

Sexual Selection in GAs
- Minor Thesis -

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1 Introduction

GAs (Genetic Algorithms) are inspired by Holland's work of the early 1970's. ([11]) The idea behind them is to mimic some of the processes observed in natural evolution in order to create powerful algorithms for optimization problems. Typically, an optimization problem requires finding a vector $\vec{x} = (x_1, \dots, x_n) \in M$ of parameters of the system under consideration, such that a certain quality criterion $f : M \rightarrow \mathbb{R}^+$ (the positive real number space) - called the *fitness function* - is maximized or minimized depending on the problem.

A solution to the global optimization problem implies finding a vector \vec{x}' such that $\forall \vec{x} \in M : f(\vec{x}) \leq f(\vec{x}')$ in the case of maximization problems and such that $\forall \vec{x} \in M : f(\vec{x}) \geq f(\vec{x}')$ for minimization problems. But even if the general global optimization problem is hard to solve, (because it is NP-complete, for example) finding a sufficiently good solution is already a big success for practical problems.

GAs are based on the idea of a population of individuals representing potential solutions for a given optimization problem and undergoing a cycle of *recombination*, *mutation* and *selection* to evolve towards increasingly better fitness values of individuals and thus better solutions for the optimization problem under consideration.

The initial population is chosen randomly and evaluated. In each iteration of the cycle pairs of individuals are randomly selected (these are the parents) and combined together with the aim of producing offspring ideally containing the most profitable traits of both parents and therefore having a higher fitness value and thus representing a better solution to the optimization problem.

After recombination, the population undergoes a mutation step. Mutation is supposed to introduce innovation into the population by generating variations of individuals and thus preserving diversity and preventing a premature convergence to a suboptimal solution.

GAs are randomized in the sense that a specified recombination and mutation probability decides whether recombination or mutation are performed and that the recombination, mutation and selection mechanisms typically make highly use of random choice. After the recombination and mutation step, individuals are selected proportionally to their quality or fitness in order to create a whole new population. However, it should be mentioned that this form of 'environmental' selection at the end of the cycle ([1]) diverges from a 'parental' selection ([9], [17], [21]) where the parents are chosen proportionally to their fitness before being recombined having no selection at the end of the cycle.

The following pseudocode algorithm represents the cycle described above:

```

t:=0;
initialize P(t);
evaluate P(t);
while not terminate do
  {
    P'(t) := recombine P(t);
    P''(t) := mutate P'(t);
    evaluate P''(t);
    P(t+1) := select (P''(t))
    t:=t+1;
  }

```

In this algorithm, $P(t)$ denotes a population of μ individuals at generation t . An offspring population $P''(t)$ of size μ is generated by means of recombination and mutation from a population $P(t)$. After that, the offspring population $P''(t)$ is evaluated by calculating the fitness values $f(x_k^*)$ for each of the solutions x_k^* represented by individuals in $P''(t)$ and selection based on the fitness values is performed to drive the process towards better solutions.

The cycle mentioned above is iterated for a number of generations until the computing time is exhausted, a sufficiently good solution has been found or some other termination criterion is fulfilled.

GAs as originally defined by Holland ([11]) use binary representation of individuals as fixed length string over the alphabet $\{0,1\}$, such that they can easily be used to handle boolean optimization problems of the form: $f : \{0, 1\}^l \rightarrow \mathbb{R}^+$.

However, they can also be applied to general discrete ($M \subseteq \mathcal{Z}^l$) and real ($M \subseteq \mathbb{R}^l$) optimization problems of the form $f : M \rightarrow \mathbb{R}^+$ by using a decoding function $h^{-1} : \{0, 1\}^l \rightarrow M$ mapping binary strings to solutions $\vec{x} \in M$. The strong preference for using binary representations of solutions in genetic algorithms is typically derived from the schema theory developed by Holland, which tries to analyze GAs in terms of their expected schema sampling behaviour. (see [11], [9], [17], [21] for a more detailed description of the schema theorem)

GAs are search algorithms based on the mechanism of natural selection and genetics. While randomized, GAs are not a simple random walk within search space, they are an example of a search procedure that uses random choice as mentioned above as a tool to guide a highly exploitative and efficient search through a coding of a parameter space.

This makes them different from traditional deterministic search methods. However, there are a few more differences. GAs work with a coding over some finite alphabet of the parameter set, not with the parameters themselves, which makes decoding functions necessary. Besides, GAs use objective payoff information in form of a fitness function rather than derivatives or other auxiliary knowledge, so that no assumption concerning continuity, derivative existence or unimodality of the fitness function is needed.

GAs have been found to provide robust search in complex spaces and are finding

more application in business, science and engineering. ([9], [17], [8]) The reason for the growing numbers of applications are clear: GAs provide a computationally simple but powerful search algorithm and furthermore are not fundamentally limited by restrictive assumptions about the search space.

However, in spite of the efficiency and robustness of GAs, they have also some weak points. Some of the main problems involved within the use of GAs for solving optimization problems are premature convergence to a non-acceptable, suboptimal solution and even no convergence at all. In fact, GAs have no convergence guarantees in arbitrary problems. In order to handle this problem, some researchers have made use of so called hybrid GAs incorporating application-specific knowledge or heuristics into their algorithms. ([8]) Basically, hybrid methods use a GA to sort out the interesting hills in the “fitness landscape” and then use locally convergent methods or heuristics to climb the local peaks. In this way the globality of a GA is combined with the more convergent behaviour of local techniques.

The problem of premature convergence bothers many people using GAs for problem optimization. A practical way of reducing premature convergence is using mutation or fitness scaling methods. ([9]) However, perhaps there is a more systematic and problem-independent approach to avoid premature convergence to a suboptimal solution. Again, maybe having a closer look at natural evolution in nature can help to find a solution to this problem.

2 Sexual Selection in Nature

Darwin clearly distinguished between natural selection and sexual selection as different kinds of processes operating on different kinds of traits according to different kinds of evolutionary dynamics. For him, natural selection improved an organism’s abilities to survive in a competitive environment while sexual selection favored abilities to attract and select mates to produce viable and attractive offspring.

In fact, organisms that reproduce sexually should avoid mating randomly because the genetic quality of one’s mate will determine half of the genetic quality of one’s offspring.

The key to choosing mates well is to evolve a mate choice mechanism that has “internalized” the long-term fitness consequences of reproducing with different kinds of potential mates. The benefit of mate choice is that negative fitness traits that threatened survival in the past can be avoided and positive ones can be exploited.

Thus, mate choice is well calibrated if the perceived sexual attractiveness of potential mates is highly correlated with the actual viability, fertility and attractiveness of the offspring they would produce.

The observable traits of potential mates that correlate primarily with offspring survival prospects have been called ‘viability indicators’ and the observable traits correlated with reproductive prospect have been called ‘aesthetic courtship displays’. ([31])

In many species, males are chosen by females in order to mate and produce offspring. This leads on the one hand to the fact that males have to compete with each other in order to be chosen as mates. On the other hand, females will be interested in picking males with high fitness as well as high attractiveness because mating with them will guarantee offspring with high probabilities of survival as well as attractive enough to be chosen as mates in future generations.

Thus, males have to find an equilibrium between developing useful traits in order to survive as well as attractive traits in order to increase their probability of mating. For this purpose males often develop detrimental or maladaptive traits. Detrimental or maladaptive traits are those which represent a certain type of 'fitness handicap' but at the same time are supposed to increase the attractiveness of an individual such as the peacock's tail for example.

Some researchers ([31]) suggest that these detrimental traits arise because they show that the fitness of an animal is enough to accept such a handicap.

Fisher's runaway selection theory ([31]) suggests that if a gene for a certain trait becomes genetically associated with the preference for it, the trait will become more common to match the female's preference for it, which can cause maladaptive traits to become common in males.

Simulations using GAs run by Werner ([31]) corroborate the theory of runaway sexual selection and show that after several generations the preferences for detrimental traits become linked with the tendency to develop them. The most striking result of his simulation is the extent to which males would sacrifice their fitness to gain features that females would find attractive.

Another interesting result is the splitting up of the population into multiple preference groups. The females' preference for different traits could split the males so that each group would "specialize" in meeting the preference for one trait at the expense of meeting preferences for another. It has been suggested that this splitting could lead to the formation of new species. ([27])

Summarizing, on the one hand natural selection puts pressure on males to reduce the feature that is handicapping them in order to increase their chance to survive which at the same time leads to a greater difficulty for a male with reduced handicaps to find a mate.

On the other hand, the females' genes for feature preferences always point in directions further away from good fitness values, which means that females prefer slightly handicapped males so that males are supposed to develop detrimental traits which increase their attractiveness.

The reasons for this are very straightforward. If females would prefer too highly attractive males having strongly evolved detrimental traits and thus being highly handicapped, their offspring (carrying their own genes) would die because of natural selection. On the other hand, if females' preferences are too close to the average male traits and thus to the average fitness, they will consequently tend to pick less highly ornamented males as mates and their offspring would be less likely to reproduce.

Thus, males have to find an equilibrium between meeting the fitness requirements which natural selection imposes on them in order to survive but also try

to meet females' preferences always lying in a slightly different direction than the natural selection forces point to.

3 Sexual Selection in GAs

Conventional GAs as defined by Holland ([11]) rely on the concept of natural selection. Individuals are selected with a probability directly proportional to their fitness following the well known principle of the 'survival of the fittest'.

However, as outlined above, evolution in nature is not only driven by natural selection but also by sexual selection forces sometimes pointing in quite different directions from each other.

As mentioned in section 2, sexual selection forces could be strong enough to pull individuals away from a fitness peak and even lead a whole population to split into certain preference groups and by this promote speciation.

Thus, the idea of incorporating sexual selection mechanisms into GAs arises almost naturally. Perhaps, populations driven by sexual selection forces could escape local 'fitness' optima and even speciate so that the problem of premature convergence could be easily and naturally overcome.

This idea has been analyzed especially by two researchers: Peter M. Todd and Geoffrey F. Miller. Within their several papers concerning sexual selection in GAs they claim that sexual selection can:

1. promote spontaneous speciation
2. promote escape from local optima with directional forms of sexual-selective drift
3. speed optimization by increasing the accuracy of the mapping from phenotype to fitness by decreasing the sampling error characteristic of natural selection
4. speed optimization by increasing the effective reproductive variance in populations even when survival-relevant differences are minimal by imposing an automatic, emergent form of fitness scaling
5. promote the emergence of complex innovations

3.1 Promoting Speciation

Todd and Miller ([27]) develop a 'Quicksilver Model' with the aim of modeling biological speciation and show through simulation that sympatric (barrierless) speciation can occur spontaneously if individuals have evolvable mate preferences based on degree of similarity to themselves and compete between each other to match the mate preferences of other individuals.

The name for the model is inspired from the behaviour of mercury ('quicksilver') shaken on a flat surface: sometimes large cohesive blobs will split into separate smaller blobs. The mercury's behaviour depends on two opposing forces: the

random shaking forces that tend to jostle blobs apart, and the cohesive surface-tension forces that tend to keep blobs intact.

Following this metaphor, the flat surface represents a fitness landscape defined over a space of possible phenotypes, the shaking forces represent random mutation and the effects of crossover and the cohesive forces represent mate-choice preferences evolved to favor phenotypically similar mates.

The Quicksilver Model suggests that, given some balance between these forces, spontaneous speciation can and will occur. This spontaneous speciation is supposed to occur without geographic barriers, other selection pressures (a flat fitness landscape is used) nor predefined mating preferences.

It should be mentioned that mate preferences can be defined directly in terms of phenotype coordinates (so called *space-relative mate preferences*) or be defined relative to the individual's current position in phenotype space (*individual-relative mate preferences*).

Each individual has an own SRP (Sexual Reference Position) somewhere in phenotype space. Basically, the SRP can be defined in four ways depending on the mechanism of sexual selection explored:

1. with *individual-relative* preferences, the SRP is identical to the individual's own phenotype-location (this has been called *assortative mating*)
2. with *parental-relative* preferences, the SRP is the phenotype of a parent
3. with *population-relative* preferences, the SRP is the average of all phenotypes in the population
4. with *space-relative* preferences, the SRP is some absolute position in phenotype space

Todd and Miller make use of individual-relative mate (assortative mating) preferences within their Quicksilver Model. This has the advantage that subpopulations splitting apart can retain the same mate preferences, which makes the Quicksilver Model more plausible because speciation requires only that the frequency distribution of phenotypes changes, the frequency distribution of mate preferences doesn't have to change at all.

In order to demonstrate the feasibility of their model, Todd and Miller define a simple GA. Each individual is represented by three genes: two encoding for phenotype attributes and one coding for a mating preference.

The reason for using two genes is to make visualization and representation easy as the phenotype of each individual can be represented as a point on a 2D plot. Phenotype space is interpreted as a 1x1 toroid and all the genes are Gray-coded, which has the nice property of making each edge of the phenotype space just one mutation away from the corresponding opposite (and toroidally connected) edge. The gene coding for a mating preference specifies a preferred mating distance.

Each individual is then associated with its own genetically coded POM (Probability of Mating) function determining the willingness to mate with other individuals. As the authors use a 2D phenotype space, the POM value can be

represented in the 3rd dimension. In fact, they define POM functions having a conical shape and a peak somewhere in phenotype space falling off linearly until zero is hit at some radial distance away from the peak.

Thus, a whole population's mate preferences can be represented as an overlapping set of such conical mountains. This abstract mountain range formed from individual's POM functions is the environment to which individuals adapt through sexual selection. As POM functions are determined by genes which can evolve, the peaks of POM functions will generally evolve towards the peaks in the current frequency distribution of individuals across phenotype space and sexual selection will drive peaks in that population frequency distribution itself to evolve towards the peaks of the POM functions without ever reaching an equilibrium but rather playing catch-up with each other.

Here's the way their GA works:

1. To create the next generation, a 'mom' individual is picked from the population using normal roulette-wheel selection.
2. Then a 'dad' is selected from the population in the same way.
3. The phenotypic distance between the mom and the dad is computed using Euclidean metric.
4. Each individual computes its probability of mating with the other using their POM-functions
5. The two probabilities are multiplied
6. A random number is generated and if it is lower than the common mating probability the pair mates and gets crossed over putting their offspring into the next generation. If the mating fails, a new dad is chosen (with replacement) and the process is repeated until the mom finds a mate. Once the mom mates, a new mom is picked randomly and the whole process is iterated until the next generation is full.

It should be noted that individuals are not meant to have a sex per se, it only depends on the order in which both individuals are picked. Todd and Miller also use a maximum number of mating attempts for a mom to find a dad and if she can't find a suitable mate within 500 attempts a new mom is chosen.

The authors also point out the fact that this '*mom-samples-dads*' schema tends to preserve the frequency distribution of phenotypes from one generation to the next. It allows different phenotypically-separate and reproductively-isolated clusters to maintain their relative numeric proportions, which is important in promoting speciation.

In contrast, a 'random-pair-sampling' schema in which a mom and a dad are picked independently and randomly at each step and thrown back if they don't like each other, would lead the next generation's frequency distribution towards currently more common phenotypes and the survival of smaller, reproductively-isolated clusters would be endangered as the probability of choosing parents

from the same small cluster simultaneously would be very low.

The authors use traditional bit-wise mutation with a mutation rate of 0.01 and two-point crossover with an implicit rate of 1.0 as once a mom and a dad are chosen recombination is performed. The population size is 100 and the population is not initialized randomly but in a small random cluster in the middle of phenotype space. Initial preferred mating distances are constrained to be in a range from 0.0 to 0.1.

When running their simulation with these settings, the authors observe the sympatric speciation effects they expected. They also find out that using large mutation rates lead to greater cluster spread while different crossover rates seem to affect merely the amount and frequency of speciation. In [28], Todd and Miller focus on another sexual selection mechanism different from assortative mating: *parental* or *sexual imprinting*. Sexual imprinting is a parent-relative preference in which the individual's SRP corresponds to the phenotype of one of the parents. Basically, the authors compare the performance of sexual/parental imprinting with the one of inherited, *evolved sexual preferences* (preferences coded in the genotype and thus subject to evolution) in terms of the following measures:

- average number of mating attempts
- time for a sexual selection preference to evolve
- mating frequency for a sexual selection preference
- ability to track changes within the population
- benefits depending on mutation rate
- ability to adapt to a 'fitness' landscape and
- ability to promote speciation

In order to compare both above mentioned sexual selection mechanisms, the authors run simulations using a GA as defined above. Each individual has a genotype made up of six genes: two 'trait' genes coding the phenotype attributes, two 'preference' genes coding the preferred phenotypic attributes of potential mates, one 'choosiness' gene coding for the amount of deviation tolerated from the specified phenotypic mate preferences and one 'learning' gene indicating whether the actual mate preferences are inherited or parentally imprinted.

When running different simulations to compare sexual imprinting vs. evolved preferences the authors come to the following conclusions:

1. The average number of mating attempts that it takes an individual to find an acceptable mate is significantly lower when using sexual imprinting.
2. When the 'learning' gene evolves together with the rest of the genotype, sexual/parental imprinting evolves in a rapid and direct manner

3. Individuals with sexual/parental imprinting have mate preferences better adapted to the evolving population and for this succeed more in finding mates
4. For a wide intermediate range of phenotypic change in the population (corresponding to intermediate mutation rates) sexual imprinting can usefully track the variation from one generation to the other. In contrast, evolved preferences work better with low mutation rates. However, when mutation rate is very high and thus phenotypic change is also very high, both mechanism fail to keep track of the population's change.
5. When introducing a moving fitness peak, the disability of sexual imprinting to keep up with it becomes clear.
6. Sexual imprinting promotes speciation much more than evolved preferences do.

3.2 Escaping Local Optima

In [19], Miller and Todd continue their work on sexual selection and show that *directional mate preferences* can cause populations to wander capriciously through phenotype space.

First, the difference between directional and *non-directional mate preferences* should be explained. With non-directional mate preferences, one's ideal mate has some degree of similarity (or dissimilarity) to one's own phenotype. With directional mate preferences, one's ideal mate is some distance away in phenotype space in a particular phenotypic direction.

Genetically coded mate preferences are supposed to exploit currently available phenotypes, and phenotypic traits evolve to fulfill currently popular mate preferences. Thus, sexual selection is expected to set up a complex reciprocal interaction between evolving mate preferences and evolving phenotypes.

Again, the authors use a GA to simulate the effect of directional mate preferences on a population. Basically, they use the same algorithm as outlined in the previous section.

However, the genotype consists of six genes: two determining the individual's phenotypic traits, two genes determining the direction in phenotype space along which the POM function is offset from the SRP and one gene coding for the distance in phenotype space by which the POM function is offset from this point. The sixth gene determines the width of the base of the POM function: the wider the base the less steeply the POM function slopes off from its peak down to zero probability and the less 'picky' the individual is about its potential mates.

There's another important difference with the algorithm described above. When computing the common mating probability, the mom's POM function is constructed based on her directional preferences while the dad's one is computed using his non-directional preferences. The reason the authors give for this is that when using the directional preferences of both individuals it is almost impossible for any individual to find a mate.

When running the simulation using sexual selection alone the results show the arbitrary nature of directional sexual selection and the way in which it can drive a population along a winding trajectory through phenotype space.

From a short-term perspective, it seems that phenotypic traits adapt to current mate preferences and mate preferences adapt to current phenotypic traits. However, the long-term course of the population is absolutely capricious: neither phenotypic traits nor mate preferences ever settle down to a stable, optimal equilibrium.

This changes when sexual selection and natural selection are combined by introducing a fitness peak into the flat fitness landscape of the simulation. Not surprisingly, natural selection leads the populations towards the fitness peak. However, directional mate preferences seem to be strong enough to pull the population away from the fitness peak making it wander through phenotype space under the momentum of these directional preferences in order to return to this single peak after a certain number of generations.

In [20] and [29], Todd and Miller concentrate on the complementary roles played by natural and sexual selection as well as the interactions between them. Basically, they explain natural selection as a hill-climbing process resulting in convergence onto a few local optima within a stable fitness landscape.

In contrast, sexual selection allows individuals to create their own peaks in the fitness landscape following their mate preferences (represented by their POM function), which are genetically coded and thus can evolve. This results in an unstable and rapidly changing landscape of sexual preference peaks that lead a population to wander capriciously around through phenotype space.

However, when natural selection and sexual selection are combined together, the forces driven by them are not always opposed to each other. In fact, sexual selection can even stabilize and reinforce natural selection. In particular, if a population is perched on a naturally selected fitness peak, then mate preferences will often evolve to favor potential mates near the actual peak. On the other hand, if a population has been evolving and moving through phenotype space then mate preferences can even evolve to point in the direction of the movement conferring more evolutionary momentum on the population than it would have under natural selection alone.

As shown by the authors ([19]), directional mate preferences lead a population to wander around, while non-directional preferences don't lead to this effect in such an extent.

3.3 Increasing the Accuracy of the Mapping from Phenotype to Fitness

Miller and Todd ([20]) point out the fact that in nature the process of natural selection is often noisy and suggest that if fitness can be internalized in form of sexual selection preferences by a population, these preferences can inhibit mating with individuals that probably survived by luck rather than by their 'fitness' and thus mate choice can be used as a method of reducing this noisiness.

However, in GA research fitness functions are specifically and artificially designed for optimization problems and thus are not noisy, so that there is no real need to increase the accuracy of the mapping.

3.4 Automatic Fitness Scaling

In GA research, populations often converge prematurely to have similar fitness values and because of this further optimization becomes difficult due to relatively small fitness differences. Miller and Todd ([20], [29]) suggest that sexual selection can provide an automatic form of fitness scaling helping populations to avoid premature evolutionary stagnation producing no improvements. Again, if sexual selection preferences can internalize long-term natural selection pressures, individuals could choose high-viability individuals in spite of the fact that variance in 'fitness' is very low. The result of this choosiness will be the above mentioned automatic form of fitness scaling.

3.5 Promoting Innovations

Mutation has been regarded as the main source of innovation within traditional GA research. However, Miller and Todd ([20], [29]) state that mutation can produce only innovation at a very low level and present sexual selection through mate choice as a much more important source of innovation than mutation can be.

As mentioned before, following the authors sexual selection can lead populations away from local fitness peaks to explore phenotype space in order to find new fitness peaks to climb and by this perhaps discover useful innovations.

4 Aim of this Work

By integrating a sexual selection mechanism into a GA and by this maybe helping a population to escape local optima as well as promoting speciation and innovation, the problem of premature convergence so often encountered within GA research could be overcome.

Besides, if as suggested by Miller & Todd, sexual selection can also stabilize and even speed up natural selection as well as act as an automatic form of fitness scaling, the efficiency and general performance of GAs as search methods within a problem space could be increased.

In order to verify the results presented by Miller and Todd, some optimization problems which have been analyzed extensively by GA researchers are needed. Also an important number of examples and their best known solution should be available in order to test the performance of GA incorporating sexual selection mechanisms. A classical optimization problem in this sense is the TSP (Traveling Salesman Problem) This optimization problem will be introduced and formally defined in the next section.

Afterwards, various sexual selection mechanisms will be explored by integrating

them into traditional GAs and analyzed in order to find out if they indeed can help a GA to escape local optima or even to speciate and therefore overcome the problem of premature convergence and thus increasing the quality of the solution. The structure of this report is as follows: section 5 formally introduces the TSP, section 6 analyzes the performance of a traditional GA applied to a 24 city TSP - the 'Grötschels24' - and sections 7 - 13 examine the effect of integrating different sexual selection mechanisms into a traditional GA in order to solve the TSP under consideration. Section 14 reports the results of a traditional GA applied to a larger problem - the 'Grötschels48' - and sections 15 and 16 analyze the performance of a GA with directional mate preferences applied to the 'Grötschels48'. Section 17 gives a conclusion and section 18 mentions further research and work to be done.

5 The Traveling Salesman Problem

The TSP (Traveling Salesman Problem) is perhaps the oldest and best studied problem in an area called combinatorial optimization. It's history can be traced as far back as Euler (1759) and Hamilton (1856), who studied similar problems. But it wasn't until the 1930's that the problem got its name.

The TSP is stated in a very simple way: given n cities and a salesman wishing to visit all the cities once and only once, which is the minimum length of the tour he must take?

From the point of view of graph theory we can state the problem more formally: let $G=(V,E)$ be a complete undirected graph with a set of nodes V representing cities and a set of edges E representing connections between them as well as a function $w : E \rightarrow \mathfrak{R}^+$ assigning weights to each edge. A Hamiltonian cycle of G is a cycle that visits each edge of the graph exactly once. The TSP is the problem of finding a Hamiltonian cycle with minimum weight.

In the symmetric version of the TSP, the number of possible tours for a n city problem is $(n - 1)!/2$, which makes solving the problem by brute-force methods almost impossible. In fact, the TSP is known to be NP-complete ([24]) which means that any problem in this class is as difficult to solve as any in the NP class (Non-deterministic Polynomial). If $NP=P$, then all the NP-complete problems would have an efficient solution, however no one has proved that this is the case and it is widely believed that it is not.

However, the TSP is very useful in areas like VLSI layout, X-ray crystallography, job scheduling and even cryptography. ([8], [17]) For this, because of the fact that the optimal solution is very hard to find, people are interested in finding a non-optimal but still good solution.

GAs have been often applied to solve different types of TSPs. The main problem of applying GAs to TSPs is that the standard crossover and mutation operators don't work as they may produce tours which are not valid. Thus, various codings, crossover and mutation operators have been developed, analyzed and compared in the last 20 years. ([15], [17], [4], [10], [12], [16], [32], [14], [26], [25], [6]) In many cases GAs have also been hybridized by using local improvement

heuristics like 2-Opt, 3-Opt and LK (Lin Kernighan). ([3], [30])

6 A Traditional GA & the 'Grötschels24'

In order to demonstrate the performance of traditional GAs based on natural selection on the TSP, the well-known and often analyzed 'Grötschels24'([23]), which is a 24 city TSP, has been examined and a GA has been developed to solve it.

6.1 Representation

The most intuitive representation for a tour, the *path representation*, has been used. ([15]) In this representation, the n cities that should be visited are put in order according to a list of n elements, so that if the city i is the j -th element of the list, city i is also the j -th city to be visited. Thus, the 'path representation' is basically a permutation of the n cities. It should also be mentioned that such a representation is not unique and one tour can be coded by $2n$ different representations.

6.2 Recombination

The recombination operator used is a modified version of the ER (Edge Recombination) crossover operator developed by Whitley et al. ([32])

This operator, which is suitable for the symmetric TSP, makes the assumption that edges are the carriers of hereditary information and attempts to preserve edges of the parents in order to pass on a maximum amount of information to the offspring. Thus, the breaking of edges is seen as an unwanted mutation.

The ER operator uses a so-called *edge map*, which gives for each city the cities adjacent to it of the parent tours.

The ER operator works as follows:

1. Choose the initial city of the parent tours with fewest entries in its edgelist. This is the 'current city'
2. Remove all occurrences of the current city from the right-hand side of the edge map
3. If the current city has no entries in its edge list go to step 4, otherwise go to step 5
4. Determine which of the cities in the edge list of the current city has the fewest entries in its own edge list. The city with the fewest entries becomes the current city. Go to step 2 (Note: if two cities have the same number of entries choose any at random)
5. If there are no remaining 'unvisited' cities, then STOP. Otherwise choose an 'unvisited' city at random and go to step 2.

This operator is modified as follows: if some city c is adjacent to a city a in both parent tours then the entry of a in the edge list of c is marked. (by a negative sign for example) The tour is then extended by choosing the next city according to the following scheme:

1. marked cities have first priority
2. cities whose own edge list has fewest entries have second priority

This modification has been sometimes referred to as Edge2 within the literature. ([16])

Consider the two example tours: (1 2 3 4 5 6) and (2 4 3 1 5 6). The edge map looks like following:

<i>City</i>	<i>Connected Cities</i>
1	2, 6, 3, 5
2	1, 3, 4, 6
3	2, -4, 1
4	-3, 5, 2
5	4, -6, 1
6	1, -5, 2

For the example tours chosen the algorithm is as following:

1. Initial cities 1 and 2 have both four edges; city 2 is chosen at random and becomes the current city. The edgemap looks now like following:

<i>City</i>	<i>Connected Cities</i>
1	6, 3, 5
2	1, 3, 4, 6
3	-4, 1
4	-3, 5
5	4, -6, 1
6	1, -5

And the actual tour is: (2)

2. The edgelist for city 2 is: 1, 3, 4, 6. Cities 3, 4 and 6 have all 2 entries in their own edgelist; assume that city 3 is randomly chosen.

And here's the edgemap:

<i>City</i>	<i>Connected Cities</i>
1	6, 5
2	1, 4, 6
3	-4, 1
4	5
5	4, -6, 1
6	1, -5

And the tour: (2 3)

3. City 3 has edges to the cities 4 and 1. Because of city 4 is marked with a negative sign it has more priority and becomes the current city. Again, city 4 is removed of the edgemap:

<i>City</i>	<i>Connected Cities</i>
1	6, 5
2	1, 6
3	1
4	5
5	-6, 1
6	1, -5

The actual tour is: (2 3 4)

4. City 4 only has an edge to city 5, thus city 5 is chosen next. Edgemap:

<i>City</i>	<i>Connected Cities</i>
1	6
2	1, 6
3	1
4	
5	-6, 1
6	1

Tour: (2 3 4 5)

5. City 5 has edges to cities 6 and 1 and because of 6 is marked it becomes the current city. Here's the resulting edgemap:

<i>City</i>	<i>Connected Cities</i>
1	
2	1
3	1
4	
5	1
6	1

Tour: (2 3 4 5 6)

6. And finally city six has only one edge to city 1.

The resulting tour is: (2 3 4 5 6 1)

6.3 Mutation

The Mutation operator used is the DM (Displacement Mutation) operator described by Michalewicz. ([17]) It first selects a subtour at random, this subtour is removed from the tour and inserted at a random point.

Consider the tour: (1 2 3 4 5 6 7 8). Suppose that the subtour (3 4 5) is selected and 5 is randomly chosen as the insertion point, which means that the subtour will be inserted at the 5th position in the tour 'displacing' the rest of the list. This results in the following tour: (1 2 6 7 3 4 5 8). It should be mentioned that the combination of the ER recombination and the DM has been empirically proven to work very well producing very good results on the 'Grötschels24'. ([15]) This is the reason why this combination has been chosen for the approach described here.

6.4 Fitness Scaling

Given the length of a tour, the fitness is calculated as follows:

$$f(\text{length}) = \left(\frac{5000}{\text{length}}\right)^4 \quad (1)$$

It should be noticed that the TSP is a minimization problem as the length of the tour is supposed to be minimized. However, when using a GA the fitness is always maximized. This explains why the fitness of an individual is inverse proportional to the length of the tour coded by it.

The optimal tour for the 'Grötschels24' has a length of 1272, so that the ratio $\frac{5000}{\text{length}}$ will have values between [0..3.93]. The reason why these values are raised to the 4th power is to magnify the differences between values that are close to each other as small 'phenotypic' differences can represent important 'genotypic' differences.

It also should be mentioned that in spite of the fact that the GA maximizes the fitness, the solution of the algorithm will always be stated in terms of the minimum length found rather than in terms of maximal fitness. For this reason, all the graphs showing the results of the GA will represent the length of the tour rather than the fitness of an individual.

6.5 Termination

The termination criterion for the GA has been chosen intuitively. As the goal is to provide better solutions with increasing generations, it seems straightforward to consider the algorithm as converged and make it stop when the best individual of each generation has not resulted in any improvement from the last t generations. (t=100 has been chosen for the 'Grötschels24')

It is important to notice that the algorithm does not stop when the global best individual has been constant for the last t generations but when the best individual found in each generation has not changed for the last t generations, which is an important difference.

Thus, the algorithm stops when reaching a certain kind of evolutionary stagnation.

6.6 Algorithm

The population is initialized randomly and traditional roulette-wheel selection ([9], [17], [21]) is used in form of a parent selection. This means that there is no environmental selection at the end of each iteration of the algorithm, but that the selection mechanism is incorporated within the recombination such that the individuals to be recombined are selected from the population proportionally to their fitness. The recombination rate is 0.75 because it has been found to work well and the mutation rate 0.01 as suggested by Miller and Todd.

The algorithm used was the following:

```

Initialize(Pop);
Evaluate(Pop);
do
{
  Pop' = Recombine(Pop);
  Pop = Mutate(Pop);
  Evaluate(Pop);
} while (not Termination_Criterion)

```

The Recombination algorithm was as following:

```

procedure Recombine(Pop)
{
  Pop" = new Population;
  for i=1 to Population_Size
  {
    ind1 = roulette-wheel-select();
    ind2 = roulette-wheel-select();
    ind = Crossover(ind1,ind2);
    insert(Pop",ind);
  }
  return Pop";
}

```

It should be mentioned that no elitist selection component has been used within the algorithm, such that good solutions can be lost if they are not selected by the parent selection mechanism. And even then, good solutions can be disrupted by the action of crossover, which means that the best tours found can even get worse with increasing generations.

For this reason, the GA doesn't converge in a mathematic sense to the best global solution found, but to the best individual found within the last 100 generations as defined within section 6.5.

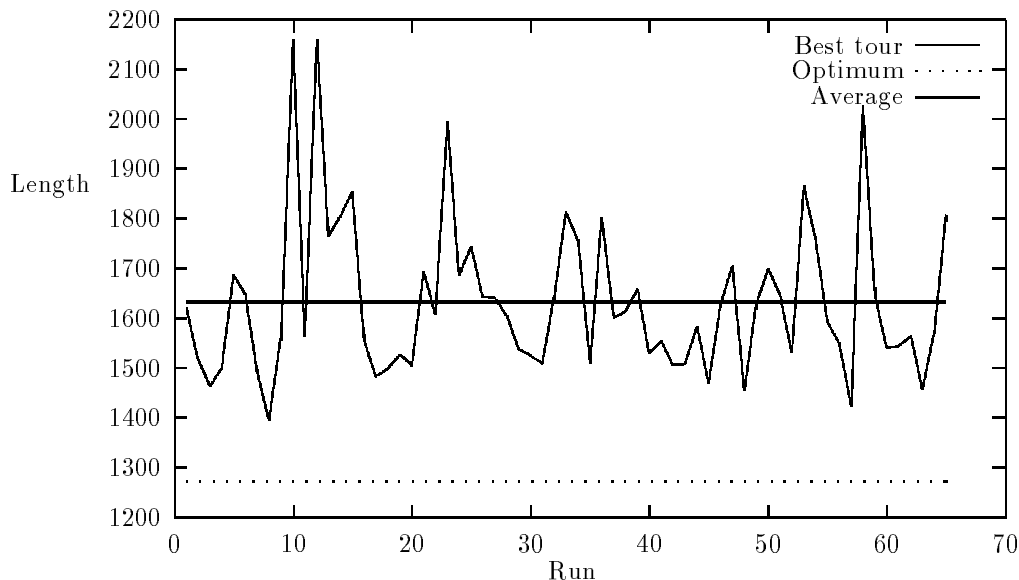


Figure 1: Results of the traditional GA: Length of best tour of each run & average of best tours over all the runs

6.7 Results

The table in Appendix A shows the results of 65 runs of the GA described above. It can be clearly seen in figure 1 that the GA doesn't find the optimal tour (1272) and thus converges to a suboptimal solution in each of the runs.

Figure 2 shows that the algorithm is biased towards smaller number of generations in the sense that some runs reach a higher number of generations but most converge after a relatively small number of generations, such that in fact it seems that the algorithm converges prematurely.

The average number of generations is 896 and the best tour has a length of 1395 and has been found in run 8 having a total number of 494 generations. The average length of the best tour over all the runs runs is 1633.

When evaluating these results, it becomes clear that the GA converges too fast and too early and is not able to find the optimal solution. In fact, it doesn't even find an acceptable solution in most of the runs as we see from the fact that the average of 1633 is 361 away from the optimum length of 1272.

It should be noticed that the quality of the solution does not depend on the number of generations. As it can be seen in Appendix A the best solution is found after only 494 runs, while the largest run with 3837 generations (run 30) produces a result tour with a length of 1524, which is 252 away from the optimum.

Thus, the way of avoiding premature convergence is not by increasing the num-

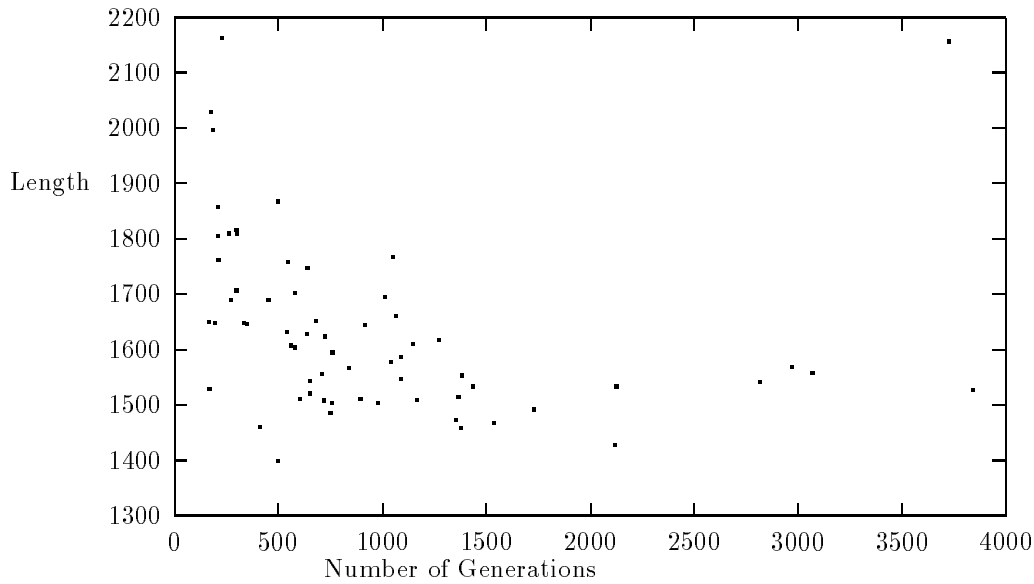


Figure 2: Results of the traditional GA: Length of best tours over number of generations

ber of generations in some way. Instead, a much more direct method of leading a population away from a local optimum and giving it a new momentum in a certain direction within phenotype space is needed.

7 A GA with Assortative Mating using a Distance Measure based on Length Difference & the 'Grötschels24'

Assortative mating as mentioned in section 3.1 is a sexual selection mechanism which makes individuals have sexual preferences to mate with individuals similar to them and thus represents a very conservative form of sexual selection.

An assortative mating mechanism has been integrated within a traditional GA for solving the 'Grötschels24' in order to find out if this sexual selection method helps a GA to escape local optima and thus to find better solutions and if it also promotes speciation.

7.1 Implementing Assortative Mating Preferences

The crossover and mutation operators, the fitness scaling and the termination criterion are the same as described in section 6. Again, the population is ini-

tialized randomly and roulette-wheel selection is used as parent selection mechanism.

The main algorithm is also the same as outlined in section 6.6.

Within the recombination step, Miller and Todd's 'mom-samples-dads' algorithm as described in section 3.1 has been used allowing a 'mom' to sample up to 10 'dads' and decide whether she wants to mate with one or not. If she decides to mate, an offspring is produced, but if she doesn't find a mate after 10 rounds she is dismissed and a new 'mom' is chosen.

It should be mentioned that the recombination rate is implicitly 100% in the sense that if a 'mom' and a 'dad' are chosen successfully, then crossover is performed.

This is completely in line with the method followed by Miller & Todd. ([27])

As mentioned above, the sexual selection mechanism used is assortative mating with the individual's SRP (Sexual Reference Position) set to its own genotype. The genotype of an individual has been extended by two genes indicating the PMD (preferred mating distance) and the WOB (width of the base of the POM function) corresponding to the 'pickiness' of the individual. (compare section 3.1) These genes will be referred to as PMD_GENE and WOB_GENE. Each of these genes consisted of 8 bits coding a value within the interval [0,1] and thus having a precision (PRECISION) of $\frac{1}{2^8-1}$.

The distance d between two individuals is computed as the difference between their tour lengths and the maximal difference (MAX_DIFFERENCE) is set to the sum of all the values of the edges of the TSP-graph divided by the number of cities and thus representing a sort of average tour length.

This approach implies the assumption that the length has some sort of unique property in the sense that if two tours have a similar length they will be similar and thus if the difference between their length is high they will be rather different.

The PMD and the WOB are computed by decoding the PMD_GENE and the WOB_GENE as following:

$$PMD = |PMD_GENE| * MAX_DIFFERENCE \quad (2)$$

where $|PMD_GENE| = PRECISION * \sum_{i=1}^8 PMD_GENE[i] * 2^{i-1}$ and $PMD_GENE[i]$ is the i -th element in the PMD_GENE.

$$WOB = |WOB_GENE| * MAX_DIFFERENCE \quad (3)$$

where $|WOB_GENE| = PRECISION * \sum_{i=1}^8 WOB_GENE[i] * 2^{i-1}$ and $WOB_GENE[i]$ is the i -th element in the WOB_GENE.

The POM (Probability of Mating) is now calculated as following:

$$POM(d) = \begin{cases} 0 & \text{if } |PMD - d| > WOB \\ 1 - \frac{|PMD - d|}{WOB} & \text{else} \end{cases} \quad (4)$$

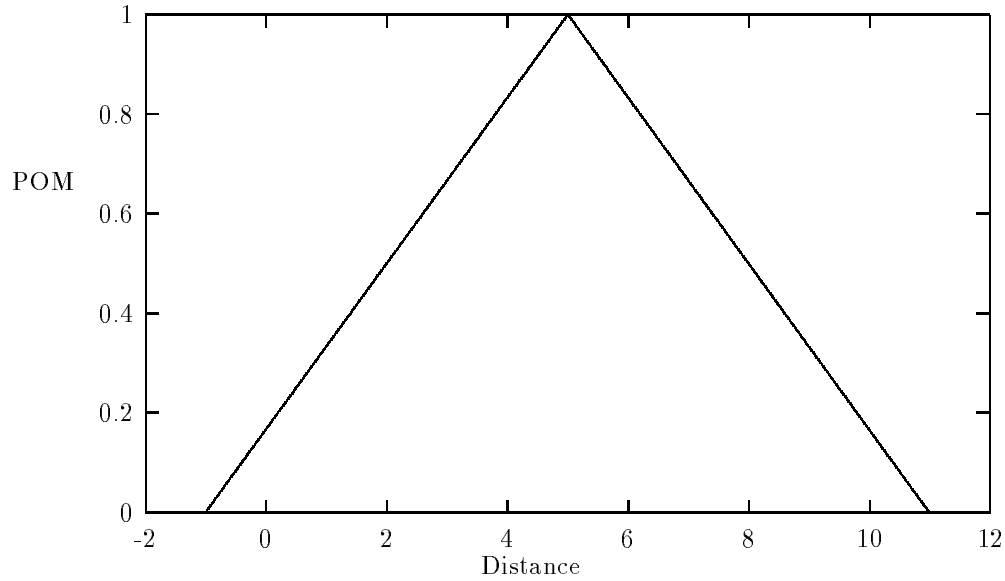


Figure 3: Example of a POM function

Thus, a PMD value of 5 and a WOB value of 6 would define a POM-function as shown in figure 3. Basically, the recombination procedure can be stated as in figure 4.

The sexual preferences are also supposed to evolve together with the rest of the genotype. This seems to be a problem when recombination is concerned. The ER operator has been especially designed to recombine TSP-tours coded by the path representation, so that it can not be intuitively extended to act on the genes coding the sexual preferences of the individual. For this reason, another crossover operator has to be used to act on the binary coded sexual preferences, which in turn could not be used to recombine TSP-tours. This leads inevitably to two recombination mechanisms acting independently on the coding of the tour and the sexual preferences. In the approach outlined here, one-point crossover has been used to recombine sexual preference genes. Of course, it could be thought of a more sophisticated crossover operator, but the aim here is to use a simple approach in order to show what effects assortative mating can have independently from the crossover operator used. This is the reason why a very simple crossover operator has been chosen.

It should be mentioned that this procedure is not in line with the one described by Miller and Todd ([27]), who basically concentrate on binary genotypes and make use of two-point crossover acting on the whole genotype. Thus, by the approach described here side effects not found by Miller and Todd could be encountered.

```

procedure Recombine(Pop)
{
Pop" = new Population;
for i=1 to Population_Size
{
  no_mating = true;
  while (no_mating)
  {
    mating_attempts = 0;
    mom = roulette-wheel-select();
    while (mating_attempts < 10)
    {
      dad = roulette-wheel-select();
      if (random ≤ POM(mom,dad) * POM(dad,mom))
      {
        child = Crossover(mom,dad);
        insert(Pop",child);
        no_mating = false;
      }
      else
      {
        mating_attempts++;
      }
    }
  }
}
return Pop";
}

```

Figure 4: 'mom-samples-dads' recombination algorithm

7.2 Results

50 runs of the GA with assortative mating preferences have been produced. The results have been evaluated in terms of convergence behaviour and speciation grade observed.

In order to get the statistical significance of the results, a undirected (two-tailed) Student's t-test has been performed. ([22], [2], [5], [13], [7]) A Student's t-test basically computes the difference between two means of two data distributions in terms of how many standard errors they are apart. The standard error of a set of values measures the accuracy with which the sample mean estimates the true mean. Typically the standard error is equal to the sample's standard deviation divided by the square root of the number of points in the sample.

The test returns a 'significance' value - called the *P-value* - within the interval [0..1]. The P-value indicates the probability that the difference observed may be due to chance. Thus, the smaller the value, the more significant is the difference between the two distributions.

There are two versions of the Student's test: an equal variance test and a unequal variance test depending on whether the variances of the two distributions are different or not.

7.2.1 Convergence

It can be clearly seen from figure 5 that the GA produces a suboptimal solution in all of the runs. Figure 6 shows that the algorithm is still biased towards smaller number of generations. So, the problem of premature convergence seems not to be overcome.

The table in Appendix B shows the results of all the 50 runs. The best solution has again a length of 1395 and it has been found during run 22. The average length of the solution over all the runs is 1644, which is 372 away from the optimum (1272) and just a bit worse than the average length of 1633 achieved with a traditional GA. (see Appendix A)

When applying a Student's t-test to the length of the best tours found by the traditional GA (Appendix A) and the GA with assortative mating (Appendix B) the following results have been obtained:

Student's t-test comparing best tours (unequal variance)	0.70618
Student's t-test comparing best tours (equal variance)	0.70863

It can be seen that the difference between the results of the traditional GA and the ones of the GA with assortative mating is not significant regardless what the difference of the variance is. Furthermore, they show that the GA with assortative mating doesn't perform much worse than the traditional one.

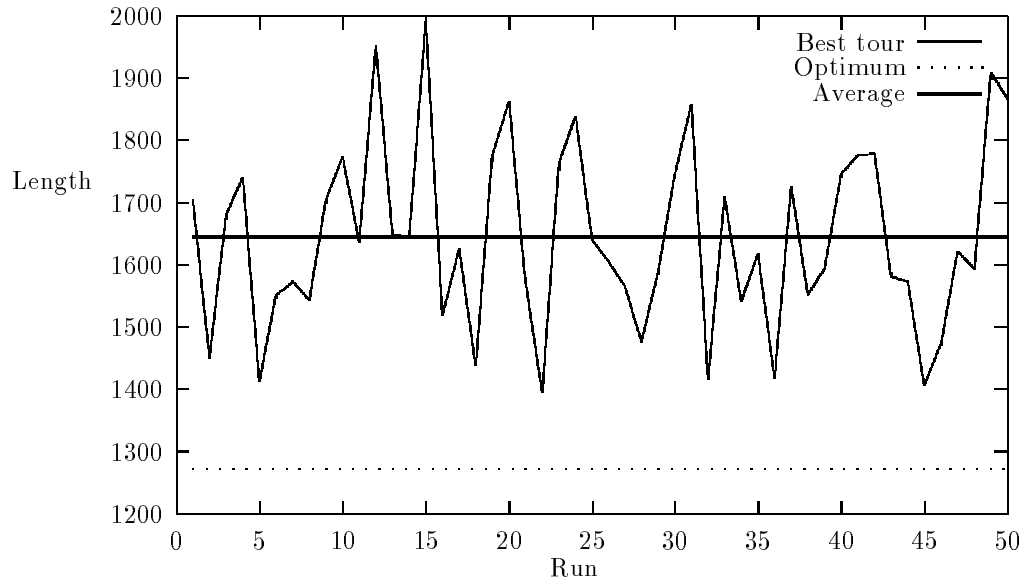


Figure 5: Results of a GA with assortative mating using a distance measure based on length difference: Length of best tour of each run & average of best tours over all the runs

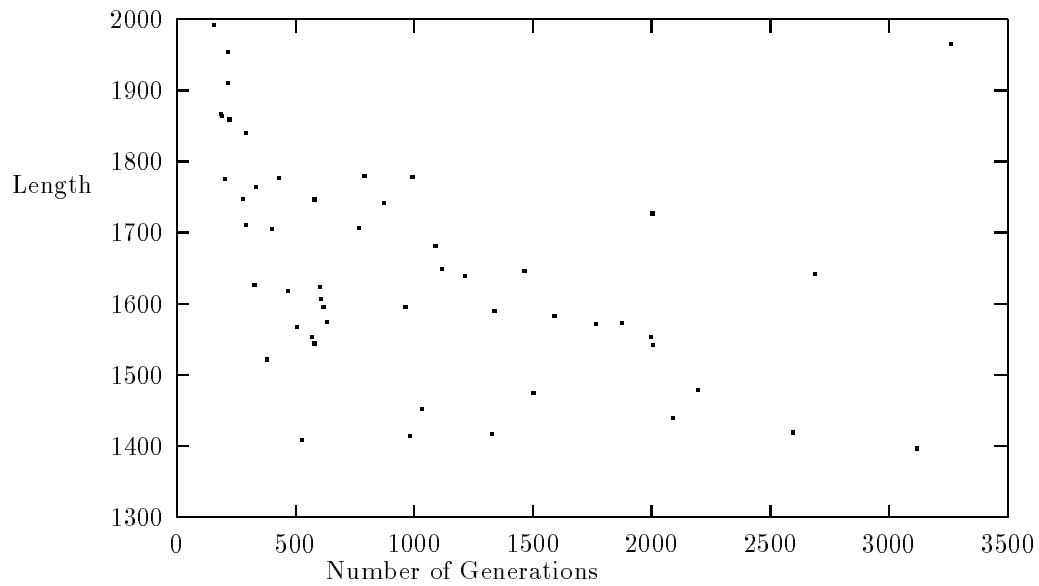


Figure 6: Results of a GA with assortative mating using a distance measure based on length difference: Length of best tours over number of generations

7.2.2 Speciation

In order to find out if assortative mating leads to speciation as suggested by Miller and Todd ([27]), the population has to be plotted in some way. Assuming again that the length of the tour is unique to a certain extent it seems enough to plot each individual together with the length of the tour coded by it in a 2D grid.

Another run has been produced plotting the population as mentioned. This run converged after 3209 generations and produced a best tour of length 1547.

After 50 generations (figure 7) the population is still spread all over phenotypic space, but after 160 generations already two different lineages seem to have formed (figure 8). After 170 generations one single lineage can be observed. (figure 9)

After 180 generations the population is again spread over phenotypic space but after 320 generations again two lineages form. (see figures 10 and 11)

This pattern of appearing and disappearing lineages sometimes decaying to chaos can be observed during the rest of the run (see figures 12 - 20) and corresponds exactly to the one observed by Miller & Todd. ([27]) It could be expected that once speciation has been achieved, it would be maintained, but obviously as search continues lineages will disappear because of extinction caused by natural selection and new lineages will form with periods of absolute chaos between the extinction of lineages and the formation of new ones.

It seems that assortative mating acts like a conservative force preventing individuals to mate with individuals phenotypically different to them and at certain stages leads to the formation of separate lineages with no matings between each other and constituting a certain type of parallel search within phenotypic space. The advantages of such a parallel search could be various. First, it could lead to a faster search as each lineage performs its own search within phenotype space and thus resulting in a greater search efficiency. Second, it also could help to maintain diversity and avoid early convergence in the sense that if one lineage disappears because of natural selection, another one can still 'continue the search' and find even better solutions.

Though the fact that in this special case analyzed, assortative mating doesn't seem to improve the solutions as suggested above, it could be thought that exchanging the distance measure between two individuals could produce different and even better results.

7.3 Conclusions

Assortative mating doesn't appear to improve a GA's ability to escape local optima and by this produce better solutions but on the other hand doesn't perform much worse than the traditional GA.

However, as predicted and shown by Miller and Todd ([27]), assortative mating can in fact lead a population to speciate and create separate and independent lineages performing a parallel search within phenotypic space.

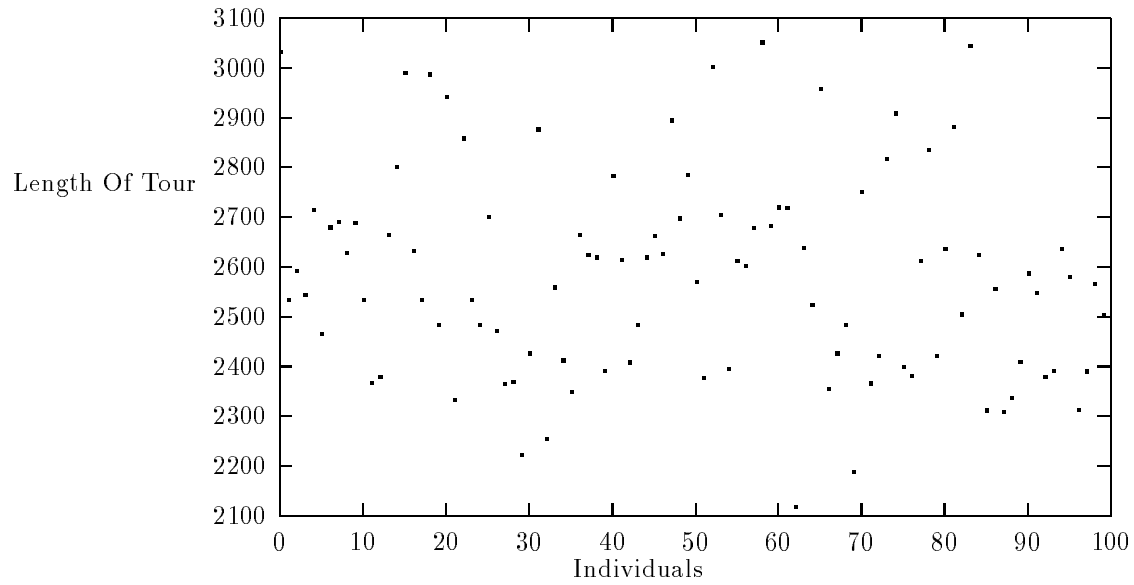


Figure 7: After 50 generations the population is spread all over phenotype space

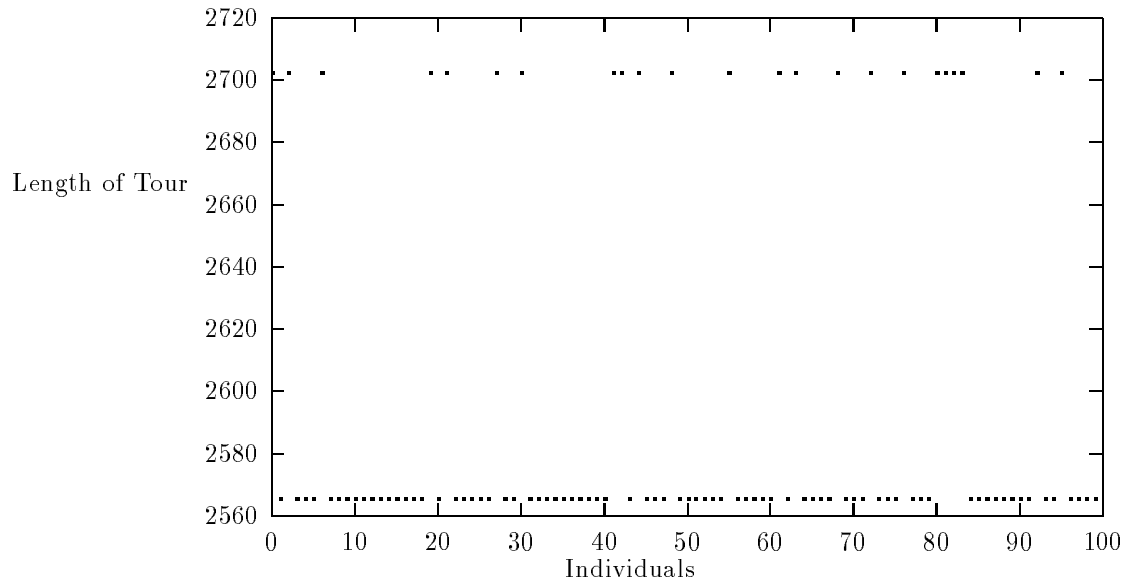


Figure 8: After 160 generations two lineages have formed

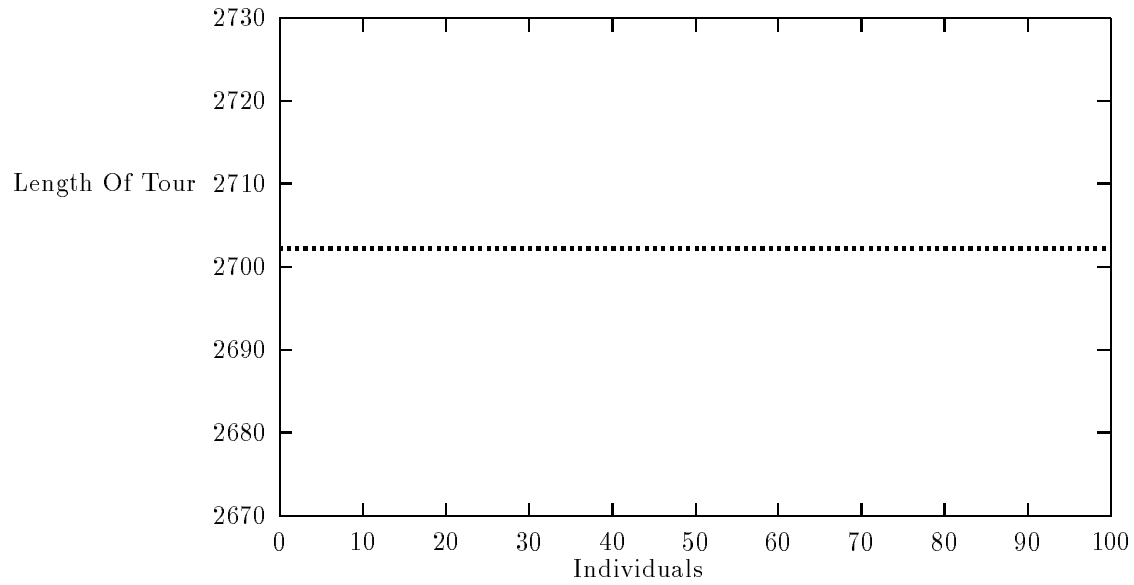


Figure 9: After 170 generations only one main lineage can be observed

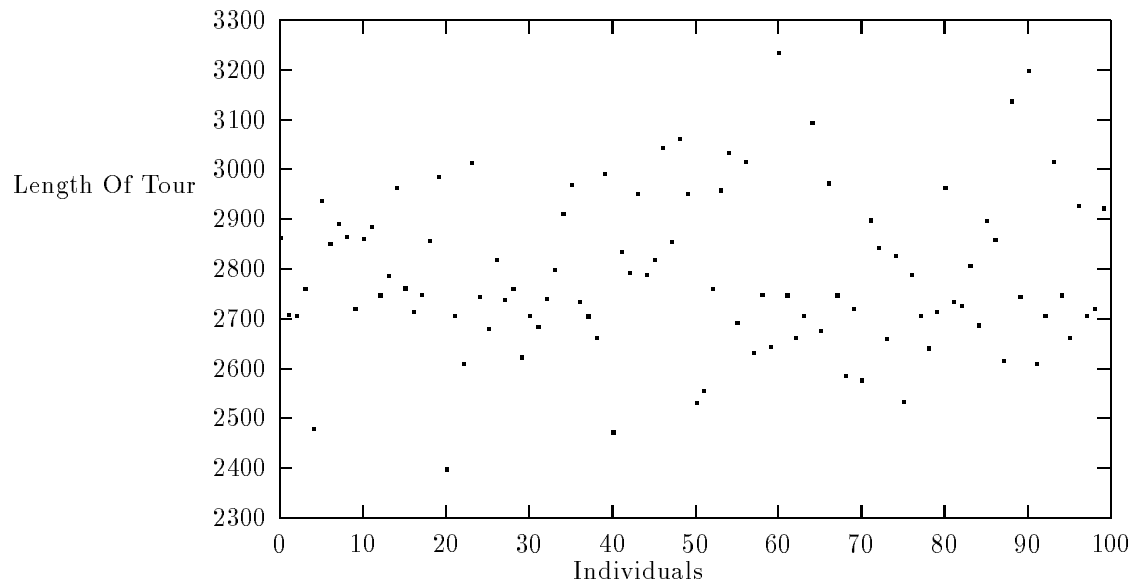


Figure 10: After 180 generations the population spreads again

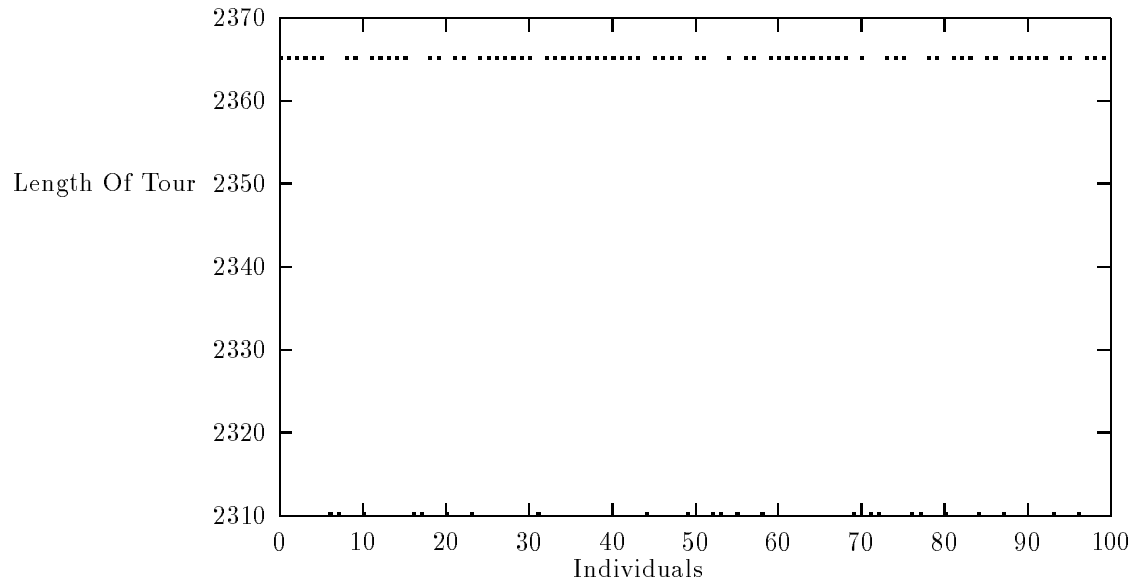


Figure 11: After 320 generations again two lineages can be observed

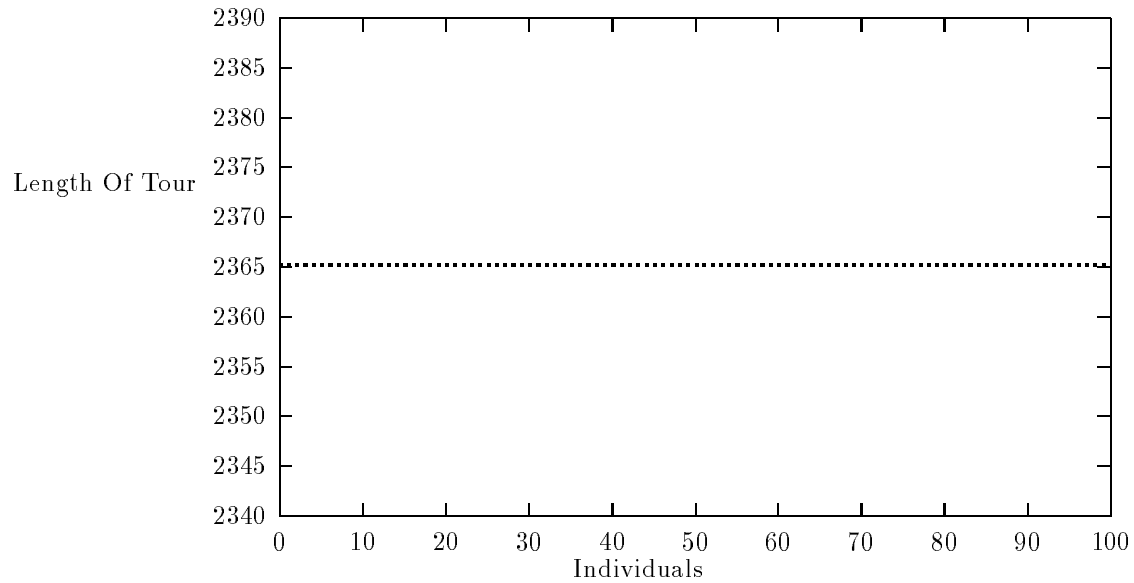


Figure 12: After 330 generations only one main lineage appears

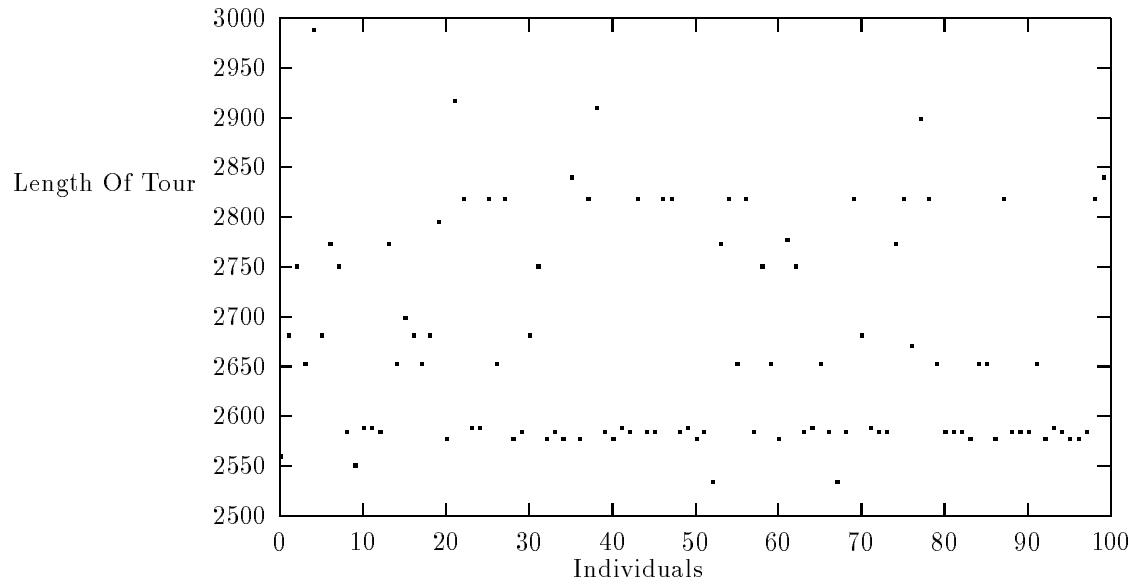


Figure 13: After 390 generations the population is spread again

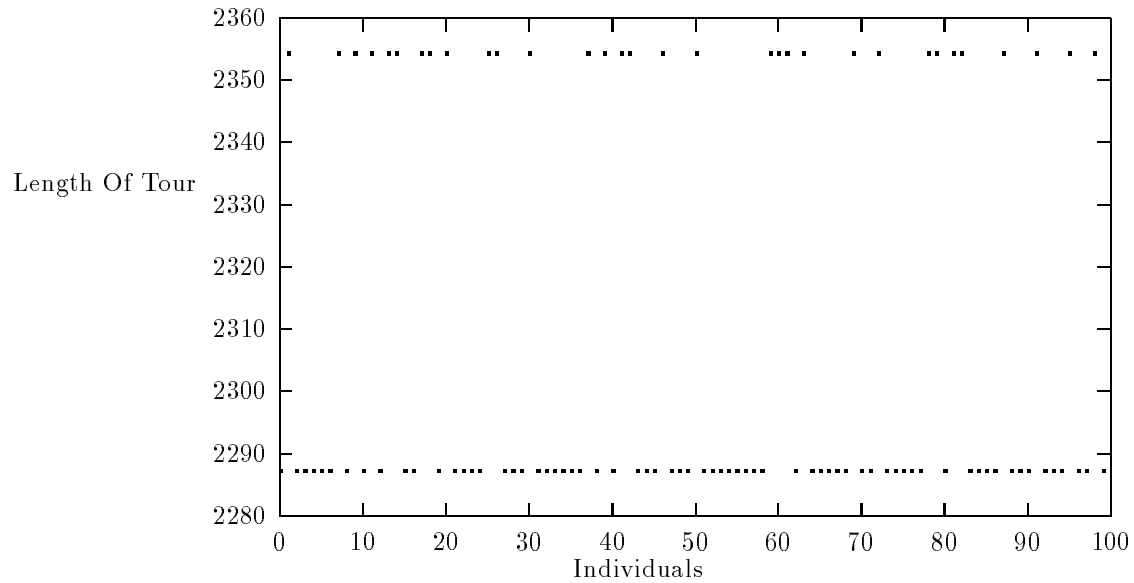


Figure 14: After 460 generations two lineages form again

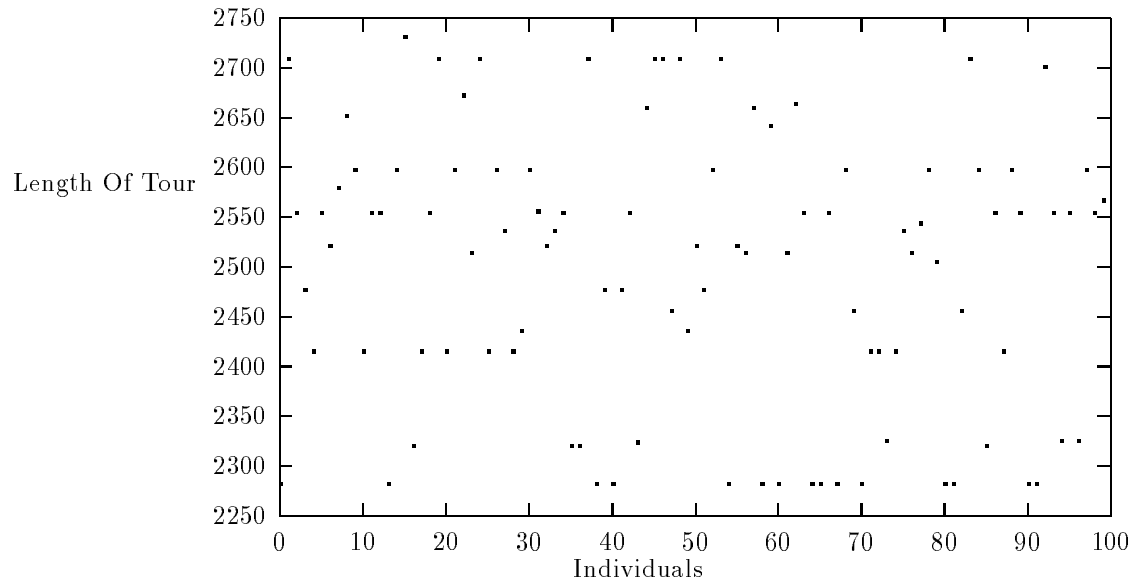


Figure 15: After 510 generations the population is spread

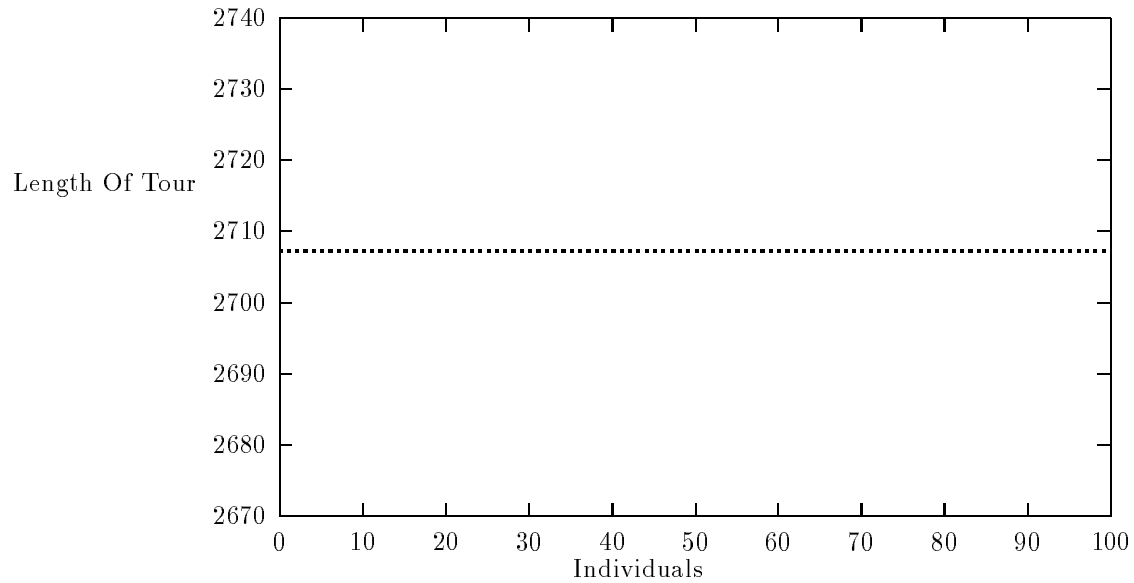


Figure 16: After 520 generations one main lineage can be seen

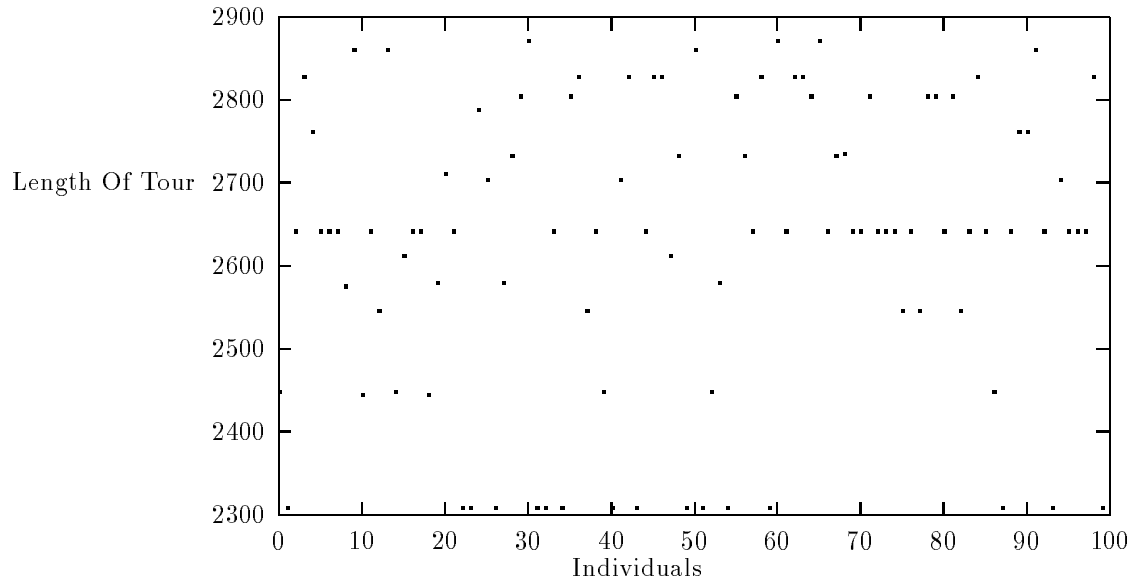


Figure 17: After 680 generations an intermediate stage is reached where the population is spread but also some lineages begin to form

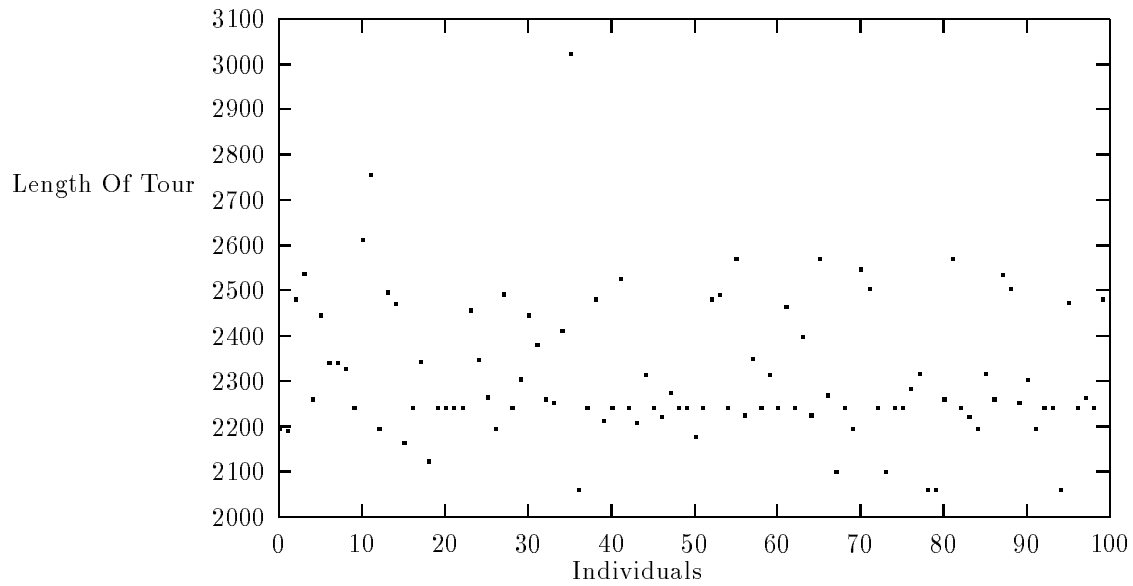


Figure 18: After 720 generations a main lineage can be observed to a certain degree

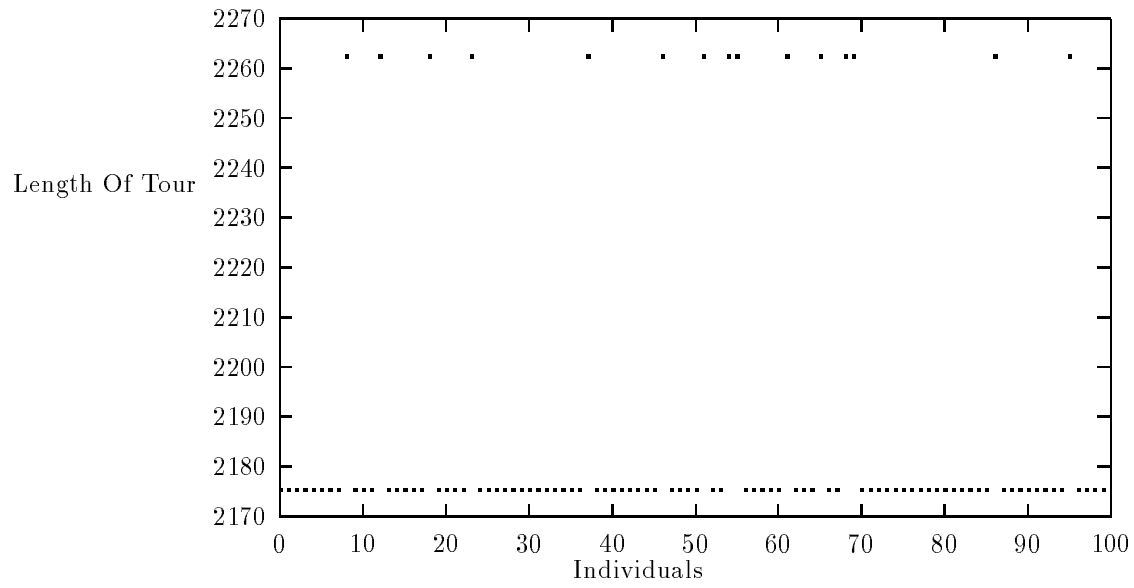


Figure 19: After 800 generations again two lineages have formed

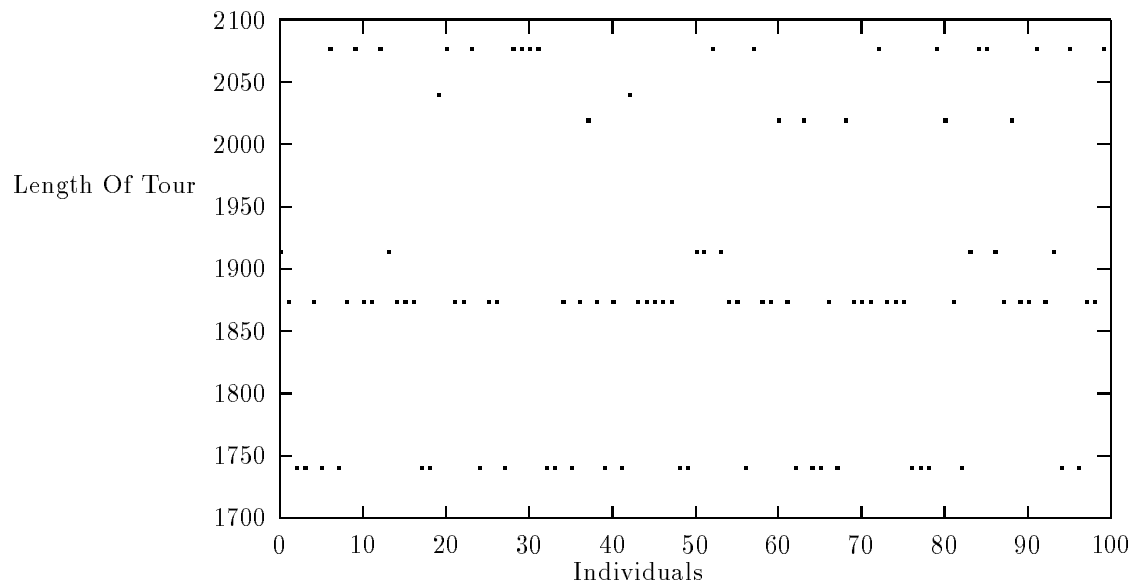


Figure 20: After 1600 generations between three and four different lineages appear

8 A GA with Aesthetic Sexual Selection using Individual-relative Mate Preferences & the 'Grötschels24'

As suggested by Miller ([18]), if aesthetic criteria or heuristics like symmetry, simplicity, streamlining, smoothness and modularity are applied to purely functional optimization problems, greater search efficiency might result in the sense that mate preferences can pick out phenotypic traits that are different from those on which natural selection acts but that are highly correlated with fitness. On the other hand, aesthetic criteria realized in form of mate preferences can select for traits or properties which the specific fitness function can not.

Taking the TSP as an example, we might be interested in finding symmetric tours in the sense that the distance between all cities is expected to be more or less the same. In fact, it should not be difficult to find applications where it could be important to meet such a criterion.

Taking the metaphor of the salesman visiting cities, it could be important for him to travel the same distance every day and end his day-tour at a city. However, the fitness function definitely can not select for symmetry, it can only select for tours with optimal length.

And even if we are not explicitly interested in finding symmetric tours, it could be imagined that the performance of the GA in terms of optimality would increase by promoting symmetry.

Mate preferences offer the possibility of implementing aesthetic criteria as outlined above. If individuals have preferences for symmetric tours, additional selective pressures are introduced that can lead a population in other directions than with natural selection pressures alone.

Thus, if aesthetic preferences for symmetric TSP-tours are implemented in form of mate preferences replacing the assortative mating mechanism described in section 7.1, it could be expected that symmetric TSP-tours are favored and selected to a much higher degree than with a traditional GA such that the quality of the solutions could be increased.

8.1 Implementing Aesthetic Sexual Preferences for Symmetry

The algorithm, operators, fitness scaling, termination criterion and the selection mechanism are the same as in section 6.

Again, the sexual preferences of an individual are coded by two genes: a `PDOS_GENE` (Preferred Degree of Symmetry) and a `WOB_GENE`; the `PRECISION`, `MAX_DIFFERENCE` and the phenotypic values $|PDOS_GENE|$ and $|WOB_GENE|$ are calculated as in section 7.1.

`MAX_DAY_TOUR` is the weight of the edge of the TSP-graph with the highest value.

This time, the SRP of each individual is set to an abstract individual having a certain degree of symmetry.

The PDOS value is now calculated as follows:

$$PDOS = |PDOS_GENE| * MAX_DAY_TOUR \quad (5)$$

and the WOB is again:

$$WOB = |WOB_GENE| * MAX_DIFFERENCE \quad (6)$$

The distance between two individuals is now not anymore their difference in length of the tour, but the average over the differences between the length of each 'day-tour' and the PDOS.

More formally, given an individual I_1 with a $PDOS_{I_1}$ and an individual I_2 coding a tour: c_1, \dots, c_n , the directed distance $\delta(I_1, I_2)$ between I_1 and I_2 is:

$$\delta(I_1, I_2) = \frac{\sum_{i=1}^{n-1} |w(c_i, c_{i+1}) - PDOS_{I_1}| + |w(c_1, c_n) - PDOS_{I_1}|}{n} \quad (7)$$

This distance is directed in the sense that it is not symmetric ($\delta(I_1, I_2) \neq \delta(I_2, I_1)$). The reason for this is that the distance $\delta(I_1, I_2)$ depends on I_2 's genotype and I_1 's PDOS while the distance $\delta(I_2, I_1)$ depends on I_1 's genotype and I_2 's PDOS.

In this way, we yield a measure of how much every day-tour length differs from the PDOS on average over the whole tour. Thus, the smaller the difference, the higher is the degree of symmetry of the individual and viceversa.

The POM is now calculated as follows:

$$POM(\delta(I_1, I_2)) = \begin{cases} 0 & \text{if } \delta(I_1, I_2) > WOB_{I_1} \\ 1 - \frac{\delta(I_1, I_2)}{WOB_{I_1}} & \text{else} \end{cases} \quad (8)$$

So, there is no PMD in this case and the POM-function is centered around distance 0.

Consider the following 6 city TSP given by the following weight matrix:

	1	2	3	4	5	6
1	5	7	4	2	6	10
2	7	3	2	8	9	1
3	4	2	5	6	2	8
4	2	8	6	4	3	9
5	6	9	2	3	5	1
6	10	1	8	9	1	6

Now consider the following two individuals I_1 and I_2 :

Individual	Tour	PDOS_GENE	WOB_GENE
I_1	1 2 3 4 5 6	0 1 0 1 0 1 0 1	1 0 1 0 1 0 1 0
I_2	2 3 5 6 4 1	1 0 1 0 1 0 1 0	0 1 0 1 0 1 0 1

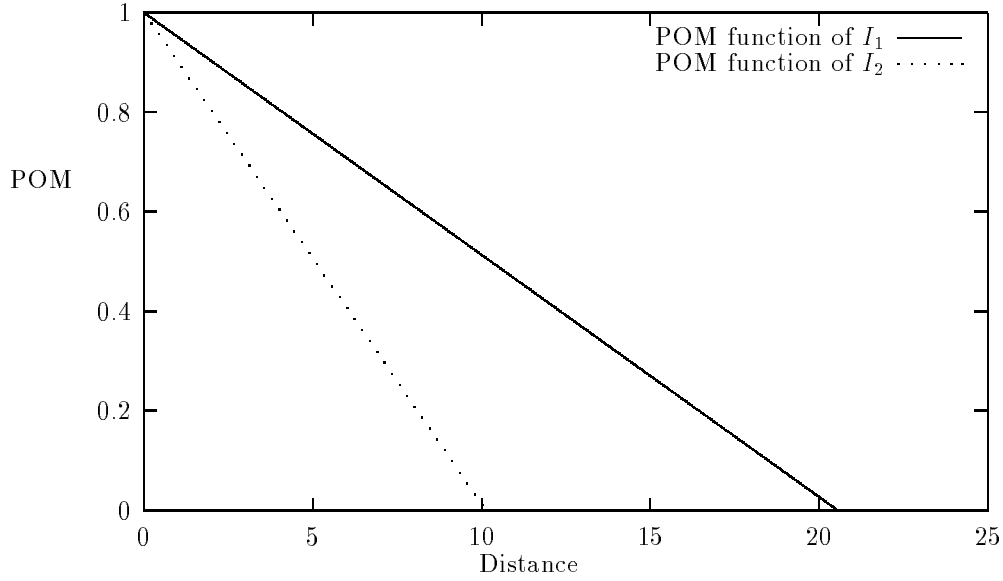


Figure 21: Using aesthetic sexual preferences for symmetry: POM function of individuals I_1 and I_2

Now we can compute the values $|PDOS|$ and $|WOB|$ for each individual:

<i>Individual</i>	$ PDOS $	$ WOB $
I_1	0.33	0.67
I_2	0.67	0.33

Having that $MAX_DAY_TOUR = 10$ and $MAX_DIFFERENCE = 30.67$ we get the following PDOS and WOB values:

<i>Individual</i>	$PDOS$	WOB
I_1	3.3	20.55
I_2	6.7	10.12

Now the distances between the two individuals can be computed:

$$\delta(I_1, I_2) = \frac{|2-3.3|+|2-3.3|+|1-3.3|+|9-3.3|+|2-3.3|+|7-3.3|}{6} = 2.6$$

$$\delta(I_2, I_1) = \frac{|7-6.7|+|2-6.7|+|6-6.7|+|3-6.7|+|1-6.7|+|10-6.7|}{6} = 3.07$$

After that we can calculate the POM that I_1 chooses I_2 as mate and vice-versa. Figure 21 shows the POM functions of each individual.

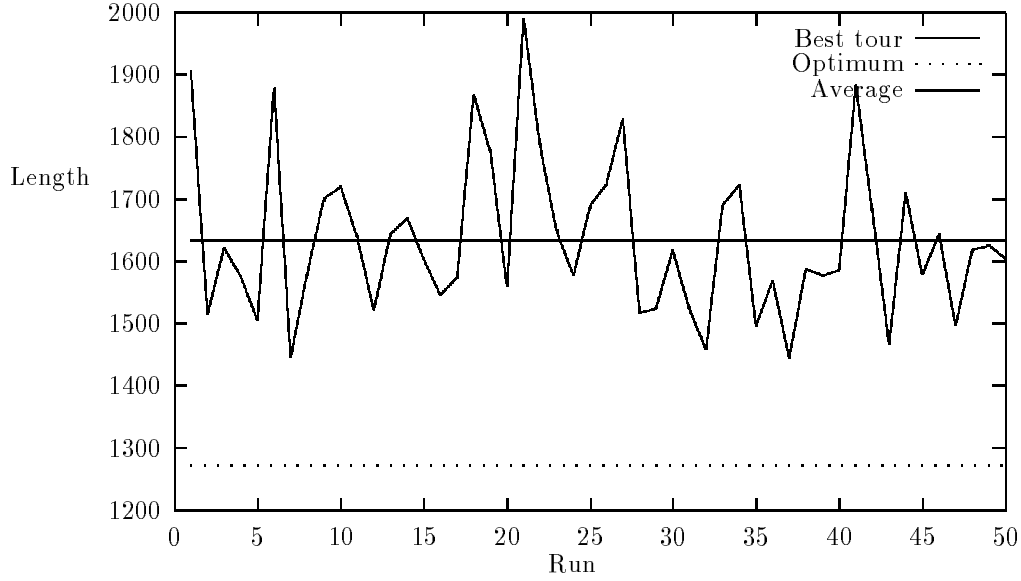


Figure 22: Results of the GA with aesthetic sexual selection using individual-relative mate preferences for symmetry: Length of best tour of each run & average of best tours over all the runs

$$POM(\delta(I_1, I_2)) = 1 - \frac{\delta(I_1, I_2)}{WOBR_1} = POM(2.6) = 1 - \frac{2.6}{20.55} = 0.87$$

$$POM(\delta(I_2, I_1)) = 1 - \frac{\delta(I_2, I_1)}{WOBR_2} = POM(3.73) = 1 - \frac{3.07}{10.12} = 0.69$$

Finally we yield the probability that both individuals mate:

$$POM = POM(\delta(I_1, I_2)) * POM(\delta(I_2, I_1)) = 0.87 * 0.69 = 0.6$$

8.2 Results

It has been expected that using a GA combining aesthetic sexual preferences for symmetric TSP tours with natural selection mechanisms would establish a certain kind of equilibrium between optimality and symmetry producing almost optimal tours with a high degree of symmetry.

In order to compare the performance of a traditional GA and a GA with aesthetic mating preferences, 50 runs of the GA with aesthetic sexual selection have been produced. A measure for the symmetry of a tour has also been introduced. The DOS (Degree of Symmetry) of a tour $t = c_1, \dots, c_n$ has been defined

as following:

$$DOS(t) = \frac{\sum_{i=1}^{n-1} w(c_i, c_{i+1} * (-1)^i) + w(c_1, c_n)}{n} \quad (9)$$

Figure 22 shows the best tours found in each of the 50 runs. The table in Appendix C summarizes the results of these runs. The best tour found has a length of 1445 and the average length of the best tours found is 1634, which is almost the same as the one achieved with the traditional GA. (see Appendix A) A Student's t-test has been used to compare both means:

Student's t-test comparing best tours (unequal variance)	0.958195
Student's t-test comparing best tours (equal variance)	0.959427

The results of the test clearly show that the difference between the results of the traditional GA and the one with aesthetic sexual preferences for symmetry is very small and thus that their performance in producing optimal tours is almost the same.

The average DOS of the best individuals produced by each run is 5.545833 and it seems to be very close to the average DOS of the traditional GA, which is 5.6147438. (see Appendix A) When using a Student's t-test to compare the DOS of the best tours of both GAs we get the following results:

Student's t-test comparing DOS (unequal variance)	0.926339
Student's t-test comparing DOS (equal variance)	0.928259

So, the difference between the DOS of the best tours seems to be also very small, so that it can be concluded that both GAs perform in a similar way what the symmetry of the best individuals produced is.

When comparing the average number of generations of both GAs, it can be seen that the average number of generations when using a GA with aesthetic sexual preferences for symmetry is slightly higher (1044) than the one of a traditional GA (896).

A Student's t-test comparing both averages yielded the following results:

Student's t-test comparing generations (unequal variance)	0.29722
Student's t-test comparing generations (equal variance)	0.29753

Thus, the difference in the number of generations seems to be significant so that it can be concluded that the GA with aesthetic sexual preferences for symmetry takes a higher number of generations than a traditional GA in producing the same results.

Besides, as it can be seen in figure 23, the algorithm is still biased towards smaller number of generations.

8.3 Conclusions

We have to be careful when evaluating these results. We can not conclude from them that aesthetic sexual selection mechanisms don't work in the sense that

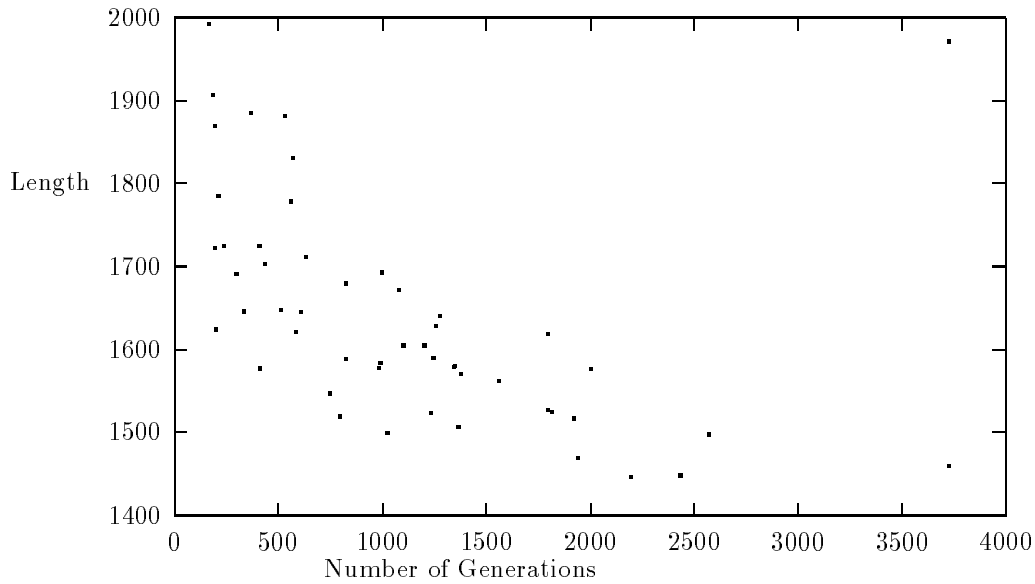


Figure 23: Results of the GA with aesthetic sexual selection using individual-relative preferences for symmetry: Length of best tours over number of generations

they fail in producing symmetric tours because of several reasons.

First, we only measured the degree of symmetry of the 'fittest' individuals. Other ways of measuring the symmetry would be taking into account the population average or even only the most symmetric individual of all the runs and compare the results produced to the ones produced by a traditional GA.

Second, each individual's PDOS is set to a certain factor within the interval $[0..1]$ multiplied with the maximum day-tour and thus getting a value within $[0..MAX_DAY_TOUR]$ such that the PDOS can be so high that no tour can fulfill it. Or let's see it the other way round, if the PDOS is very high and a tour fulfills it, then this tour will certainly have a high length and thus have a very low fitness and represent a very bad solution to the optimization problem. Thus, in the way aesthetic sexual preferences for symmetry have been implemented, symmetry and optimality could be excluding each other, which could explain why the aesthetic selection mechanism as implemented here fails in producing symmetric as well as optimal tours.

So, after these first experiments and results, it seems intuitive to define the distance to another individual using directly the DOS-measure and introducing a PMD so that each individual can 'decide' to which degree it prefers symmetry. Furthermore, even an absolute (in the sense of individual-independent) DOS criterion could be used by mapping the DOS-value of the individual to mate with into an interval between $[0..1]$ and using it directly as POM.

It also seems necessary to develop other criteria to evaluate the performance of the GA with aesthetic preferences for symmetry in terms of producing symmetric results as mentioned above.

9 A GA with Directional Mate Preferences using a Distance Measure based on Length Difference & the 'Grötschels24'

The idea behind directional mate preferences is that an individual's POM function center is set off in some direction and distance within phenotype space from the SRP. (see section 3.2)

However, when applying directional mate preferences to the TSP we encounter a fundamental problem. For the TSP, the search space is N^n (where $N = \{1, \dots, n\}$), while the number of valid tours is $n!$. Thus, if the center of the POM function is just set off from the individual's SRP in some direction (given by a vector $\vec{v} \in N^n$) and a distance within phenotype space, we might yield a non-valid tour as center of the POM function.

For this reason, in the method described here an individual's SRP is directly set to a valid tour.

9.1 Implementing Directional Mate Preferences

In the approach followed, an individual consists of 4 genes: a TOUR_GENE coding the tour, a SRP_GENE coding the tour to which the individual's SRP is set, a PMD_GENE coding the distance from which the center of the POM function is set off from the SRP and a WOB_GENE coding the width of the base of the POM function.

Again, the algorithm, operators, fitness scaling, termination criterion and the selection mechanism have been chosen as in section 6. Also the PRECISION and MAX_DIFFERENCE values are calculated as previously defined in section 7.1. and the PMD and WOB values have been computed as in formulas 2 and 3.

Basically, each individual has a specific ideal mate coded by his SRP_GENE, which is nothing else than the path representation of a valid TSP-tour.

The distance measure used is the one used with the assortative mating preferences, which means that the distance is calculated based on the difference between the length of the tours.

However, in this case the distance between two individuals is directed because of the length difference is calculated between the tour coded by the individual to mate with and the tour coded by the own SRP.

Thus, the distance measure used is the following:

$$\delta(I_1, I_2) = |\text{length}(SRP_GENE_{I_1}) - \text{length}(TOUR_GENE_{I_2})| \quad (10)$$

And the POM is defined as following:

$$POM(\delta(I_1, I_2)) = \begin{cases} 0 & \text{if } |PMD_{I_1} - \delta(I_1, I_2)| > WOB_{I_1} \\ 1 - \frac{|PMD_{I_1} - \delta(I_1, I_2)|}{WOB_{I_1}} & \text{else} \end{cases} \quad (11)$$

As the individuals' sexual preferences are supposed to evolve, the ER operator is also applied to this SRP_GENE. Thus we have now three crossover operators acting separately on the TOUR_GENE, on the SRP_GENE and on the PMD and WOB genes together.

Consider again the 6 city TSP of section 8.1 and the following two individuals:

Individual	TOUR_GENE	SRP_GENE	PMD_GENE	WOB_GENE
I_1	1 2 3 4 5 6	1 3 5 2 4 6	0 1 0 1 0 1 0 1	1 0 1 0 1 0 1 0
I_2	2 3 5 6 4 1	1 2 3 4 5 6	1 0 1 0 1 0 1 0	0 1 0 1 0 1 0 1

The tour coded by the TOUR_GENE of individual I_1 has a length of 29 and the one coded by its SRP_GENE has a length of 23. The TOUR_GENE of individual I_2 codes a tour with a length of 42 and the SRP_GENE codes a tour with a length of 29.

The values $|PMD_GENE|$ and $|WOB_GENE|$ now can be computed:

Individual	$ PMD $	$ WOB $
I_1	0.33	0.67
I_2	0.67	0.33

Having that MAX_DIFFERENCE = 30.67 we get the following PMD and WOB values:

Individual	PMD	WOB
I_1	10.12	20.55
I_2	20.55	10.12

The distances between the two individuals now are:

$$\delta(I_1, I_2) = |length(SRP_GENE_{I_1}) - length(TOUR_GENE_{I_2})| = |23 - 42| = 19$$

$$\delta(I_2, I_1) = |length(SRP_GENE_{I_2}) - length(TOUR_GENE_{I_1})| = |29 - 29| = 0$$

Figure 24 shows the POM functions of individuals I_1 and I_2 .

Now we can calculate the POM that I_1 chooses I_2 as mate and viceversa:

$$POM(\delta(I_1, I_2)) = 1 - \frac{|10.12 - 19|}{20.55} = 0.57$$

$$POM(\delta(I_2, I_1)) = 0, \text{ because } |20.55 - 0| > 10.12$$

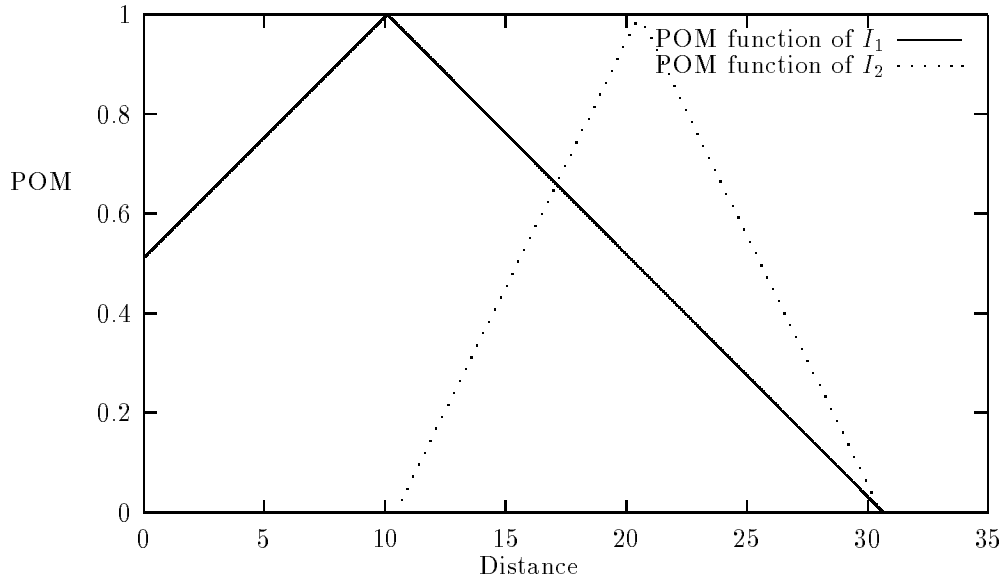


Figure 24: Using directional mate preferences: POM functions of individuals I_1 and I_2

So, the POM that the two individuals mate together is:

$$POM = POM(\delta(I_1, I_2)) * POM(\delta(I_2, I_1)) = 0.57 * 0 = 0$$

9.2 Results

When comparing figure 25 with figure 1 both showing the best tours found in each of the runs, it seems at a first glance that the GA with directional mate preferences performs much better than the traditional GA in terms of finding optimal solutions. The table in Appendix D shows the results of 50 runs of a GA with directional mate preferences implemented as described above.

The best tour produced has a length of 1286, which is only 14 away of the optimal tour, and has been found in run 46 having 888 generations. The average length of the best tours of each run is 1433, which is much better than the average achieved by the traditional GA. (see Appendix A) In order to get a statistical significance for this difference, a Student's t-test has been again used yielding the following results:

Student's t-test comparing best tours (unequal variance)	$3.31 * 10^{-14}$
Student's t-test comparing best tours (equal variance)	$5.69 * 10^{-13}$

These results are very impressive and clearly show that in fact the GA with

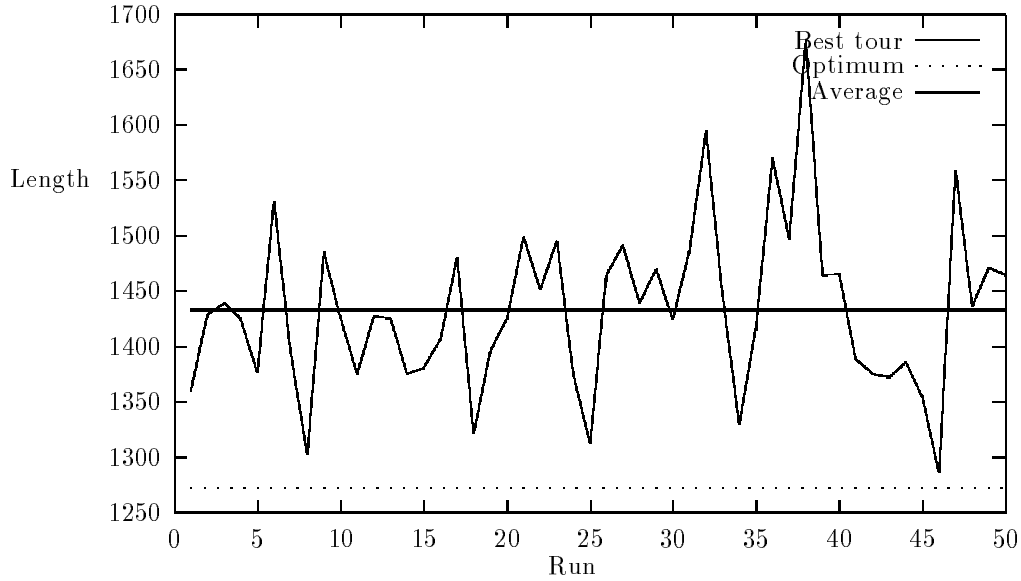


Figure 25: Results of the GA with directional mate preferences using a distance measure based on length difference: Length of best tour of each run & average of best tours over all the runs

directional mate preferences performs much better than a traditional GA in producing optimal tours.

When comparing the number of generations of each GA and using a Student’s t-test in order to get a statistically correct interpretation of the results, we obtain the following:

Student’s t-test comparing number of generations (unequal variance)	0.15877
Student’s t-test comparing number of generations (equal variance)	0.18744

Thus, it can be seen that there is quite a significant difference between the average number of generations, which is 738 for the GA with directional mate preferences and 896 for the traditional GA. Figure 26 shows that the algorithm is not anymore so biased towards smaller number of generations in the sense that the variance in the number of generations is lower than with a traditional GA.

9.3 Conclusions

The results above clearly show that the GA with directional mate preferences performs better than the traditional GA producing much better results with a smaller average number of runs, which is a very impressive result.

The fact that much better solutions are achieved shows that directional mate

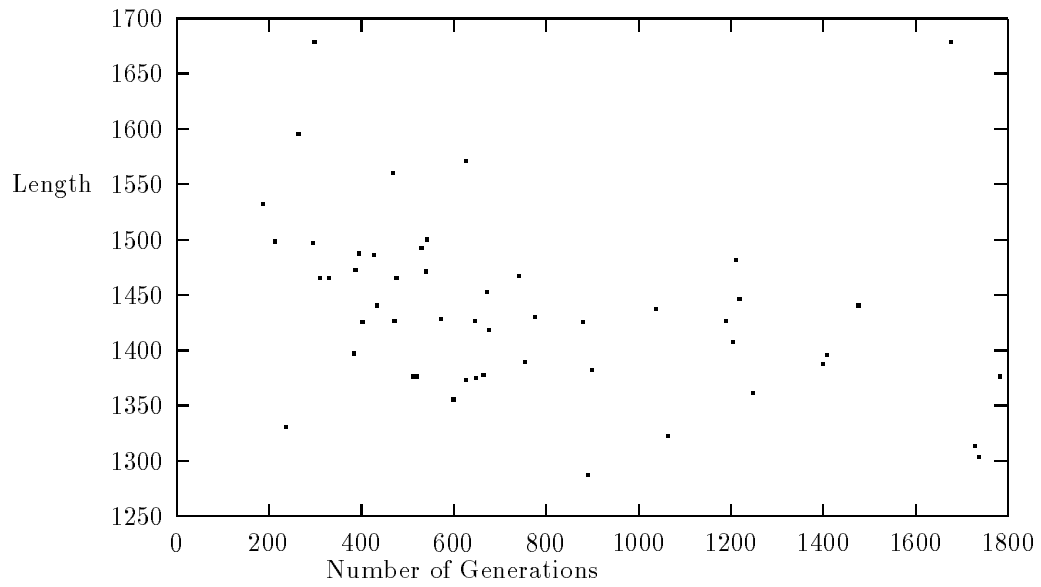


Figure 26: Results of the GA with directional mate preferences using a distance measure based on length difference: Length of best tours over number of generations

preferences can in fact help a GA to escape local optima making it still converge to a suboptimal solution but on average much better than the ones achieved with a traditional GA.

On the other hand, the fact that the number of generations is quite significantly lower shows that directional mate preferences also seem to reinforce natural selection resulting in a much more efficient and directed search. Thinking further, it seems that directional mate preferences somehow have internalized natural selection pressures and steadily lead a population towards high fitness peaks within the fitness landscape. Thus, directional mate preferences could indeed be acting as an automatic fitness scaling by favoring good individuals while penalizing bad ones as suggested by Miller and Todd. ([20], [29])

10 The Traditional GA & the 'Grötschels24' II

For many applications it is important to know how much time the GA takes in order to converge and produce a solution. For this purpose, 50 more runs of the traditional GA as defined in section 6 have been produced recording also the time each run takes.

It has been also recorded in which generation the best tour has been found and also the average DOS of the population over all generations has been calculated for each run. (see Appendix F)

10.1 Results

The results of these 50 runs are similar to the ones achieved before. (compare Appendices A and F) The best tour found has a length of 1319 and has been found in run 32 after 1461 out of 1629 total generations.

The average length of the best tours found is 1630, the average number of generations is 1046 and the average time consumed by each run is 1181.7 seconds on a SUN Ultra-4 Sparcstation. The Average-Best-Tour-Length-Diagram in figure 27 shows the length of the best tour of each generation on average over all the runs. It should be mentioned that because of the fact that each run has a different number of generations, the number of runs averaged gets less with increasing number of generations such that the diagram ends up representing one single run.

It can be clearly seen that the algorithm converges prematurely to a suboptimal solution.

Figure 28 shows the best tours found in each run as well as the average length of the best tours of all the runs and the optimum.

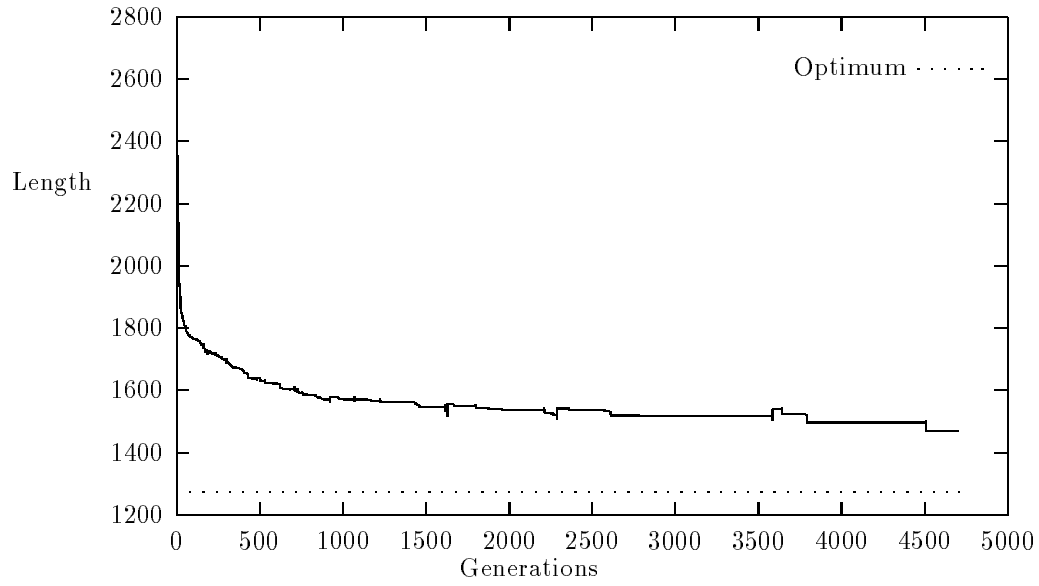


Figure 27: Results of a traditional GA II: Average-Best-Tour-Length-Diagram & Optimum

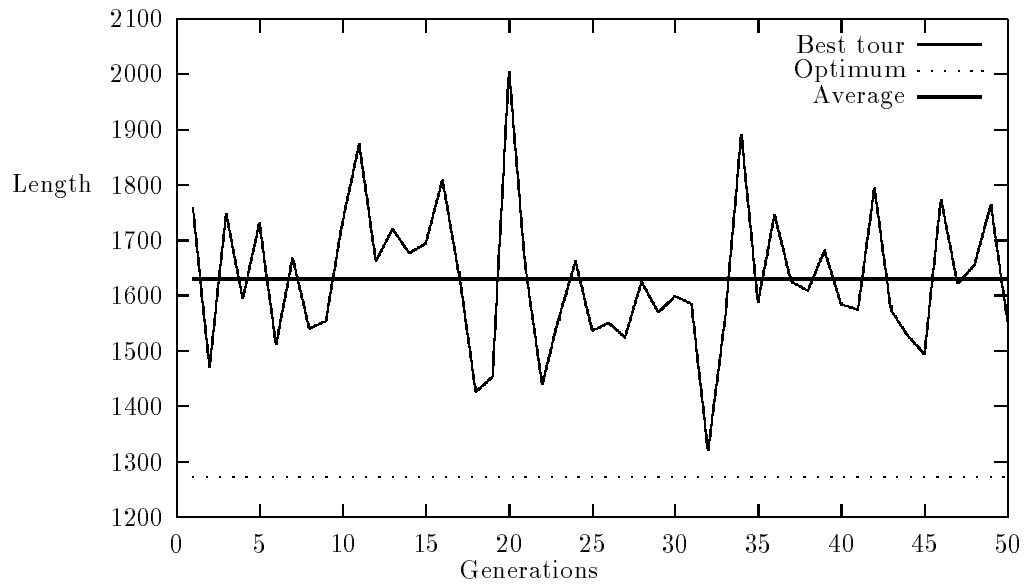


Figure 28: Results of a traditional GA II: Length of best tour of each run & average of best tours over all the runs

11 A GA with Assortative Mating using a Distance Measure based on Common Edges & the 'Grötschels24'

In the first experiment using assortative mating as sexual selection mechanism, the distance between two individuals has been calculated based on the difference between the length of the tours coded by them. This approach assumes that the length of the tour is unique in the sense that a certain length corresponds more or less uniquely to a certain tour, which must not be the case. It also assumes that if tours have similar lengths they are also similar themselves which must not be the case either. So, it seems necessary to develop a different measure for the distance between two individuals not making use of this assumption.

A rather intuitive and straightforward way of defining similarity would be in terms of common edges between the tours. So, the more common edges two tours have, the more similar they are and the less is the distance between them. By this, we yield an undirected distance measure between two individuals based only on their genotype.

11.1 Implementing the New Distance Measure

A TSP-tour can be represented as a set of edges between n cities in the following way:

$$t = \{(c_1, c_2), (c_2, c_3), \dots, (c_{n-1}, c_n), (c_n, c_1)\} \quad (12)$$

Now the undirected distance $\delta(I_1, I_2)$ between two individuals I_1 and I_2 coding tours t_{I_1} and t_{I_2} is defined as follows:

$$\delta(I_1, I_2) = n - \sum_{e \in t_{I_1}} \begin{cases} 1 & \text{if } e \in t_{I_2} \\ 0 & \text{else} \end{cases} \quad (13)$$

Basically only the distance measure has been changed having now a MAX_DIFFERENCE of n as the maximal number of different edges between two tours of n cities is also n .

The rest of the algorithm is as defined in section 7.1 with the only exception that the 'mom-samples-dads' schema has been slightly modified in the sense that only the mom decides whether a mating takes place or not. So, the POM that the mom and the dad mate is only determined by the POM that the mom wants to mate with the dad. The reason for this is that by multiplying both POMs very low probabilities have been yielded and thus the average number of mating attempts and the time the GA runs are very high as suggested by Miller and Todd. ([19])

11.2 Results

The table in Appendix G shows the results of the 40 runs of the GA with assortative mating using the distance measure based on common edges as defined in (13). It contains the following information:

- Simulation: number of the run
- Generations: number of generations
- Best: length of the best tour found
- Fitness: fitness of the best tour found
- Found: generation at which the best tour was found
- Average Matings: number of average mating attempts
- Time: computational time in seconds

The best tour found has a length of 1397 and has been produced in run 11 after 1999 out of 2535 generations.

The average length of the best tours found in each run is 1639 with an average number of 1205 generations. Each run takes on average 7479 seconds on a SUN Ultra-4 Sparcstation, which is more or less two hours. At a first glance, when having a look at figure 29, it seems that the performance of both GAs is rather similar.

In order to verify these results statistically, a Student's t-test has been used to compare the length of the best tours produced in each run with the following results:

Student's t-test comparing best tours (unequal variance)	0.74478673
Student's t-test comparing best tours (equal variance)	0.748667801

So, in fact there is not much difference between the quality of the solutions produced.

When comparing the time each run of the GA takes on average over all the runs with a Student's t-test, we get the following results:

Student's t-test comparing average time (unequal variance)	$5.96306 * 10^{-8}$
Student's t-test comparing average time results (equal variance)	$3.97605 * 10^{-6}$

It becomes clear that the GA with assortative mating preferences takes much longer than the traditional GA. Having a look at the time averages in Appendix G, it can be stated that the traditional GA is almost seven times faster than its counterpart with assortative mating preferences, which is a very striking difference.

Figure 31 shows that the algorithm appears still to be biased towards smaller number of generations in the sense that the variance in the number of generations is very high but only a few tours reach a number of generations higher

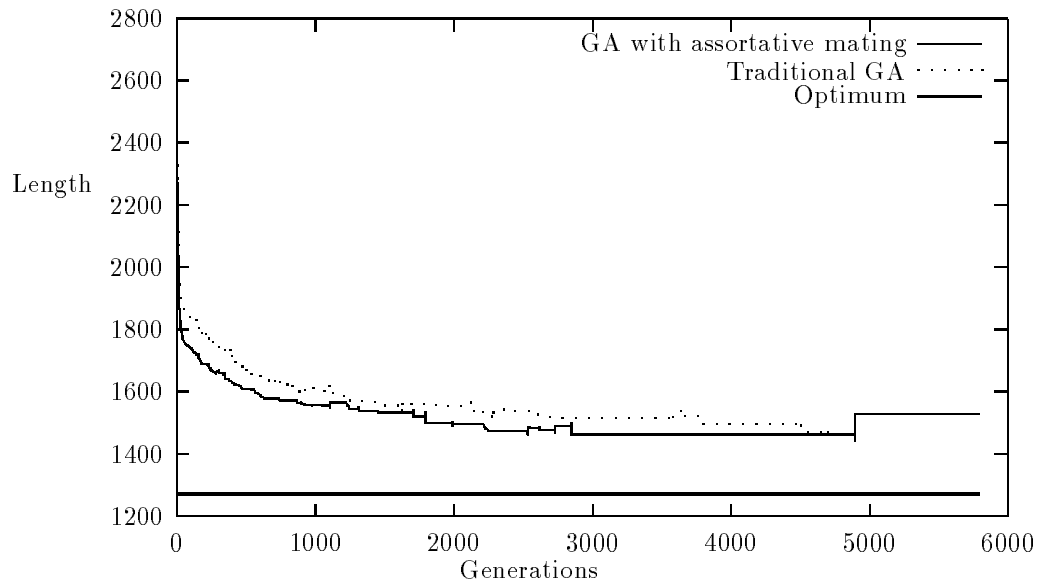


Figure 29: Results of a GA with assortative mating using a distance measure based on common edges: Average-Best-Tour-Length-Diagram comparing the GA with assortative mating and the traditional GA & Optimum

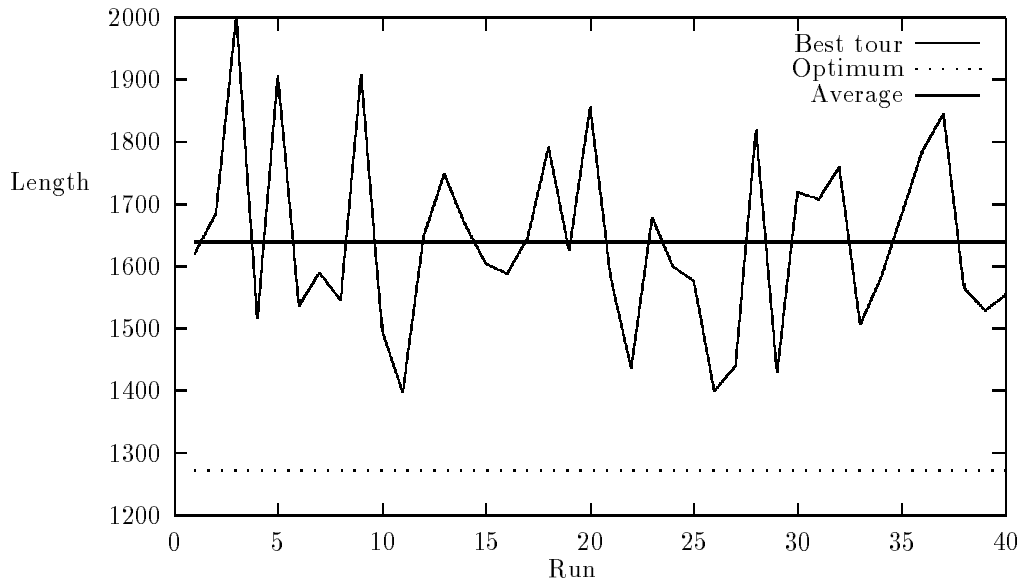


Figure 30: Results of a GA with assortative mating using a distance measure based on common edges: Length of best tour of each run & average of best tours over all the runs

than the average.

The average number of mating attempts, which is basically the number of times a 'dad' is sampled or evaluated by a 'mom' before a mating takes place or not is 6.33557.

It seems straightforward that if we multiply the total number generations of a run with the average number of mating attempts for this run, this number, which we will be called the *samplings*, will be proportional to the time (in seconds) the run took.

In fact, it can be seen from figure 32 that the factor of the proportion is very close to 1.

Figure 33 shows that the total number of generations is also proportional to the time but that this proportion is quite away from a factor of 1.

Figure 34 shows the length of the best tours produced by each run over the number of samplings. It clearly can be seen that the quality of the solutions is not linearly proportional to the number of samplings, but that the quality seems to increase with increasing number of generations. However, for high number of generations the quality seems to decrease again.

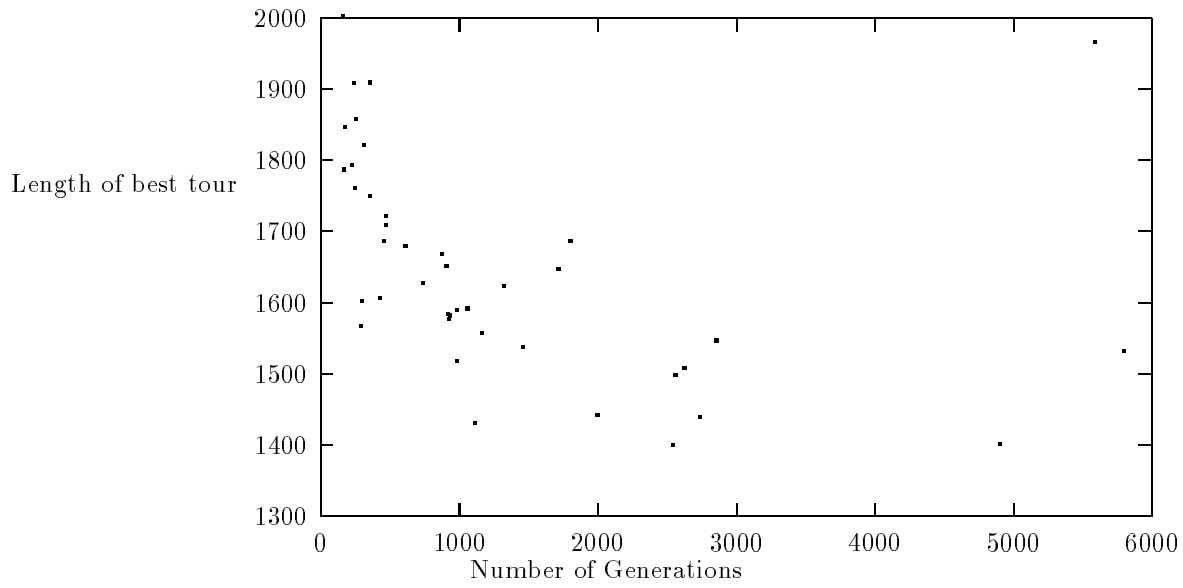


Figure 31: Results of a GA with assortative mating using a distance measure based on common edges: Length of best tours over number of generations

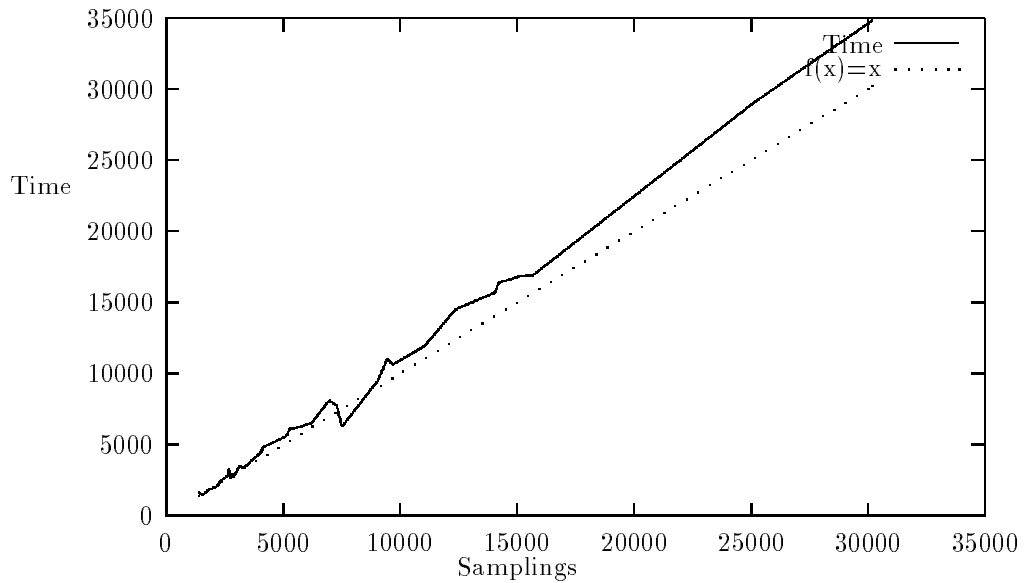


Figure 32: Results of a GA with assortative mating using a distance measure based on common edges: Time (in seconds) over number of samplings

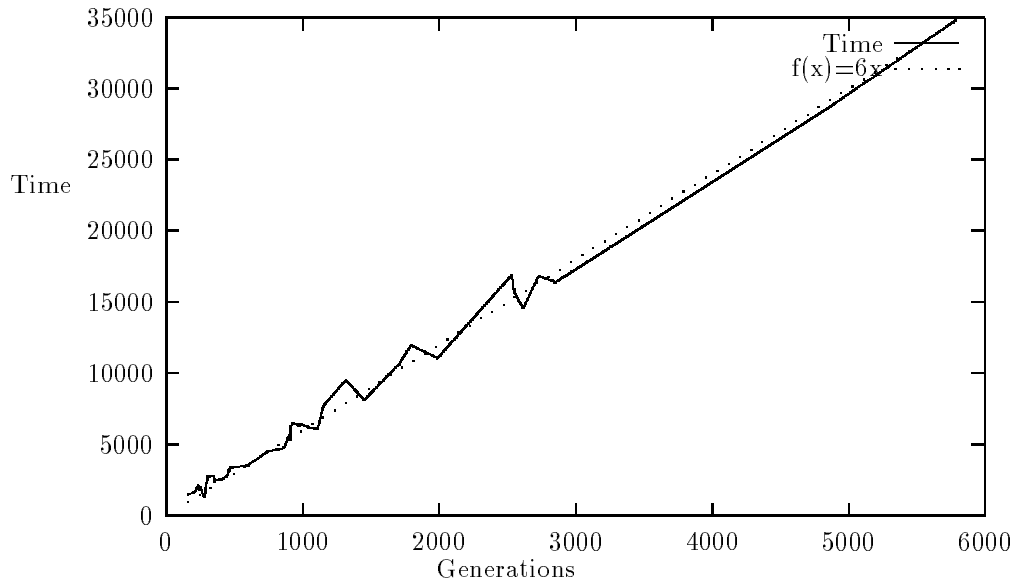


Figure 33: Results of a GA with assortative mating using a distance measure based on common edges: Time (in seconds) over number of generations

11.3 Conclusions

The GA with assortative mating preferences performs very similar as a traditional GA in terms of producing optimal solutions. However, it takes much longer in producing comparable results, which is very bad.

12 A GA with Aesthetic Sexual Selection using Absolute Mate Preferences for Symmetry & the 'Grötschels24'

In the second series of experiments applying a GA with aesthetic sexual preferences for symmetry to the 'Grötschels24' the POM has been calculated based only on the DOS of the individual to mate with.

By this, we move away from what Miller and Todd have called individual-relative preferences (see section 3.1) and introduce a concept of absolute preferences in the sense that all individuals share the same aesthetic ideal and basically have the same SRP: an individual with absolute symmetry, i.e. with a DOS of 0.

As can be seen from the results of earlier experiments (see Appendices) the DOS of individuals is within the interval $[0..MAX_DOS=20]$. For this reason, an individual with a DOS of 0 will be considered as absolutely attractive such

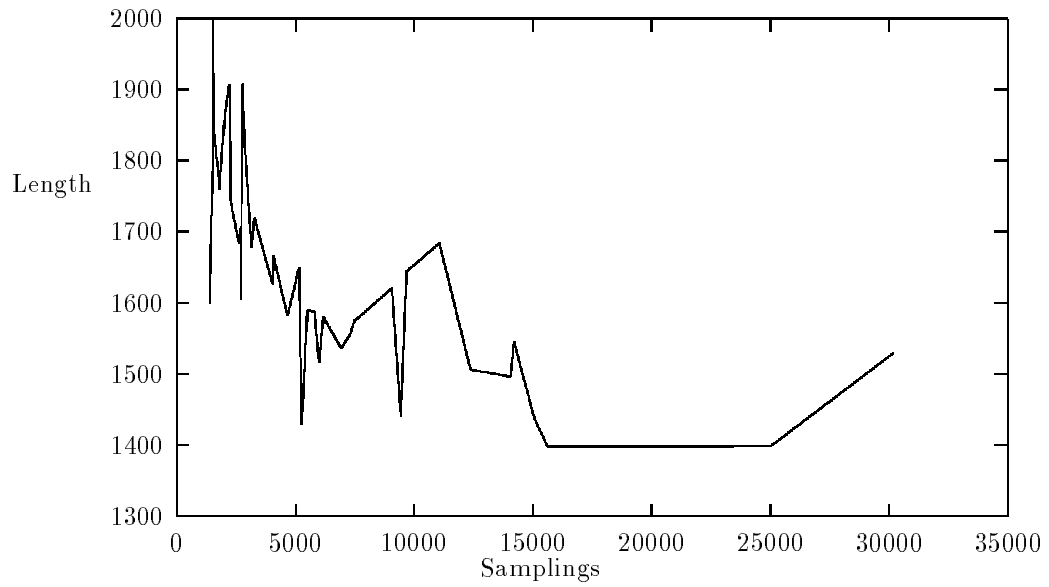


Figure 34: Results of a GA with assortative mating using a distance measure based on common edges: Length of best tour of each run over number of samplings

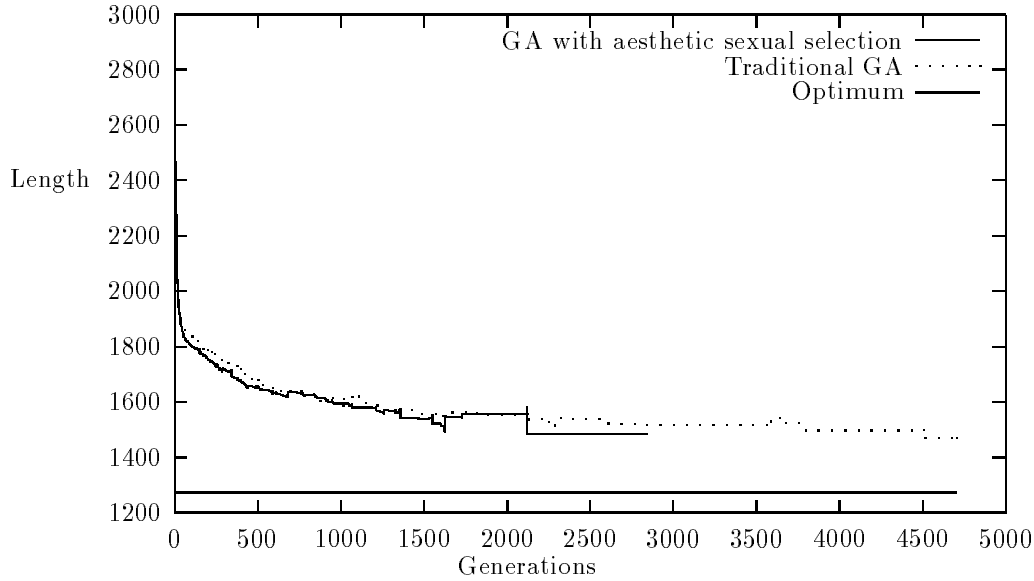


Figure 35: Results of a GA with aesthetic sexual selection using absolute mate preferences for symmetry: Average-Best-Tour-Length-Diagram comparing the GA with aesthetic sexual selection and the traditional GA & Optimum

that the POM of mating with it will be 1, while as one with a DOS of > 20 will be considered as absolutely disgusting, so that the POM of mating with him will be 0.

This idea leads directly to the following formula for the POM of mating with an individual I :

$$POM(I) = \begin{cases} DOS(I) * \frac{1}{MAX_DOS} & \text{if } DOS(I) \leq MAX_DOS \\ 0 & \text{otherwise} \end{cases} \quad (14)$$

12.1 Results

The length of the best tour is 1411 and has been found in run 15 after 471 out of 1624 generations. (see Appendix H)

The average length of the best tours found is 1654, which seems to be just a little worse than the average of 1630 achieved with the traditional GA (see Appendix F).

Figure 35 shows a Average-Best-Tour-Length-Diagram and figure 36 shows again the best tours found in each run. A Student's t-test comparing the best tours obtained leads to the following:

Student's t-test comparing best tours (unequal variance)	0.376857
Student's t-test comparing best tours (equal variance)	0.376884

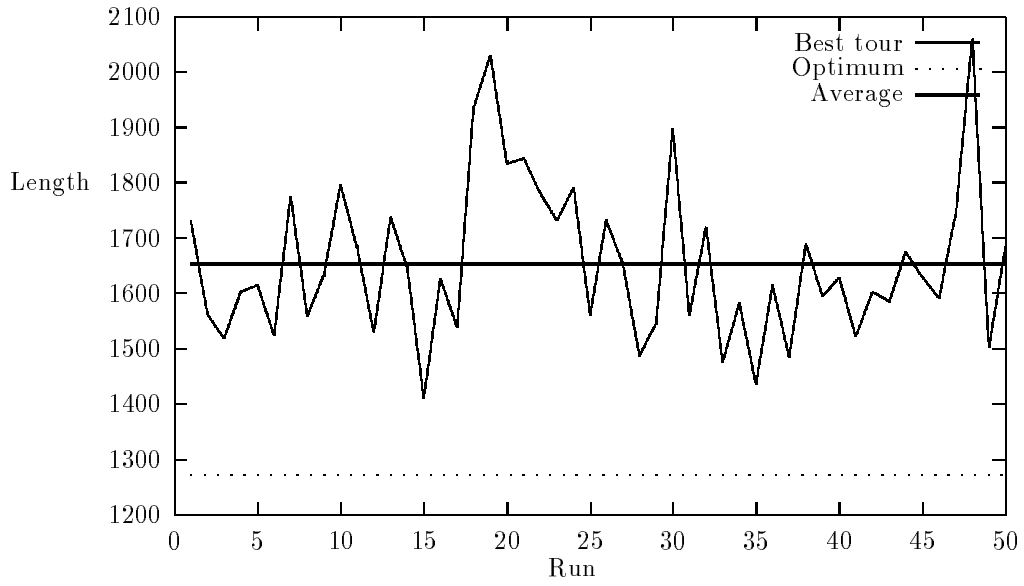


Figure 36: Results of a GA with aesthetic sexual selection using absolute mate preferences for symmetry: Length of best tours of all runs

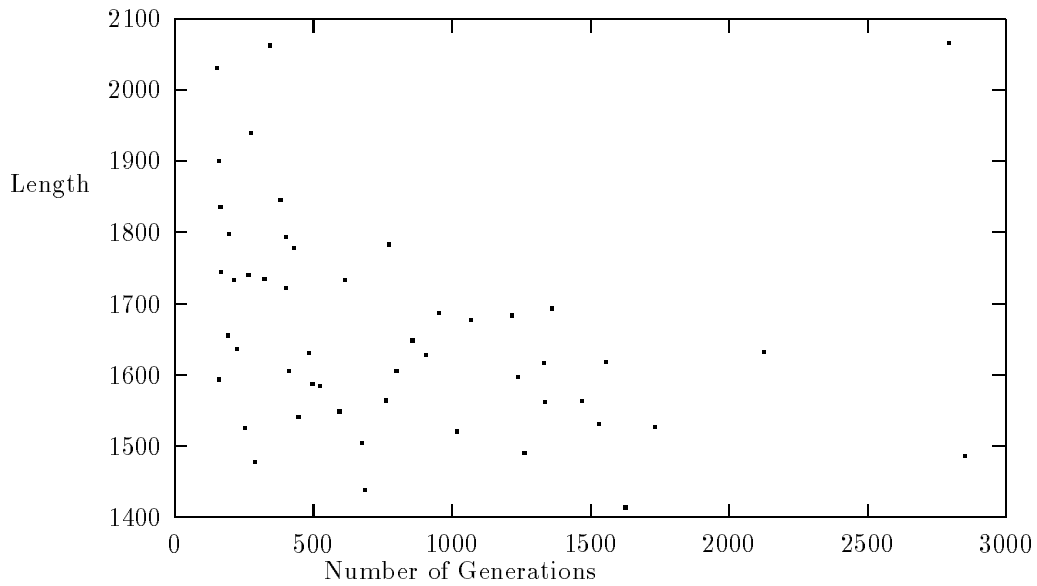


Figure 37: Results of a GA with aesthetic sexual preferences for symmetry II: Length of best tours over number of generations

So, it can be concluded that the GA with aesthetic sexual preferences for symmetry performs just a bit worse than the traditional GA.

Similar results have been achieved when comparing the time both GAs take on average over all the runs:

Student's t-test comparing time (unequal variance)	0.386298
Student's t-test comparing time (equal variance)	0.386298

The average number of matings is 0.862924, which is significantly lower than the average number of matings of the GA implementing assortative mating preferences (6.33557).

The most striking results have been yielded when comparing the DOS of the best tours found and the average DOS of each generation over all the runs:

Student's t-test comparing DOS of best tours (unequal variance)	0.153394
Student's t-test comparing DOS of best tours (equal variance)	0.153396

Student's t-test comparing DOS of population (unequal variance)	$1.41 * 10^{-18}$
Student's t-test comparing DOS of population (equal variance)	$1.6 * 10^{-17}$

It can be concluded from these results that the GA with aesthetic sexual selection preferences for symmetry produces best tours which are significantly more symmetric than the ones produced by a traditional GA.

Furthermore, the average DOS of each generation over all the runs is very significantly lower than the one of the traditional GA.

Figure 38 shows the relationship between the samplings and the time. Again it can be seen that the time is proportional to the number of samplings, but this time with a factor around 2

Figure 39 shows the quality of the solutions over the number of samplings. It can be clearly seen that they are not linearly proportional. However, it seems that the quality increases again with increasing number of samplings, which is an interesting observation.

Figure 37 shows that the algorithm is again biased towards smaller number of generations as described in previous sections.

12.2 Conclusions

The fact that the individuals of the GA with aesthetic sexual preferences for symmetry are more symmetric on average in comparison to the ones of the traditional GA shows that aesthetic sexual preferences are in fact introducing additional pressures different from natural selection ones into the population by favoring symmetric individuals against non-symmetric ones.

Following this line, the fact that the best tours produced are on average more symmetric than the ones produced by the traditional GA could be seen as a direct consequence of it.

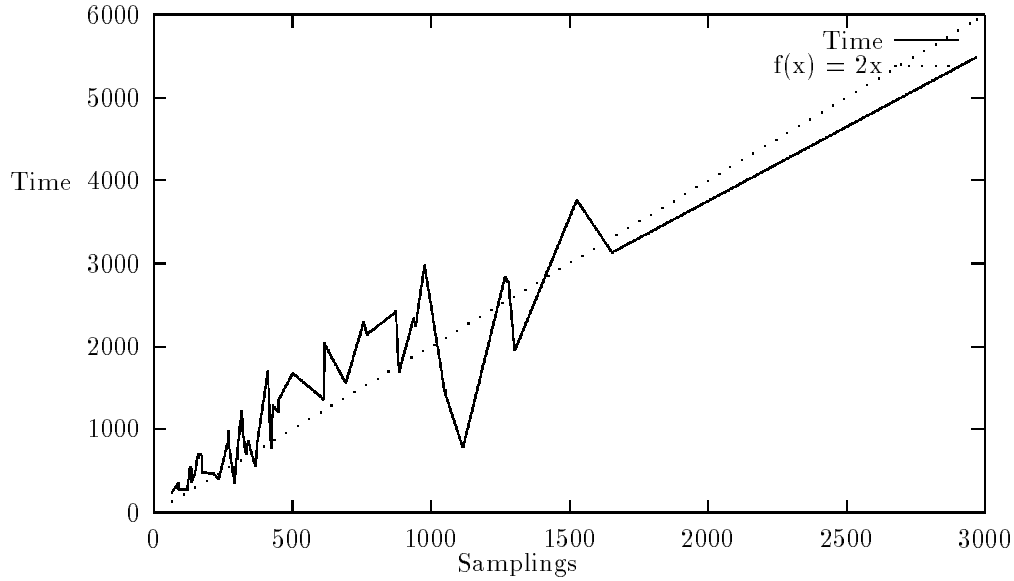


Figure 38: Results of a GA with aesthetic sexual selection using absolute mate preferences for symmetry: Time (in seconds) over number of samplings

Moreover, it would also explain why the GA with aesthetic sexual preferences for symmetry produces slightly worse results than the traditional GA. The introduced sexual preferences for symmetry are probably leading the population away from fitness peaks towards 'symmetry' peaks created by the genetically coded sexual preferences of each individual, but not too far away from them such that a certain equilibrium is established between optimality and symmetry.

In the line of Miller & Todd's sexual selection theory described in section 3.2, it could be said that individuals are adapting not only to the fitness landscape but also to the evolving sexual selection landscape specified by each individual's POM-function.

Furthermore, these results seem to be completely in line with the sexual selection theory outlined in section 2. Talking metaphorically, it could be said that indeed 'moms' seem to prefer attractive 'dads' (i.e. with high symmetry) possibly having a lower fitness by this, but not too attractive as their fitness is expected to be within an acceptable range such that a perfect equilibrium is established between fitness (= optimality) and attractiveness (=symmetry).

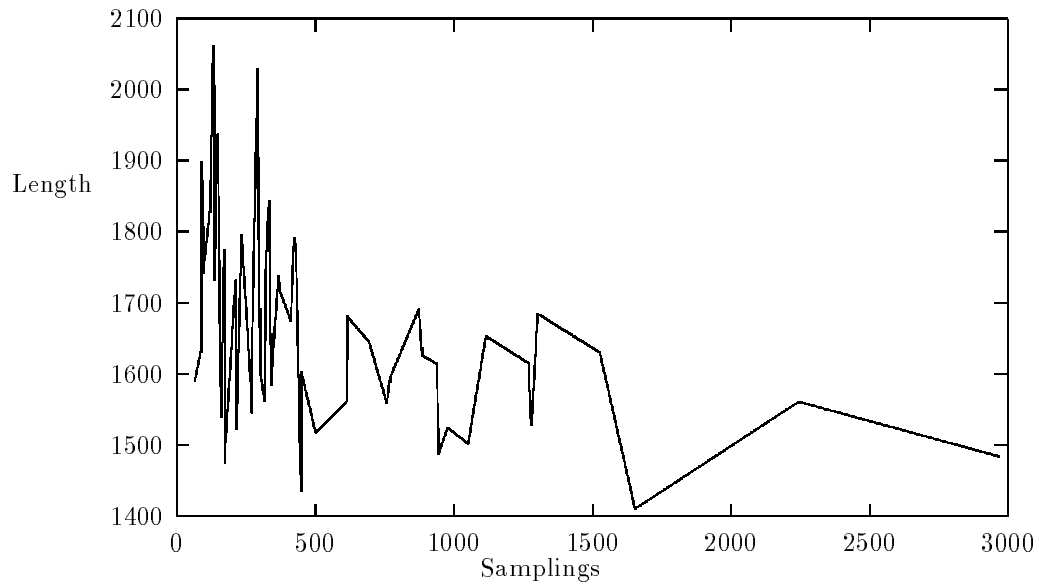


Figure 39: Results of a GA with aesthetic sexual selection using absolute mate preferences for symmetry: Length of the best tour of each run over number of samplings

13 A GA with Directional Mate Preferences using a Distance Measure based on Common Edges & the 'Grötschels24'

In the first experiment applying a GA with directional mate preferences to the 'Grötschels24', a distance measure based on the length difference between the tours coded by two individuals has been used.

However, it may also be interesting to use directional mate preferences in combination with a distance measure based on common edges as defined by (13) in section 11.

The only difference with the algorithm described in section 9.1 is that the distance measure has been replaced by the one based on common edges. Of course, when using directional mate preferences, this distance measure will be directed as the distance is calculated between the tour of the individual to mate with and the tour coded by the SRP_GENE. (see section 9.1).

13.1 Results

40 runs of the GA with directional mate preferences using the distance measure based on common edges have been produced.

It can be seen on figures 40 and 41 that the GA with directional mate preferences performs much worse in terms of producing optimal tours than the traditional GA.

The best tour found has a length of 1541 and has been found in run 21 after 285 out of 1767 total generations. The average length of the best tours found is 1870.

When using a Student's t-test to compare these results with the ones obtained with the traditional GA, the bad performance of the GA with directional mate preferences becomes obvious:

Student's t-test comparing best tours (unequal variance)	$2.83306 * 10^{-11}$
Student's t-test comparing best tours (equal variance)	$2.51716 * 10^{-10}$

Besides producing very bad results, the GA with directional mate preferences also takes much longer as the results of a Student's t-test comparing the time of both algorithms shows:

Student's t-test comparing time (unequal variance)	$2.83306 * 10^{-10}$
Student's t-test comparing time (equal variance)	$1.38648 * 10^{-7}$

In contrast to the results obtained with the directional mate preferences using a distance measure based on tour length difference, the algorithm is still biased towards smaller numbers of generations. (figure 42)

The average number of matings was very high (12.5262) in comparison to the one of the other sexual selection mechanisms. (Appendices G, H and I).

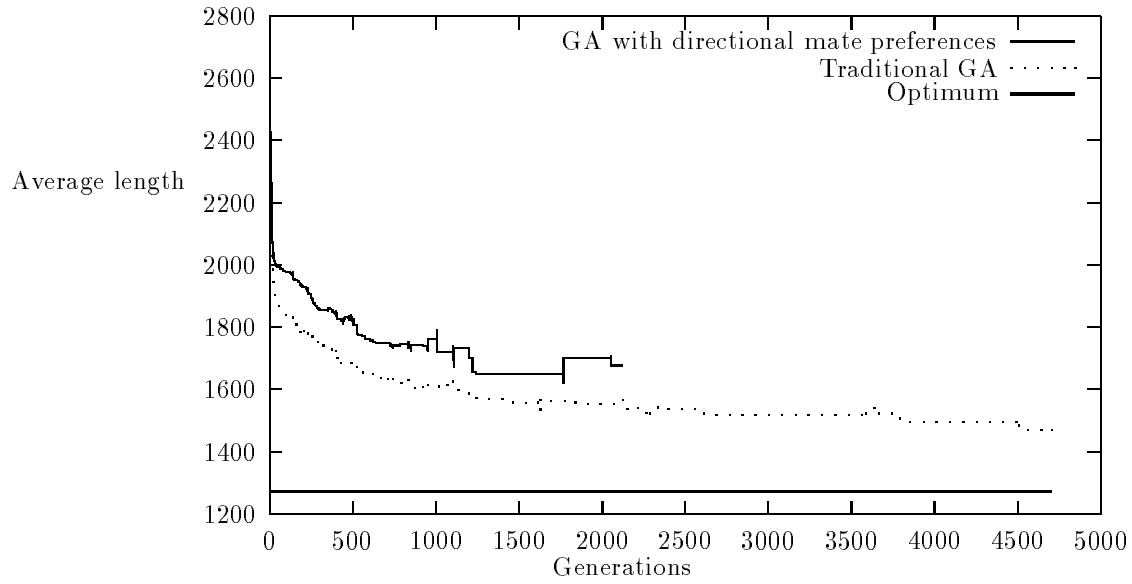


Figure 40: Results of a GA with directional mate preferences using a distance measure based on common edges: Average-Best-Tour-Length-Diagram comparing the GA with directional mate preferences and the traditional GA & Optimum

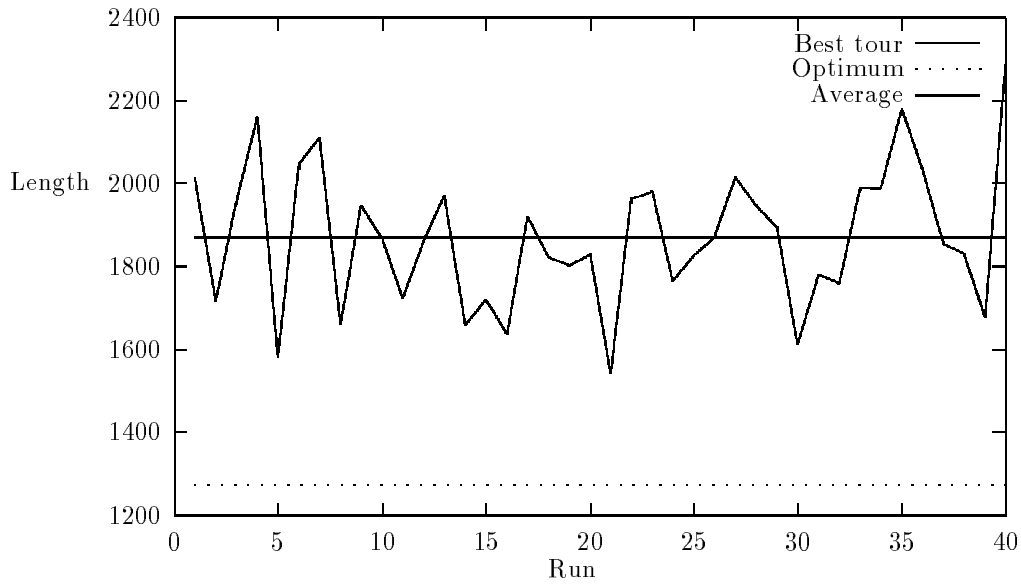


Figure 41: Results of a GA with directional mate preferences using a distance measure based on common edges: Length of best tour of each run & average of best tours over all the runs

It can be seen on figure 43 that the time is proportional to the number of samplings with a factor close to 1.5.

Figure 44 shows that again the quality of the solutions increases with increasing number of generations but that there is no linear relationship.

13.2 Conclusions

It has become clear that changing the distance measure based on the length of the tour by the one based on common edges has important effects on the performance of the GA with directional mate preferences.

It has been expected that the GA with directional mate preferences would again perform better than the traditional one but it turns out to be the other way round.

In fact, the new GA implementing directional mate preferences performs much worse and even takes significantly longer than the normal GA.

It seems that directional preferences are still acting as a certain kind of fitness scaling reinforcing natural selection but they don't seem to be able to help the GA to escape local optima. Moreover, it appears as if they are even leading the population faster on to the fitness peaks and keep the population there such that the whole algorithm converges too early.

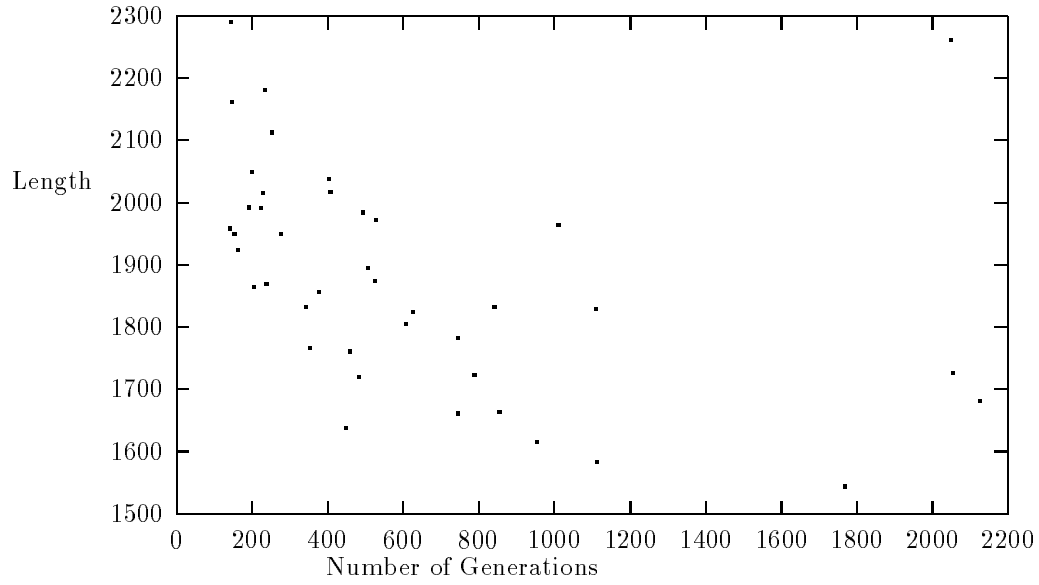


Figure 42: Results of a GA with directional mate preferences using a distance measure based on common edges: Length of best tours over number of generations

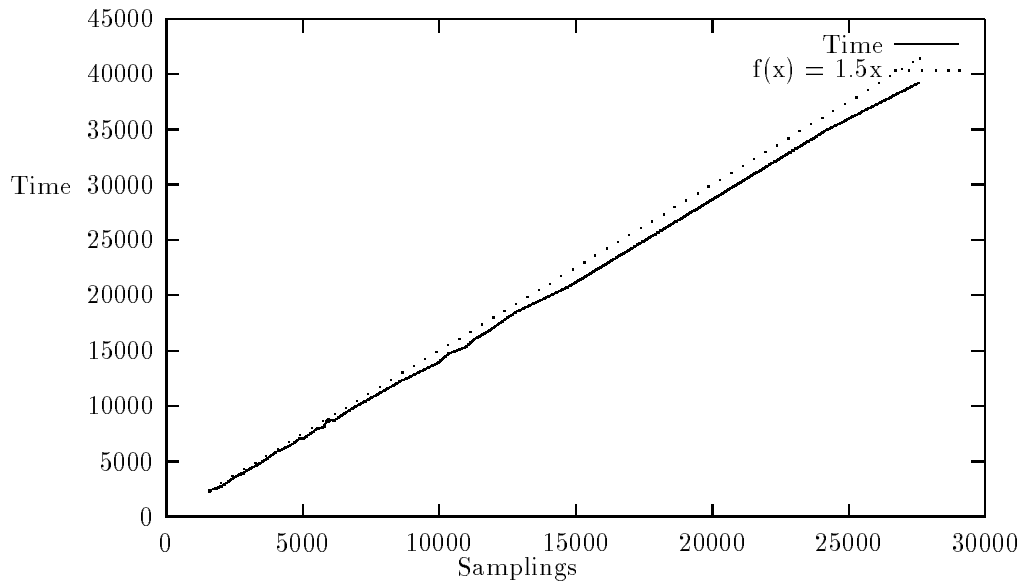


Figure 43: Results of a GA with directional mate preferences using a distance measure based on common edges: Time (in seconds) over number samplings

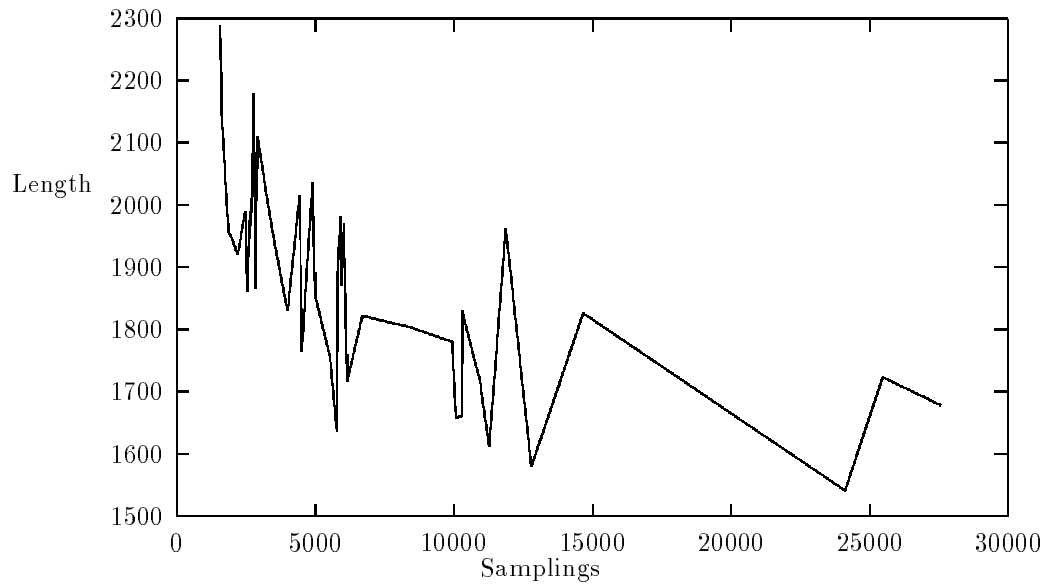


Figure 44: Results of a GA with directional mate preferences using a distance measure based on common edges: Length of the best tours of each run over number of samplings

This is also suggested by the fact that the number of average generation each run took (584) is almost half of the average each run of the traditional GA took (1046). So it can be concluded that the directional mate preferences as implemented here lead to a rapid premature convergence.

The obvious reason why the algorithm takes so long is because the average number of matings is so high. The reason for this is that the POMs seem to be very low.

In order to overcome this problem, only the POM that the 'mom' wants to mate with the 'dad' could be used to determine if a mating takes place or not as defined in section 11. This would at least avoid that two low POMs are multiplied yielding an even lower POM.

On the other hand, the PMD could be eliminated such that the POM function is centered around distance 0 from the SRP.

A third possibility mentioned by Miller & Todd (compare section 3.2) would be to use the mom's directional preferences while the dad's non-directional preferences, which means that the SRP of the dad is set to the TSP-tour he represents.

14 A Traditional GA & the 'Grötschels48'

In order to verify the results obtained in previous sections, directional mate preferences, which can be seen as the most controversial and unstable form of sexual selection examined, have been applied to a larger problem, the 'Grötschels48', which is a 48 city TSP. ([23]) Again, first the performance of a traditional GA has been analyzed.

14.1 Algorithm

The algorithm used is basically the same as the one defined in section 6. The representation, mutation and crossover operators as well as the termination criterion are also the same as described in the section mentioned. The population size is again 100, the crossover and mutation probabilities 0.75 and 0.01 respectively. However, the fitness scaling has been changed to make it suitable for the 'Grötschels48'. The fitness f of an individual is calculated as follows:

$$f(\text{length}) = \left(\frac{20000}{\text{length}}\right)^4 \quad (15)$$

As mentioned in section 6.4, the fitness is inverse proportional to the length of the tour. The optimal tour length for the 'Grötschels48' is 5046, so that the ratio $\frac{20000}{\text{length}}$ will have values within the interval [0..3.96] and consequently the fitness will always be within [0..245.91].

14.2 Results

The performance of the algorithm is very bad and it converges again to a sub-optimal solution in all of the 50 runs produced as can be seen in figures 45 and 46.

The best tour found has a length of 9194 which is 4148 away from the optimum of 5046. This solution has been found in run 46 after 748 of 5545 generations and a total time of 14254 seconds. (see Appendix J)

The average length of the best tours found over all the runs is 11308 and the average time each run takes is 4936 seconds on a SUN Ultra-4 Sparcstation.

Thus, it is obvious that the algorithm converges too early to a solution which is very far away from being acceptable in all the runs.

The average DOS of the best individuals found in each run is 16.6371 and the average DOS of each generation over all the runs is 22.1099.

Figure 47 shows that the variance in the number of generations is very high and only a few runs reach a number of generations above the average, so that it can again be stated that the algorithm is biased towards smaller number of generations.

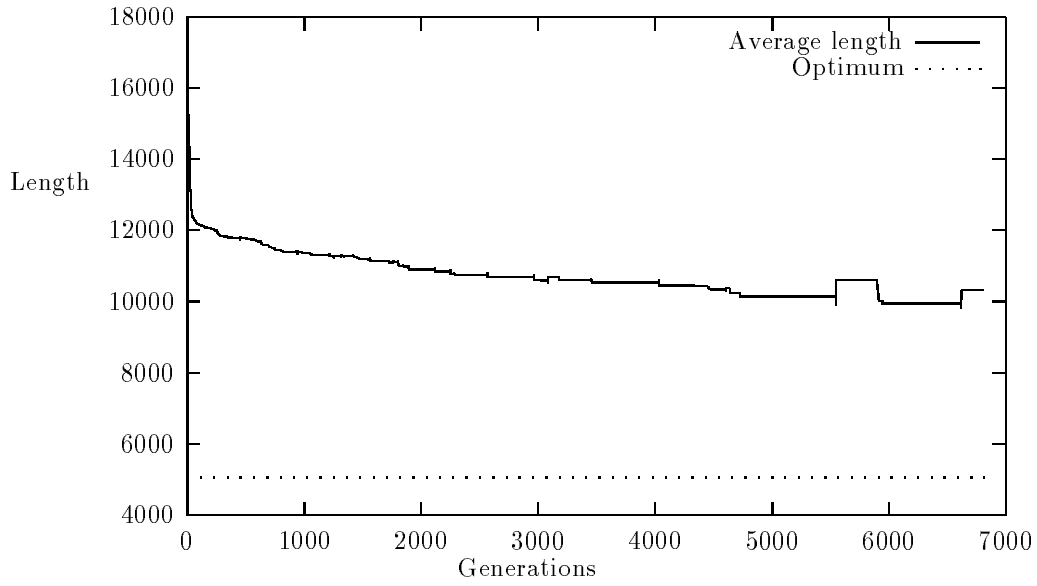


Figure 45: Results of a traditional GA applied to the 'Grötschels48': Average-Best-Tour-Length-Diagram

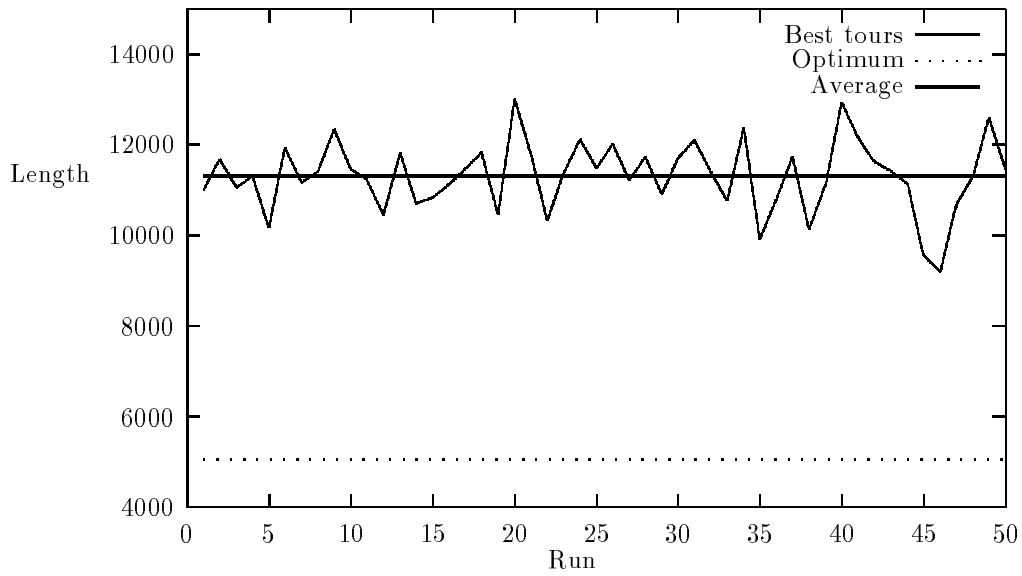


Figure 46: Results of a traditional GA applied to the 'Grötschels48': Length of best tour of each run & average of best tours over all the runs

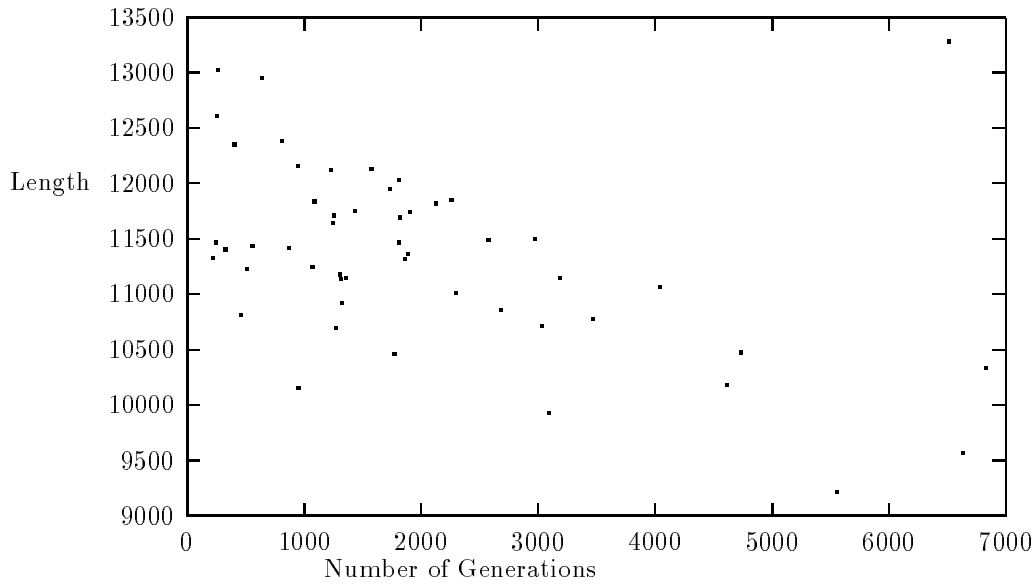


Figure 47: Results of a traditional GA applied to the 'Grötschels48': Length of best tours over number of generations

15 A GA with directional mate preferences using a distance measure based on length difference & the 'Grötschels48'

A GA with directional mate preferences using the distance measure based on length difference as defined in section 9.1 has been applied to the 'Grötschels48'. However, in order to decrease the time the GA runs, the POM function has been centered around distance 0 ($PMD = 0$) and the 'mom-samples-dads' algorithm has been modified such that again only the mom's POM determines whether a mating takes place or not.

15.1 Results

The best tour found has a length of 8930 and has been found in run 30 after 372 out of 786 generations.

The average length of the best tours produced in the 40 runs is 11315 and thus is very similar to the one of 11308 achieved by the traditional GA. (compare Appendices J and K)

In order to find out how similar the results of both GAs are from a statistical point of view, a Student's t-test has been performed comparing both means with the following results:

Student's t-test comparing best tours (unequal variance)	0.979874
Student's t-test comparing best tours (equal variance)	0.981239

These results show that in fact both GAs perform almost the same in terms of producing optimal tours.

However, it is interesting to observe that when taking into account the best tour of each generation over all the runs, the GA with directional mate preferences seems to perform better than the traditional one. (figure 48) Besides, there seems to be an important difference in the average time each of the runs takes. The GA with directional mate preferences takes on average 2230 seconds, which is less than half the time the traditional GA takes on average (4936). When using a Student's t-test to confirm that this difference is in fact significant, we get the following significance values:

Student's t-test comparing time (unequal variance)	0.000142102
Student's t-test comparing time (equal variance)	$5.17719 * 10^{-5}$

These results show that the difference is very significant, so that it can be concluded that the traditional GA takes twice as longer as the one with directional preferences in producing comparable results.

Figure 50 shows the time over the number of samplings. It can be seen that the linear relationship between time and number of samplings is not that clear anymore.

When having a look at figure 51 it becomes clear that the quality of the solutions improves with increasing number of samplings.

Figure 52 shows the best tours over the number of generations. It shows that the variance in the number of generations is much lower than with the traditional GA (figure 47) such that it can be concluded that directional mate preferences as implemented manage to 'unbiase' the algorithm and keep the number of generations more or less constant in comparison to the traditional GA.

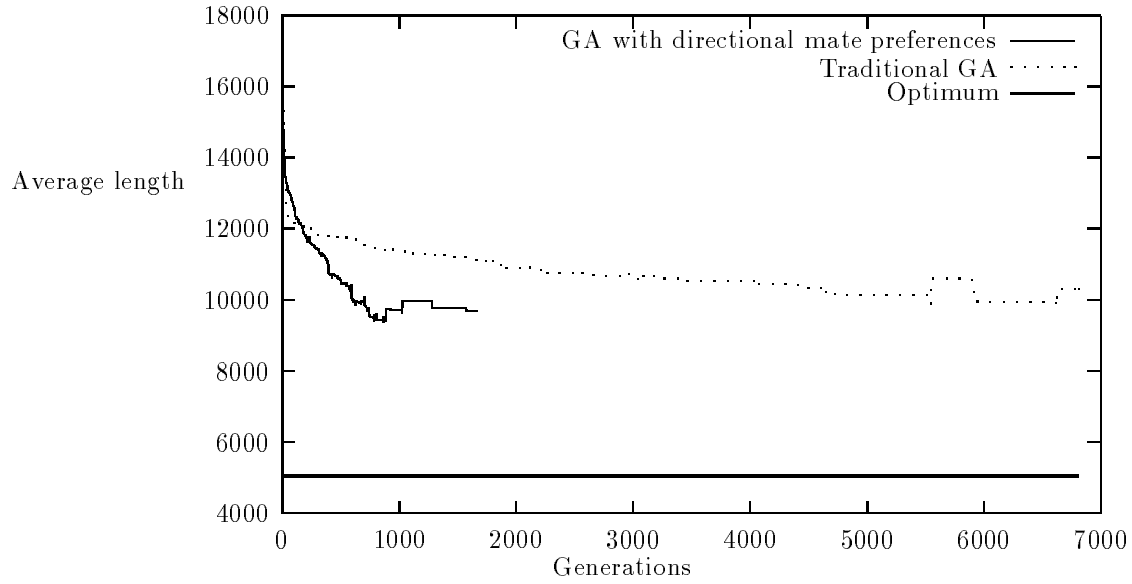


Figure 48: Results of a GA with directional mate preferences using a distance measure based on length difference applied to the 'Grötschels48': Average-Best-Tour-Length-Diagram comparing the GA with directional mate preferences and the traditional GA & Optimum

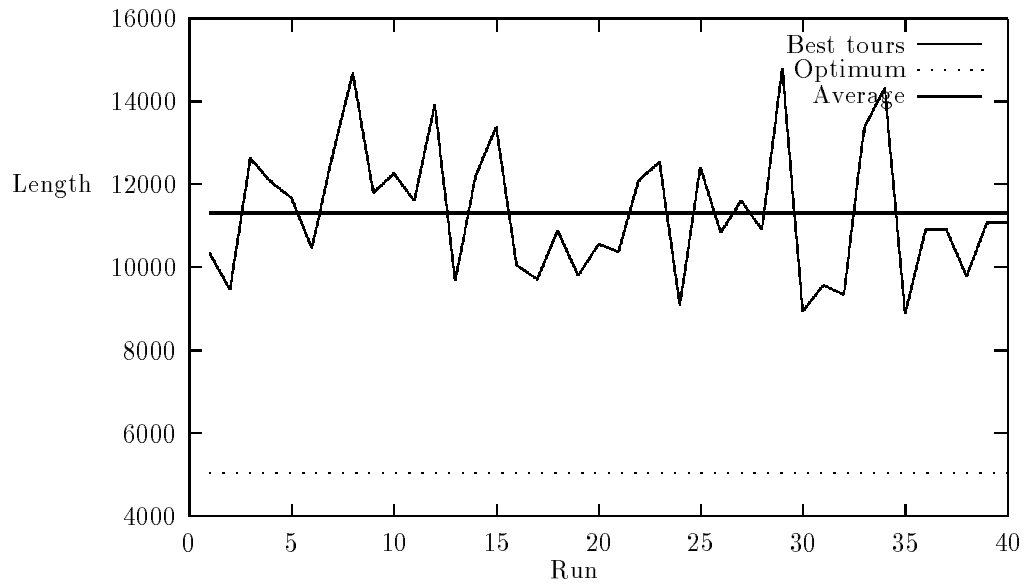


Figure 49: Results of a GA with directional mate preferences using a distance measure based on length difference applied to the 'Grötschels48': Length of best tour of each run & average of best tours over all the runs

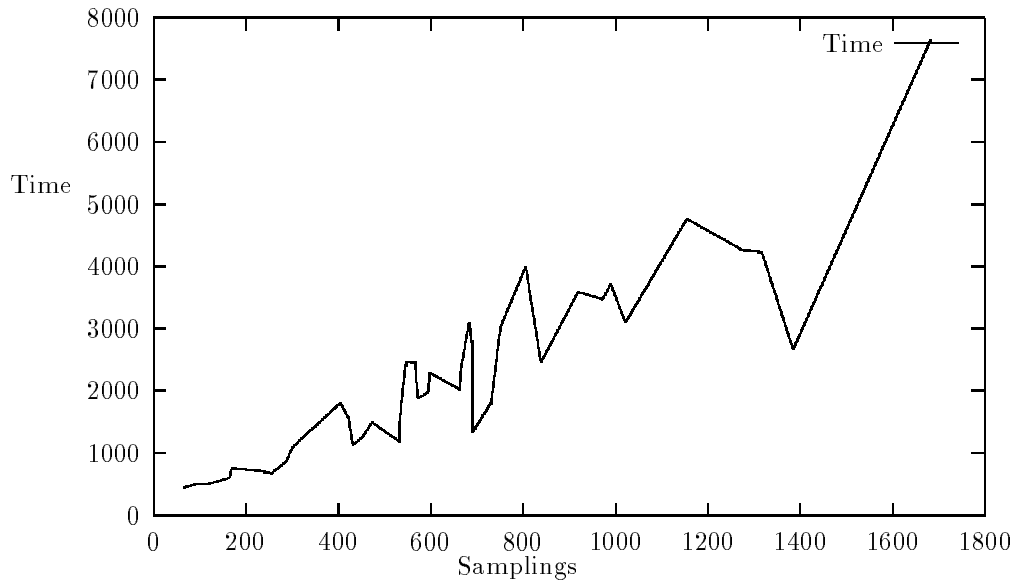


Figure 50: Results of a GA with directional mate preferences using a distance measure based on length difference applied to the 'Grötschels48': Time (in seconds) over number of samplings

15.2 Conclusions

When applying the GA with directional mate preferences using the distance measure based on tour length difference to the 'Grötschels48', it becomes clear that the quality of the solutions doesn't improve in comparison to the results produced by a traditional GA.

This result is in contrast to the one of section 9.1, where it has been concluded that the GA with directional mate preferences performs much better than the traditional GA when applying it to the 'Grötschels24'.

However, if we take into account the best tours of each generation on average over the runs, it seems that the GA with directional mate preferences performs much better than the traditional GA.

In fact, it appears that directional mate preferences are stabilizing and reinforcing natural selection for the following reasons:

1. there is less variance in the number of generations in comparison to the traditional GA
2. the average of the best tours of each generation over the runs is much closer to the global best solution found so that it seems that directional mate preferences are making the whole population converge to the global best tour

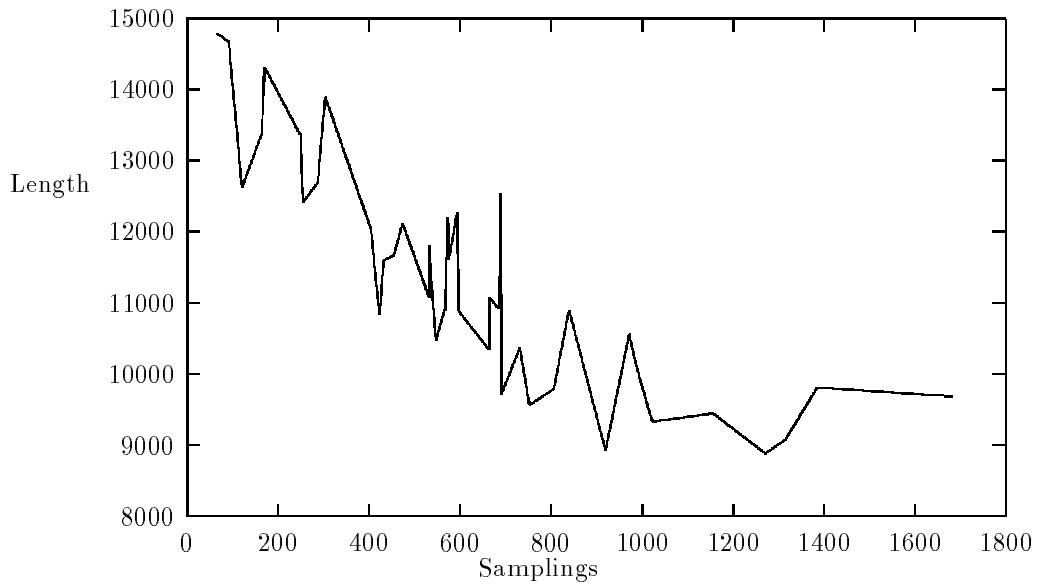


Figure 51: Results of a GA with directional mate preferences using a distance measure based on length difference applied to the 'Grötschels48': Length of the best tour of each run over number of samplings

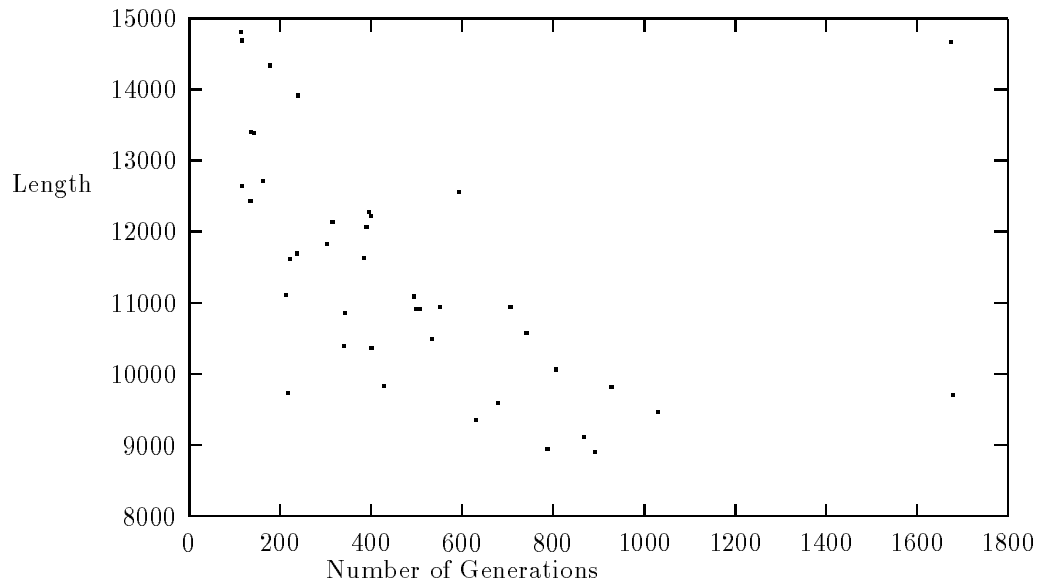


Figure 52: Results of a GA with directional mate preferences using a distance measure based on length difference applied to the 'Grötschels48': Length of best tours over number of generations

3. the number of generations is much lower such that it can be concluded that the search is much more directed than with to a traditional GA
4. the time consumed is less than with a traditional GA

16 A GA with Directional Mate Preferences using a Distance Measure based on Common Edges & the 'Grötschels48'

The GA with directional mate preferences using a distance measure based on common edges as defined in section 13 has been applied to the 'Grötschels48' producing 40 runs.

Again, the POM function has been centered around distance 0 ($PMD = 0$) and the 'mom-samples-dads' algorithm has been modified such that again only the mom's POM determines whether a mating takes place or not.

16.1 Results

The Average-Best-Tour-Length-Diagram in figure 53 shows that the performance of the traditional GA and the one with directional mate preferences using a distance measure based on common edges is almost the same.

The best tour found has a length of 9614 and has been found in run 35 after 1100 of 1998 generations. The average best tour has a length of 11163, the average number of generations is 1947 and the average time consumed is 17928.15 seconds. (see Appendix L) Figure 54 shows the best tours of each run, the average best tour and the optimum.

Comparing the best tours of each run of the traditional GA and the one with directional mate preferences using a distance measure based on common edges with a Student's t-test leads to the following results:

Student's t-test comparing best tours (unequal variance)	0.991146646
Student's t-test comparing best tours (equal variance)	0.991146646

Thus, there seems to be no difference in the best tours produced such that it can be concluded that both GAs perform the same in terms of producing optimal tours.

When comparing the number of generations and the time consumed we yield the following:

Student's t-test comparing number of generations (unequal variance)	0.418940437
Student's t-test comparing number of generations (equal variance)	0.418940437

Student's t-test comparing time (unequal variance)	$2.39429 * 10^{-7}$
Student's t-test comparing time (equal variance)	$7.82049 * 10^{-6}$

It seems that the difference in the number of generations is not very significant

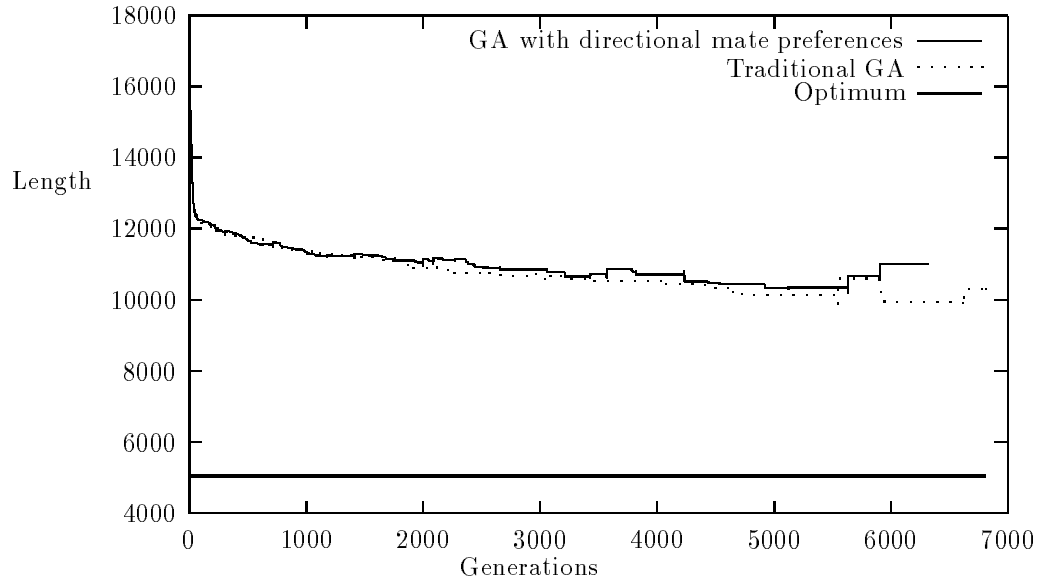


Figure 53: Results of a GA with directional mate preferences using a distance measure based on common edges applied to the 'Grötschels48': Average-Best-Tour-Length-Diagram comparing the GA with directional mate preferences and the traditional GA & Optimum

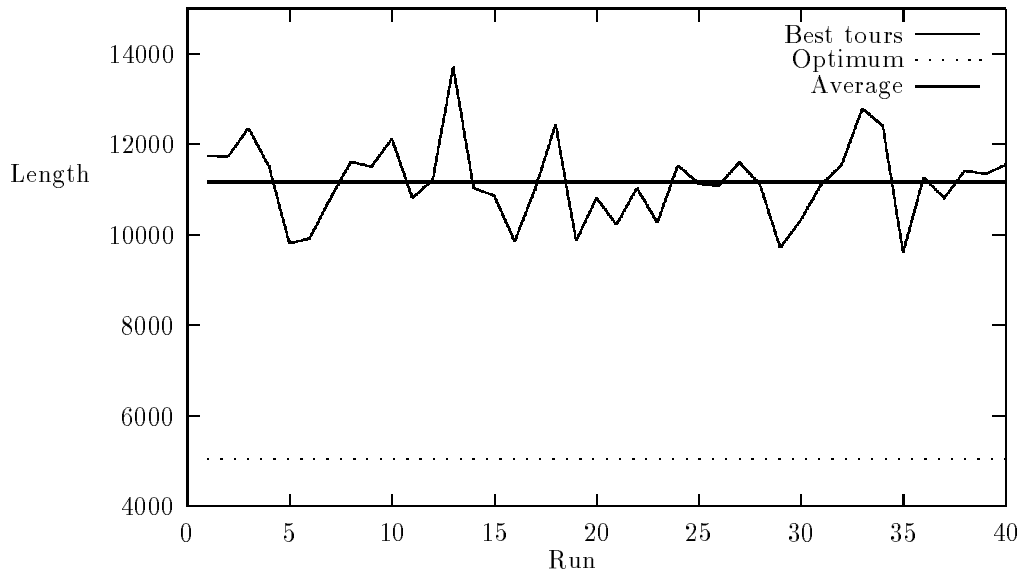


Figure 54: Results of a GA with directional mate preferences using a distance measure based on common edges applied to the 'Grötschels48': Length of best tour of each run & average of best tours over all the runs

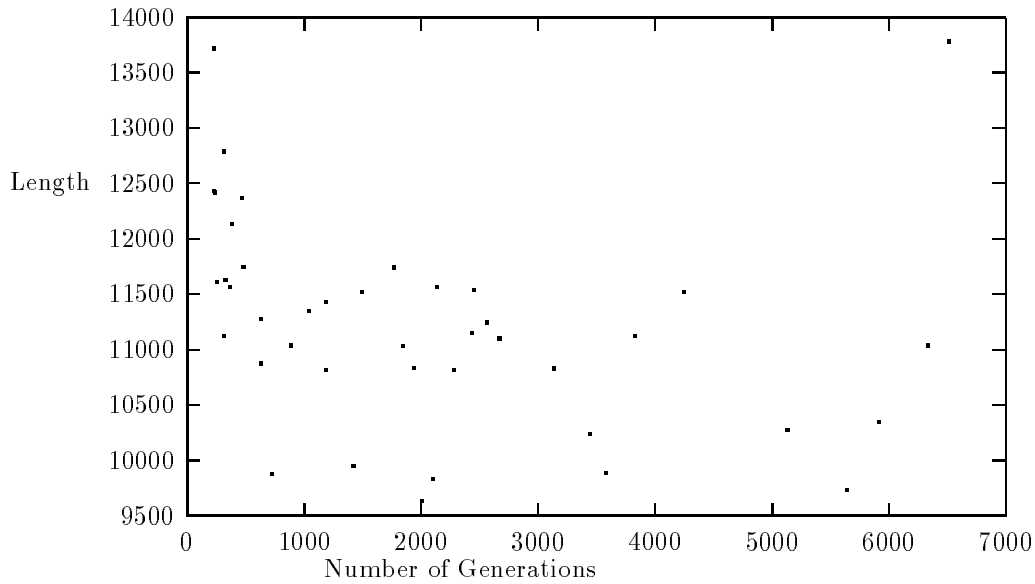


Figure 55: Results of a GA with directional mate preferences using a distance measure based on common edges applied to the 'Grötschels48': Length of best tours over number of generations

but that the difference in time is very significant so that we can conclude that the GA with directional mate preferences takes almost four times longer than the traditional GA. (compare Appendices J and L) The number of samplings on average is 0.175754, which is much lower than the average yielded when using the distance measure based on length difference, which is 1.46361815. Thus, it can be concluded that the distance measure based on common edges makes it much easier for individuals to find a mate. Of course, this means in turn that the selection pressure imposed by the distance measure based on common edges is much weaker than the one introduced by the distance measure based on length difference. This would explain why the performance of the GA with directional mate preferences using the distance measure based on common edges is worse.

Figure 55 shows that the algorithm is biased towards smaller numbers of generations and that the variance is very high. It becomes clear that directional mate preferences using the distance measure based on common edges are not helping the population to escape local optima.

It can be seen in figure 56 that there is a linear relationship between the time and the number of samplings and that the factor of the relationship is 50.

Figure 57 shows that the relationship between the quality of the solutions produced and the number of samplings is very weak and unstable.

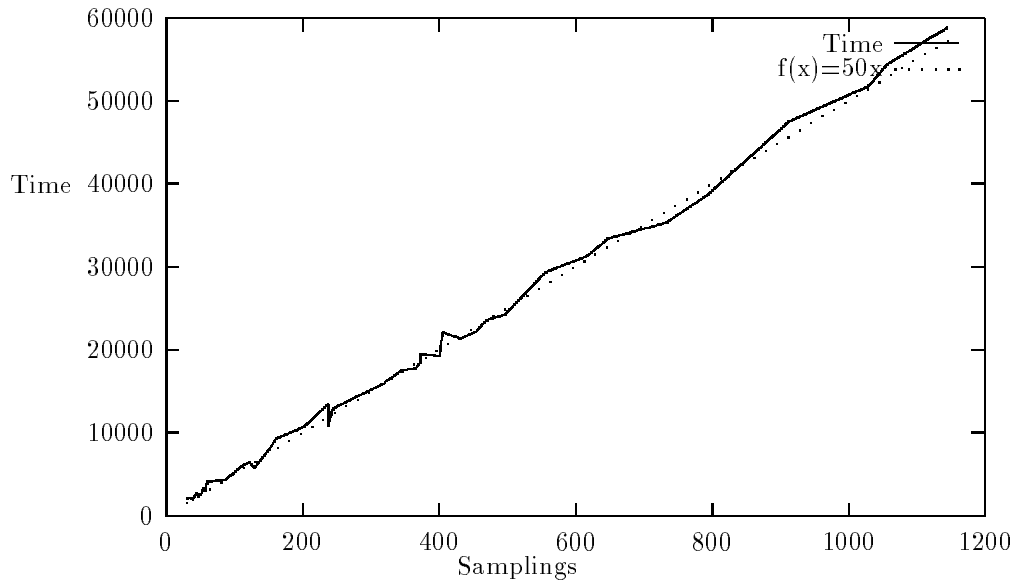


Figure 56: Results of a GA with directional mate preferences using a distance measure based on common edges applied to the 'Grötschels48': Time (in seconds) over number of samplings

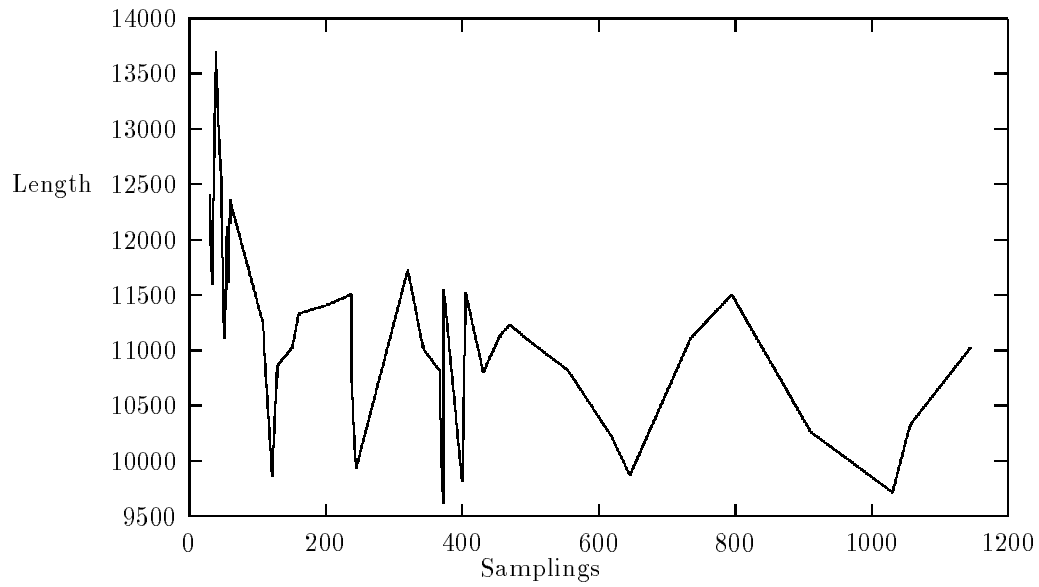


Figure 57: Results of a GA with directional mate preferences using a distance measure based on common edges applied to the 'Grötschels48': Length of the best tour of each run over number of samplings

16.2 Conclusions

The GA with directional mate preferences using a distance measure based on common edges and the traditional GA perform almost the same when applied to the 'Grötschels48'.

So, in contrast to the results observed for the 'Grötschels24', when applied to a larger TSP, the GA with directional mate preferences at least doesn't perform worse than a traditional GA.

However, it seems that directional mate preferences using the distance measure based on common edges:

1. do not help a population to escape local optima
2. do not manage to 'unbiase' the algorithm reducing the variance in the number of generations
3. do not reinforce natural selection in the sense that they don't reduce the number of generations
4. increase the time consumed

17 Conclusions

It has become clear that sexual selection can have important effects on the convergence behaviour of a GA. However, the effects depend highly on the sexual selection method and the measure used to compute the distance between two individuals.

Assortative mating has been found to be the most conservative of the sexual selection methods analyzed. When integrating an assortative mating sexual selection mechanism into a GA, the quality of the results doesn't seem to improve but also doesn't seem to get worse.

Though the fact that there is no change in the quality of the solutions found, the GA with the assortative mating mechanism takes much longer than the conventional GA. This is due to the fact that the recombination step takes longer as several 'dads' are sampled by a 'mom' before two individuals are recombined. These results are not striking in the sense that it seems obvious that if two very similar individuals mate, their offspring will also be very similar to them, such that no real innovations can be expected. The surprising result is that though the fact that innovations are unlikely to be produced, the GA with the assortative mating mechanism doesn't perform much worse than a traditional GA.

On the other hand, the results obtained by a GA with an aesthetic sexual selection mechanism are very impressive. It seems that aesthetic sexual selection offers a way of integrating additional search criteria or constraints the fitness function can't select for into a GA. In fact, it has been shown that when introducing additional criteria in form of aesthetic sexual selection preferences, the whole population will tend to fulfill these additional criteria. Thus, when thinking of an application where optimality is important, but also other requirements

have to be met, aesthetic sexual selection preferences offer an easy and intuitive way of implementing them.

Sexual selection based on directional mate preferences is probably the most unstable and controversial sexual selection method examined in the sense that its performance and effects seem to be highly dependent on the distance measure used.

With a distance measure based on phenotype difference (the tour length in the case of the TSP), it seems that directional mate preferences applied to a smaller TSP - the 'Grötschels24' - improve the performance of a GA to a very high degree when comparing the quality of the solutions found.

When applied to a larger TSP - the 'Grötschels48' - the GA with directional mate preferences using the distance measure based on length difference performs at least as good as a conventional GA in terms of finding optimal solutions and when taking into account the best tour of each generation on average over all the runs, it even seems to perform better.

In both cases it seems that directional mate preferences are reinforcing and stabilizing natural selection in the sense that:

1. the GA with directional mate preferences converges in less number of generations producing at least as good results and thus representing a much more directed search compared to a traditional GA
2. the number of generations the algorithm takes is more or less constant over the runs
3. the GA with directional mate preferences performs better on average over the generations

In fact, it seems that directional mate preferences using a distance measure based on length difference are acting as an automatic form of fitness scaling by favoring good individuals against bad ones as suggested by Miller and Todd. ([20], [29])

When using a distance measure based on common edges, the performance of the GA with directional mate preferences applied to the smaller TSP is very bad, while when applied to the larger TSP it is almost the same as with a traditional GA.

Directional mate preferences with a distance measure based on common edges don't seem to help a population to escape local optima or to stabilize and reinforce natural selection as directional mate preferences with a distance measure based on length difference.

This may be due to the fact that the first one is a distance measure based on phenotype while the latter one is based on genotype difference. Further research is definitely needed to clarify this and other questions.

18 Further Research and Work

The aim of this work has been to examine different sexual selection mechanisms and find out how they can influence the convergence of a GA.

It has been shown that sexual selection can have very strong effects on the convergence behaviour of a GA. As suggested within this work and originally by Miller & Todd ([27]), assortative mating seems to be able to lead a population to speciate. Further research is needed: (1) to examine the conditions under which a populations can speciate, (2) to develop measures to formalize and evaluate the degree of speciations observed and (3) to find out which are the advantages such a speciation has.

Concerning aesthetic sexual selection, different problems requiring additional criteria which the fitness function can't select for should be examined and solved using a GA integrating an aesthetic sexual selection component.

The effect of assortative mating and directional mate preferences highly depends on the distance measure used. Within GA research lots of representations, recombination and mutation operators as well as combinations of them have been examined for various problems in order to find out which ones work best. Something similar should be done with the distance measure in order to find out which sexual selection method together with which distance measure works well on a specific problem.

Besides, the effect of varying the recombination and mutation rates as well as the population size should be examined in context of a certain sexual selection method.

Moreover, new measures and evaluation methods should be developed in order to find out to which degree sexual selection can: (1) reinforce and stabilize natural selection, (2) help a population to escape local optima, (3) act as an automatic form of fitness scaling and (4) replace mutation by introducing innovations.

19 Appendix A: Results of a Traditional GA applied to the 'Grötschels24'

<i>Run</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>
1	722	1620	90.7444	16.4167
2	648	1517	118.015	9.875
3	1532	1464	136.055	1
4	751	1500	123.457	7.25
5	268	1686	77.3481	0.166667
6	161	1647	84.9387	6.29167
7	1725	1489	127.146	8.54167
8	494	1395	165.038	0.458333
9	833	1564	104.456	0.583333
10	223	2159	28.7653	6.125
11	833	1564	104.456	0.583333
12	223	2159	28.7653	6.125
13	1048	1764	64.5484	9.08333
14	297	1806	58.7502	0.666667
15	203	1854	52.8982	13.5833
16	705	1553	107.447	5.79167
17	744	1483	129.216	6.95833
18	972	1500	123.457	1.5
19	163	1526	115.256	0.583333
20	714	1505	121.824	3.79167
21	1008	1692	76.2568	0.0833333
22	1141	1607	93.7166	0.0416667
23	183	1994	39.5348	6.5
24	445	1686	77.3481	18
25	633	1744	67.5607	2.5
26	343	1642	85.978	3.75
27	913	1641	86.1878	8.875
28	553	1604	94.4197	13.1667
29	2811	1538	111.7	4.91667
30	3837	1524	115.862	2.16667
31	597	1508	120.858	0.75
32	331	1645	85.3525	4.04167
33	291	1813	57.8481	15.7083
34	539	1755	65.8827	3.45833
35	1362	1510	120.219	8.41667
36	204	1802	59.2735	1.16667
37	575	1601	95.1294	8.125
38	1265	1614	92.1013	2.66667
39	1058	1657	82.9068	8.29167

<i>Run</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>
40	2121	1530	114.055	1.5
41	3064	1555	106.895	4.20833
42	1161	1506	121.501	8.08333
43	890	1508	120.858	0.5
44	1085	1583	99.5305	4.20833
45	1348	1469	134.212	4.45833
46	537	1629	88.7556	8.70833
47	291	1704	74.1313	4.33333
48	1372	1455	139.453	2.375
49	632	1625	89.6327	9.54167
50	574	1699	75.0078	5.79167
51	674	1648	84.7327	8.16667
52	1431	1530	114.055	9.08333
53	494	1865	51.6612	11.375
54	206	1758	65.4342	9.16667
55	753	1591	97.5437	4.125
56	1381	1550	108.281	0.583333
57	2114	1424	151.999	4.75
58	170	2027	37.0224	3.70833
59	189	1645	85.3525	11.7917
60	648	1541	110.833	12.7083
61	1085	1544	109.974	1.75
62	2964	1565	104.189	3.125
63	408	1457	138.689	6.29167
64	1038	1574	101.827	0.916667
65	256	1807	58.6202	5.70833
Average	896	1633	95	5.6147438
Best	494	1395	165.038	0.458333

20 Appendix B: Results of a GA with Assortative Mating using a Distance Measure based on Length Difference applied to the 'Grötschels24'

<i>Run</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>
1	395	1704	74.1313
2	1029	1451	140.997
3	1085	1680	78.459
4	869	1741	68.0276
5	978	1413	156.787
6	565	1552	107.724
7	631	1573	102.086
8	577	1543	110.26
9	764	1705	73.9575
10	200	1774	63.1053
11	1211	1637	87.0333
12	212	1953	42.9607
13	1114	1647	84.9387
14	1461	1645	85.3525
15	153	1991	39.7736
16	378	1520	117.086
17	323	1626	89.4124
18	2086	1439	145.759
19	989	1777	62.6802
20	185	1862	51.995
21	1763	1570	102.868
22	3111	1395	165.038
23	332	1763	64.695
24	288	1839	54.6453
25	2684	1640	86.3982
26	604	1606	93.9502
27	501	1566	103.923
28	2191	1477	131.328
29	1333	1589	98.0357
30	577	1745	67.406
31	217	1858	52.4442
32	1324	1416	155.463
33	289	1709	73.2676
34	2002	1541	110.833
35	466	1617	91.4197
36	2589	1418	154.588
37	1998	1726	70.4234
38	1993	1552	107.724
39	614	1594	96.8115
40	274	1746	67.2517

<i>Run</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>
41	427	1776	62.8215
42	786	1779	62.3988
43	1586	1582	99.7824
44	1869	1572	102.346
45	522	1407	159.479
46	1497	1474	132.401
47	599	1622	90.2977
48	959	1594	96.8115
49	213	1909	47.0605
50	183	1866	51.5506
Average	980	1644	92.72
Best	3111	1395	165.038

21 Appendix C: Results of a GA with Aesthetic Sexual Selection using Individual-relative Mate Preferences for Symmetry applied to the 'Grötschels24'

<i>Run</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>
1	181	1905	47.457	12.2917
2	1918	1515	118.64	4.125
3	193	1622	90.2977	4.25
4	408	1575	101.568	3.625
5	1361	1505	121.824	2.625
6	528	1879	50.1387	9.95833
7	2429	1446	142.957	3.08333
8	986	1582	99.7824	5.91667
9	431	1701	74.6557	8.375
10	189	1720	71.4112	5.66667
11	1271	1638	86.8209	5.33333
12	1228	1521	116.779	5.33333
13	331	1644	85.5604	5.83333
14	1076	1670	80.3552	11.9167
15	1097	1603	94.6555	10.4583
16	741	1545	109.69	3.125
17	1998	1574	101.827	0.166667
18	188	1867	51.4402	7.29167
19	553	1776	62.8215	5.91667
20	1555	1560	105.531	5.33333
21	161	1990	39.8536	11.8333
22	206	1783	61.8407	4.70833
23	507	1646	85.1453	2.75
24	1341	1577	101.054	0.0416667
25	291	1689	76.8	4.95833
26	402	1723	70.9151	8.95833
27	568	1829	55.8503	2.54167
28	792	1517	118.015	7.45833
29	1793	1525	115.558	7.04167
30	1791	1617	91.4197	7.54167
31	1810	1523	116.166	9.04167
32	3722	1458	138.309	1.5
33	995	1691	76.4373	0.0416667
34	233	1722	71.08	9.83333
35	2568	1496	124.782	3.08333
36	1373	1569	103.131	4.70833
37	2193	1445	143.354	0.625
38	1240	1588	98.2829	11.5833
39	980	1576	101.311	0.333333
40	819	1587	98.5309	2.79167

<i>Run</i>	<i>Generations</i>	<i>Best</i>	Fitness	<i>DOS</i>
41	362	1883	49.714	5.29167
42	820	1678	78.8338	3.16667
43	1938	1467	134.946	3.20833
44	627	1709	73.2676	8.45833
45	1344	1578	100.798	9.33333
46	604	1643	85.7689	0.125
47	1020	1497	124.449	1.375
48	580	1619	90.9688	12.0417
49	1252	1626	89.4124	3.16667
50	1197	1603	94.6555	9.125
Average	1044	1634	92.4972	5.545833
Best	2193	1445	143.354	0.625

22 Appendix D: Results of a GA with Directional Mate Preferences using a Distance Measure based on Length Difference applied to the 'Grötschels24'

<i>Run</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>
1	1246	1360	182.694
2	775	1429	149.883
3	1474	1439	145.759
4	879	1424	151.999
5	662	1376	174.344
6	186	1531	113.757
7	1407	1394	165.512
8	1735	1302	217.488
9	426	1485	128.521
10	645	1425	151.573
11	1780	1375	174.851
12	569	1427	150.725
13	1188	1425	151.573
14	510	1375	174.851
15	898	1381	171.832
16	1203	1406	159.933
17	1210	1480	130.267
18	1062	1321	205.243
19	382	1396	164.565
20	470	1425	151.573
21	541	1499	123.787
22	671	1451	140.997
23	293	1495	125.117
24	646	1373	175.872
25	1726	1312	210.933
26	307	1464	136.055
27	528	1491	126.465
28	431	1439	145.759
29	537	1470	133.848
30	400	1424	151.999
31	392	1486	128.175
32	262	1594	96.8115
33	1217	1445	143.354
34	234	1329	200.346
35	673	1417	155.025
36	625	1570	102.868
37	211	1497	124.449
38	297	1677	79.022
39	327	1464	136.055
40	739	1466	135.314

<i>Run</i>	Generations	<i>Best</i>	<i>Fitness</i>
41	753	1388	168.392
42	518	1375	174.851
43	624	1372	176.386
44	1398	1386	169.366
45	597	1354	185.954
46	888	1286	228.516
47	465	1559	105.802
48	1035	1436	146.981
49	385	1471	133.484
50	474	1464	136.055
Average	738	1433	152.3
Best	888	1286	228.516

23 Appendix F: Results of a Traditional GA applied to the 'Grötschels24' II

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>	<i>Found</i>	<i>Average DOS</i>	<i>Time</i>
1	533	1759	65.2855	1.125	37	9.35246	596
2	4705	1469	134.212	0.875	1010	8.61433	5371
3	236	1748	66.9444	3.25	82	7.31666	264
4	1801	1594	96.8115	5.75	1668	9.44748	2032
5	208	1731	69.6132	10.5417	14	6.32039	235
6	186	1511	119.901	5.04167	29	7.50346	210
7	1614	1667	80.9352	6.20833	122	9.24426	1826
8	889	1540	111.121	1.16667	749	7.75595	999
9	2361	1555	106.895	6.04167	257	7.95032	2670
10	621	1733	69.2924	2.125	119	10.9585	698
11	182	1873	50.7842	0.125	10	6.00851	204
12	605	1661	82.111	5.45833	430	8.32789	679
13	728	1720	71.4112	3.25	43	9.51456	817
14	200	1677	79.022	8.79167	67	5.59991	225
15	191	1695	75.7184	3.875	23	15.165	213
16	301	1809	58.3614	1.29167	130	13.1669	337
17	412	1638	86.8209	4.25	256	10.5121	462
18	2288	1427	150.725	3.79167	427	8.83769	2582
19	3586	1453	140.222	7.625	2615	9.25964	4082
20	162	2004	38.7516	4.75	23	7.21615	181
21	376	1647	84.9387	4.70833	35	7.66591	419
22	925	1439	145.759	0.0416667	411	6.5682	1036
23	487	1560	105.531	0.833333	184	9.29896	545
24	758	1661	82.111	1.875	72	8.19524	849
25	681	1537	111.991	7.20833	552	9.58002	762
26	909	1551	108.002	7.04167	341	11.5524	1017
27	4509	1524	115.862	4.08333	3793	9.07821	5135
28	1226	1624	89.8537	15.4167	285	8.43052	1378
29	3642	1570	102.868	7.41667	2783	8.84338	4140
30	2212	1599	95.6062	10.9583	359	10.5269	2494
31	592	1584	99.2794	5.58333	234	8.87413	662
32	1629	1319	206.491	6.95833	1461	9.53579	1833
33	1671	1552	107.724	1.58333	509	9.9169	1874
34	432	1891	48.8781	0.458333	78	12.3579	484
35	976	1588	98.2829	2	862	7.392	1092
36	708	1746	67.2517	8.58333	93	10.3288	793

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>	<i>Found</i>	<i>Average DOS</i>	<i>Time</i>
37	176	1624	89.8537	4.08333	38	11.3574	196
38	924	1608	93.4837	4.58333	284	7.50466	1036
39	205	1681	78.2725	14.125	25	16.4477	229
40	794	1584	99.2794	11.0833	639	7.50618	889
41	233	1574	101.827	2.75	38	13.255	262
42	273	1793	60.4726	6.04167	12	12.5633	306
43	713	1574	101.827	9.16667	332	9.01369	797
44	304	1527	114.954	8.375	174	11.1247	340
45	1070	1494	125.452	3.16667	52	8.7651	1242
46	426	1774	63.1053	1.41667	81	7.68215	482
47	783	1621	90.5207	7.70833	658	10.1479	884
48	583	1655	83.3083	4.04167	445	8.36932	654
49	329	1763	64.695	0.958333	52	12.9556	368
50	1958	1554	107.171	8	124	8.75631	2204
Best	1629	1319	206.491	6.95833	1461	9.53579	1833
Average	1046	1630	93.9918	5.111667	462.34	9.43333	1181.7
Std. Dev.	1096	128	29.7425	3.592739	763.248	2.24428	1247.876

24 Appendix G: Results of a GA with Assortative Mating using a Distance Measure based on Common Edges applied to the 'Grötschels24'

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
1	1316	1621	90.5207	569	6.89125	9510
2	1797	1684	77.7162	557	6.16648	11952
3	159	2000	39.0625	34	9.66456	1458
4	974	1516	118.327	446	6.16855	6431
5	237	1906	47.3575	29	9.39407	2117
6	1454	1536	112.283	474	4.79009	8085
7	1053	1590	97.7893	179	5.23384	6185
8	2852	1545	109.69	226	4.98843	16367
9	347	1907	47.2582	25	8.07225	2769
10	2553	1496	124.782	1161	5.50627	15698
11	2535	1397	164.095	1999	6.17482	16888
12	899	1649	84.5274	199	5.74388	5613
13	352	1748	66.9444	143	6.43875	2372
14	869	1666	81.1297	179	4.72811	4764
15	421	1604	94.4197	176	6.49345	2612
16	974	1588	98.2829	148	5.98458	6280
17	1708	1645	85.3525	564	5.67838	10629
18	217	1791	60.7432	30	8.11111	1728
19	735	1626	89.4124	181	5.5218	4458
20	248	1856	52.6706	121	8.11741	1975
21	910	1582	99.7824	49	5.15732	5283
22	2732	1437	146.573	2244	5.52472	16822
23	606	1678	78.8338	30	5.22645	3535
24	292	1600	95.3674	45	4.80756	1613
25	917	1575	101.568	599	6.49345	6234
26	4897	1399	163.158	380	5.11091	28927
27	1991	1440	145.355	1230	4.75226	11021
28	306	1819	57.0886	19	9.43934	2747
29	1110	1429	149.883	744	4.75924	6127
30	468	1719	71.5775	19	7	3344
31	464	1707	73.6115	20	6.70842	3224
32	238	1759	65.2855	22	7.5654	1800
33	2618	1506	121.501	1455	4.73825	14550
34	927	1580	100.289	29	6.69546	6476
35	450	1684	77.7162	42	5.87751	2848

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
36	160	1785	61.564	19	9.56604	1442
37	171	1845	53.938	10	9.18824	1491
38	281	1565	104.189	63	3.4	1256
39	5791	1529	114.354	155	5.21261	34818
40	1153	1555	106.895	399	6.3316	7696
Best	2535	1397	164.095	1999	6.17482	16888
Average	1205	1639	93.2724	375	6.33557	7479
Std. Dev.	1251	147	31.9195	538	1.56614	7395

25 Appendix H: Results of a GA with Aesthetic Sexual Selection using Absolute Mate Preferences for Symmetry applied to the 'Grötschels24'

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>	<i>Found</i>	<i>Average DOS</i>	<i>Av. Matings</i>	<i>Time</i>
1	612	1731	69.6132	6.625	333	4.98988	0.523732	1026
2	759	1562	104.992	1	592	4.57089	0.420844	1227
3	1017	1518	117.704	5	756	4.40669	0.496063	1673
4	409	1603	94.6555	12.875	171	4.20313	0.740196	707
5	1552	1615	91.8734	11.875	304	5.38204	0.818827	2840
6	1729	1524	115.862	9	924	5.06687	0.565972	2974
7	428	1775	62.9632	6.125	33	4.34687	0.405152	696
8	1333	1559	105.802	1.04167	964	5.07076	0.56982	2289
9	221	1634	87.6742	16.0833	18	3.79862	0.404545	349
10	194	1796	60.0696	9.33333	76	7.25313	1.21762	392
11	1214	1681	78.2725	2.125	857	4.77536	0.508656	2038
12	1530	1528	114.653	10	88	5.23324	0.838457	2771
13	264	1738	68.4985	5.5	27	7.39288	1.40304	546
14	855	1646	85.1453	6.16667	56	5.07468	0.813817	1560
15	1624	1411	157.678	5.70833	471	5.67705	1.0191	3130
16	904	1626	89.4124	12.3333	593	5.37425	0.981174	1681
17	444	1539	111.41	1.125	139	3.8628	0.365688	702
18	272	1937	44.3978	6.45833	132	4.7134	0.553506	457
19	150	2029	36.8767	10.2083	31	8.84115	1.95973	349
20	161	1834	55.2437	7.66667	37	3.66674	0.75625	271
21	378	1844	54.0551	6.08333	27	5.77688	0.883289	693
22	768	1781	62.119	9.375	648	4.62385	0.563233	1286
23	210	1731	69.6132	1.875	31	4.88191	0.660287	365
24	399	1791	60.7432	0.708333	53	6.23065	1.06281	772
25	760	1561	105.261	3.45833	249	5.31812	0.807642	1359
26	322	1732	69.4526	8.33333	22	5.49718	0.669782	560
27	189	1653	83.7122	6.70833	46	11.7764	5.91489	782
28	1258	1487	127.831	2.45833	772	5.29332	0.752586	2239
29	591	1546	109.406	8.75	86	5.20014	0.461017	991
30	156	1898	48.161	3.41667	28	5.69887	0.587097	278
31	1467	1561	105.261	0.541667	359	6.31687	1.53001	3189
32	398	1719	71.5775	7.54167	268	5.6094	0.934509	750
33	287	1475	132.042	2.04167	95	4.70461	0.604895	485
34	520	1582	99.7824	1.16667	236	4.23461	0.520231	849
35	683	1436	146.981	6.33333	372	5.57998	0.658358	1207

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>	<i>Found</i>	<i>Average DOS</i>	<i>Av. Matings</i>	<i>Time</i>
36	1328	1614	92.1013	3.66667	1207	5.34593	0.707611	2335
37	2848	1484	128.868	4.58333	1602	5.30261	1.0432	5481
38	1358	1691	76.4373	8.20833	519	5.00582	0.644068	2422
39	1236	1594	96.8115	7	357	5.14034	0.624291	2146
40	481	1628	88.9739	4.66667	356	4.85011	0.56875	816
41	252	1522	116.472	8.83333	115	6.71678	0.864542	472
42	796	1603	94.6555	2.79167	654	4.85842	0.566038	1345
43	494	1584	99.2794	9.66667	350	5.38786	0.693712	862
44	1068	1674	79.5899	7.25	37	3.93432	0.388004	1694
45	2122	1629	88.7556	3.54167	1300	5.53142	0.720886	3764
46	156	1591	97.5437	6.20833	20	3.57863	0.432258	242
47	164	1742	67.8715	4.08333	47	5.73902	0.588957	289
48	342	2060	34.7065	5.75	150	4.46544	0.390029	551
49	673	1502	122.801	6.25	194	7.22026	1.56548	1436
50	949	1684	77.7162	9.16667	422	5.96057	1.37553	1952
Best	1624	1411	157.678	5.70833	471	5.67705	1.0191	3130
Average	767	1654	89.2276	6.134165	344.48	5.38962	0.862924	1386
Std. Dev.	588	143	27.5184	3.513437	375.514	1.3612	0.804431	1092

26 Appendix I: Results of a GA with Directional Mate Preferences using a Distance Measure based on Common Edges applied to the 'Grötschels24'

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
1	225	2013	38.0632	83	12.1295	3833
2	479	1717	71.9116	178	12.8933	8672
3	139	1956	42.6977	20	13.6522	2615
4	144	2159	28.7653	30	11.2867	2375
5	1109	1580	100.289	61	11.5505	18463
6	197	2047	35.5966	66	14.4031	3865
7	251	2110	31.5319	11	11.664	4079
8	852	1660	82.3091	734	12.1011	14647
9	150	1946	43.5822	13	13.4027	2740
10	236	1867	51.4402	40	12.0638	3951
11	2053	1723	70.9151	378	12.4215	36564
12	202	1862	51.995	21	12.6468	3567
13	525	1970	41.4968	381	11.5382	8707
14	742	1658	82.7069	475	13.5992	14169
15	785	1720	71.4112	302	13.9503	15279
16	445	1636	87.2463	270	13.0338	8080
17	159	1921	45.8955	28	13.9114	2997
18	624	1822	56.7135	395	10.7528	9623
19	605	1802	59.2735	488	14.096	12132
20	341	1830	55.7283	225	11.7824	5800
21	1767	1541	110.833	285	13.6614	34811
22	1007	1962	42.1778	511	11.8161	16906
23	491	1981	40.5828	308	12.802	8821
24	351	1764	64.5484	204	12.9086	6365
25	1107	1826	56.2182	368	13.2767	20684
26	524	1871	51.0017	35	11.3614	8533
27	404	2014	37.9876	138	11.0422	6328
28	272	1947	43.4927	137	12.941	4906
29	504	1893	48.6718	274	11.5348	8269
30	950	1612	92.5593	577	11.8957	16041
31	742	1780	62.2587	96	13.4224	13891
32	456	1758	65.4342	145	12.1538	7923
33	188	1989	39.9338	65	13.2299	3501
34	221	1988	40.0142	52	12.1136	3819
35	231	2179	27.7237	10	12	3928

<i>Simulation</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
36	401	2035	36.4437	216	12.24	7046
37	375	1854	52.8982	243	13.3743	7001
38	838	1829	55.8503	639	12.3214	14679
39	2124	1678	78.8338	1254	12.9939	39199
40	141	2288	22.8064	22	11.0786	2185
Best	1767	1541	110.833	285	13.6614	34811
Average	584	1870	55.496	244	12.5262	10425
Std. Dev.	492	171	20.6793	250	0.94365	9104

27 Appendix J: Results of a Traditional GA applied to the 'Grötschels48'

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>	<i>Found</i>	<i>Average DOS</i>	<i>Time</i>
1	2285	10994	10.9521	22.2917	1550	20.6894	5857
2	1812	11676	8.60882	4.33333	34	23.3437	4720
3	4035	11052	10.724	20.375	521	21.386	10749
4	208	11311	9.77498	20.2708	74	29.9681	522
5	4611	10164	14.9921	19.5	4484	21.1448	11932
6	1725	11938	7.8776	15.2917	42	19.4153	4313
7	1296	11163	10.3038	27.1875	1048	24.4598	3230
8	548	11424	9.39393	4.29167	78	15.5897	1355
9	393	12338	6.90464	15.0833	222	16.8181	970
10	234	11454	9.2959	2.20833	33	22.5051	577
11	1061	11230	10.0601	15.2917	571	22.4455	2637
12	1760	10447	13.4324	21.5625	1581	19.3586	4432
13	1080	11820	8.19691	9.66667	44	22.4507	2697
14	3019	10702	12.1972	35.1667	280	21.4602	7615
15	2679	10838	11.5964	7.29167	1308	22.806	6723
16	1306	11122	10.4566	11.7917	812	24.7005	3246
17	2968	11482	9.20555	15.2917	1669	20.2875	7473
18	2252	11833	8.16095	35.8125	30	19.3838	5662
19	4724	10456	13.3862	22.2917	26	22.2275	12154
20	253	13007	5.59	9.39583	38	18.8557	630
21	2120	11807	8.23307	23.7708	54	22.5684	5344
22	6817	10320	14.1059	1.58333	5943	19.8307	17771
23	1876	11348	9.64812	6.91667	958	20.7422	4687
24	1563	12120	7.41497	5.5	1099	23.8527	3898
25	2568	11473	9.23447	3.97917	1479	19.4105	6477
26	1801	12019	7.66737	10.9375	572	20.1263	4534
27	497	11211	10.1284	36.4792	345	19.8494	1229
28	1421	11736	8.43412	40.625	305	21.544	3542
29	1314	10903	11.3223	18.4375	215	22.4096	3275
30	1240	11695	8.55301	8.14583	669	20.1678	3083
31	1218	12104	7.45426	19.2083	773	19.6597	3029
32	319	11387	9.51662	26.3958	155	19.5171	794
33	3457	10757	11.9497	20.7292	256	21.123	8735
34	800	12373	6.82684	16.0625	614	18.0123	1981
35	3081	9915	16.5558	8.89583	281	23.5047	7798
36	451	10798	11.7692	1.54167	91	24.9052	1120

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>DOS</i>	<i>Found</i>	<i>Average DOS</i>	<i>Time</i>
37	1892	11732	8.44562	2.04167	1338	18.7216	4734
38	944	10133	15.1764	20.2708	643	24.8193	2355
39	1344	11126	10.4415	13.4583	721	19.7024	3364
40	631	12939	5.70844	3.14583	45	31.8714	1567
41	934	12142	7.36138	13.1667	104	24.3761	2337
42	1239	11626	8.75787	25.2083	540	21.328	3095
43	862	11402	9.46664	17.5	40	21.8829	2146
44	3174	11132	10.419	16.9583	1811	23.0058	8065
45	6620	9549	19.2437	31.9792	5909	23.703	17232
46	5545	9194	22.3925	2.58333	748	22.5857	14254
47	1257	10678	12.3072	33.2917	393	24.42	3133
48	1848	11300	9.8131	35.75	1324	20.8088	4620
49	248	12590	6.36821	24.75	27	40.1631	612
50	1802	11451	9.30564	8.14583	1570	21.5887	4506
Best	5545	9194	22.3925	2.58333	748	22.5857	14254
Average	1943	11308	10.3026	16.6371	869	22.1099	4936
Std. Dev.	4866	790.1	3.24825	10.6289	1295	3.83469	4093

28 Appendix K: Results of a GA with Directional Mate Preferences using a Distance Measure based on Length Difference applied to the 'Grötschels48'

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
1	398	10338	14.0079	274	1.66751	2020
2	1027	9453	20.0374	615	1.12476	4763
3	112	12625	6.29788	8	1.08108	501
4	387	12053	7.58122	257	1.04404	1809
5	233	11672	8.62063	118	1.94828	1270
6	532	10466	13.3351	420	1.03013	2468
7	161	12691	6.16789	49	1.7875	874
8	112	14668	3.4565	7	0.81982	499
9	300	11803	8.24423	194	1.17726	1431
10	393	12260	7.08204	105	1.51276	1987
11	382	11611	8.80322	265	1.50656	1885
12	236	13896	4.29102	99	1.28511	1112
13	1678	9683	18.2004	1573	1.00298	7641
14	397	12203	7.21529	163	1.44192	1903
15	134	13376	4.99822	10	1.23308	607
16	804	10042	15.734	612	1.23163	3717
17	215	9708	18.0136	113	3.21495	1322
18	504	10886	11.3932	390	1.18489	2292
19	425	9805	17.3113	225	3.26179	2662
20	739	10552	12.9057	631	1.31572	3465
21	338	10367	13.8518	218	2.16617	1808
22	313	12109	7.44195	210	1.51603	1495
23	591	12538	6.47451	473	1.1678	2725
24	866	9093	23.4041	749	1.52139	4225
25	132	12411	6.74362	18	1.9313	670
26	340	10838	11.5964	228	1.24484	1558
27	220	11598	8.84275	35	1.96347	1134
28	704	10913	11.2809	538	0.972973	3101
29	111	14788	3.34566	5	0.590909	443
30	786	8930	25.1602	372	1.1707	3591
31	676	9566	19.1073	563	1.11407	3030
32	627	9335	21.0699	497	1.63099	3095
33	139	13361	5.0207	15	1.78986	688
34	175	14312	3.81346	9	0.971264	762
35	889	8885	25.6738	776	1.43018	4269

<i>Simulation</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
36	497	10898	11.3431	366	1.68952	2457
37	549	10912	11.285	382	1.03285	2455
38	926	9791	17.4105	792	0.87027	3988
39	491	11072	10.6467	388	1.3551	2316
40	209	11082	10.6083	108	2.54327	1181
Best	786	8930	25.1602	372	1.1707	3591
Average	469	11315	11.6954	321.75	1.46361815	2230
Std. Dev.	323	1599	6.15108	311.436	0.571029	1463

29 Appendix L: Results of a GA with Directional Mate Preferences using a Distance Measure based on Common Edges applied to the 'Grötschels48'

<i>Run</i>	<i>Gen</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
1	470	11735	8.43699	68	0.185501	4295
2	1759	11724	8.4687	36	0.182594	16071
3	460	12355	6.86671	336	0.130719	4090
4	1483	11508	9.12264	30	0.159919	13507
5	2088	9812	17.2619	1007	0.191663	19167
6	1413	9931	16.4493	989	0.173513	12892
7	1179	10800	11.7605	510	0.201188	10801
8	318	11609	19.7708	96	0.179811	2881
9	4234	11499	9.15123	2053	0.18781	38816
10	373	12121	7.41253	43	0.147849	3308
11	1926	10817	11.6867	775	0.190649	17786
12	2556	11227	10.0708	1521	0.183953	23544
13	220	13705	4.53528	39	0.178082	1953
14	877	11024	10.8334	227	0.172374	7946
15	626	10862	11.4943	142	0.206831	5706
16	711	9857	16.9489	371	0.171831	6462
17	1831	11018	10.857	506	0.187432	17459
18	218	12422	6.71976	23	0.21659	2159
19	3567	9871	16.8529	3214	0.181155	33296
20	3123	10812	11.7084	1860	0.178091	29318
21	3429	10224	14.6432	1680	0.180572	31406
22	6320	11020	10.8491	4439	0.1812	58877
23	5124	10258	14.45	4918	0.178021	47461
24	2439	11526	9.06579	1956	0.16612	22051
25	2426	11129	10.4303	237	0.188041	22256
26	2658	11085	10.5969	2167	0.187429	24325
27	248	11591	8.86413	45	0.137652	2176
28	308	11110	10.5018	26	0.166124	2724
29	5632	9716	17.9544	2433	0.183094	51826
30	5904	10326	14.0732	3791	0.179061	54401
31	3821	11110	10.5018	1549	0.192408	35418
32	2130	11549	8.99378	1446	0.1752	19413
33	307	12775	6.00726	120	0.147059	2712
34	227	12403	6.76103	69	0.132743	1984
35	1998	9614	18.7285	1100	0.186279	18372

<i>Simulation</i>	<i>Generations</i>	<i>Best</i>	<i>Fitness</i>	<i>Found</i>	<i>Av. Matings</i>	<i>Time</i>
36	623	11260	9.95328	43	0.173633	5754
37	2273	10803	11.7474	1938	0.189701	21298
38	1178	11412	9.4335	792	0.172472	10773
39	1027	11333	9.6993	61	0.15692	9245
40	357	11553	8.98133	37	0.148876	3197
Best	1998	9614	18.7285	1100	0.186279	18372
Average	1947	11163	11.2161	1067	0.175754	17928.15
Std. Dev.	1701	886	3.7042	1280	0.018803	15770.55

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