has a four times better fitness than individual$_2$ and therefore has a four times larger probability of being selected.

4.2.4 Genetic Operations

This subsection gives an overview over the genetic operations used to produce the next child generation. Three crossover methods, elitism and four mutation methods are implemented and will be presented.

4.2.4.1 Crossover and Elitism

Crossover is the recombination method utilized by the genetic algorithm to perform sexual reproduction. A crossover operation produced two children

by recombining genes of two parent individuals. The genetic algorithm implemented for this thesis has three crossover methods to chose from: Single point crossover, two point crossover and uniform crossover [Magalhaes-Mendes, 2013]. These are all presented in figure 4.9. As shown in figure 4.9a, single point crossover uses randomly generated position, called the crossover point, to perform recombination. All genes from the first parent prior to the crossover point are copied to the first child, and all genes after the crossover point are copied to the second child, and all genes from the second parent prior to the crossover point is copied to the second child, and all genes after the crossover point is copied to the first child. Two point crossover is similar to single point crossover, except that it uses two crossover points instead of one. This is shown in figure 4.9b. In uniform crossover, there is a fifty percent probability that each gene will be drawn from each parent as shown in figure 4.9c. This crossover method mix up the parent genes more than the two others, therefore more gene patterns will be lost using this method. Even though crossover is the main recombination method it is not used for creating every child individual. Some child individuals are copies of their parents with potential small mutation in their genes. The number of individuals created using crossover is decided by the crossover rate. Crossover rates are usually kept pretty high since the goal is to evolve new and better solutions, however test runs presented in chapter 5 do confirm that it is good to let a percentage of the children be produced without crossover.
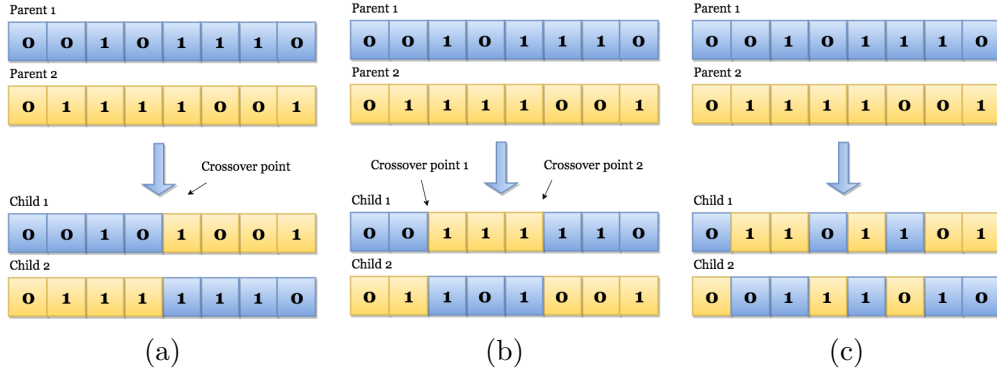

Figure 4.9: Crossover methods: (a) Single point crossover, (b) two point crossover, and (c) uniform crossover.

A method used to make sure that the best individuals in the population

does not get killed of by accident is called *elitism*. Elitism simply takes the best individual(s) from the parent population and copies it(them) directly into the new child population without performing any genetic operations on it(them). Elitism is commonly used with genetic algorithm and will be used in this thesis.

4.2.4.2 Mutation

Although crossover is a powerful genetic operator that makes sure that child individuals inherit genes from the best parent individuals, it is not enough by itself. Without any way to mutate genes, one can end up with a population where every individual has the same gene value in the same position, this means that no recombination method will be able to change the value of that gene. Mutation is the operation used by the genetic algorithm to make sure that the population do not get sterile. In nature, genes can be mutated in numerous ways. In this thesis, three mutation methods are implemented to mimic the mutation methods that can happen in genes [Soni and Kumar, 2014], these are called: Flip mutation, interchanging mutation, and inversion mutation. Flip mutation, shown in figure 4.10a, is the most common mutation method used in genetic algorithms. As it's name implies, flip mutation works by flipping the value of bits in the genotype. Usually, mutation rates are low since one do not want mutation to make to many changes to the good genes inherited from parent individuals, but simply introduce some diversity. Therefore, only a couple of bits are mutated in each genotype each generation. Interchange mutation and inversion mutation are rarely used in genetic algorithms, however they are included in this thesis to introduce even more diversity in the population and hopefully help the genetic search finding even better solutions. They both introduce more change than flip mutation, and will be assigned rates even lower than the mutation rate for flip mutation. Figure 4.10b and 4.10c shows interchange- and inversion mutation respectively. Interchange mutation works by picking two random genes and interchange their values, while inversion mutation works by picking two random positions and invert each gene between those positions.

4.2.5 Wind-, Wake- and Power Model

The evaluation class uses the same wake-, wind- and power model as Kusiak and Song [2010]. The wake model used is the classical Jensen model [Jensen,
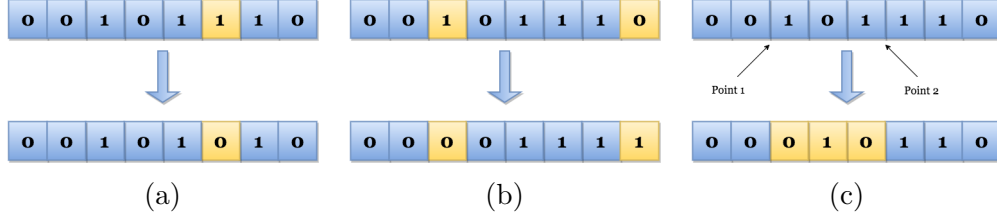
Figure 4.10: Mutation methods: (a) Single point crossover, (b) two point crossover, and (c) uniform crossover.

1983], which is used in almost every study of the wind farm layout optimization problem, as can be seen in table 3.3.

Wind distribution is modeled using the Weibull distribution, a continuous probability distribution shown to model wind distribution quite well [Justus et al., 1978]. The probability density function is shown in equation 4.1

$$f(x; c, k) = \begin{cases} \frac{k}{c} \left(\frac{x}{c}\right)^{k-1} e^{-\left(\frac{x}{c}\right)^{k}} & \text{if } x \geq 0 \\ 0 & \text{if } x < 0 \end{cases} \tag{4.1}$$

where k is called the shape parameter and c is the scale parameter, and $k, c > 0$. In most of the wind scenarios provided by GECCO 2016, $k \approx 2$, this is shown empirically to be a good value for wind speed distribution [Justus et al., 1978]. On the other hand, the shape parameter vary for each wind direction. Figure 4.11 shows the Weibull distribution plotted for $k = 2$ and for different values of c.

The wind scenarios used in this thesis are therefore a specification of the shape- and scale parameters for every wind direction, where wind direction is partitioned into 24 different directions. Twenty wind scenarios are provided by GECCO 2016, 10 which simply specify wind distribution parameters, and 10 that specify wind distribution parameters and locations of obstacles.

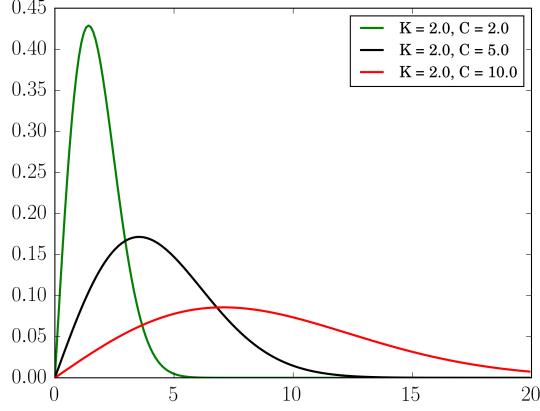The power curve used is also the same as used in Kusiak and Song [2010], it

Figure 4.11: The Weibull distribution plotted for $k = 2$ for different values of the scale parameter c.

is the linear function shown in equation 4.2,

$$f(v) = \begin{cases} 0 & \text{if } v < v_{cut-in} \\ \lambda v + \eta & \text{if } v_{cut-in} \leq v \leq v_{rated} \\ P_{rated} & \text{if } v_{cut-out} > v > v_{rated}. \end{cases} \tag{4.2}$$

Here λ is the slope parameter, v the wind speed, η the intercept parameter, P_{rated} is the fixed power output, and v_{cut-in} is the cut-in speed; the minimum speed for which the turbine produces power, and $v_{cut-out}$ is the cut-out speed; the maximum wind speed for which the turbine is kept on.

4.2.6 Fitness Function

The main task of the evaluation classes is to calculate the fitness of each individual based on the fitness function. The fitness function to be minimized is provided by GECCO 2016, and is displayed in equation 4.3.

$$fitness = \frac{\left(c_t \cdot n + c_s \cdot \left\lfloor \frac{n}{m} \right\rfloor\right)\left(\frac{2}{3} + \frac{1}{3} \cdot e^{-0.00174 n^2}\right) + c_{OM} \cdot n}{\left(\frac{1-(1+r)^{-y}}{r}\right)} \cdot \frac{1}{8760 \cdot P} + \frac{0.1}{n} \tag{4.3}$$

Description and numerical values of all parameters given in equation 4.3 are displayed in table 4.1. As can be seen in this table, the values of n, the number of turbines, and P, farm energy output, are not given. This is because the number of turbines, together with the turbine positions, are the parameters to be optimized by the genetic algorithm. Farm energy output is the indirect parameter that we are trying to optimize. It is dependent on turbines count, position, wind scenario and so on, and is of course therefore not provided in table 4.1 either.

Table 4.1: Description and value of each parameter used in the objective function provided by GECCO 2015.

Parameter	Description	Value
c_t	Turbine cost (usd)	750 000
c_s	Substation cost (usd)	8 000 000
m	Turbines per substation	30
r	Interest rate	0.03
y	Farm lifetime (years)	20
c_{OM}	Yearly operating costs per turbine	20 000
n	Number of turbines	
m	Farm energy output	

Intuitively, the objective function can be divided into different parts. The first parenthesis in the nominator of the first fraction is the construction cost, while the second parenthesis is the economies of scale and the third part of the nominator is yearly operating costs. The denominator represents the interests. The denominator of the second fraction describes yearly power output, while the number 0.1 in the nominator of the last fraction is a farm size coefficient.

4.3 Scenarios

GECCO 2016 has provided the contestants with 20 different wind scenarios for which the genetic algorithm can be tested on. Each wind scenario contain
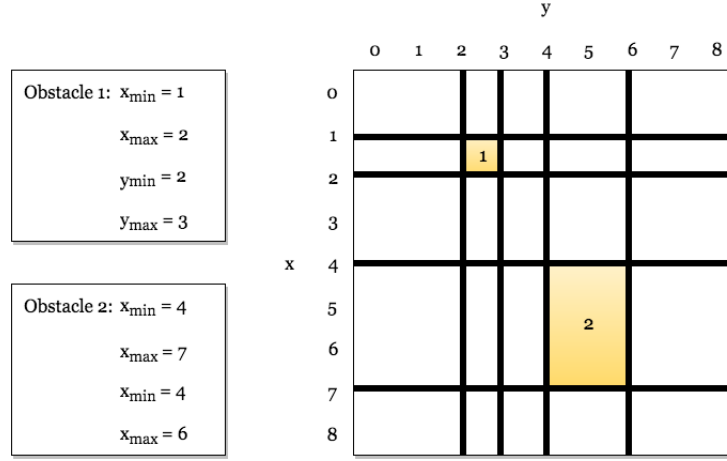
Figure 4.12: Obstacles are described in the scenarios with its (x, y)-boundaries.

shape and scale parameters, k and c respectively, for each wind directions where wind direction is partitioned into slots that cover an 15 degree angle each, so that there are 24 different wind directions. Unavailable areas are described in the scenario by the parameters x_{min}, x_{max}, y_{min} and y_{max} as shown in figure 4.12. In the figure, two obstacles are described giving their (x, y)-boundaries. The boundaries of the obstacles are marked with black lines. The yellow area in the middle of the lines are the illegal areas. Each wind scenario also contain values for the constants "width", "height", "number of turbines" and "wake free energy". The scenarios are read from file at the beginning of each run of the genetic algorithm.

4.4 Population Distributed Genetic Algorithms Implementation Details

Now that the reader is familiar with how individuals are represented, which selection mechanisms and genetic operators that are implemented, how fitness is calculated, and how the scenarios look, it is time to go into details of how the population distributed genetic algorithms are implemented. Although the population distributed genetic algorithms were introduced in

chapter 2, the details of how each step in figure 4.2 are implemented for each model was not given. Therefore, this section contains a detailed description of how the population distributed genetic algorithms are implemented.

One decision that can be mentioned here, because it applies to all the models below, is whether the three population distributed genetic algorithms are heterogeneous or homogeneous. In an homogeneous environment, the same rules apply to the entire model. This means that the same adult- and parent selection mechanisms, the same genetic operators and the same fitness function is used for the entire model, it is not different for different Islands (Island model), threads (Pool model) or areas (Cellular model). Even thought it would be very interesting to implement heterogeneous models, it is not done in this thesis. The reason behind this decision is that it is best to let the same rules apply to every part of every model when different models are compared.

4.4.1 The Island Model Design Decisions

The Island model works as follows: A population of individuals are partitioned into sub populations which are distributed onto different Islands. An Island can be connected to one or more Islands and individuals on one Island can migrate to other Islands following one of the migration routes. Table 4.2 gives an description of the Island model parameters. For a number of generations, decided by the variable *migration interval*, the population on one Island follow the steps of the simple genetic algorithm from figure 4.2. However, when the population has evolved for *migration interval* generations some individuals from one Island can migrate to another Island. These two steps continue until the total number of generations reaches some predefined value.

As mentioned in chapter 2 the Island model can be implemented with either synchronized or asynchronized migration. Synchronized migration means that migration is performed at the same generation for all Island, and asynchronized migration means that migration can be performed whenever an Island is ready. In this thesis, the Island model is implemented with synchronous migration in order to not over-complicate the migration function.

As mentioned, migration means that individuals migrates to another Island.

Table 4.2: Island model parameter description.

Parameter	Description
Deme size	Number of individuals on each Island (deme)
Deme count	Number of Islands (demes)
Migration rate	Number of individuals that migrate
Migration interval	Number of generations between migration.
Number of migrations	Total number of times migration is performed.
Topology	Circular

In this thesis, migration from one Island to another means that the best individuals in Island i is copied onto Island j to replace the individuals with lowest fitness on Island j. In other words, migration does not mean that the best individuals in Island i leaves that Island, but that copies of them replace the individuals with worst fitness on Island j. The number of individuals that migrate is decided by the parameter *migration rate*.

As described in table 4.2 the topology implemented in this thesis is circular. This can be seen in figure 4.13 where the legal migration routes are indicated by arrows. Since individuals are only allowed to migration in one direction with this topology it will take time (many generations) for the individual on the upper-right Island to travel to the upper-left Island since they have to go through both Islands on the bottom. This means that different parts of the solution space can be explored on different Island before individuals from one Island take over the entire population.

4.4.2 Pool Model Design Decisions

In the Pool model, the individuals are distributed in a resource pool. The resource pool is partitioned into equal size partitions so that one thread is responsible for one partition. Each thread selects x individuals from the entire population, where x is equal to the total population size divided by the total number of threads. Next, each thread generates a child pool by performing genetic operations on the selected individuals. After the new child pool is generated, each child individual is compared against the individual in the resource pool currently occupying its designated position. If the fitness of the new individuals is better than the fitness of the old individual the new child individual overwrites the old individuals. This is illustrated in figure 4.14.
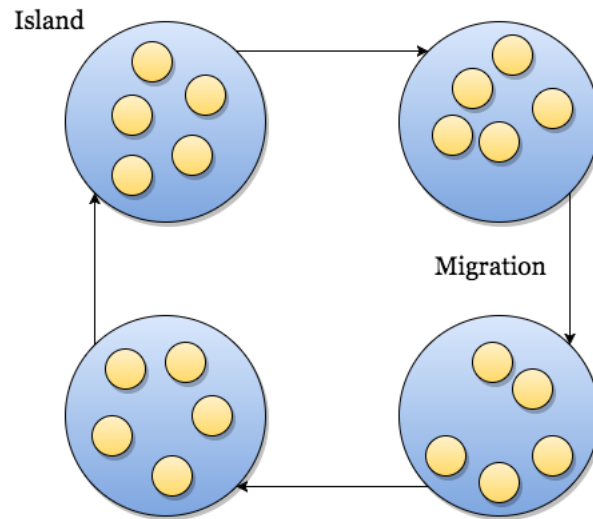
Figure 4.13: Island model topology.

As can be seen in the figure thread i overwrites the individuals in positions 1, 3 and 4 in the partition it is responsible for.
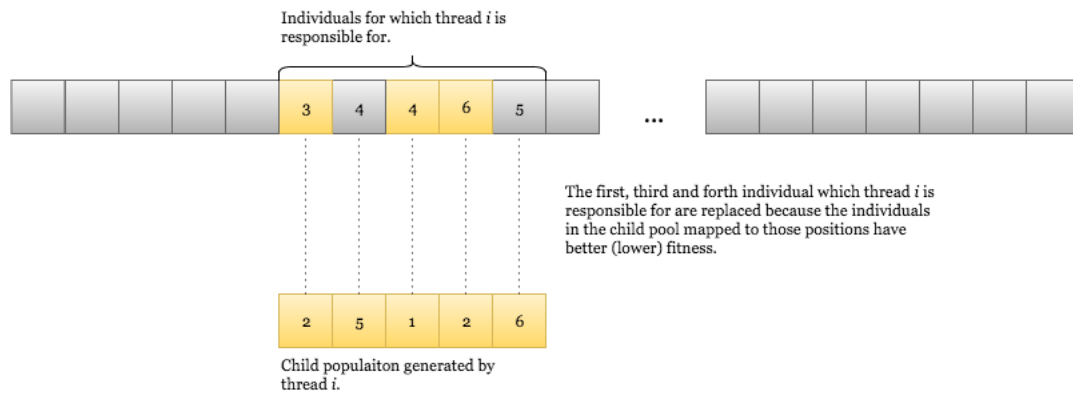

Figure 4.14: Pool model updating function. For each generation, each thread updates its region if the new individuals are better than the individuals currently occupying the position.

The pool model is asynchronous by nature. The threads operate unaware of each other. Since each thread only writes to its own positions in the resource pool, it is not a problem that the threads work independently without any form of synchronization. By implementing the Pool model this way some parts of the resource pool might have better fitness that others because they have evolved for more generations than other parts. This property ensures that different parts of the search space is explored in different regions of the resource pool.

As mentioned above, parent individuals are selected from the entire resource pool. However, parents are not picked completely at random. For each parent selected a group of potential parents are selected at random from the resource pool, and these individuals compete for the spot in the parent pool by tournament selection. This guides the evolution in the right direction. Picking individuals at random might also work for this model since the new individuals are only written back if they are better than the previous individuals, however, this would make evolution extremely slow, and it would not make sense from an evolutionary point of view because the fittest individuals are not prioritized.

4.4.3 Cellular Model Design Decisions

The Cellular model distributes the population in a square grid. Each individual has its own cell which corresponds to an (x, y)-position. For each generation, each cell is updated. Each cell in the grid is updated by selecting parent individuals that are close to the given cell, perform genetic operations on those parents and write the newly generated individual back to the cell.

As mentioned in the background, the cells in the Cellular model could either be updated in a synchronous fashion or an asynchronous fashion. In this thesis the updating is synchronous, meaning that the cells are updated simultaneously.

The topology used in this thesis is a square topology, as shown in figure 4.15. Only individuals within the square can be selected as parents for the middle cell. Parent selection are performed by tournament selection within the square. By distributing individuals in a grid different parts of the grid will explore different regions of the search space.
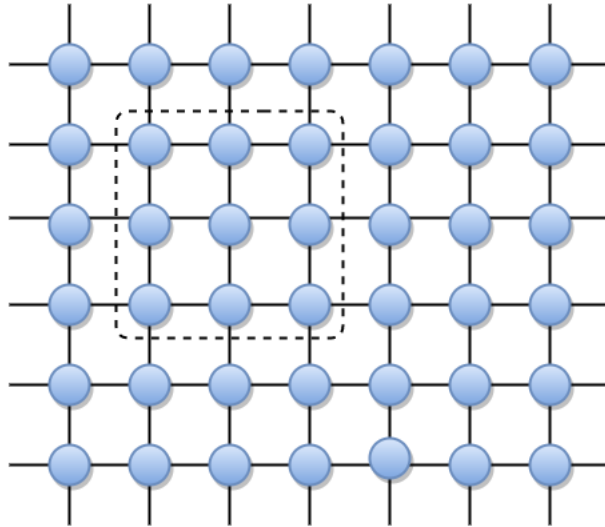
Figure 4.15: Cellular model topology. Only individuals within the marked square are allowed to become parents for the middle cell.

4.5 Motivation behind Implementing the Genetic Algorithm from Scratch

Even though GECCO 2016 has provided each contestant with an API which could be used directly, or improved upon and used in the competition, the decision to implement the genetic algorithm from scratch was made. Even though this decision lead to more work for the author, several arguments supported the decision. First of all, even though the provided API was implemented in Java, it was not very object oriented nor was it modular, something that made it very difficult to add new features to the code without having to do major changes. In addition, the provided genetic algorithm was extremely simple with no room for making any decisions about which method to use for any of the steps in figure 4.2. Other problems such as hard-coded variables and too long methods made it very difficult to make changes and add new features.

The new genetic algorithm is implemented so that new selection methods

can be added by simply implementing the AdultSelection- or ParentSelection interface, and new crossover methods can be added by extending the Crossover class. This makes the program much more flexible, if one wish to try something new. No variables are hard-coded in the new program, but taken as parameters to the GeneticAlgorithm constructor, leaving no room for making errors. The major improvement, and most important motivation behind the decisions of implementing the genetic algorithm from scratch is that it gives the author total control over every aspect of the code, and it was very important with modular code when the population distributed genetic algorithms were implemented.

In summary, this chapter contains the implementation detail of the genetic algorithm implemented for this thesis. Now that the reader is familiar with how the different genetic algorithm models are implemented it is time to take a closer look at the results obtained in this thesis.

Chapter 5

Results and Discussion

This chapter includes presentation and analysis of the results obtained in this thesis. Section 5.1 presents results from testing different parameter settings for the genetic algorithm, and briefly discusses each results. Section 5.2 presents the main results obtained when running the different population distributed genetic algorithms. Section 5.3 contains a discussion and comparison of the results obtained in section 5.2.

5.1 Parameter settings

Parameter settings are crucial for obtaining good results with the genetic algorithm, therefore, this whole section is devoted to the process. Simulations were run to find the best adult selection method, parent selection method, crossover method, crossover rate and mutation rate for the given problem. Even though it would take much less time and effort to test these values on a toy problem, such as One Max, the decision was made to test them on the real problem. The reason for this is that it is not necessarily true that the parameter values most fit to solve the One Max problem is the same as those most fit to solve the wind farm layout optimization problem. In the wind farm layout optimization problem the relative positions of the turbines are extremely important, this property distinguishes wind farm layout optimization from other problems and could mean that it needs different parameter values than a toy problem with different properties.

It is important to note that even though effort was made to find the right

Table 5.1: Values that were kept fixed while one by one were optimized to find the correct settings for the find farm layout optimization problem.

Parameter	Value
Wind scenario	00.xml
Evaluator	KusiakLayoutEvaluator
Population size	100
Generations	100
Elitism	true
Flip mutation rate	0.01
Inversion mutation rate	0.0
Interchange mutation rate	0.0
Parent selection	Tournament selection
Tournament size	5
Epsilon	0.1
Crossover method	Uniform crossover
Crossover rate	0.9

parameter values for the genetic algorithm, it is impossible to obtain the optimal ones. Just imagine trying to test every single value of the continuous parameter crossover rate, just that would be impossible! Therefore, the values that are tested for each parameter are based on the authors previous knowledge and experience with genetic algorithms.

For each simulation presented in this section one parameter were optimized while the others were kept fixed with the values shown in table 5.1. The parameters in the table are common for all the genetic algorithm models implemented in this thesis, however, they are only optimized when run on the Master/Slave model. Ideally, they should be optimized for all of the models, but that would not be possible within the time frame of this thesis.

As can be seen in table 5.1, other parameters such as wind scenario, population size, number of generations, whether elitism should be used and mutation rate for interchange mutation and inversion mutation could also be optimized. However, as explained above, the time frame of this thesis prevented the author from running these simulations. These variables are therefore set using the authors previous experience with genetic algorithms. Testing different

parameter values on a single wind scenario might lead to values that are tailored for the given scenario and that are not as well suited for some of the other scenarios. However, the author does not believe this to be crucial for the final results. Population size is a value that heavily influence the performance of the genetic algorithm, because greater population size increase the probability of finding the global best solution. When testing parameter values, the population size was kept at 100 for two reasons: First, a population size of 100 is large enough so that many different solutions can be explored. Second, when the population size was kept at 100, the adult selection mechanism overproduction would require 200 evaluations each generation. This doubles the evaluation time, the step that is already the bottleneck of the algorithm. Elitism was set to true for every run, meaning that the best individual of each generation will survive. This decision is based on the authors previous experience with genetic algorithms, where experiments has shown that elitism leads to better results because the best individual is not lost due to coincidences. Three different mutation methods were implemented, but experiments were only run to find the optimal value for the flip mutation rate. Usually, flip mutation is the only mutation method used with genetic algorithms and it is therefore also used as the main mutation method in this thesis. Inversion mutation and interchange mutation will also be used, but they will be assigned low enough probabilities so that they will not make trouble, but hopefully, lead to occasional, rare jumps from one part of the solution space to another so that the population do not get stuck in a local minima.

In summary, the sub-sections below contain simulations run to find the parameter values most suited for the wind farm layout optimization problem. The resulting parameter values will be used for all 4 genetic algorithm models in section 5.2. In order to get trustworthy results, each simulation is run 10 times and the plots shown in the subsequent sub-sections are averaged over these 10 simulations. Even though all the models are implemented to run in parallel it takes half a day to run one simulation on an 8 core computer, this is the reason why only the most crucial parameters are optimized and why they are only optimized on the Master/Slave model even thought they will be used by the other models as well.

5.1.1 Adult Selection

Figure 5.1 shows the results of running the genetic algorithm with the three different adult selection methods. Sub-figure 5.1a, 5.1b, and 5.1c shows the results for full generational replacement, generational mixing and overproduction respectively.

The results show that full generational replacement ends up with worse fitness than both generational mixing and overproduction, and that overproduction is the method that is able to achieve the best fitness of the three. These results agrees with the authors previous experience. Note that with generational mixing, only the solutions from the new child population that are better than those in the previous adult population are allowed to enter the adult pool. This means that from one generation to another the average fitness of the new adult population can never be worse than the average fitness of the previous adult population. If every new solution generated is worse than those from the previous generation, the previous generation is given another attempt to reproduce and the fitness from one generation to another is left unchanged. However, if one or more of the new solutions are better than those in the previous generation they will be allowed into the adult pool, and the new adult pool will have better fitness than the previous. Full generational replacement does not take this greedy approach. It replaces the entire previous adult population, even though that might lead to worse average fitness from one generation to another. This does not however mean that full generational replacement always obtains worse final results than generational mixing. On this problem however, it seems like the greedy approach taken by generational mixing works well for wind farm layout optimization. Overproduction will, as full generational replacement, replace the entire previous adult pool with new individuals. However, with overproduction, the probability that the new adult population will have better average fitness is much higher since it has twice as many children to choose from. This means that even though it is not guaranteed, it is likely that the new adult population will have higher fitness than the previous one. The results show that overproduction is the most suitable adult selection method for the wind farm layout optimization problem.
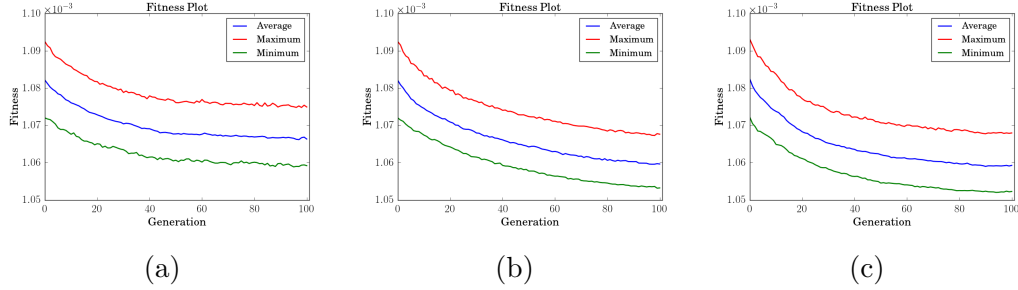
Figure 5.1: Adult selection methods: (a) Full generational replacement, (b) generational mixing and (c) overproduction. Each plot shows the averaged results obtained when running each scenario 10 times.

5.1.2 Parent Selection

Figure 5.2 shows the results for running the genetic algorithm with parent selection methods roulette wheel in sub-figure 5.2a, and tournament selection in sub-figures 5.2b - 5.2f. Tournament selection is run with five different values for the variable *tournament size*. Clearly, roulette wheel do not work well for this problem. Roulette wheel assigns each individual a probability of being selected proportional to its fitness, and since there is not a large different in fitness of the different individuals the selection becomes almost random. With tournament selection on the other hand, this problem is taken care of because it finds the best individuals out of those competing, even though there is not much different in their fitness.

As can be seen in the figure, the fitness gets better as the variable *tournament size* increases. However, a larger tournament size than 25 is not tested. The reason for this is that 25 is already a very large tournament size. With 25 % of the individuals competing in every tournament the population will not have much time to explore different solutions because the best individuals will take over the entire population extremely fast. As can be seen in the figure, a tournament size of 25 is not significantly better than a tournament size of 20, and therefore 20 is chosen as the final tournament size to slow down the take-over time.

As mentioned before, *epsilon* is the probability that the selected individual is selected at random from the adult pool instead of by tournament selection.

Figure 5.3 shows the result for testing the values 5 %, 10 %, and 15 %. As can be seen in the figure, varying epsilon does not have a significant impact on the fitness of the wind farm layout optimization problem.
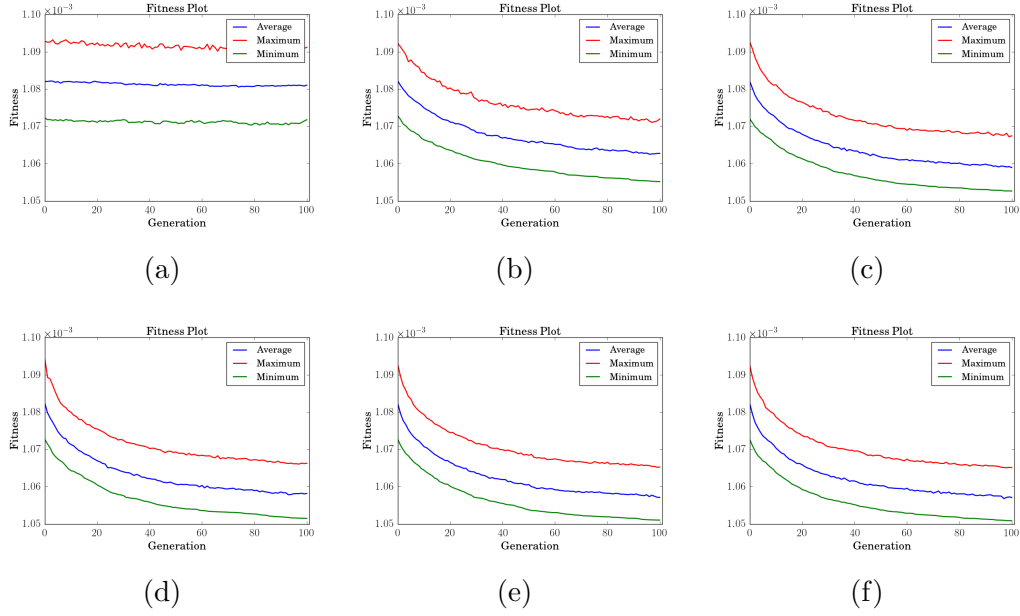

Figure 5.2: Parent selection methods: (a) Roulette wheel, (b) tournament selection, tournament size 5 (c) tournament selection, tournament size 10, (d) tournament selection, tournament size 15, (e) tournament selection, tournaments size 20, and (f) tournament selection, tournament size 25. Each result is an average over 10 runs.

5.1.3   Crossover Methods

Figure 5.4 show the results when running the genetic algorithm with single point crossover, two point crossover, and uniform crossover as can be seen in sub figures 5.4a, 5.4b, and 5.4c respectively. The experiment show that no crossover method is significantly better than the others in solving the wind farm layout optimization problem. This result is unexpected. Intuitively, one would expect uniform crossover to perform worse because it mixes up the relative positions of the wind turbines more than single point crossover
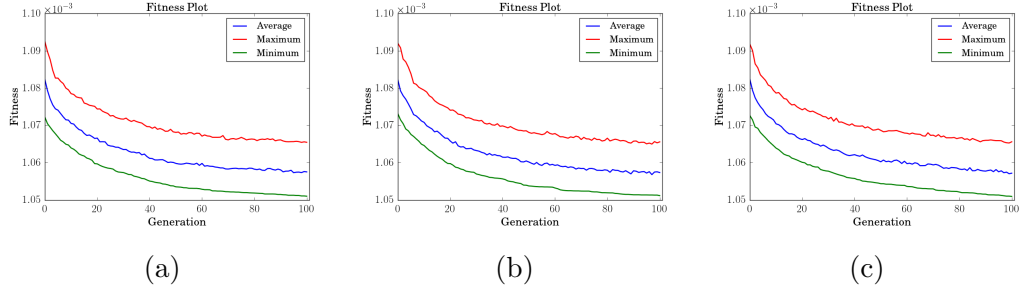
Figure 5.3: Different epsilon values: (a) Epsilon 0.05, (b) epsilon 0.10, and (c) epsilon 0.15. The tournament size was kept fixed at 20 since that was proven to give the best results. Each plot is an average over 10 runs.

and two point crossover. However, the results contradicts this hypothesis.
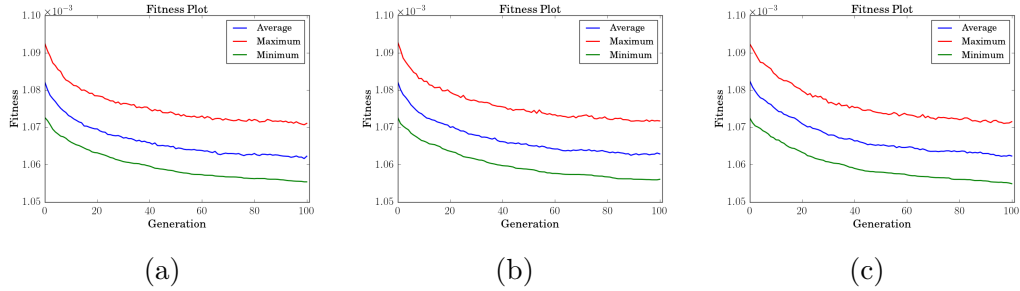

Figure 5.4: Crossover methods averaged over 10 runs: (a) Single point crossover, (b) two point crossover and (c) uniform crossover.

5.1.4 Crossover Rate

Figure 5.5 displays the results of running the genetic algorithm with different crossover rates. As can be seen in the figure, the crossover rate do not have a large impact on the fitness for this problem. A crossover rate below 0.4 gives slightly worse fitness than a crossover rate above 0.6. However, it is not obvious which crossover rate is best out of those presented in sub-figures 5.5d, 5.5e, and 5.5f. The differences in the results obtained when running the algorithm with these crossover rates are not significant, and it can not

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be stated that one is better than the others based on these results. It can only be stated that a crossover rate above 0.6 should be used.
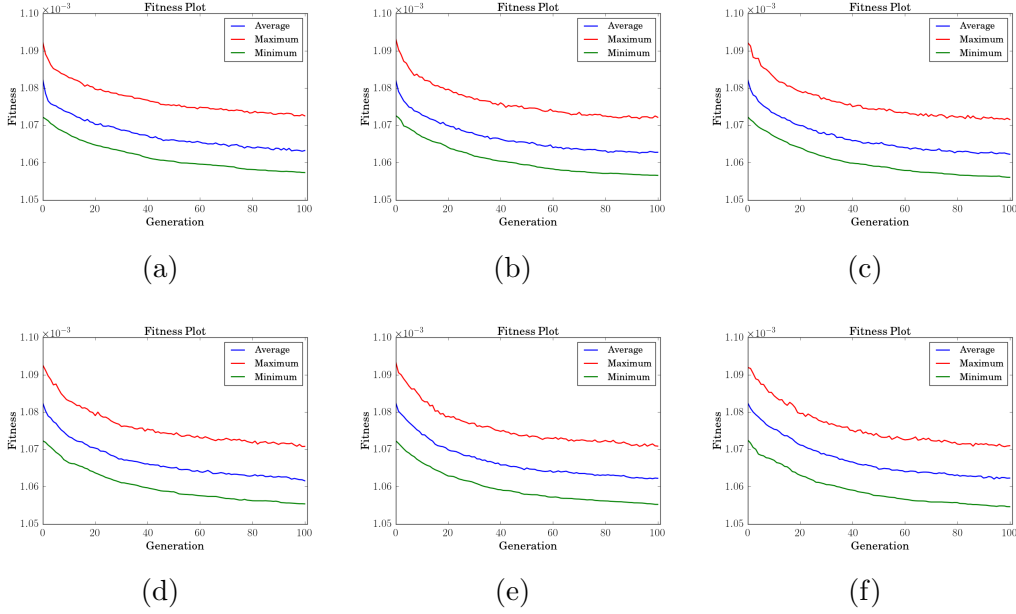

Figure 5.5: Crossover rates average over 10 runs: (a) Crossover rate 0.0, (b) crossover rate 0.2, (c) crossover rate 0.4, (d) crossover rate 0.6, (e) crossover rate 0.8, and (f) crossover rate 1.0.

5.1.5 Mutation Rate

In figure 5.6, the effect of varying the mutation rate can be seen. As the figure shows, if the mutation rate is very low as shown in sub-figure 5.6a, the population is clearly not able to find a good solution. Mutation means adding or removing a turbine. As sub-figure 5.6a show, with a mutation rate that is too low the genetic algorithm will not be able to add or remove enough turbines and therefore the population ends up in a local minima. On the other hand, when the mutation rate gets too high, as shown in sub-figure 5.6e, the population is able to explore many different solutions something that increases its chance of finding the global minima. However, since mutation is performed too frequently, it is not able to stay there even if it finds the global

optimal solution. These results show that mutation rate largely impacts the fitness, and that a mutation rate of 0.001 clearly gives the best results.
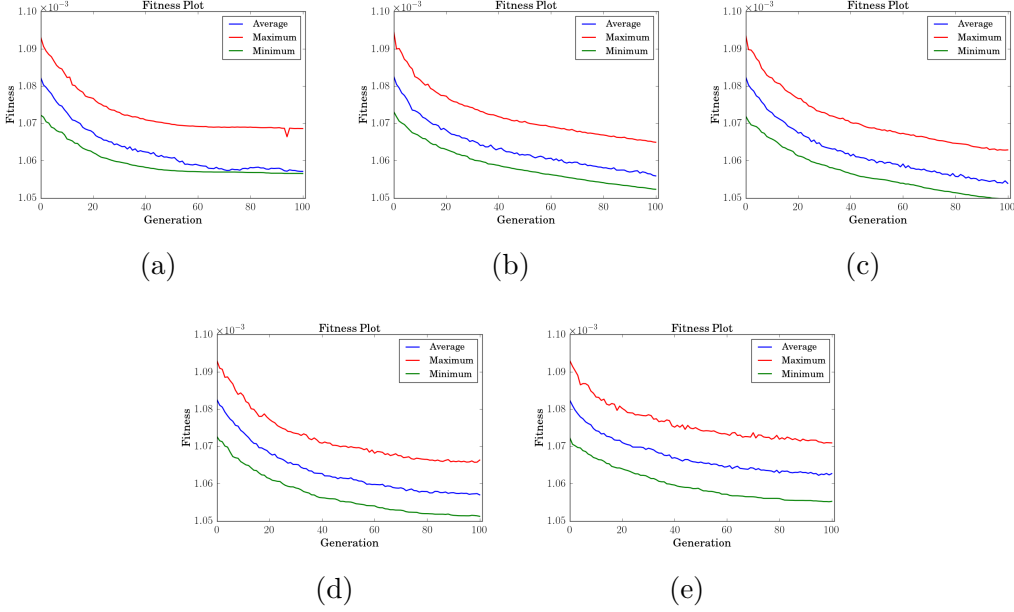

(a)

(b)

(c)

(d)

(e)

Figure 5.6: Mutation rate averaged over 10 runs: (a) Mutation rate 0.0001, (b) mutation rate 0.0005 and (c) mutation rate 0.001, (d) mutation rate 0.005 and (e) mutation rate 0.01s.

5.2   Results

5.2.1   Final Parameter Values

This sub-section gives an overview of the final parameter values that will be used in the subsequent sub-section when running the different models. Table 5.2 provides an overview of the parameter values that will be used when running the Master/Slave model. The adult selection method, parent selection method, parent selection parameters, crossover method, crossover rate and mutation rate are those that was proven to work best for the Master/Slave model in section 5.1. As table 5.2 show, the population size was set to 100 and the number of generations to 200. A population size of 100 is

quite small, but since overproduction is the selected adult selection method, a population size of 100 leads to evaluation of 200 individuals for each generation. Since evaluation is the bottleneck for wind farm layout optimization, a larger population size would not be possible to evaluate for 200 generations within the time limits of this thesis. A possibility could be to pick a larger population size and a smaller number of generations, but since the objective of this thesis is to explore population distributed genetic algorithms a large number of generations is crucial. Population distributed genetic algorithms need more time to find good solutions because they spend more time than simple genetic algorithms on exploring different parts of the search space.

Table 5.2: Parameter values used for the Master/Slave model.

Parameter	Value
Population size	100
Generations	200
Crossover method	Single point crossover
Crossover rate	0.9
Elitism	True
Flip mutation rate	0.001
Inversion mutation rate	0.000001
Interchange mutation rate	0.000001
Adult selection mechanism	Overproduction
Parent selection mechanism	Tournament selection
Tournament size	20% of population size
Epsilon	0.1

The parameter values in table 5.2 will also be used for all of the population distributed models if not otherwise stated. Table 5.3 contains the additional parameter values used by the Island model, and those parameters from table 5.2 that have new values for the Island model. The parameter *deme size*, the number of individuals on each Island, is set to 26 resulting in a total population size of 104, not 100 as in table 5.2. The reason behind this is that the implementation requires a population size of even numbers on each Island, this is not a problem since a few additional individuals will not be enough to impact the final results. The parameter *migration rate* was set to 2, meaning that only 7 % of the individuals on an Island are replaced

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by new individuals each migration. This number was set to be low so that the new individuals would not be able to take over the new population too fast. The parameter *deme count* is set to 4 and the topology is circular as presented in figure 4.13 in chapter 4. In order to let the populations on the different Islands explore different parts of the search space 20 generations are run between each migration. Migration is performed 10 times so that the total number of generations becomes 200 as for the Master/Slave model.

Table 5.3: Parameter values used for the Island model.

Parameter	Value
Deme size	26
Total population size	104
Deme count	4
Migration rate	2
Number of migrations	10
Migration interval	20
Topology	Circular (figure 4.13)

As can be seen in table 5.5, the Cellular model is run with population size of 225. At a first glance this might seem like an odd decision since the models above has a population size of about 100 individuals, but the reason is simple. For the Master/Slave model, and Island model overproduction is used as the adult selection technique because it was proven the best technique in section 5.1. For the Cellular model however, it does not make sense to use overproduction because of the way the grid is updated. Each new individual is generated to occupy a particular spot in the grid, because it has its own area for which its parents can be chosen from. Since each new individual is mapped to one position in the grid, overproduction does not make sense to use and it is therefore not used for the Cellular model. Because of this, the population size is set to approximately 200 individuals, so that the Cellular model performs the same number of evaluations as the other models each generation. The reason why the population size is 225 and not 200 is because a quadratic grid is used to distribute the production and 225 is equal to 15^2. As explained in the methodology chapter, the topology used is a simple square containing nine individuals. The individual in the middle square can only be replaced by individuals generated by recombining individuals within

Table 5.4: Parameter values used for the Cellular model.

Parameter	Value
Population size	225
Topology	Square (figure 4.15)

the square grid. The decision to make the neighborhood this small is that it will give different solutions the opportunity to dominate different areas of the grid, giving the algorithm the time to explore.

Table 5.5 shows the parameter values used by the Pool model that differs from those in table 5.2. The population size is set to 200 so that 200 evaluations are performed for each of the 200 generations. As for the Cellular model, the individuals of the Pool model occupy specific positions. Child generation consist of producing one new individual for each position that a worker is responsible for. If overproduction was used, it would be no clear mapping between new child individuals and the old individuals of the worker because twice as many individuals as position would be generated, this does not make sense for the Pool model. Because of this a population size of 200 individuals where used so that 200 evaluations are performed for each generation as for the other models.

Table 5.5: Parameter values used for the Pool model.

Parameter	Value
Population size	200
Number of workers	4

In summary, in order to make the comparison as fair as possible, the parameter values of each models is set so that approximately 200 individuals are evaluated for each of the 200 generations. This ensures that every model gets approximately the same processor time.

5.2.2 Performance Metrics

Each of the 4 genetic algorithm models are tested on 4 wind scenarios. The wind scenarios are provided by GECCO 2016 and can be seen in table 5.6. As can be seen, the first two scenarios are without obstacles, while the two last scenarios are with obstacles.

Table 5.6: Test scenarios provided by GECCO 2016.

Scenario Name	Obstacles
00.xml	No obstacles.
05.xml	No obstacles.
obs00.xml	Obstacles.
obs05.xml	Obstacles.

The performance of the 4 models on each of the four scenarios are measured using the performance metrics shown in table 5.7. The first performance metric is the results of the fitness function presented in chapter 4. The efficiency is a measure of how much energy the given layout is able to produce out of the power the layout would have been able to produce had there been no wake effect, as shown in equation 5.1

$$\text{efficiency} = \frac{\text{yearly power output}}{\text{wake free yearly power output}}. \tag{5.1}$$

The performance metrics cost and power represent the cost and power part of the fitness function. Figure 5.7, shows which parts of the fitness function presented in chapter 4 that represents cost and which represents power. The last metric, number of turbines, is intuitively the total number of turbines in the layout.

In chapter 2, one of the resulting layouts from [Grady et al., 2005] was shown as an example layout. The resulting layouts from this project are however too large to include in this thesis. Luckily, will the performance metrics presented above give a much more clear understanding of the performance of the models than any resulting layout would.

$$fitness = \frac{\overbrace{\left(c_t \cdot n + c_s \cdot \lfloor \frac{n}{m} \rfloor\right)\left(\frac{2}{3} + \frac{1}{3} \cdot e^{-0.00174n^2}\right) + c_{OM} \cdot n}^{\text{Cost}}}{\left(\frac{1-(1+r)^{-y}}{r}\right)} \cdot \underbrace{\frac{1}{8760 \cdot P}}_{\text{Power}} + \frac{0.1}{n}$$

Figure 5.7: A screen shot of the fitness function presented in chapter 4 where the cost and power metrics are shown.

Table 5.7: For each scenario, results are measured in these measurements.

Results measured	Description
Fitness	Fitness of the best individual
Efficiency	Amount of power produced out of maximum
Cost	Total cost (USD)
Power	Yearly power output (kWh)
Number of turbines	Total number of turbines

5.2.3   Results Scenario 00

The results when all the models were run on scenario 00.xml is shown in figure 5.8. It is important to note that each of the plots displays results averaged over 10 simulations so that the discussion below is based on the models' average behavior. The fitness plot is shown in sub-figure 5.8a. The Master/Slave model is able to get the best fitness, the Pool model comes in second, quite close to the Master/Slave model, the Island model comes in third, and the Cellular model comes in forth, clearly not able to keep up with the other models.

Sub-figure 5.8b shows the performance of the different models in terms of efficiency. Efficiency is a very interesting measure, since it shows the models' ability to live up to their potential. It is interesting to note that even thought the Master/Slave model, Island model and Cellular model end up with approximately the same number of turbines they are not able to produce equally efficiency layouts. This shows that the Island model and Cellular model are

not able to position the given number of turbines in the wind farm as well as the Master/Slave model.

As shown in sub-figures 5.8c and 5.8e, the plots for cost and number of turbines have identical shape. This makes sense off course since the cost increase and decrease with the number of turbines. The plot in sub-figure 5.8e show that the Pool model on average end up with layouts that have a higher number of turbines. Solutions with many turbines will be able to produce much energy, despite the fact that they suffer more from wake loss than layouts with fewer turbines. The Pool model ends up with layouts that score well on fitness, even thought they are more expensive than those obtained by the other models because they in return produce more energy.

As shown in figure 5.8e, the Island model spends the first 40 generations or so, exploring layouts with higher number of turbines before it realizes that settling on a layout with fewer turbines decrease the cost at the same time as it increases efficiency because of reduced wake loss. The cost and number of turbines plots of the Island model are very interesting because they show the effect of migration. As sub-figures 5.8e and 5.8c shows, the model jumps from one solution space to another at generation 20 and 40, the generations when migration is performed.

As opposed to the other model, the Cellular model is able to explore different number of turbines for many generations as can be seen in sub-figure 5.8e. For the other models, it seems like individuals with a given number of turbines soon has monopolized the entire population, but for the Cellular model different parts of the grid still explored different number of turbines after 200 generations. Even thought this property is desirable, the Cellular model takes it too far. While the other models are able to optimize the positions of turbines in their layouts after stabilizing on a given number of turbines, the Cellular model never reaches this phase.

The performance of the different models can be viewed in terms of power in sub-figure 5.8d. Power, as mentioned above, is closely related to the number of turbines. As the Pool model has discovered, a solution with more turbines leads to higher energy output. As the sub-figure show, after the models have stabilized on a particular number of turbines, the power is slowly increasing. This is because the turbines are slowly moved into positions with less wake

loss. It is interesting to observe that even thought the Island model and Cellular model has found layouts with as few turbines as the Master/Slave model, they are not able to optimize the turbine positions as well as the Master/Slave model in the same number of generations.

In summary, the optimization can be viewed as consisting of two phases. The first phase is the search for the optimal number of turbines, while the second phase consist of moving turbines around in order to reduce wake loss. The Island model stays in phase one longer than the Master/Slave model and the Pool model. The Cellular model never leaves phase one. While the population of the other models are monopolized by individuals with the same number of turbines in a few generations, the Cellular model is still exploring different numbers of turbines after 200 generations.

5.2.4 Results Scenario 05

The results for running the different models on scenario 05.xml is shown in figure 5.9. The fitness plot is shown in sub-figure 5.9a. As for scenario 00.xml, the Master/Slave model obtains the best fitness closely followed by the Pool model. The Island model comes in third again, and the Cellular model is not able to keep up with the other models on this scenario either. After 200 generations the Cellular model has a fitness which each of the other models had beaten already at generation 10.

The efficiency plot is shown in sub-figure 5.9b. As before, the Master/Slave model and Pool model is able to find a solution with approximately the same efficiency. The Island model is a few steps behind, while the efficiency of the Cellular model is increasing extremely slowly.

Sub-figures 5.9c and 5.9e shows cost plot and number of turbines plot respectively. As can be seen, all the models end up with different number of turbines on average. This could indicate that this layout is harder to optimize than the one above where 3 of the models ended up with the same average number of turbines. As was the case for the scenario above, the Master/Slave model and Pool model have decided on the number of turbines in approximately 10 generations, the population of the Island model has not been monopolized before after 40 generations, and the Cellular model never
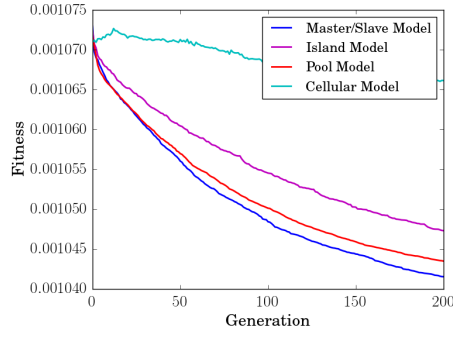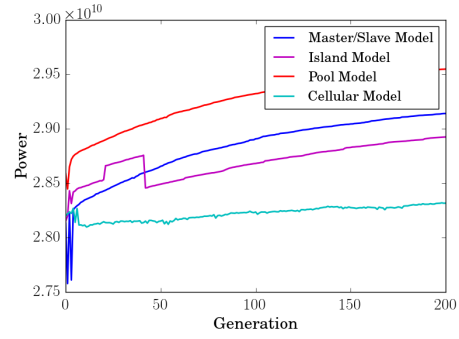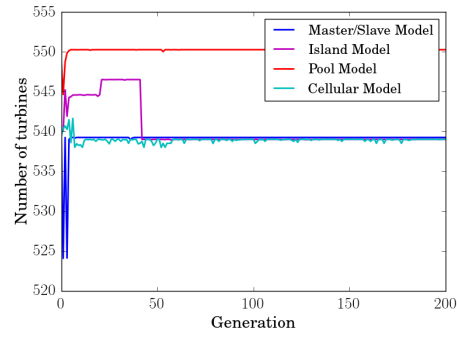
(a) Fitness
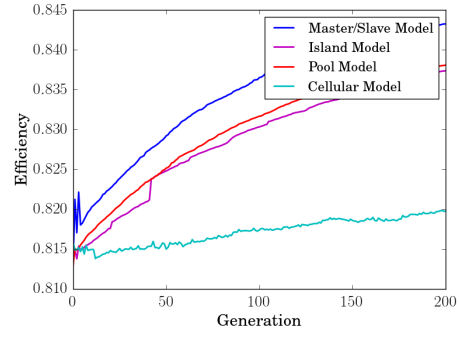
(b) Efficiency
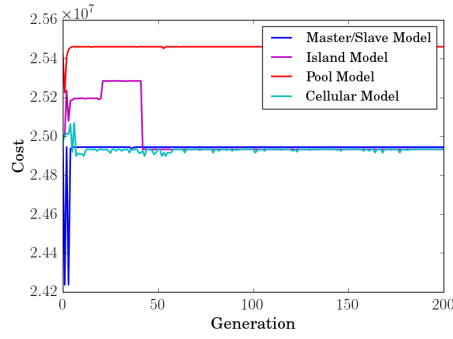
(c) Cost

(d) Power

(e) Turbies

Figure 5.8: Scenario 00.xml averaged over 10 runs: (a) Fitness plot, (b) efficiency plot, (c) cost plot, (d) power plot, and (e) number of turbines.

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stabilize on a given number of turbines.

Power is closely related to the number of turbines, and as can be seen in sub-figure 5.9d, the Island model, which is the model that found layouts with the highest number of turbines on average, is able to produce most energy. The Cellular model ends up with the second highest number of turbines on average, yet, it ends up with the layouts that produce less power on average. This should not be possible, and shows the Cellular model's inability to position turbines in positions that reduce wake loss. The Master/Slave model finds solutions with a larger number of turbines than the Pool model, and is therefore also able to produce a little more energy as expected.

5.2.5   Results Scenario obs00.xml

Figure 5.10 shows the results obtained when running the models on scenario obs00.xml. As for scenairo 00.xml and 05.xml, the Master/Slave model obtains the best fitness, the Pool model the second best, the Island model third best and the Cellular model the fourth best, as can be seen in sub-figure 5.10a.

As for efficiency, the results are similar as those observed for scenario 05.xml as can be seen in sub-figure 5.10b. Both the Master/Slave model and the Pool model are able to optimize their solutions so that they produce more than 84.5 % of the wake free energy. The Island model however, is only able to produce just above 83.5 % of the wake free energy.

As shown in sub-figures 5.10c and 5.10e the Island model ends up with a higher number of turbines on average than the other models. The Cellular model ends up with the second highest number of turbines, the Master/Slave model with the third highest number of turbines and the Pool model with the lowest number of turbines. These results are similar to the ones obtained on scenario 05.xml. The high number of turbines obtained by the Island model explains why the model scored so badly on efficiency.
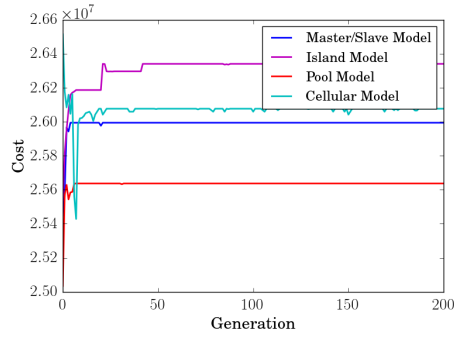
The Island model finds the solutions which produces most power, a reasonable result since no other model ends up with more turbines. However, the Island model is closely followed by the Master/Slave model even though it finds a solution with fewer turbines. This shows that the Master/Slave model
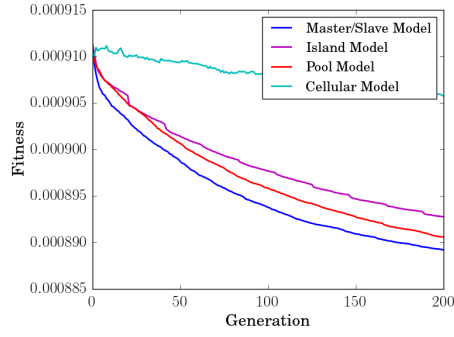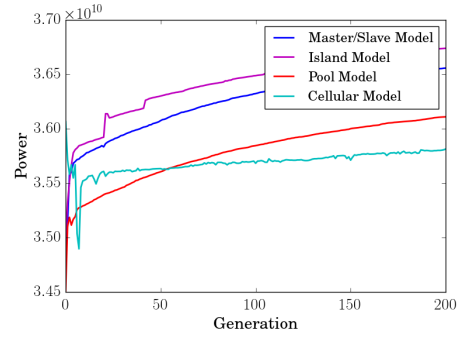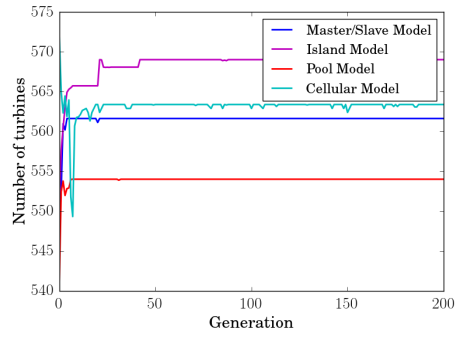
(a) Fitness
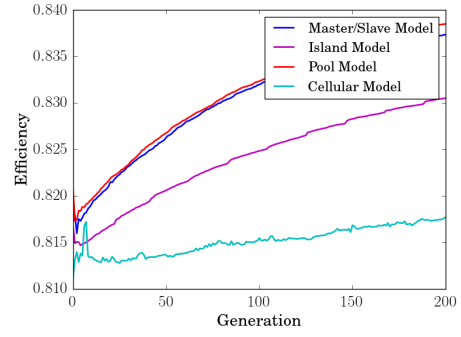
(b) Efficiency

(c) Cost

(d) Power

(e) Turbies

Figure 5.9: Scenario 05.xml averaged over 10 runs: (a) Fitness plot, (b) efficiency plot, (c) cost plot, (d) power plot, and (e) number of turbines.

is way better at optimizing the turbine positions. On problematic observation is that the Cellular model ends up with a solution that produces less power than all the other models even thought it ends up with a solution with the same number of turbines as the Island model. This results show that the Cellular model is not able to find a solution that position the turbines well within 200 generations.

5.2.6   Results Scenario obs05.xml

Figure 5.11 shows the results from scenario obs05.xml averaged over 10 runs. Fitness is shown in sub-figure 5.9a. As can be seen, the result are similar to those observed for the other scenarios and they will therefore not be discussed here.

In summary, the results show that the Master/Slave model is able to optimize wind farm layout better than the population distributed models. The Master/Slave model and Pool model only spend a few generations testing solutions with different number of turbines before settling for a given number and start optimizing turbine positions. The Island model reaches this step a little later, while the Cellular model new do. It is very unlikely that any of the models have found the global optimal solution for any of the scenarios given how few number of turbines they explore compared to how large the search space is.

5.3   Discussion

In the previous section it was shown that the non-population distributed Master/Slave model consistently was able to evolve layouts with better fitness than the 3 population distributed models. The Pool model came in second, the Island model came in third and the Cellular model came in fourth and last. There can be many reasons for this, and they will all be discussed in this section. The main results are summaries below.
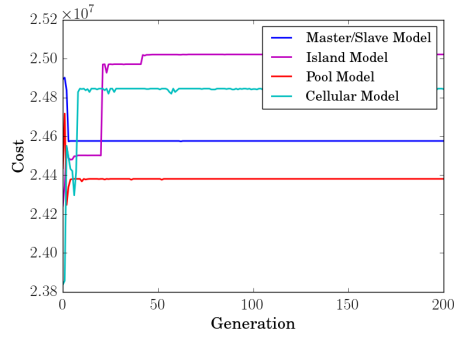
- The non-population distributed Master/Slave model was the model able to obtain the best results.
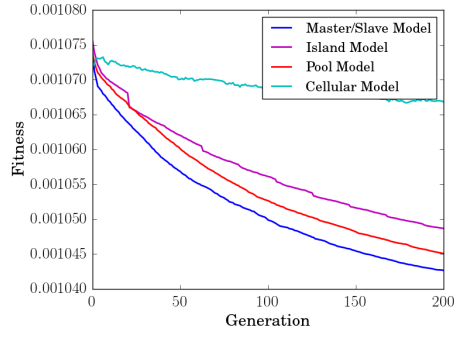
(a) Fitness
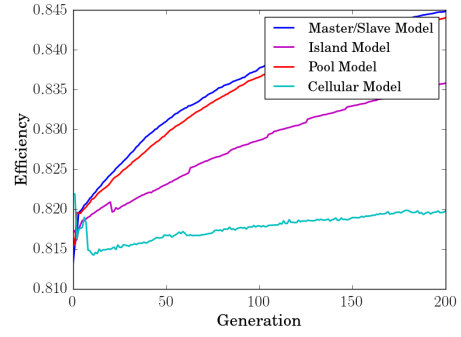
(b) Efficiency

(c) Cost

(d) Power

(e) Turbies

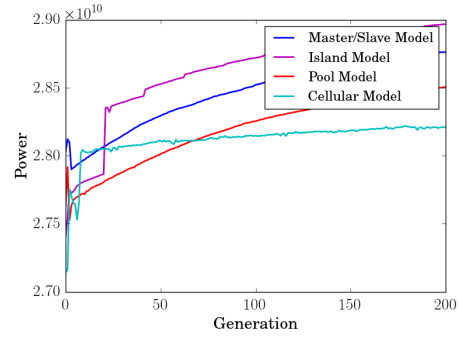Figure 5.10: Scenario obs00.xml averaged over 10 runs: (a) Fitness plot, (b) efficiency plot, (c) cost plot, (d) power plot, and (e) number of turbines.
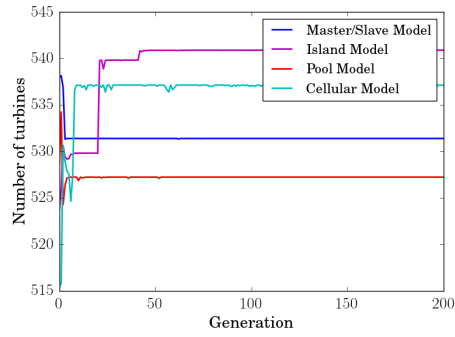
(a) Fitness

(b) Efficiency

(c) Cost
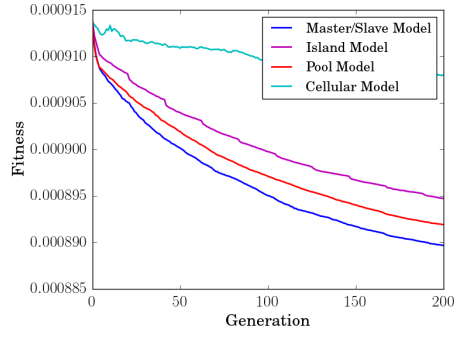
(d) Power
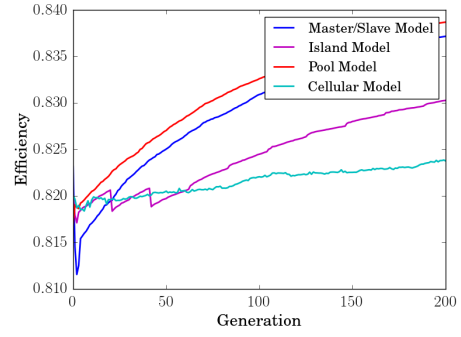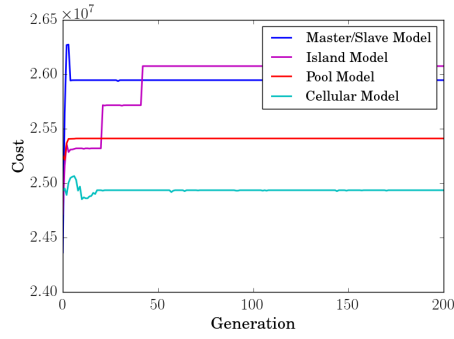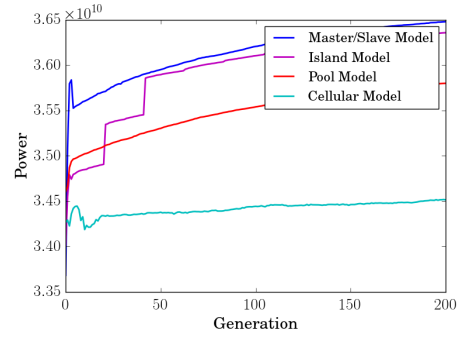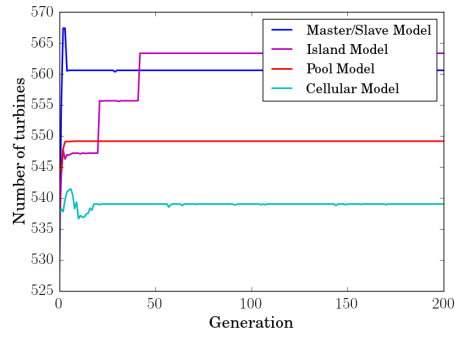
(e) Turbies

Figure 5.11: Scenario obs05.xml averaged over 10 runs: (a) Fitness plot, (b) efficiency plot, (c) cost plot, (d) power plot, and (e) number of turbines.

- The Pool model obtained the second best results, with fitness values close to those obtained by the Master/Slave model.

- The Island model obtained the third best results. This model spent more time exploring different number of turbines than the Master/Slave model and the Pool model.

- The Cellular model obtained the forth best results. This model was not able to produce efficient wind farm layouts.

As mentioned earlier, the wind farm layout optimization problem is extremely hard, if not impossible, to solve analytically. The solution space is simply too huge for any computer to evaluate every possible wind farm layout to find the best one. For a wind farm with only 500 legal turbine positions, 2^{500} different layouts exists! With a solution space this large, it is very unlikely that a genetic algorithm is able to find the global optimal solution. As the results show, the Master/Slave model spend less than 10 generations before individuals with a given number of turbines have monopolized the population. It is therefore unlikely that it has found the global optimal number of turbines. One would expect that a model that spends more time testing different number of turbines would be able to come up with better solutions. However, the results contradicted this hypothesis. The Island model is the only model, except from the Cellular model, able to explore different number of turbines for a significant amount of time. Still, the model is not able to find layouts as good as those found by the Master/Slave model and the Pool model. These results suggest that the models benefit from settling for a sub-optimal number of turbines fast so that they have more time to spend optimizing the positions of the turbines.

It could also be the case that the Master/Slave model were able to obtain better results than the population distributed models because the parameter values were tailored for this model. This is definitively an advantage for the Master/Slave model. Even though the parameters, selection mechanisms, and genetic operations are common for all the models, it is not certain that the settings that works best for the Master/Slave model works best for the other models. If these settings had been tailored for each model it could have been the case that one or more of the population distributed genetic algorithms would be able to perform better. But, as explained before, the 20-week time frame of this project prevented the author form tailoring these

settings for each of the population distributed model. However, since each model is solving the same problem it is not very likely that there would be huge differences in the settings for the different models.

Another reason that might explain why the population distributed models were not able to keep up with the Master/Slave model is that the parameters that are unique for the different population distributed models were not optimized. Parameters such as *deme size*, *deme count*, *migration rate*, *migration interval*, and *number of migrations* for the Island model, and *number of workers* for the Pool model were selected based on values that have worked well on other problems. Different topologies for the Island model and the Cellular model should also have been tested in order to find out which where the optimal ones. However, as mentioned in the paragraph above, time limitations prevented the author from testing and optimizing these values.

In spite of the fact that the results show that the traditional non-population distributed Master/Slave model works best for the wind farm layout optimization problem it is important to note that these results could be different under different circumstances. It has only been proved that it performs best when each model is provided the same resources, with the parameter values presented in sub-section 5.2.1. One challenge with using genetic algorithms is that they can be implemented in so many different ways. As shown in section 5.1, different selection mechanisms, genetic operations and parameter values influence the performance of the genetic algorithm. It is impossible to find the optimal combination of the parameters, because it would require testing every value of every parameter against every value of all other parameters. Therefore, it can only be concluded that non-population distributed models perform better than population distributed models under the given circumstances.

Even though providing each of the models with the same amount of computer resources seems fair it also introduces challenges. The main property that distinguishes population distributed genetic algorithms from non-population distributed genetic algorithms is that they spend more time exploring different solutions in order to hopefully find the global optimal solution. This means that population distributed genetic algorithms by nature require more time than non-population distributed genetic algorithms. In order to satisfy this requirement, but also provide a fair comparison one could allow the the

models to run for the same number of generations after the population has decided on the number of turbines it wish to pursue. This way, the population distributed genetic algorithms would not be punished because they spend more time exploring different number of turbines. As mentioned earlier, the Pool model is not able to explore different number of turbines for a significant amount of time, this adjustment would therefore not affect the results of the Pool model. The Island model on the other hand would probably benefit from this scheme. The Cellular model would probably also benefit from this scheme, however, it would require that it run for so many more generations that it would be impossible to do in practice.

In chapter 3, Grady et al. [2005] and Huang [2007] showed that under different circumstances, the Island model were able to find better wind farm layouts than a traditional non-population distributed model. It was therefore a little surprising that the Island model were outperformed by the Master/Slave model in this project, but there can be many reasons for this. Grady et al. [2005] implement an Island model and compare the results obtained with those of Mosetti et al. [1994], which was obtained with a traditional non-population distributed genetic algorithm. However, Grady et al. [2005] increased both the population size and the number of generations in their experiment. It can therefore not be stated with certainty that the Island model were the key to their success, it could just as likely be the increase in population size or the increase in the total number of generations. Huang [2007] on the other hand, implemented one traditional genetic algorithm and one Island model and compare their results when both models were run for the same number of generations with the same population size. It is therefore more surprising that the results obtained in this thesis were different from those obtained by Huang [2007], but there can be many reasons for this. In the experiments done by Huang [2007], the population size were 3 times as large as in this project and the total number of generations were more than 12 times the total number of generation used in this thesis. Obviously, a larger population size is an advantage for genetic algorithms. The probability of finding the global best solution increase with the population size. This is also true for the number of generations, increasing the total number of generations increases the probability of finding the global optimal solutions. It could therefore be the case that if the Island model in this thesis were run with a larger population size, or for more generations it could surpass the Master/Slave model. Another difference between this project and the

project of Huang [2007] is the topology. In the topology of Huang [2007], 20 Islands were used, five times as many as in this project. This means that it would take longer for individuals from one Island to monopolized the entire population something that also could benefit the model. Yet another difference between this project and the project of Huang [2007] is the fitness function. In this project, the fitness function that the models try to optimize is much more complex than the one used in Huang [2007] Therefore, it could be the case that while the Island model is able to outperform the simple genetic algorithm with a simple fitness function, it comes up short when the function to be optimized is more complex, realistic and time consuming.

The Pool model stands out as the population distributed genetic algorithm fittest for solving the wind farm layout optimization problem. One reason why this might be is that out of the 3 population distributed models, the Pool model is the one most similar to the Master/Slave model. As mentioned above, the parameter values were optimized when tested on the Master/Slave model, and since the Pool model is most similar to the Master/Slave model it is likely that the same parameter values would work for this model. As the Master/Slave model, the Pool model does not waste many generations searching for the optimal number of turbines. It makes the decision in less than 15 generations, and spends the rest of its time optimizing solutions with that given number of turbines. This worked well for the Master/Slave model, and it worked well for the Pool model too.

The Cellular model is outperformed by all the other models. It is not able to get results that are close to those obtained by the others. One reason for this is that the Cellular model is by far the model that needs most generations to find a good solution. For example, for the individual in the upper left corner, it would take a minimum of 14 generations to spread its genes to the lower right corner, and that is just the lower bound. The Cellular model is simply too slow to compete with the other models. A solution to this problem could be to use a larger square for which parents for each individual can be selected from. This would however make the model more similar to the Master/Slave model, and make it lose its unique features. As mentioned in chapter 4, the updating function used by the Cellular model works so that each individual is replaced each generation, even when the new individual has worse fitness than the current individual. This explains why the Cellular model fitness get worse for the first 5-10 generations, before it slowly starts to get better. If

the updating function had been similar to the one used by the Pool model, so that each individual were only replaced if the new individual had better fitness, the results might have been better. However, it could also be the case that this greedy approach would lead to worse results in the end.

Even though it is outside the scope of this thesis, it is interesting to discuss the fitness function. It is very hard to find the optimal fitness function, i.e. the fitness function that guides the population towards the layout that will make the owners most money. The fitness function is based on cost estimates, power estimates and wind predictions. Therefore, it might not be the case that those who came up with the fitness function is 100% certain that it is optimal. Because of this, it would probably be interesting for the owners of the wind farm to take a look at the different results obtained by the different models and make up their own decision about which they would want to implement.

In summary, it has been showed that population distributed genetic algorithms are not always able to come up with better results than the traditional, non-population distributed genetic algorithm. Now that the results are presented and discussed it is time to go back and answer the research questions.

Chapter 6

Conclusion

In this thesis, different genetic algorithm models have been implemented and tested. The goal of the thesis was to investigate how population distributed genetic algorithms would perform when used to solve the wind farm layout optimization problem. The performance of the population distributed genetic algorithms were compared to the performance of the simple genetic algorithm as well as to each other. In this chapter, an overview of the thesis will be presented in section 6.1. In section 6.2 the goal and research questions are discussed and answered. Section 6.3 contains a discussion of how this thesis contribute to the field of wind farm layout optimization using genetic algorithm technology, and section 6.4 contains suggestions to further work.

6.1 Overview

In chapter 2, the wind farm layout optimization problem was introduced and challenges to wind farm construction were presented. A thorough review of the genetic algorithm was also given, and the 3 population distributed genetic algorithms investigated in this thesis were introduced.

Chapter 3 contains a thorough review of research within the field of wind farm layout optimization using genetic algorithm technology. In table 3.3 the most important features of each publication is presented. Chapter 3 also contain a brief overview of other artificial intelligence methods that have been

used to optimize wind farm layout. During the research phase, it became apparent that no attempt had been made to investigate the performance of the Pool model and the Cellular model on wind farm layout optimization. The only population distributed genetic algorithm reported tested was the Island model [Gao et al., 2015, Grady et al., 2005, Huang, 2007, Şişbot et al., 2010, Wan et al., 2009]. The fact that no attempt had been made in testing other population distributed genetic algorithms than the Island model on the wind farm layout optimization problem, even though the Island model performed so well was the main motivation behind the choice of the goal statement and research questions.

Chapter 4 presents the methodology for investigating the goal- and research questions. The decision was made to implement the genetic algorithm from scratch and connect it to the wind farm simulator provided by GECCO 2016. The chapter first gives a system overview. Next, the implementation details for the simple genetic algorithm are presented and discussed. The wind-, wake-, and power model, fitness function and test scenarios are also given. Additionally, the design decisions for the 3 population distributed genetic algorithms are presented and explained.

The final results of the experiments are presented in chapter 5. The first part of the chapter contains the results of testing different parameter values, selection mechanisms and recombination mechanism. The second part of the chapter contains the results obtained when running the different genetic algorithm models on 4 different wind scenarios, 2 containing obstacles and 2 not containing obstacles. A discussion of the results are provided at the end of the chapter. The results show that the Master/Slave model is able to find better results for each of the 4 scenarios. The Pool model performs second best, the Island model third best and the Cellular model forth best.

6.2   Goal Evaluation

The goal of this thesis was to investigate the possible advantages of using population distributed genetic algorithms in optimizing wind farm layout. In this section, the research questions will be reviewed, answered and discussed.

Research question 1

> *Can distributed genetic algorithms improve the quality of the so-lution to the wind farm layout optimization problem as compared to a simple genetic algorithm?*

The results from this thesis show that population distributed genetic algorithm does not necessarily find better solutions than the simple genetic algorithm for the wind farm layout optimization problem. In this thesis, the Master/Slave model consistently found better wind farm layouts than the population distributed genetic algorithms.

As mentioned in chapter 1 the wind farm layout optimization problem is impossible to solve analytically because the search space is too big. For a wind farm site with 500 legal turbine positions 2^{500} different layouts exist, that is, more layouts than the number of particles in the universe! This analogy explains just how complex the wind farm layout optimization problem is, and it illustrates how unlikely it is that a genetic algorithm is able to come up with the global optimal solution. The Master/Slave model is the model that spends the least time exploring different number of turbines. It settles on a given number of turbines after approximately 10 generations and starts optimizing the turbine positions within that solution space. This strategy of settling for a local minima fast and optimize turbine positions for as many generations as possible seem to work! And, as the results imply, this might be the property that makes the Master/Slave model outperform the other models.

Another possible explanation why the Master/Slave model obtain better results than the population distributed genetic algorithms could be that the genetic algorithm parameters and selection strategies were optimized running this model. It might be the case that the population distributed models could obtain better results if these settings where tailored for every model. Sadly, the time frame of this thesis prevented the author to perform these experiments for every model.

It is important to note that this thesis have only proven that the Master/Slave model performs better than population distributed genetic algorithms when each model is provided the same amount of resources. As mentioned in

the discussion, it could be argued that it is wrong to compare population distributed models with the Master/Slave model with the same amount of resources. The essential property of population distributed models is that they spend more time exploring different number of turbines before they settle on a given number and start optimizing turbine positions. However, it would be very difficult to compare the results of the models were they not given the same amount of resources.

Another fact that might explain why the population distributed genetic algorithms were not able to come up with results as good as the Master/Slave model could be that the parameters that are specific for the population distributed models were not optimized, but set based on the authors previous experience with genetic algorithms. As mentioned many times before, there was no time to perform these experiments in this project.

Research question 2

> *Which distributed genetic algorithm works best for the wind farm layout optimization problem? What properties are essential for its success?*

Out of the population distributed genetic algorithms, the Pool model was able to find the best solutions. The Island model also came up with acceptable results, while the Cellular model had trouble keeping up with the other models.

Above it was discussed that the property that made the Master/Slave model superior to the other models could be that it does not waste time searching for the optimal number of turbines, but settles fast in a local minima, and spends most of its time optimizing wind turbine positions. The results obtained by the Pool model supports this explanation. The Pool model is the population distributed genetic algorithm that resembles the Master/Slave model most. The results show that it settles on a given number of turbines almost as fast as the Master/Slave model and spend an extensive amount of time optimizing turbines positions. The difference in fitness between the Master/Slave model and the Pool model is small enough so that it might be reasonable to conclude that if the settings had been tailored for the Pool model, it would have been able to obtain similar results.

As mentioned, as opposed to the Pool model, the Island model was able to take advantage of its population distributed property by using it to explore different number of turbines. It was expected that this property would be crucial for the success of the populating distributed genetic algorithms. However, this thesis have proven that under the given circumstances this property was not an advantage. As discussed before, a number of reasons could explain this result. First, it might be the case that this property is only advantageous when the model is allowed to run for more generations, and is allowed to optimize each solution longer. It might also be the case that this exploration is a waste of time because the algorithms are not able to find the global optimal solution anyway, and should concentrate on optimizing a local minima.

The Cellular model was not able to come up with good solutions for the problem. The model performed so much worse than the other models that it is safe to say that it is not suited for wind farm layout optimization. The problem with the Cellular model is that it would require so much more time than the other models that it would be unfit to use, at least when run on a personal computer.

In summary, genetic algorithms have been used trying to solve the wind farm layout optimization problem for more than 20 years. Genetic search algorithms have become the primary artificial intelligence technique in wind farm optimization because the problem is too complex to solve analytically. However, the complexity of the problem is also apparent when genetic algorithms are used. It is shown that properties that usually are advantageous for genetic algorithms such as their ability to explore different solutions might not benefit wind farm optimization. However, the suggestions presented in section6.4 should be investigated before it can be said with certainty that population distributed models are less suited for wind farm layout optimization than simple genetic algorithms.

6.3   Contributions

This thesis contribute to the field of wind farm layout optimization in a number of ways. First of all, chapter 3 contains the most complete survey of

the state of the art within wind farm layout optimization and genetic algorithms. Even thought the survey was mainly a byproduct of the thesis meant to provide the author and reader with an overview, it has become one of the biggest contributions of this thesis. Samorani [2013] includes a small survey of different techniques used to optimize wind farm layouts, but it only covers a fraction of the research presented in the survey in chapter 4. A survey of the state of the art would be very useful for other researchers working on wind farm layout optimization.

The survey in chapter 3 have shown that genetic algorithms are suitable for wind farm layout optimization. However, no attempt, has been made in investigating the performance of the Pool model and Cellular model on the wind farm layout optimization problem. Therefore, this thesis contributes to the field by being the first project attempting to show which, if any, of the population distributed genetic algorithms are best equipped for wind farm layout optimization. The results obtained in this thesis can be used as a basis for further research within the field. Section 6.4 contains suggestions on how the research presented in this thesis could be investigated further. Many interesting directions can, and should, be taken in order to find out which method is truly the primary method for wind farm layout optimization.

The main lesson from this project:

> *Using population distributed genetic algorithms to solve the wind farm layout optimization problem will not necessarily lead to better fitness than with simple genetic algorithms. Population distributed genetic algorithm demand more computational resources and will therefore have trouble beating a simple genetic algorithm with the same amount of resources. Population distributed genetic algorithms are more advanced than simple genetic algorithms and it will therefore be more difficult to find the correct settings for them. However, when handed more resources it is clear that population distributed genetic algorithms are powerful algorithms that should be investigated further on the wind farm layout optimization problem.*

6.4 Further work

As far as the author knows, this is the first time different population distributed genetic algorithms have been compared against each other and against a simple genetic algorithm in their ability to solve the wind farm layout optimization problem. This thesis can be view as a first attempt to understand how population distributed genetic algorithm can affect wind farm layout optimization, and it should be explored further.

Both research questions should be further investigated. As has been mentioned, further work should be done in optimizing the parameters that are specific for each of the population distributed models. For the Island model, experiments should be performed to optimize *deme size*, *deme count*, *migration rate*, *migration interval* and the *topology*. Especially, the author believes that optimizing the *migration interval* would have a major impact on the performance of the Island model. As the results showed, the Island model was the only model able to explore different number of turbines for a significant amount of time. However, it was not given enough time to optimize each of these number of turbines, and therefore it was not able to realize the potential of the solution it has found before it jumped to another solution. Increasing the migration interval could have changed the final results. For the Cellular model, different topologies should be investigated and compared. A larger square, or another form of topology would affect the results. The replacement strategy of replacing every individual at every generation even thought the new individual had worse fitness than the previous individual should probably be revised. It might also be the case that a different parent selection function, such as roulette wheel, would work better for this model, even though it did not work for the Master/Slave model. For the Pool model, different number of workers should be tested. It would also be very interesting to take control over the scheduling of the different workers, and investigate the effect of letting one or more of the workers to get far ahead of the others in evolution and compare this to simulations where the workers are at about the same generation.

In addition to optimize the parameters that are specific for each model it would also be desirable to redo the parameter settings from section 5.1 for each of the population distributed genetic algorithms. This would make sure

that the Master/Slave model does not have an advantage because the settings used for every model is only tested on that model. Even though the author does not believe this part to be as important as the improvements recommended above, it could have an impact on the final results.

All 3 population distributed genetic algorithms were implemented as homogeneous models. It would be very interesting to observe how implementing these as heterogeneous models would affect the results. This would require an extensive amount of work because so many different settings could be used, that it might be wise to start with only one of the models. It would be very interesting to observe how the Island model could be improved by using different parameter settings, selection mechanisms and recombination methods on each Island and compare the results against a homogeneous implementation. It would also be very interesting to let the workers of the Pool model run with different settings, and to let different settings apply to different parts of the grid in the Cellular model.

The Island model and Cellular model were both synchronous. Implementing these as asynchronous models could also be interesting to investigate, although the author does not believe that this would impact the results as much as implementing them as heterogeneous models.

Since this thesis is a contribution to GECCO 2016, where the goal is to optimize the objective function provided by the contest, a multi-objective function was not implemented. However, it would be very interesting to solve the wind farm layout optimization problem with a multi-objective genetic algorithm, and combine this with population distributed genetic algorithms. Finding the best objective function is a difficult job, which includes a lot of estimation. It is extremely difficult to come up with a fitness function that guide the population to the optimal solution. Because of this, it is often more accurate to use a multi-objective function because then you do not have to weight the importance of the different objective against each other. A population distributed genetic algorithm would be perfect for optimizing a multi-objective function because each Island, worker or area could be assigned a different objective function.

Gong et al. [2015] also present population distributed genetic algorithms which are combinations of each other. The Island model implemented for this

thesis was actually one of the models mentioned, because the Master/Slave model was run on each Island. However, the population distributed genetic algorithms were not combined. [Gong et al., 2015] suggest combining the Island model with the Cellular model (one cellular model on every Island) or running an Island model on each Island in the Island model. These models go even further in their attempt to slow down take over time, and investigate different solutions.

Saavedra-Morena et al. [2011] used a greedy heuristic to decide the initial position of the wind turbines, and then used the genetic algorithm to improve the results. Saavedra-Morena et al. [2011] showed that the final results were better than those obtained by the genetic algorithm when it started out with random solutions. This strategy could also be implemented together with the models implemented in this thesis to investigate if this would improve the final results obtain by the population distributed genetic algorithms.

In section 3.2 it was shown that greedy heuristics, simulated annealing, ant colony algorithms and other swarm algorithms could also be used to solve the wind farm layout optimization problem. A study comparing different artificial intelligence methods in solving the wind farm layout optimization problem would be very interesting. It would also be possible to combine the different algorithms either by letting a genetic algorithm run first at trying to let one of the other methods improve the final results, or the other way around.

As discussed, this thesis has answered some questions and left the author with many new questions that it would be very interesting to investigate and answer. This thesis has laid the foundation for further work within population distributed genetic algorithms and wind farm layout optimization.

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