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# **Evaluation of a Genetic Algorithm on generating critical Scenarios in a Traffic Simulation**

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# Abstract

This is a placeholder for the abstract. It summarizes the whole thesis to give a very short overview. Usually, this the abstract is written when the whole thesis text is finished.



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# 1 Introduction

This Thesis will use a Genetic Algorithm in order to generate critical Driving Scenarios for testing ADAS/AD Functionality in vehicles. While generating these scenarios is the objective, the main task of the thesis will evolve around the implementation of the Genetic Algorithm as well as the Optimization of its Hyperparameter.

## 1.1 Research Questions

### 1.1.1 Research Question 1

*Is a Genetic Algorithm suitable for generating critical driving scenarios compared to a random generation?*

### 1.1.2 Research Question 2

*Is it possible to improve the performance of a Genetic Algorithm using Taguchi Orthogonal Array Testing?*

Taguchi Orthogonal Arrays allow for minimal experiment runs when testing across different settings Roy, 1990). It will be analyzed if this method can be used to

### 1.1.3 Research Question 3

*Can a hypertuned Genetic Algorithm generalize on different start scenarios?*

Due to performance considerations, only one start scenario was defined. When evaluating the optimized Genetic Algorithm, its performance will be compared across different start scenarios.

## 1.2 Shortcomings

This Master Thesis started with the development of the Traffic Manager and thus progress was closely linked. Without a working simulation, no genetic algorithm could be tested. Due to time and performance constraints, it is not possible to test a full driving stack like autoware, as well as other professional ADAS/AD functions. In this Thesis, internal functions like Time-To-Collision and Emergency Braking will be optimized. The learned information on e.g. optimal hyperparameter settings can then be applied in further steps to test these functions. This will however not be tackled by this thesis.

Performance is also a problem and will lead to many shortcuts that need to be taken. There is a huge number of possible combinations of hyperparameters, so only a handful can be tested. In further chapters, these shortcuts will be explained and their relevancy will be discussed.

## 2 Foundations

### 2.1 Genetic Algorithm

**General** Pioneered by John Holland (1974) , [Genetic Algorithms \(GAs\)](#) imitate natural selection and the Darwinian principle called "survival of the fittest". Genetic Algorithms search the solution space using a population of individuals. Each individual contains one chromosome, which serves as a candidate solution. Using genetic operations, the individuals mate among themselves and mutate independently. Which individual is chosen depends on a fitness function, which defines the search problem. Individuals that do poorly on the given problem die out, while "strong" individuals propagate. Genetic Algorithms iteratively (each iteration is call "generation") optimize by manipulating a population of potential solutions (Srinivas and Patnaik, 1994). Chromosomes consist of individual genes, which form a solution to the search problem. Over generations using genetic operations, gene values and position will be optimized, resulting in iteratively better solutions (Srinivas and Patnaik, 1994). This masters thesis will utilize generational genetic algorithms, where each generation, the entire population is replaces. Contrary to that, steady state genetic algorithms only replace a small fraction of the population at a time (Srinivas and Patnaik, 1994).

[Find paper](#)

Genetic algorithms are a subclass of evolutionary algorithms (Mills, Filliben, and Haines, 2015).

" The Fitness Function: The fitness function in Genetic Algorithm represents the objective function and the fitness value corresponds the performance of an individual chromosome. "Majumdar and Ghosh, 2015

**Pros** This search method on the basis of biological principles allows trough its population for a global and dispersed search which avoids various shortcommings of local search techniques (Grefenstette, 1986). Especially on difficult search spaces with lots of local optima, a genetic alogorithm is less prone to get stuck on a substandard solution (Katoch, Chauhan, and Kumar, 2021, Xia et al., 2019, Majumdar and Ghosh, 2015). Genetic Algorithms offer advantages for complex optimization and non-deterministic polynomial (NP-hard) problems (Hussain and Muhammad, 2020).

“GAs can find good solutions within a large, ill-defined search space, and can be readily adapted to a wide variety of search problems (Mitchell, 1998)” (Mills, Filliben, and Haines, 2015)

Grefenstette, 1986 further emphasis its ability to outperform gradient techniques on difficult problems such as "as optimizations involving discontinuous, noisy, high-dimensional, and multimodal objective functions." Adding, that base Genetic Algorithms their effectiveness on their "ability to exploit efficiently this vast amount of accumulating knowledge by means of relatively simple selection mechanisms".

“The most attractive feature of GA is that it has the ability to explore the search space with the help of the entire population of individuals.” (Hussain and Muhammad, 2020)

Further advantages are the "high implicit parallelism", which makes genetic algorithms "numerically very efficient" (Marsili Libelli and Alba, 2000).

“The power and simplicity of GA make it popular for even largescale optimization problems. The main advantage of GA is that it does not require neither mathematical expression of response surfaces nor any derivative or gradient information” (Boyabatli and Sabuncuoglu, 2004)

**Basic Structure** At its core, a genetic algorithm uses a list of simple evolution inspired functions. A basic genetic algorithm can be seen here, according to Srinivas and Patnaik, 1994.

Probably ref  
Holland or De-  
jong

```
1  simple_genetic_algorithm()  
2  {  
3      initialize_population();
```

```
4     evaluate_population();
5     for(int i = 0; i < num_of_generations; i++)
6     {
7         select_individuals_for_next_population();
8         perform_crossover();
9         perform_mutation();
10        evaluate_population();
11    }
12 }
```

First, the population is initialized randomly and its individuals are subsequently evaluated using the fitness function. The following steps are now repeated until some stopping criterion is triggered (Grefenstette, 1986) (in this case, it is just a maximum on the number of generations). The individuals are chosen using a selection operation, which takes their fitness value under consideration. Next, under some crossover probability, the selected individuals mate, producing new offspring. This serves the purpose of exchanging information between the chromosomes as genes. Further, a handful of individuals (selected using a mutation probability) get mutated, which adds small variations to the chromosomes, thus adding new variation to the population. Finally the new population gets evaluated.

" Stopping criteria: Stopping criteria determines what causes the algorithm to terminate-generations, time limit, fitness limit etc. "Majumdar and Ghosh, 2015

**Problems** According to Hussain and Muhammad, 2020, genetic algorithms suffer from an exploration vs exploitation dilemma. If the algorithm converges too quickly to a solution, most of the search space might not have yet been explored, thus increasing the probability of getting stuck at only a local optimum. In contrast to that, a low convergence rate will be time consuming and result in wasted computational resources.

"Finding a balance between exploration and exploitation has been a difficult-to-achieve goal from the beginning." (K. De Jong, 2007)

Genetic algorithms also require an application specific encoding of genes, which requires time and domain specific knowledge. Due to know real

consensus on the "best parameter settings" (see section 4, their optimal selection proves to be difficult.

" Premature convergence is a common issue for GA. It can lead to the loss of alleles that makes it difficult to identify a gene [15]. Premature convergence states that the result will be suboptimal if the optimization problem coincides too early. "Katoch, Chauhan, and Kumar, 2021

### 2.1.1 Genes

The encoding of the genes proved to be, besides the hyperparameter tuning, the main challenge of setting up a genetic algorithm pipeline. A simple and commonly used representation for genes is binary encoding. As suggested by its name, a gene can take the form of 0 or 1. Further common encodings are octal and hexadecimal representations (Srinivas and Patnaik, 1994, Katoch, Chauhan, and Kumar, 2021).

In case a custom encoding needs to be used, the genetic operation crossover and mutation have to be tailored accordingly. Srinivas and Patnaik, 1994 suggests, to use integer representations in case a optimization problem has real-valued continuous variables. These variables are linearly mapped to integers defined in a specific range. It is also possible to again represent these integers as binary encodings.

Various other encodings are available, often very problem specific. For example tree encodings allows for genes to represent programming functions, leading to a path of genetic algorithms called "genetic programming" (Katoch, Chauhan, and Kumar, 2021).

### 2.1.2 Control Parameter of a Genetic Algorithm

Hyperparameters have a huge influence on the performance of a Genetic Algorithm. They have an impact on the "convergence" ... It has been shown, that there is no universal hyperparameter set and that it needs to be optimized on a per "problem" basis.



### **Num of generations**

The Number of Generation defines the duration of a GA. As long as the algorithm has not converged, ....? For my testing, using a generation size of 30 was almost always sufficient, and will thus mostly be used.

### **Population Size**

Controlling the Population Size, which defines the number of individuals per generation, has a direct impact on the performance of the genetic algorithm. Research seems to be in agreement, that a small population leads to less diverse individuals and might provide an insufficient sample size. This can lead to a premature convergence to a local optimum. Increasing the population size will allow the genetic algorithm to perform a more informed search. However computation time will suffer due to the larger number of individuals per generation as well as slower convergence to an optimum (Grefenstette, 1986, Katoch, Chauhan, and Kumar, 2021, K. De Jong, 2007). K. De Jong, 2007 also suggest, that "complex, multi-peaked landscapes may require populations of 100s or even 1000s of parents in order to have some reasonable chance of finding globally optimal solutions" This Exploration-Exploitation problem is at the core of the Genetic Algorithm.

Increasing population size will increase the degree of parallelism, as each individual represents one search point (Mills, Filliben, and Haines, 2015).

" As a consequence, most EAs used in practice today run with a fixed population size, the value of which may be based on existing off-line studies (e.g., [34]) or more likely via manual tuning over multiple runs. "K. De Jong, 2007

### **Selection**

The selection operator chooses two parents for crossover and mutation operation until the list of offsprings has reached the desired population size. The selection operator will favour individuals based on their fitness value, ensuring their increased representation from generation to generation

(Srinivas and Patnaik, 1994). Weak solutions thus will be discarded over time.

The selection algorithm again needs to satisfy two requirements. On the one hand, high selection pressure will lead to decreased diversity in the population resulting in premature convergence (Katoch, Chauhan, and Kumar, 2021). This results in the algorithm behaving more like a local search method like a hill-climber or a “greedy” algorithm (K. De Jong, 2007). The initial low average fitness value of the population will in combination with a few good performing individuals will lead to them overtaking the population, drastically reducing diversity. On the other hand, a low selection pressure will struggle to converge at an optimum.

Hussain and Muhammad, 2020 propose a selection method where initially a low selection pressure is applied, while increasing it to the end, arguing, that “trade-off between these two competing criteria, an adjustable selection pressure must desired”.

Different selection methods like stochastic uniform remainder, random selection, rank selection, roulette wheel selection and tournament selection exist (Majumdar and Ghosh, 2015). The choice of selection method highly affects the performance of the Genetic Algorithm (Hussain and Muhammad, 2020).

Roulette wheel selection is a popular mechanism, where each individual corresponds to an area on the roulette wheel, based on its fitness value ( $f_i$ ). Grefenstette, 1986 points out the scaling problem as a major drawback, which means, that as the algorithm progresses, its fitness variance to mean ratio becomes increasingly small, which leads to low selection pressure. This problem can be mitigated by using ranks instead of the fitness value (Katoch, Chauhan, and Kumar, 2021).

cite Holland,  
else: Hussain  
and Muham-  
mad, 2020

Tournament selection is a popular alternative to roulette selection. First, a tournament size  $t$  has to be chosen. Until the desired number of offsprings is achieved,  $t$  individuals will be chosen at random from the population. Only from this smaller list, the best individual is selected. A popular tournament size is 2, larger sizes might enhance competition among individuals, however it also has an impact on the diversity of the population (Hussain and Muhammad, 2020). In a comparison of different selection methods

by Jinghui Zhong et al., 2005, tournament selection was deemed to be the most performant, converging more quickly than for example roulette wheel selection.

Hussain and Muhammad, 2020 provide an extensive comparison of different selection techniques.

Elite is an additional method to help the selection process, proposed by K. A. De Jong, 1975. Here the best  $n$  individuals are automatically chosen to go into the next generation. This can help improve performance, as the best individuals are not removed by randomness.

### Crossover

The crossover operation serves as the mating process between two individuals (chosen from the population by the selection operation). Its resulting offspring has a combination of both parents' genes. Grefenstette, 1986 highlights, that this "First, it provides new points for further testing within the hyperplanes already represented in the population." and "Second, crossover introduces representatives of new hyperplanes into the population".

Different types of crossovers can be chosen, the most simple approach being the single-point crossover. Here a randomly chosen point along the length of the chromosome is chosen. The two parents will swap their genetic information at this point, generating two new offsprings (Katoch, Chauhan, and Kumar, 2021). Extensions are the two- or multipoint crossover operations, where chromosomes are divided by  $k$  segments, which will get exchanged. They eliminate a disadvantage of "the single-point crossover bias toward bits at the ends of strings." (Srinivas and Patnaik, 1994)

A second crossover operation is the uniform crossover, here, based on a probability, it randomly decides to swap genes between the parents, independent of the exchange of other genes (Katoch, Chauhan, and Kumar, 2021).

To classify techniques, we can use the notions of positional and distributional biases. A crossover operator has positional bias if the probability that a bit is swapped depends on its position in the string. Distributional

bias is related to the number of bits exchanged by the crossover operator. If the distribution of the number is nonuniform, the crossover operator has a distributional bias. Among the various crossover operators, single-point crossover exhibits the maximum positional bias and the least distributional bias. Uniform crossover, at the other end of the spectrum, has maximal distributional bias and minimal positional bias. (Srinivas and Patnaik, 1994)

According to Srinivas and Patnaik, 1994 the ignoring of the genes position results in a higher disruptiveness, which has potential drawbacks. However it will be more exploratory in homogeneous populations where k-point crossovers might struggle to explore. Srinivas and Patnaik, 1994 also suggests that uniform crossover is more useful in small populations. Larger populations inherently are more diverse, making k-point crossover more suitable.

Find good research paper, maybe Katoch, Chauhan, and Kumar, 2021

Other crossover operations are analysed in paper .

Not only the crossover type has to be chosen, a crossover probability (or crossover rate) also needs definition. This value defines, how likely a single crossover operation is to be applied on the parent population. If no crossover will be applied, the parents will directly be used as children. The problem of choosing a crossover probability again comes back to the exploration/-exploitation balance. Higher crossover rates will introduce new structures quickly into the population, however good structures might get disrupted. A low crossover rate will result in a low exploration, resulting in stagnation (Grefenstette, 1986).

"If reproductive variation is too strong, the result is undirected random search." (K. De Jong, 2007)

### **Mutation**

The Mutation operation is applied after crossover as a means to maintain the diversity of the gene pool. Through small random changes, the variability of the population increases. Each individual can be exposed to a mutation, irrespective of their fitness value (Srinivas and Patnaik, 1994). Mutation is controlled by a "MutationProbability" which chooses the individuals that

are mutated. An "IndividualMutationProbability" will decide which genes of the chosen chromosome are mutated.

"If the mutation is not considered during evolution, then there will be no new information available for evolution."(Katoch, Chauhan, and Kumar, 2021)

Depending on the gene encoding, the mutation operation might vary. In case of binary gene encoding, mutation will only flip certain bits. For custom encodings, the mutation operation needs to be tailored accordingly.

The setting of the mutation probabilities again needs to be chosen carefully. If it is too high, the genetic algorithm might transform into random testing, too low and the population will not be able to maintain diversity and reintroduce genetic material. (Klampfl, Klück, and Wotawa, 2023, Grefenstette, 1986). "A low level of mutation serves to prevent any given bit position from remaining forever converged to a single value in- the entire population." (Grefenstette, 1986)

" DeJong believes that EAs pre-tuned with default parameter values for particular problem classes will continue providing better performance than EAs that attempt to dynamically adapt too many control parameters for specific problems. So, even after 30+ years of research, the question of best settings for EA and GA control parameters has no widely agreed answer. "Mills, Filliben, and Haines, 2015

### **Adaptive Control Parameters**

#### **GENERALL**

" My sense is that, for static optimization problems, it will to continue to be the case that particular types of EAs that have been pre-tuned for particular classes of problems will continue to outperform EAs that try to adapt too many things dynamically. "K. De Jong, 2007

" Parameter settings optimal in the earlier stages of the search typically become inefficient during the later stages. Similarly, encodings become too coarse as the search progresses, and the fraction of the search space that the GA focuses its search on becomes progressively smaller. To overcome these

drawbacks, several dynamic and adaptive strategies for varying the control parameters and encodings have been proposed. One strategy exponentially decreases mutation rates with increasing numbers of generations, to gradually decrease the search rate and disruption of strings as the population converges in the search space. Another approach considers dynamically modifying the rates at which the various genetic operators are used, based on their performance. Each operator is evaluated for the fitness values of strings it generates in subsequent generations. Very often, after a large fraction of the population has converged (the strings have become homogeneous), crossover becomes ineffective in searching for better strings. Typically, low mutation rates (0.001 to 0.01) are inadequate for continuing exploration. In such a situation, a dynamic approach for varying mutation rates based on the Hamming distance between strings to be crossed can be useful. The mutation rate increases as the Hamming distance between strings decreases. As the strings to be crossed resemble each other to a greater extent, the capacity of crossover to generate new strings decreases, but the increased mutation rate sustains the search. "Srinivas and Patnaik, 1994

" The purist might argue that inventing feedback control procedures for EAs is a good example of over-engineering an already sophisticated adaptive system.

A better strategy is to take our inspiration from nature and design our EAs to be self-regulating. For example, individuals in the population might contain "regulatory genes" that control mutation and recombination mechanisms, and these regulatory genes would be subject to the same evolutionary processes as the rest of the genome. "K. De Jong, 2007

" Perhaps the most interesting thing to note today, after more than 30 years of experimenting with dynamic parameter setting strategies, is that, with one exception, none of them are used routinely in every day practice. The one exception are the strategies used by the ES community for mutation step size adaptation. "K. De Jong, 2007

" My own view is that there is not much to be gained in dynamically adapting EA parameter settings when solving static optimization problems. The real payoff for dynamic parameter setting strategies is when the fitness landscapes are themselves dynamic (see, for example, [4], [5], or [32]). "K. De Jong, 2007

" For instance, in a GA, one may want to decrease the probability of crossover and mutation over time to avoid too high reproductive variation hindering convergence to local optima. However, in that case, one would need to set new parameters that define how much and how often each probability is decreased. Research has not yet concluded if one technique has a clear advantage over the other. "Klampfl, Klück, and Wotawa, 2023

MUTATION "It is shown in this paper that making mutation a function of fitness produces a more efficient search. This function is such that the least significant bits are more likely to be mutated in high-fitness chromosomes, thus improving their accuracy, whereas low-fitness chromosomes have an increased probability of mutation, enhancing their role in the search. In this way, the chance of disrupting a high-fitness chromosome is decreased and the exploratory role of low-fitness chromosomes is best exploited. " Marsili Libelli and Alba, 2000

" The weak point of "classical" GAs is the total randomness of mutation, which is applied equally to all chromosomes, irrespective of their fitness. Thus a very good chromosome is equally likely to be disrupted by mutation as a bad one. On the other hand, bad chromosomes are less likely to produce good ones through crossover, because of their lack of building blocks, until they remain unchanged. They would benefit the most from mutation and could be used to spread throughout the parameter space to increase the search thoroughness. So there are two conflicting needs in determining the best probability of mutation. Usually, a reasonable compromise in the case of a constant mutation is to keep the probability low to avoid disruption of good chromosomes, but this would prevent a high mutation rate of low-fitness chromosomes. Thus a constant probability of mutation would probably miss both goals and result in a slow improvement of the population. "Marsili Libelli and Alba, 2000

" This paper has presented an improved search algorithm to reduce the chance that high-fitness chromosomes are muted during the search, thus losing their favourable schemata. In GAs, mutation is usually assigned a constant probability and thus all chromosome have the same likelihood of mutation irrespective of their fitness. Conversely, making mutation a function of fitness produces a more efficient search. "Marsili Libelli and Alba, 2000

" significant bits are likely to be muted in high-fitness chromosomes, thus improving their accuracy, whereas low-fitness chromosomes are much more likely to change, enhancing their exploratory role in the search. "Marsili Libelli and Alba, 2000

" In all cases the new algorithm showed a faster improvement of the maximum fitness, which was always greater than the one produced by the classical GA at the same generation. "Marsili Libelli and Alba, 2000

" In 2007, DeJong took a broader view, considering what was known with respect to the wider community of evolutionary algorithms (EAs). He observed that while it appears that adapting mutation rate on-line during execution provides advantages, most EAs are deployed with a default set of static parameter values that have been found quite robust in practice. "Mills, Filliben, and Haines, 2015



## 3 Implementation

### 3.1 Traffic Manager

A custom developed Traffic Manager will be used to simulate an environment, that can subsequently be controlled by the Genetic Algorithm. The Traffic Manager is not part of this thesis and will be regarded as a "blackbox", only receiving a brief introduction. In general, it will simulate traffic starting from a predefined scenarios which defines the positions and types of vehicles and pedestrians(i.e. actors). A simulation always consist of at least one EGO vehicle. Additionally any number of NPCs can be used.

While the NPCs are only controlled by the Traffic Manager, the ego vehicle can be either partly or completely controlled by an ADAS/AD function. The goal of the Genetic Algorithm is to test these functions for safety.

For all simulations done by this thesis, the Traffic Manager was set to 100Hz and the simulation duration set to 35 seconds.

#### 3.1.1 Action Interface

To control the behaviour of the actors inside the simulation, actions can be requested over the "Action Interface", which is provided by the Traffic Manager. An action will initiate a certain behaviour from an actor. It can be set to at any timestep for any actor<sup>1</sup>. Pedestrians and vehicles have a different set of actions.

Insert graph of  
action interface

---

<sup>1</sup>depending on the ADAS/AD function under test, the Action Interface might be disabled for the EGO vehicle

If no action is set, the actor will behave in a normal manner inside the simulation. This means that the actor will follow along its path until a new action changes its behaviour.

The following list are all actions provided by the traffic manager that were available for the genetic algorithm at the time of this master thesis.

- JunctionSelection
  - Parameters: Vehicle ID: int, Junction\_selection\_angle: float
  - Angle is set in radiant. Default value is 0. Vehicles will choose which direction to take at a junction based on this angle.
- LaneChange
  - Parameters: Vehicle ID: int, ...
  - Initiates a LaneChange based on its given parameters.
- AbortLaneChange
  - Parameters: Vehicle ID: int, ...
  - If a LaneChange is currently happening, it will get aborted.
- ModifyTargetVelocity
  - Parameters: Vehicle ID: int, ...
  - Modifies the internal Target Velocity of the Traffic Manager by a percentage. If it is for example 0, the vehicle will stop.
- TurnHeading
  - Parameters: Pedestrian ID: int, ...
  - The pedestrian will turn 180 degrees and walk in the opposite direction
- CrossRoad
  - Parameters: Pedestrian ID: int, ...
  - The pedestrian will cross the road immediately.
- CrossAtCrosswalk
  - Parameters: Pedestrian ID: int, ...
  - The pedestrian will cross the road at the next crosswalk.

All these actions are accessed by the Genetic Algorithm and the Behavior tree. The Behaviour tree sets only actions for the EGO vehicle, while the Genetic Algorithm will set all actions for the other actors in the simulation.

### 3.1.2 Map and Starting Scenario

The map is Town10 from Carla. It was chosen, because 1. its roads are self contained, 2. its not too big, yet still complex and 3. its supported by Carla and thus visualization looks better.

The Starting Scenario defines the number and type of all actors as well as their position. It needs to be created manually.

## 3.2 Genetic Algorithm

The task of the Genetic Algorithm is to search for sequences of actions that will result in the most interesting scenarios according to its cost function. For implementing the Genetic Algorithm, DEAP<sup>2</sup> was chosen. It is a popular tool for academia and allows for high customisability. As has been stated in section 3.1.1, the algorithm has full access over setting actions for all NPCs. Searching for sequences of actions, it tries to optimize a cost function. This section aims to explain how the genetic algorithm was implemented and which different hyperparameters are variable. In chapter 4, the best hyperparameter combination will be generated, further analysis is done in 5.

A few default settings for the genetic algorithm had to be chosen. It was decided that the genetic algorithm will set an action per actor every 50 steps, which translates to 0.5 seconds (simulation runs at 100hz). In other words, every 50 steps of the simulation is 1 timestep for the genetic algorithm. The time of a simulation is always set to 35 seconds. Each genetic algorithm will run for 30 generations. These to settings were chosen with the aim of reducing the amount of needed computations.

---

<sup>2</sup><https://deap.readthedocs.io/en/master>

If the GA decides to not set an action for the integer, it sets "NoAction" as a placeholder.

#### 3.2.1 Usage for GA

maybe remove

insert ref to discussion

Due to the fact, that there is no full stack available for the EGO vehicle, a solution had to be found. In order to have the Genetic Algorithm control only NPCs and not the EGO vehicle itself, a behaviour tree is used. The behaviour tree is used to control the EGO vehicle over the action interface provided by the Traffic Manager. This is the same as the Genetic Algorithm is doing.

The behaviour tree will define which direction the EGO should take at junctions and it will realistically dodge obstacles introduced by the Genetic Algorithm. The main goal of the BT is to make the EGO vehicle behave in a realistic way.

#### 3.2.2 Encoding

When implementing a Genetic Algorithm, it is necessary to implement an encoding that fits to the problem. Each individual basically thus needs to include all actions that the genetic algorithm wants to apply. Different encodings presented in section 2.1.1, however none directly fitted to the problem presented. A custom encoding for both chromosomes and genes needed to be generated.

##### Chromosome

ref

Each individual has 1 chromosome which consists of a list of genes, which has been explained in section . Starting out, 2 different encodings came to mind, in both cases, the genes position in the chromosome defined the time an action is set.

**Time** The first encoding is will be called "Time". Each gene corresponds to 1 timestep (so 1 gene per every 0.5 seconds). One gene has a list of the length of the number of all NPCs. This list is populated with actions. The index of an action in the list corresponds to the NPC id (index + 1 as the ego has id == 0, thus a start at 1 is needed). A visualization is seen in figure 3.1.

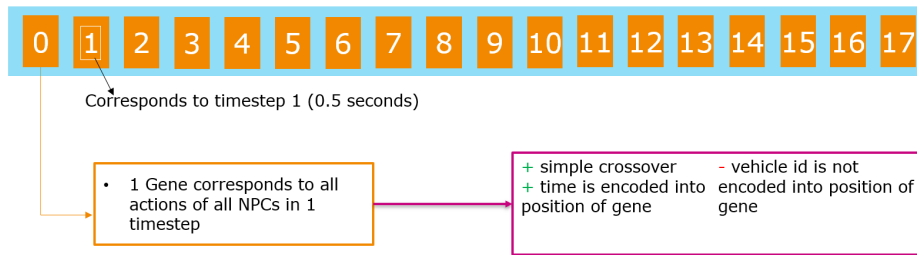


Figure 3.1: Time

Given the previously stated simulation time of 35 seconds, each chromosome has a length of  $35 * 2 = 70$  genes. Each gene consists of *number\_of\_actors* actions. Crossover can thus only move all actions of a timestep at once, modifying between actions of the same timestep can only be done using mutation. If this is desired will be seen in the next chapters.

**TimeNPC** The second encoding has the name "TimeNPC", and is somewhat differently structured. Now, genes only hold 1 action, encoding now not only the timestep, but also the actor id in the position of the gene inside the chromosome. Now, each actors actions will be listed one after another. This is visualized in figure 3.2.

Now, each gene has a length of 1 and each chromosome now has a length of  $35 * 2 * \text{number\_of\_actors}$ , which makes them much longer compared to the previous encoding. This now allows the crossover operation to modify only specific actions of one timestep. Previously this was not possible.

However for this encoding to make sense, the crossover operations "One-Point" and "TwoPoint" had to be modified as follows. In an example of 10

### 3 Implementation

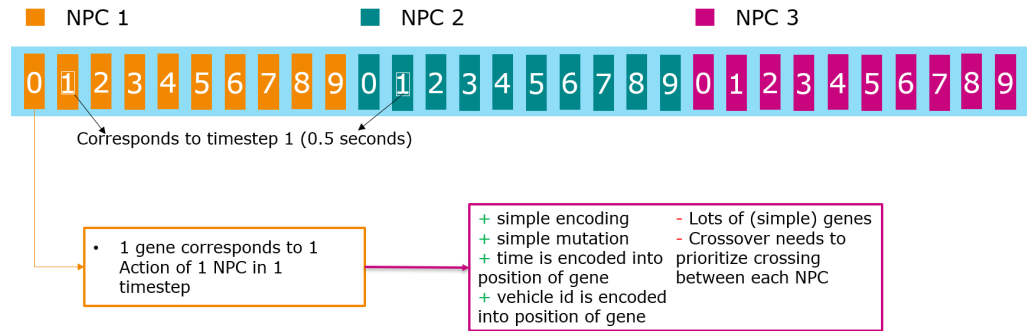


Figure 3.2: Time + NPC

NPCs, the operations will be executed for each NPC separately. Otherwise these two operations would have only had an effect on 1 or 2 different NPCs. For the remaining NPCs, their actions would stay the same.

#### Gene

Two different encodings for genes were implemented as well. A gene always consists of a list, which depending on the chromosome type either has a length of *number\_of\_actors* (In case *ChromosomeEncoding* == *Time*) or of length 1 (in case *ChromosomeEncoding* == *TimeNPC*). The following two encodings thus show the type of object, which is in these lists.

**Integer** The first encoding uses integer, which are translated into actions when the simulation is started. For each action, a range of integers is assigned, the larger the range, the more likely the action is chosen by the GA. Actions that have parameters are split into different ranges, according to which parameters make sense. For example *ModifyTargetVelocity* is split into five different parts, with different percentages, namely 50, 70, 100, 130, 160. The range of integers assigned to these parts is different. A percentage setting of 100 for example has the largest integer range assigned. In Appendix , the probability of an action can be seen. In Appendix ... the probability per actions of the parameters can be viewed.

These ranges were assigned based on intuition and trial and error. The encoding is visualized in 3.3.

TODO: Due to the cliff problem, it was decided to not use binary representations for these integers. Due to the mutation choosing the integers randomly, it is not a problem that the variables are not really "continuous".

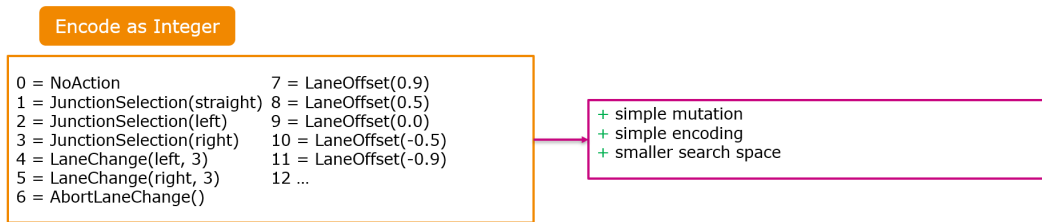


Figure 3.3: Integer

**Dictionary** The second encoding is much similar to the actual actions used in the simulations. Now, no translation is necessary anymore. During generation of the individuals, each action is again selected based on different probabilities assigned to actions, which again can be viewed in Appendix ... . These probabilities are the same as for the integer encoding. However the difference is, in case an action has parameters that need to be chosen. For each parameter, a range and a randomness function was chosen. For example in case of the percentage parameter in ModifyTargetVelocity, the values are selected from a GausDistribution, with  $\mu=100$ ,  $\sigma=25$  and a range limit between 0 and 300.

Again, these probability functions with settings were assigned based on intuition as well as trial and error. Detailed information can be seen in Appendix...

Figure 3.4 shows a visualization.

### 3.2.3 Cost Function

### 3 Implementation

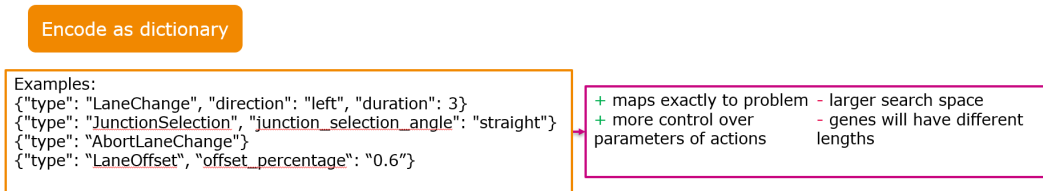


Figure 3.4: Dictionary

Cost function is a bit difficult, as we are only using internal values. No ADAS/AD system is tested and we thus have to work with what we got. This is the code of the cost function:

```
1 SEPS_PER_SECOND = 100
2 # allow emergency breaks to last only 3 seconds
3 MAX_DURATION = 3 * STEPS_PER_SECOND
4
5 cost = 0
6 duration_counter = 0
7 for i in range(len(result["ego_emergency_stop"])):
8     if not result["ego_emergency_stop"][i]:
9         # base cost in case of no current emergency break
10        cost = cost + 1
11        duration_counter = 0
12    else:
13        if duration_counter > MAX_DURATION:
14            # increase cost if emergency break max
15            # duration is exceeded
16            cost = cost + 10
17            duration_counter += 1
18 return cost
```

`result["ego_emergency_stop"]` is a list with the length  $100 * \text{simulation\_duration\_seconds}$  (because 100hz). It contains a boolean per step, if the EGO vehicle has initiated an emergency stop.

It would have been interesting to not only test for emergency stops (which will make the NPCs try to get the EGO to hard break often) but also improve time to collision (TTC), as was done by . However by the time of starting

Ref florian



the testing, no working TTC functionality was implemented. Thus, only the emergency break cost function is used by the GA to be optimized.

## 3.3 Behavior Tree

A behavior tree is a decision tree. Depending on the functionality under test, it is possible to let the EGO vehicle be controlled by a Behaviour Tree. This makes sense if for example a functionilty like AEB is tested, where only the breaks are controlled. In case of a full driving stack, no Behaviour Tree would be used.

insert a good introduction to BT

The general idea is to have an EGO vehicle moving in a "relateable" manner trough the world. It will try to dodge standing or slow moving obstacles. This needs to be done in a determinisitic manner in order to no introduce randomness into the simulation.

For this, Behaviour Tree is used. While it has access to the same Action Interface (described in section 3.1.1) as the Genetic Algorithm, it is more tightly integrated with the Traffic Manger. While the Genetic Algorithm only ingests the results generated by the Simulation with the cost function, the Behaviour Tree needs access to internal functions during the simulation. The following figure shows the behaviour tree implemented.

Starting out, \_\_\_\_\_

Explain BT

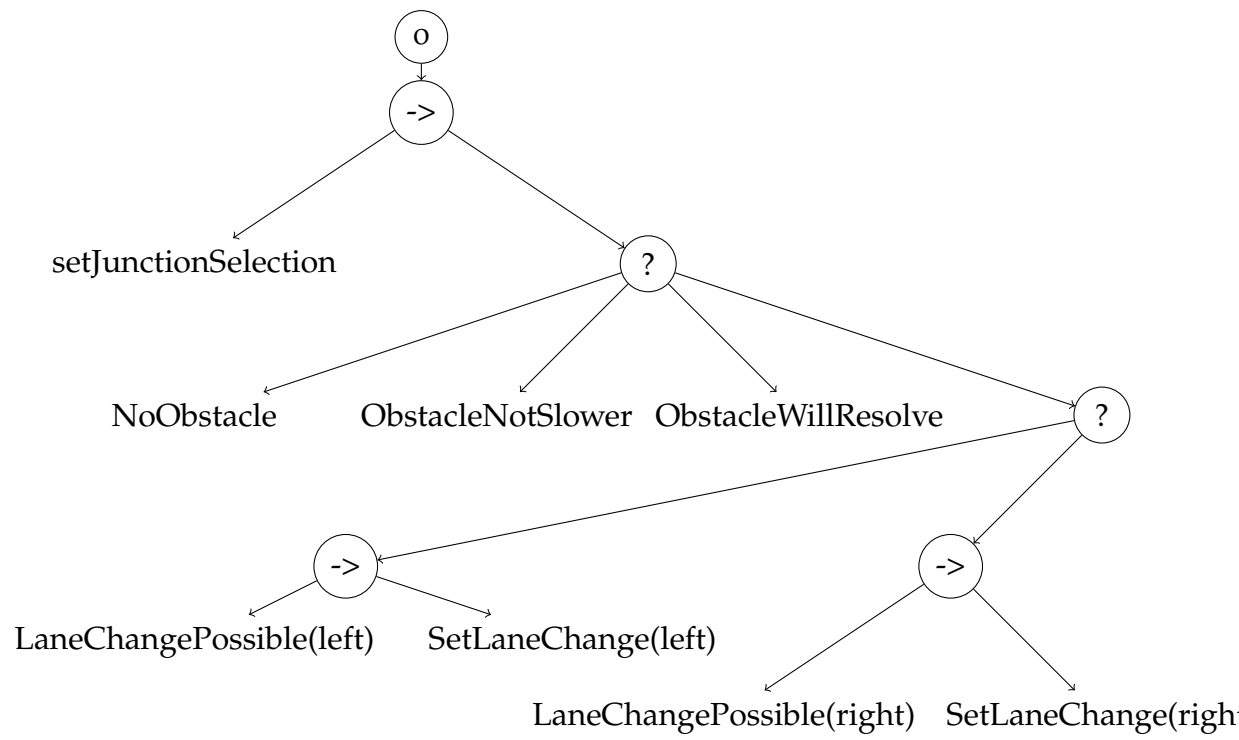


Figure 3.5: Used Behaviour Tree

## 4 Hyperparameter Tuning

The performance of a Genetic Algorithm is significantly influenced by its control parameters. Performant settings on a particular fitness landscape might not be appropriate on a different one (K. De Jong, 2007).

According to the "No Free Lunch Theorem", no single algorithm will outperform all other algorithms on a single class of problem (K. De Jong, 2007). According to K. De Jong, 2007, "the No Free Lunch results place an obligation on the EA practitioner to understand something about the particular properties of the problems that (s)he is trying to solve that relate to particular choices of EA parameter settings." Further stating that a human-in-the-loop approach is needed to fine-tune parameter settings to a particular problem.

This chapter will focus on tuning the Genetic Algorithm to perform on the given cost function. First, an agreement on the optimal population size is made and second, a Taguchi Orthogonal Array is used for tuning the remaining hyperparameter.

In order to reduce the required number of tests, it was decided to only use one starting scenario for tuning. It can be seen in appendix 6.2. In chapter 5, the performance on different start scenarios will be investigated.

### 4.1 Population

Setting a suitable population size is of high importance to a Genetic Algorithm, which has been discussed in section 2.1, especially considering the limited processing resources available. On one hand, a population that is too

small might result in less diverse runs of the genetic algorithm, on the other hand, if population is too high, the simulations will become too costly.

In order to test for the best population size, other hyperparameters first have to be fixated using an educated guess. While reviewing the literature, trends of general settings for genetic algorithms can be found. Grefenstette, 1986 suggests that a range of control parameter will already lead to acceptable performance, yet optimal performance needs tuning. K. De Jong, 2007 complements these findings, adding that the "sweet spot" for hyperparameters of genetic algorithms is reasonably large and easy to find. A default set of static parameter values is generally speaking sufficient.

Following this advice, the most suitable population parameters will now be evaluated by fixating the remaining hyperparameters to a small range of suggested values from the literature.

### 4.1.1 Suggested hyperparameter from the literature

Use best values also from :  
Using genetic algorithms for automating automated lane-keeping system testing

After reviewing various literature regarding control parameter of Genetic Algorithms, no clear consensus emerged. Mills, Filliben, and Haines, 2015 also mention the inconsistencies between findings during their literature review, highlighting the conflicting evidence regarding "key GA control parameter".

Table 4.1 aims to provide a short, though not exhaustive, overview on different control parameter settings used in the literature. This compilation does not claim to cover the entire scope of available research in this domain, rather it served as a focused effort to identify usable hyperparameters.

Generally speaking, a low mutation rate is recommended. For example Grefenstette, 1986 suggest poor performance using a rate over 0.05. Using a low mutation rate is also suggested by Whitley, 1994 and Jinghui Zhong et al., 2005. On the other hand, Boyabatli and Sabuncuoglu, 2004 found higher mutation rates for their application to be more suitable.

Srinivas and Patnaik, 1994 differentiates between higher and lower population numbers, claiming that a smaller population needs higher mutation rates in order to maintain a sufficient diversity.

Table 4.1: Summary of Genetic Algorithm Hyperparameters

Parameter Set	Pop	Cross
K. A. De Jong, 1975	50	0.6
Mills, Filliben, and Haines, 2015	200	?
Grefenstette, 1986	30	0.95
Grefenstette, 1986	80	0.45
Almanee et al., 2021	50	0.8
Srinivas and Patnaik, 1994	30-100	0.9
Fazal et al., 2005	50	0.5
Dao, Abhary, and Marian, 2016	200	0.7
<b>assistant_professor_amity_university_jaipur_rajasthan_india_parameter_2019</b>	200	0.4
Jinghui Zhong et al., 2005	50-250	0.1-0.9

### 4.1.2 Comparison of Population Size

This now leads to a difficult decision in choosing the right parameters. Based on the extensive research, we will compare population size of 32, 48, 64 and 96. We will compare the different crossover rates: 0.8 and 0.6. For mutation, 0.01 and 0.2 will be discussed. Further we will use tournament selection with 2 and 4. Individual Mutation Probability will stay at 0.1. Chromosome Encoding is set to Time and Gene Encoding is set to Integer. Each run will be executed 5 times to reduce randomness and to make the results more robust. Each simulation will last for 30 generations.

Settings	Code	32	48	64	96
C: 0.6, M: 0.01, TS: 2	A	3051	3016	2851	2871
C: 0.6, M: 0.01, TS: 4	B	3111	3021	3079	2937
C: 0.6, M: 0.20, TS: 2	C	3062	3010	3002	2831
C: 0.6, M: 0.20, TS: 4	D	3020	2967	2891	2850
C: 0.8, M: 0.01, TS: 2	E	3063	2892	2971	2916
C: 0.8, M: 0.01, TS: 4	F	3052	3049	3054	2897
C: 0.8, M: 0.20, TS: 2	G	3099	2940	2959	2869
C: 0.8, M: 0.20, TS: 4	H	3058	3005	2794	2809

Figure 4.1: Comparison of Population Size - mean

## 4 Hyperparameter Tuning

In figure 4.2, the results per population are plotted. The line corresponds to the mean, while the bars show the spread (min to max) of all 5 repetitions.

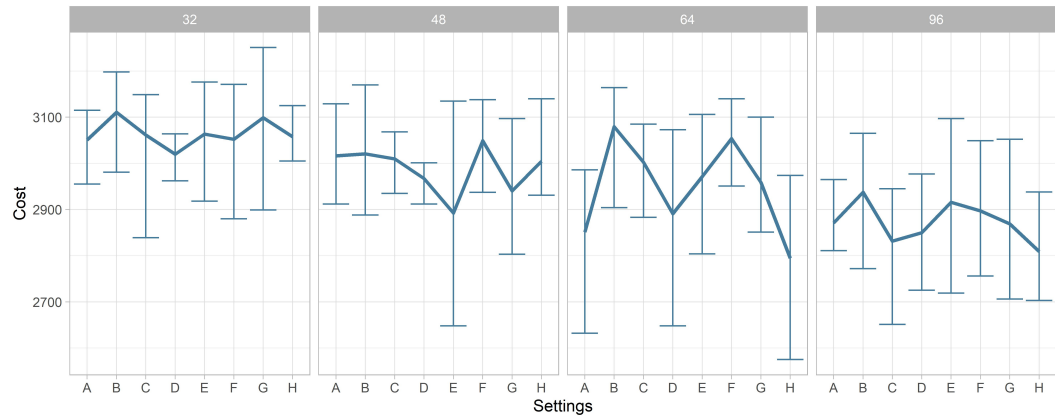


Figure 4.2: mean and error bars per population

A higher spread in the results can be seen when looking at small population sizes. Considering these findings, a population size of 96 was chosen. While such a high value will result in a performance impact, it was deemed to be more important to keep the variation low.

## 4.2 Design of Experiment

This section aims to find optimal settings for the remaining control parameters for the given problem. Following the conclusion from the previous section 4.1, a population size of 96 will be used.

In order to tune the control parameter of the genetic algorithm, various different strategies can be used. Using automated approaches like "Grid Search", "Bayesian Optimization", "Simulated Annealing" or "Hyperband" might lead to good results with minimal effort (tuning hyperparameter of these search algorithms is still needed), however they each require a high number of runs (K. De Jong, 2007). K. De Jong, 2007 even suggest using a

find more (better) references

second, higher level Genetic Algorithm for the optimization process.

Due to performance considerations, many optimization methods however did not fit the requirements. Executing one run for 30 generations currently takes around 3:50 hours. Although two different workstations were available, the time required to execute the needed number of runs for these automated tests would exceed the available time budgeted. This is without considering a minimum required number of repetitions to remove randomness in the results.

A different approach called "design of experiment" (DOE), also known as statistically designed experiments. DOE tries to find the cause and-effect relationship between the factors and the output of experiments. It uses factorial design where each experiment has factors, of which each consists of at least two settings, with the actual number of settings being called "levels" (Yang and El-Haik, 2009). Design of experiment needs manual expertise to define which factors are possibly of importance and which settings each factor should have.

"If the range of variable is too small, then we may miss lots of useful information. If the range is too large, then the extreme values might give infeasible experimental runs." (Yang and El-Haik, 2009)

Afterwards, main effects and interactions can be calculated to find the best settings per factor. It provides a graphical representation of these relationship by using interaction as well as main-effects charts. Using ANOVA (Analysis of Variance) it is possible to identify the significance of each factor and interaction, which enables the ranking of these factors. More details on these analysis tools will be provided in section 4.2.3.

A full factorial design will test over all possible combinations of the manually selected factor levels. Looking at the proposed factors in table 4.2.1, we would require 1024 runs<sup>1</sup>, which not feasible performance wise. A full factorial design has the drawback, that as the number of factors  $k$  gets increased, the number of needed experimental runs increases exponentially, thus resulting in lengthy experiments. Yang and El-Haik, 2009 state, that most of the results obtained by testing over all combinations are only

---

<sup>1</sup>number of runs calculated using: <https://datatab.net/statistics-calculator/design-of-experiments>

used for estimating higher-order interactions, which are in most cases insignificant.

Short explanation

Fractional factorial experiments require less runs ...

“Techniques such as fractional (or partial) factorial experiments are used to simplify the experiment. Fractional factorial experiments investigate only a fraction of all possible combinations. This approach saves considerable time and money but requires rigorous mathematical treatment, both in the design of the experiment and in the analysis of the results. (Roy, 1990)”

### 4.2.1 Taguchi Design

Various improvements to Design of experiment have been put forward by Dr. Genichi Taguchi, such as reducing the influence of uncontrollable (noise) factors on processes and products and reducing variability. Some of these methods evolve around Signal-to-noise (S/N) analysis and utilizing cost functions to "express predicted improvements from DOE results in terms of expected cost saving" (Roy, 1990). This master thesis will not discuss all of Taguchi's proposed considerations, for more detail Roy, 1990 as well as Yang and El-Haik, 2009 is highly recommended.

Find examples of Papers that use taguchi for ga

Using a Taguchi design for evaluating the best hyperparameter has been successfully performed by Dao, Abhary, and Marian, 2016 as well as [naruka\\_parameter\\_2019](#).

“ There are many similarities between “regular” experimental design and Taguchi's experimental design. However, in a Taguchi experiment, only the main effects and two-factor interactions are considered. Higher-order interactions are assumed to be nonexistent. In addition, experimenters are asked to identify which interactions might be significant before conducting the experiment, through their knowledge of the subject matter.” (Yang and El-Haik, 2009)

This master's thesis will mainly utilize Taguchi's orthogonal arrays (OAs), "which represent the smallest fractional factorials and are used for most common experiment designs." (Roy, 1990). This means, that only a fraction of combinations needs to be tested which drastically improves performance.



Each row of these matrices contains the factors of one experiment, while the columns correspond the factors Hamzaçebi, 2021.

Different orthogonal arrays have been proposed by Taguchi. The researcher has the responsibility to select an array based on the individual needs (Hamzaçebi, 2021). Using these orthogonal arrays instead of full factorial experiments will lead to needing a much smaller amount of simulation runs (in our case only 16 compared to 1024), while the latter "might not provide appreciably more useful information" Roy, 1990.

An orthogonal array has multiple properties: " OFF and OLH experiment designs sample a full factorial design space in a balanced and orthogonal fashion. Balance ensures good effect estimates by reducing an estimator's bias and variability. Orthogonality ensures good estimates of two-term interactions. Balance is achieved by ensuring that each level of every factor occurs an equal number of times in the selected sample. Orthogonality is achieved by ensuring that each pair of levels occurs an equal number of times across all experiment parameters in the selected sample. OFF and OLH designs exhibit good space-spanning properties, which aid screening, sensitivity, and comparative analyses. On the other hand, highly fractionated OFF or OLH designs can have poor space-filling properties, which are necessary for optimization analyses.

Definition orthogonal array

"Mills, Filliben, and Haines, 2015

As has been stated, probably the biggest drawback of using Taguchi orthogonal arrays is on the one hand to increased manual labour and on the other hand the fact, that higher order interactions ignored.

Roy, 1990 explains why this might not be a big problem: "Generally speaking, OA experiments work well when there is minimal interaction among factors; that is, the factor influences on the measured quality objectives are independent of each other and are linear. In other words, when the outcome is directly proportional to the linear combination of individual factor main effects, OA design identifies the optimum condition and estimates performance at this condition accurately. If, however, the factors interact with each other and influence the outcome, there is still a good chance that the optimum condition will be identified accurately, but the estimate of

performance at the optimum can be significantly off. The degree of inaccuracy in performance estimates will depend on the degree of complexity of interactions among all the factors."

This is complimented by Yang and El-Haik, 2009, who states, that: "During many years of applications of factorial design, people have found that higher-order interaction effects (i.e., interaction effects involving three or more factors) are very seldom significant. In most experimental case studies, only some main effects and two-factor interactions are significant."

However, K. De Jong, 2007 claim, that "tuning EA parameters can itself be a challenging task since EA parameters interact in highly non-linear ways." It remains to be seen in it is possible to use this method for optimizing parameters of a genetic algorithm.

**Selection of orthogonal array** When choosing a suitable Taguchi orthogonal array, we need to take various factors into account, which can make the process tricky. According to Yang and El-Haik, 2009, we will have to follow a three step procedure:

1. Calculate the total degree of freedom (DOF).
2. Following two rules, standard orthogonal array should be selected:
  - a) Total DOF need to be smaller than the number of runs provided by the orthogonal array.
  - b) All required factor level combinations need to be accommodated by the orthogonal array.
3. Factors have to be assigned using these rules:
  - a) In case the factor level does not fit into the orthogonal array, methods such as column merging and dummy level can be used to modify the original array.
  - b) Using the linear graph and interaction table, interactions can be defined.
  - c) In case some columns are not assigned, its possible to keep these columns empty.

For this genetic algorithm, 7 factors (3 Factors of Level 4 and 4 Factors of Level 2) have been selected. Which factors to choose and with which level was done based on experience gained on section 4.1. When selecting levels, it is important to have them "as far away from either side of the current working condition as possible." (Roy, 1990) In table 4.2.1, every factor with corresponding levels has been listed,

Factors	Code	Level 1	Level 2	Level 3	Level 4
CrossoverType	A	one point	two point	uniform 0.1	uniform 0.5
CrossoverProp	B	0.2	0.5	0.8	0.9
MutationProp	C	0.01	0.1	0.3	0.5
ChromosomeType	D	Time	Time+NPC	-	-
GeneType	E	int	dict	-	-
TournamentSize	F	2	4	-	-
IndMutationProp	G	0.1	0.5	-	-

Figure 4.3: List of Hyperparamters (Factors) matched to a Code and defined settings (Levels)

Using this table, we will now find the best standard orthogonal array in section 4.2.2. Before doing so, it is important to state, that Taguchi allows to test for possible (pre determined) two-level interactions (Yang and El-Haik, 2009). Analysing interactions comes at a cost of Degrees of freedom. If we look at the table, an interaction between ChromosomeType and GeneType might be of interest. Using the power of hindsight, we know, that a second two factor interaction is possible within our chosen array, thus we will have a look at the interaction between Tournament Size and IndMutationPropability as well.

#### 4.2.2 Selection of a suitable standart orthogonal array

The total degree of freedom can be quickly calculated using the rules provided by Yang and El-Haik, 2009:

1. 1 DOF is always used for the overall mean.
2. Each factor has a DOF of NumberOfLevels - 1.

#### 4 Hyperparameter Tuning

3. Two-factor interactions use this equation to calculate DOF:  $(n_{factor1} - 1)(n_{factor2} - 1)$  where  $n$  = number of levels.

This leads to the following calculation for the needed 3 Factors of Level 4 and 4 Factors of Level 2 as well as the two interactions between ChromosomeType-GeneType and TournamentSize-IndMutationProp:

$$\begin{aligned} DOF &= 1 + 3 * (3 - 1) + 4 * (2 - 1) + 2 * (2 - 1) * (2 - 1) \\ &= 13 \end{aligned} \quad (4.1)$$

A  $L_{16}$  array seems suitable to accommodate the required 13 DOF, which can be seen in 4.2.2.

NO.	$L_{16}(2^{15})$														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
3	1	1	1	2	2	2	2	1	1	1	1	2	2	2	2
4	1	1	1	2	2	2	2	2	2	2	2	1	1	1	1
5	1	2	1	1	1	2	2	1	1	2	2	1	1	2	2
6	1	2	2	1	1	2	2	2	2	1	1	2	2	1	1
7	1	2	2	2	2	1	1	1	1	2	2	2	2	1	1
8	1	2	2	2	2	1	1	2	2	1	1	1	1	2	2
9	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
10	2	1	2	1	2	1	2	2	1	2	1	2	1	2	1
11	2	1	2	2	1	2	1	1	2	1	2	2	1	2	1
12	2	1	2	2	1	2	1	2	1	2	1	1	2	1	2
13	2	2	1	1	2	2	1	1	2	2	1	1	2	2	1
14	2	2	1	1	2	2	1	2	1	1	2	2	1	1	2
15	2	2	1	2	1	1	2	1	2	2	1	2	1	1	2
16	2	2	1	2	1	1	2	2	1	1	2	1	2	2	1

Figure 4.4:  $L_{16}(2^{15})$  Taguchi orthogonal array taken from Roy, 1990

This graph now needs to be fitted and modified to accommodate the needed factors. 4 Level Factors need additional space which will be generated using

column merging, while interactions will need to be assigned as well. For this, either an interaction table or linear graphs of the  $L_{16}$  array can be used (NazanDanacioğlu, 2005). The linear graph approach is straight forward and will be selected. While there are multiple linear graphs for  $L_{16}$  array, 4.2.2 describes the graph which best fits the requirements from table 4.2.1. If no graph with the perfect fit is found, these graphs can be modified as well, using rules described by NazanDanacioğlu, 2005.

"In each of Taguchi's orthogonal arrays, there are one or more accompanying linear graphs. A linear graph is used to illustrate the interaction relationships in the orthogonal array." Yang and El-Haik, 2009

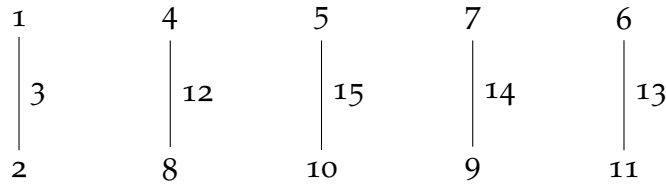


Figure 4.5: Linear Graph of  $L_{16}(2^{15})$  taken from Yang and El-Haik, 2009

In a Taguchi linear graph, the nodes as well as the connections both represent columns in the orthogonal array. An interaction between two columns that are represented as nodes "comes out to" the connecting line column Taguchi et al., 2005. This is useful for both analysing interactions between columns as well as combining (merging) interacting columns in case a higher factor is needed.

**Column Merging** A, B and C are both 4 level factors. The currently selected orthogonal only fits 2 level factors. Using column merging, it is possible to extend columns to accommodate higher order levels.

As calculated in 4.1, a four-level column requires three degrees of freedom, thus three two-level columns need to be merged. For column merging, it is required, that the to be merged columns are part of an interaction group (Yang and El-Haik, 2009).

So, 3 interaction 2-level columns need to first be selected. One column is discarded, the remain two columns need to be merged using the rules in tabular 4.6.

OLD COLUMN			NEW COLUMN
1	1	->	1
1	2	->	2
2	1	->	3
2	2	->	4

Figure 4.6: Rules taken from Roy, 1990

The four-level factor can then be assigned to this newly generated column. Because three four-level factors are needed for the current experiment, nine two-level columns need to be merged in total.

**Assigning Interactions** Interactions between two-level factors can be assigned using the linear graph as well. Here, select two connected nodes. The column describing their connection will subsequently contain the interaction (Taguchi et al., 2005).

An interaction between ChromosomeType and GeneType seems possible, thus D and E will be assigned to connected nodes in the linear graph. As we still have some unused space in the graph, we will also look at the interaction of TournamentSize and IndMutationProp (F and G). The resulting graph can be seen in 4.2.2.

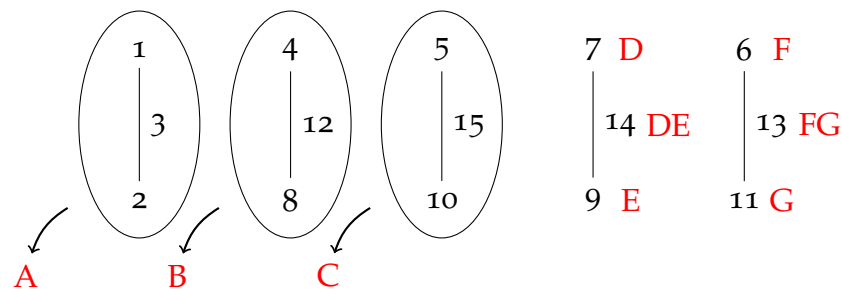


Figure 4.7: Modified Linear Graph to fit our needs

Combining columns 1 2 3 to A, 4 8 12 to B and 5 10 15 to C using rules defined by table 4.6 is done in 4.8.

NO.	1 2 3	4 8 12	5 10 15
1	11 > 1	11 > 1	11 > 1
2	11 > 1	12 > 2	12 > 2
3	11 > 1	21 > 3	21 > 3
4	11 > 1	22 > 4	22 > 4
5	12 > 2	11 > 1	12 > 2
6	12 > 2	12 > 2	11 > 1
7	12 > 2	21 > 3	22 > 4
8	12 > 2	22 > 4	21 > 3
9	21 > 3	11 > 1	21 > 3
10	21 > 3	12 > 2	22 > 4
11	21 > 3	21 > 3	11 > 1
12	22 > 3	22 > 4	12 > 2
13	22 > 4	11 > 1	22 > 4
14	22 > 4	12 > 2	21 > 3
15	22 > 4	21 > 3	12 > 2
16	22 > 4	22 > 4	11 > 1

Figure 4.8: Building 4 Level columns from 2 Level columns

Removing the old and inserting the new columns in the table and transcoding 7 to D, 9 to E, 14 to DE, 6 to F, 11 to G and 13 to FG results in the final table 4.9. This combinations table will subsequently be used as settings for the simulation runs.

### 4.2.3 Analysing the results

Table 4.9 can now be used for running all the needed testcases (the interaction columns can be ignored until the evaluation). Transcoding all factors and levels to get the corresponding setting can be done using in the table from 4.2.1. We will repeat every setting 8 times to reduce randomness and gain information about variance. Running the Genetic Algorithm using

NO.	A	B	C	D	E	F	G	FG	DE
1	1	1	1	1	1	1	1	1	1
2	1	2	2	1	2	1	2	2	2
3	1	3	3	2	1	2	1	2	2
4	1	4	4	2	2	2	2	1	1
5	2	1	2	2	1	2	2	1	2
6	2	2	1	2	2	2	1	2	1
7	2	3	4	1	1	1	2	2	1
8	2	4	3	1	2	1	1	1	2
9	3	1	3	2	2	1	2	2	1
10	3	2	4	2	1	1	1	1	2
11	3	3	1	1	2	2	2	1	2
12	3	4	2	1	1	2	1	2	1
13	4	1	4	1	2	2	1	2	2
14	4	2	3	1	1	2	2	1	1
15	4	3	2	2	2	1	1	1	1
16	4	4	1	2	1	1	2	2	2

Figure 4.9: Final version of used Taguchi orthogonal array

ref to section

these 16 different settings each repeated 8 times took 10 days on the two previously described workstations.

The results are found in the appendix at 6.2.

### Main-effects and interaction chart

Identifying the optimal conditions is done by analyzing the main effects per factor. Using them, it is possible to predict the factors, that lead to the best result Roy, 1990.

Yang and El-Haik, 2009 explains them well: “The main-effects chart is a plot of average responses at different levels of a factor versus the factor levels”

Example for D

So, for every factor, sum up the mean of all results per level, then divide by the number of runs per level.

The resulting main-effect charts can be seen here:



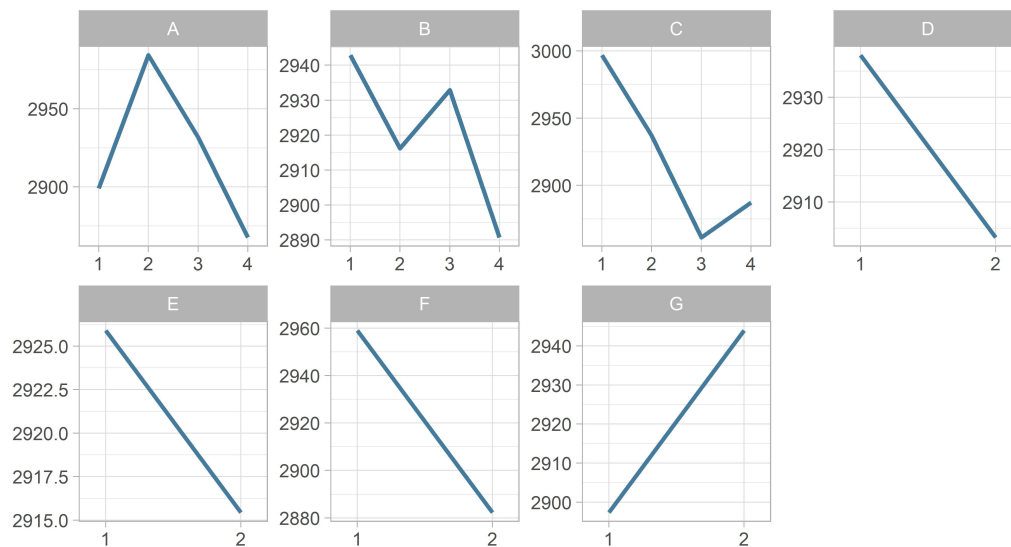


Figure 4.10: Main Effects

In case there is no interaction, the optimal setting is easily determined by using the main effects chart. Go over every factor in the chart and use the best level (in case of this experiment, the level with the lowest cost value). If interactions exist, they might have an influence on the best settings and need to be investigated (Yang and El-Haik, 2009).

To investigate previously defined interactions, a test of interactions can be used. Their calculation is similar to calculating main effects.

Example for DE

If lines cross, an interaction between the two factors exists. The more parallel the lines are, the less likely an interaction. Magnitude of the angle between the lines corresponds to the degree of interaction presence, according to Roy, 1990.

## ANOVA

Before choosing the best settings, ANOVA analysis (analysis of variance) should be performed on the results. Among other things, this will provide

## 4 Hyperparameter Tuning

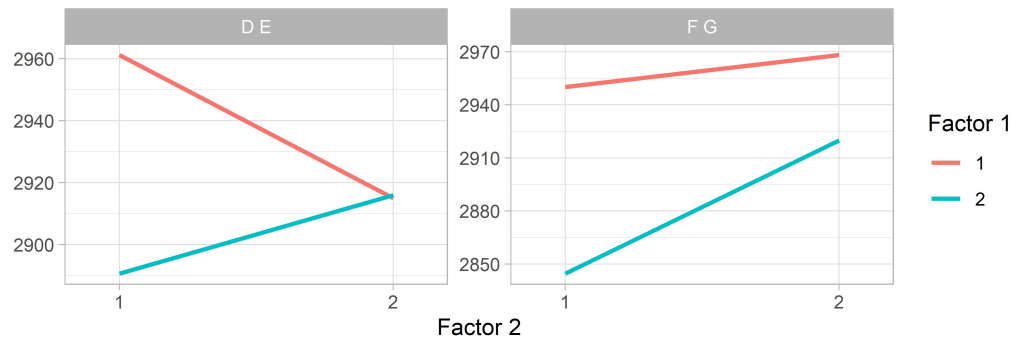


Figure 4.11: Test of interactions

Summary after  
reading "Intro-  
duction into R"

information on the magnitude of contribution of each main effects and interactions. The calculation of ANOVA is the same as for a classical design of experiment, according to Yang and El-Haik, 2009.

"In analysis of variance, mean squares are used in the F test to see if the corresponding effect is statistically significant." Yang and El-Haik, 2009 "F ratio is a better measure for relative performance" Yang and El-Haik, 2009

". The most commonly used criterion is to compare the p value with 0.05, or 5%, if p value is less than 0.05, then that effect is significant." Yang and El-Haik, 2009

"The variance ratio, commonly called the F statistic, is the ratio of variance due to the effect of a factor and variance due to the error term. (The F statistic is named after Sir Ronald A. Fisher.) This ratio is used to measure the significance of the factor under investigation with respect to the variance of all of the factors included in the error term. The F value obtained in the analysis is compared with a value from standard F-tables for a given statistical level of significance." Roy, 1990.

Due to our number of repetitions, the number of DOF increases according to the following equation (taken from Roy, 1990):

$$\begin{aligned}
 DOF &= totalNumberofResults - 1 \\
 &= numberOfTrials * numberOfRepetitions - 1 \\
 &= 16 * 8 - 1 = 127
 \end{aligned}
 \tag{4.2}$$

Calculating ANOVA can be done simply be done using R, which will result in table 4.2.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
A	3	238901.41	79633.80	6.66	0.0004
B	3	49972.09	16657.36	1.39	0.2488
C	3	343169.03	114389.68	9.56	0.0000
D	1	38781.12	38781.12	3.24	0.0745
E	1	3507.03	3507.03	0.29	0.5893
F	1	189112.50	189112.50	15.81	0.0001
G	1	69751.13	69751.13	5.83	0.0174
D:E	1	41041.12	41041.12	3.43	0.0666
F:G	1	26277.78	26277.78	2.20	0.1411
Residuals	112	1339693.00	11961.54		

Table 4.2: ANOVA results

A, C, F and G have a relatively high F value, which suggests high influence on the model.

The Multiple R-squared: 0.4275, Adjusted R-squared: 0.3509 ... both are bad.

We can also look at the percentage contribution of each factor, using the formula gathered by Yang and El-Haik, 2009:

$$SS_T = SS_A + SS_B + SS_C + \dots + SS_{error} \quad (4.3)$$

$$contribution_A = SS_A / SS_T * 100 \quad (4.4)$$

The percentage contribution is plotted in 4.2.3 (Sum of all factor contributions == Multiple R-squared in theory)

We can clearly see a high contribution of the residuals (error), which is concerning.

explain using R book

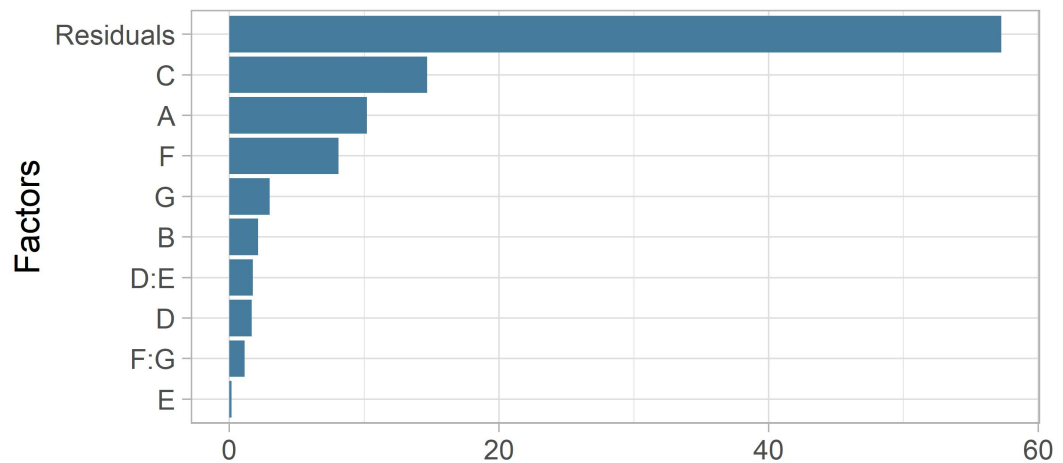


Figure 4.12: Percentage Contribution

### Selection of optimal setting

When choosing the optimal setting, the first step is to look at the best main effects combination. For this experiment, the best combination would be the following: A<sub>4</sub>, B<sub>4</sub>, C<sub>3</sub>, D<sub>2</sub>, E<sub>2</sub>, F<sub>2</sub>, G<sub>1</sub>. Looking the ANOVA table, the interaction D:E has seems to have significance, especially compared to E. We will try to integrate this interaction. Compared to D:E, the second interaction (F:G) has a lower influence. This is also the case when looking at the individual factors F and G. The interaction F:G will thus not further be discussed.

The test of interaction in figure 4.2.3 suggest D<sub>2</sub> and E<sub>1</sub> as the best combination. This is optimal, as D<sub>2</sub> is also suggested by the main effects. E<sub>1</sub> is different to the suggested main effects, however its low F value in the anova table suggests low significance for using E<sub>2</sub>. Concluding this line of thought, the combination A<sub>4</sub>, B<sub>4</sub>, C<sub>3</sub>, D<sub>2</sub>, E<sub>1</sub>, F<sub>2</sub>, G<sub>1</sub> looks to be optimal.

**Optimum performance calculation** Using optimal performance calculation  
 1. using only main effects or 2. using main effects with applied interaction

can be applied. The equation provided by Roy, 1990.

Better bars

$$\begin{aligned}
 Y_{opt} &= \bar{T} + (\bar{A}_4 - \bar{T}) + (\bar{B}_4 - \bar{T}) + (\bar{C}_3 - \bar{T}) + (\bar{D}_2 - \bar{T}) + (\bar{E}_2 - \bar{T}) + (\bar{F}_2 - \bar{T}) + (\bar{G}_1 - \bar{T}) \\
 &= 2693.984
 \end{aligned}
 \tag{4.5}$$

$$\begin{aligned}
 Y_{opt} &= \bar{T} + (\bar{A}_4 - \bar{T}) + (\bar{B}_4 - \bar{T}) + (\bar{C}_3 - \bar{T}) + (\bar{D}_2 - \bar{T}) + (\bar{E}_1 - \bar{T}) + ([D\bar{x}E]_2 - \bar{T}) + (\bar{F}_2 - \bar{T}) + (\bar{G}_1 - \bar{T}) \\
 &= 2686.547
 \end{aligned}
 \tag{4.6}$$

Using the interaction D:E, the performance estimation improves from 2693.984 to 2686.547. Considering this result, interaction will be taken into account and the optimized settings are as follows: CrossoverType: Uniform 0.5, CrossoverPropability: 0.9, MutationPropability: 0.3, ChromosomeType: Time+NPC, GeneType: integer encoding, TournamentSize: 4 and Individual-MutationPropability: 0.1.

**signal-to-noise (S/N)** As previously discussed when looking at the anova model, the error is very high, which suggests high randomness. Taguchi recommends using signal-to-noise (S/N) ratio to reduce the variability, as using only the mean of the results does not take the variation into account (Roy, 1990). The greater the signal-to-noise ratio, the smaller the variance. Roy, 1990 further states, that the "use of the S/N ratio offers an objective way to look at the two characteristics (consistency and average value) together."

When using S/N, todo: talk about equation.

Afterwards, generating main effects and anova table is the same as using the mean. However the DOF calculation done in equation 4.2 is no longer valid, as repetitions get combined to 1 value per run. So, the DOF for anova changes to the following equation in 4.7 according to Roy, 1990.

$$\begin{aligned}
 DOF &= totalNumberOfResults - 1 \\
 &= numberOfTrials * 1 - 1 \\
 &= 16 - 1 = 15
 \end{aligned}
 \tag{4.7}$$

Find out why  
15 DOF is not  
enough

This is not enough residuals for generating the F value in anova. Thus in order to reduce the current DOF, the anova table was generated without the interaction F:G considered, which can be seen in 4.3.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
A	3	0.26	0.09	3.01	0.3953
B	3	0.05	0.02	0.60	0.7139
C	3	0.38	0.13	4.44	0.3326
D	1	0.04	0.04	1.48	0.4378
E	1	0.00	0.00	0.12	0.7845
F	1	0.21	0.21	7.35	0.2250
G	1	0.08	0.08	2.80	0.3429
D:E	1	0.04	0.04	1.56	0.4296
Residuals	1	0.03	0.03		

Table 4.3: S/N ANOVA results

When looking at the p values of this table, it is very obvious that no factor can discard the null - hypothesis, which states that a factor has no significant effect. Considering this, it was deemed to be not necessary to perform further investigations. Somehow argument, that having less variability is only to an extend important. It is always possible to restart a simulation, if the variability is not too large, it is important that the results have a good mean overall. Less variability is in producing products much more important.

**Elite** Although the optimal hyperparameter setting will be discussed in chapter 5, a problem was obvious when analyzing a run using the optimized GA. Figure 4.2.3 shows for a few selected repetitions the best individual cost per generation.

The lines show that setbacks in the optimal cost between two generations happens frequently. In order to mitigate this problem, it was decided to

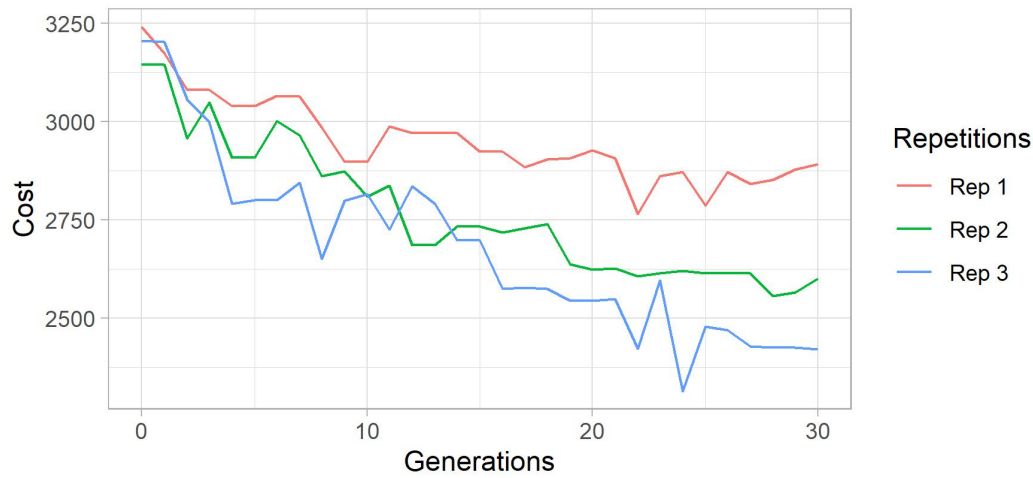


Figure 4.13: Genetic Algorithm without Elite

implement elite selection with a size of 2. This means, that per generation, the two best individuals are copied into the next generation without modifications, which makes worse performance between generations not possible. It is important to note, that the two best individuals can still be selected by tournament selection for modification, its just that a copy of them is saved. Figure 4.2.3 shows the effect of these changes.

Comparing the 10 repetitions also provides a clear picture in figure 4.2.3. It is thus concluded that the slightly modified version of the optimized Ga now using Elite of 2 will be used for chapter 5.

## 4 Hyperparameter Tuning

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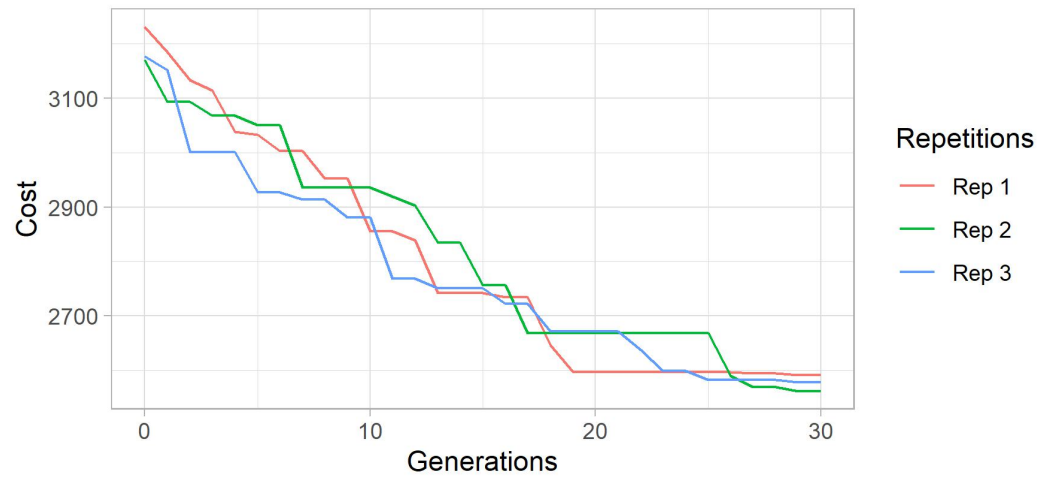


Figure 4.14: Genetic Algorithm with Elite

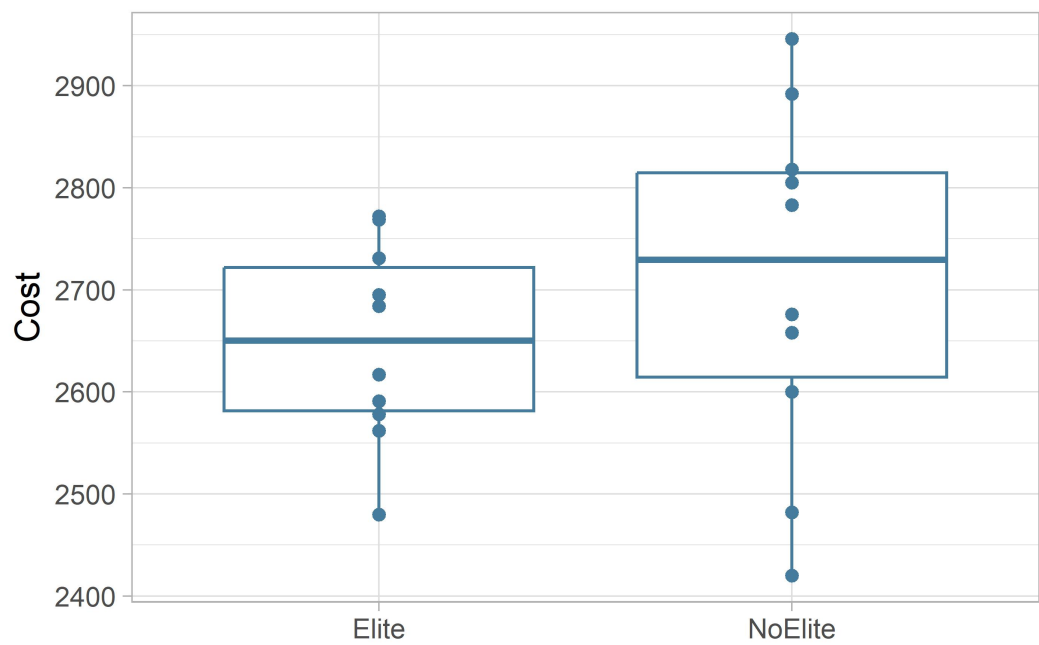


Figure 4.15: Comparison Elite vs No Elite



## 5 Evaluation

in this chapter, we evaluate and compare various different settings

"We found crossover and mutation most influential in GA success."Mills, Filliben, and Haines, 2015

"The cross over operator is found to be the most influential parameter in both the case studies, followed by mutation rate, population size for case study-1 and population size and selection process for case study-2. It is evident that the robust GA parameter settings are sensitive" Majumdar and Ghosh, 2015

Boyabatli and Sabuncuoglu, 2004 also suggest a high mutation rate.

It seems like the high variations does not allow for more complex traffic situations, giving a clear priority to pedestrian actions

TODO: chart: emergency break due to pedestrians vs vehicles

In the last chapter 4, values from the cost function (shown in section 3.2.3) were displayed. These values however are difficult to interpret. Considering this, in this chapter, these values will be modified using this equation:

$$(3500 - \text{cost}) / 100$$

This will result in a value called Emergency Brake Duration, which will from now on be using instead of cost. The higher the Emergency Brake Duration, the better. It is important to consider, that this value might not exactly correspond to the actual Emergency Brake Duration time from the simulation, as the cost function applies a penalty for emergency breaks lasting longer then 3 seconds (again, see section 3.2.3).

# 5.1 Comparison with random and default ga Values

scenario 1: default : 9v 5p

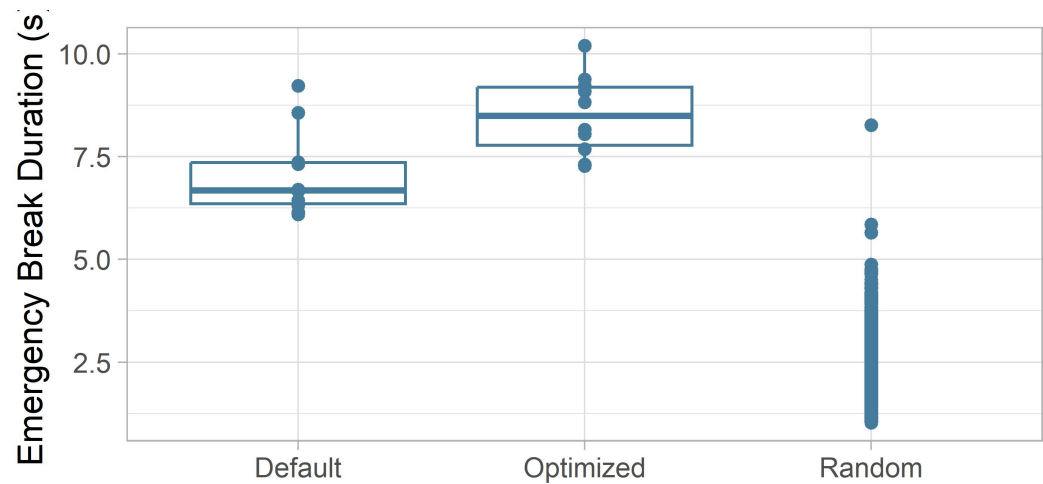


Figure 5.1: Comparison simulation 1: Default GA vs Optimized GA vs Random

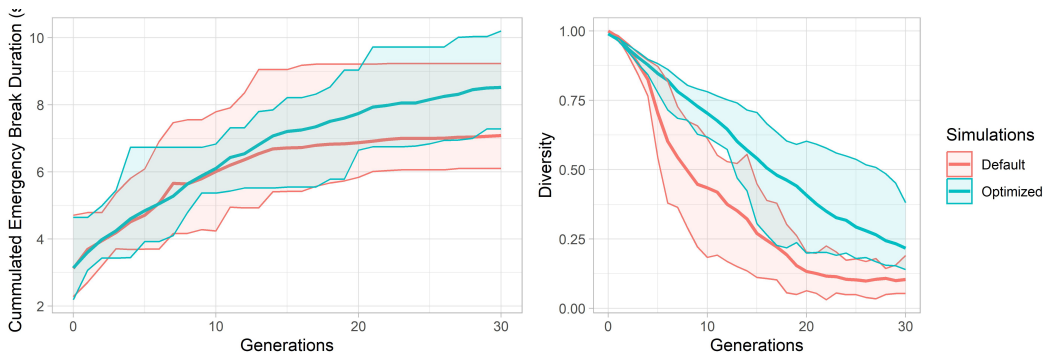


Figure 5.2: Comparison over generations. simulation 1

## 5.2 Generalization on different start scenarios

### Scenario 2

scenario 2: 9v 5p

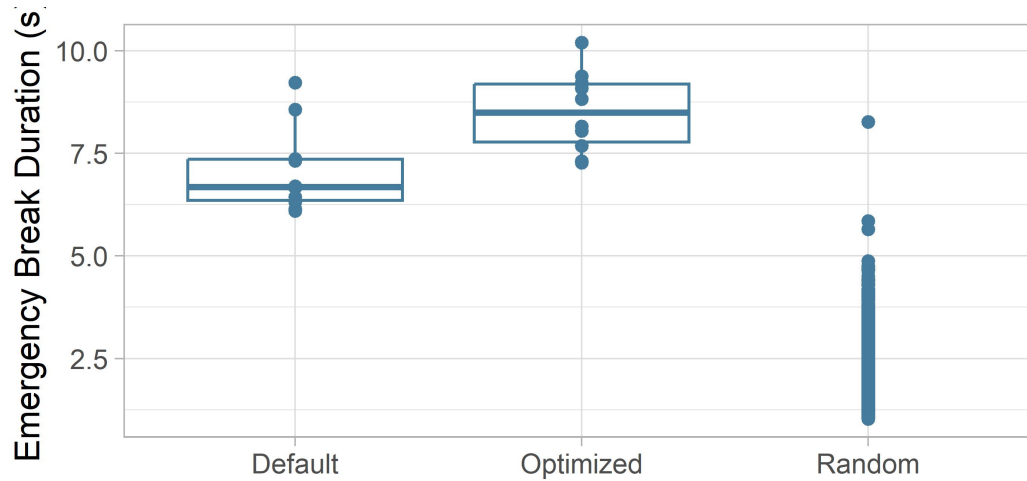


Figure 5.3: Genetic Algorithm with Elite

### Scenario 3

scenario 3: 5v 3p

### Scenario 4

scenario 4: 18v 10p

also compare  
(average) diver-  
sity?

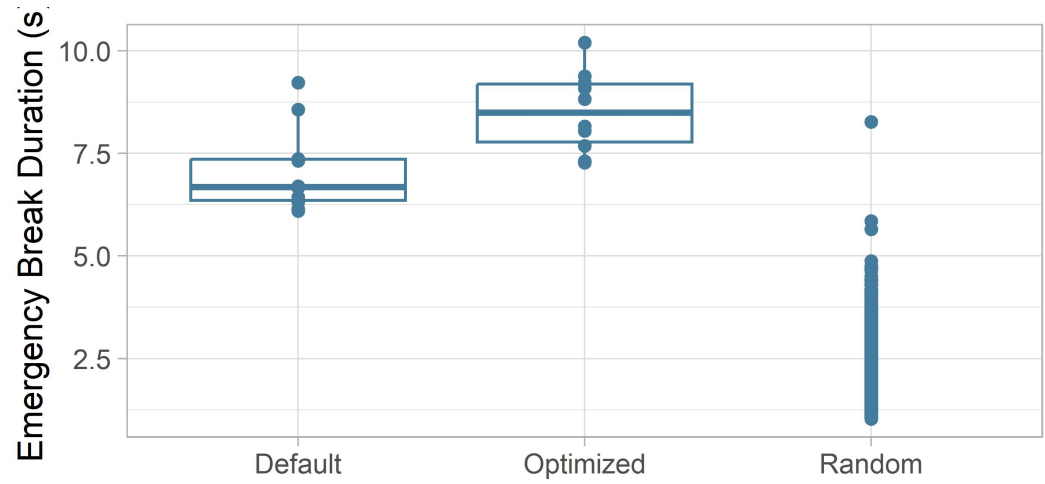


Figure 5.4: Genetic Algorithm with Elite

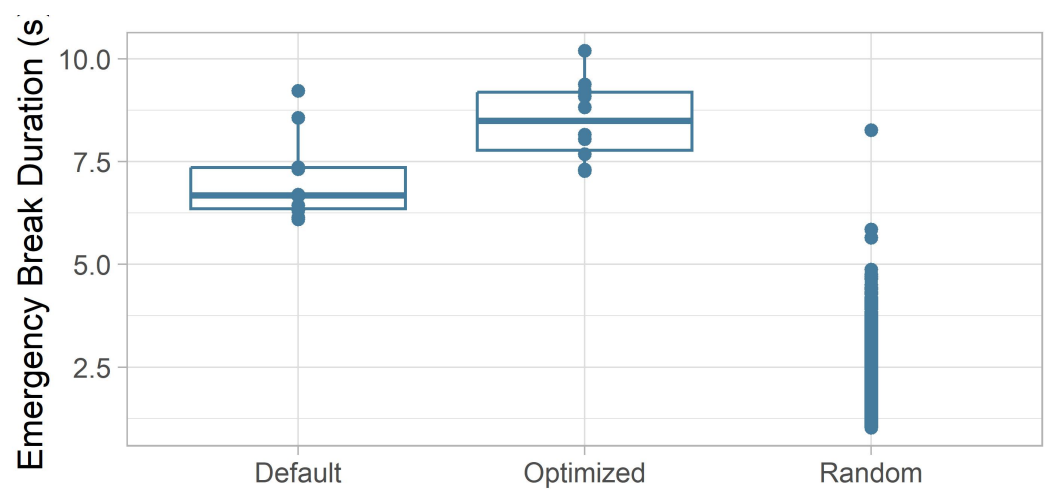


Figure 5.5: Genetic Algorithm with Elite

# **6 Conclusion**

## **6.1 Future Work**

### **6.1.1 Oracles**

While not implemented here, Oracles are needed in order to get a list of good scenarios.

## **6.2 Final words**



# Appendix





# Appendix A.

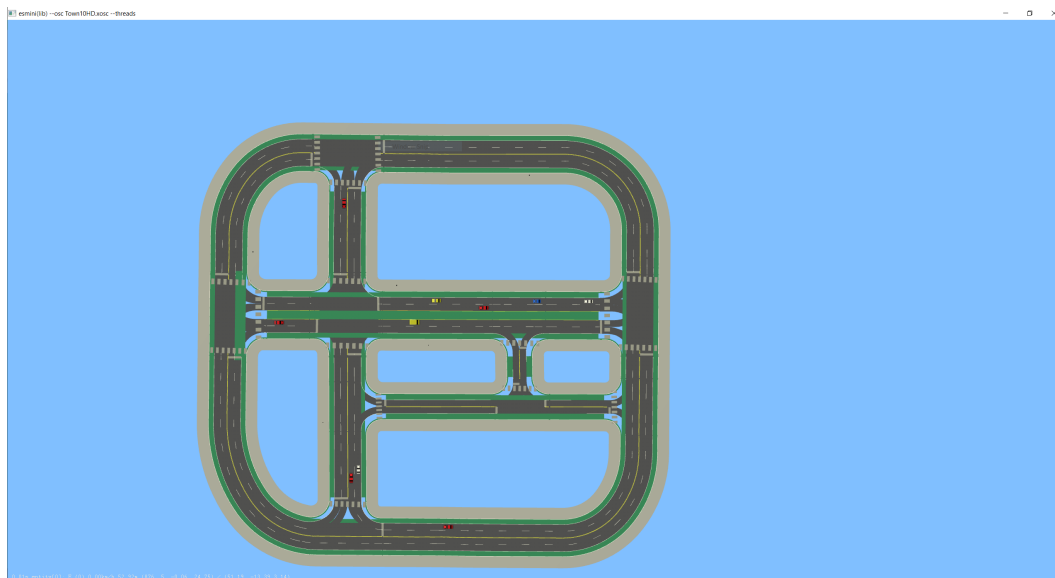


Figure 1: Start scenario 1

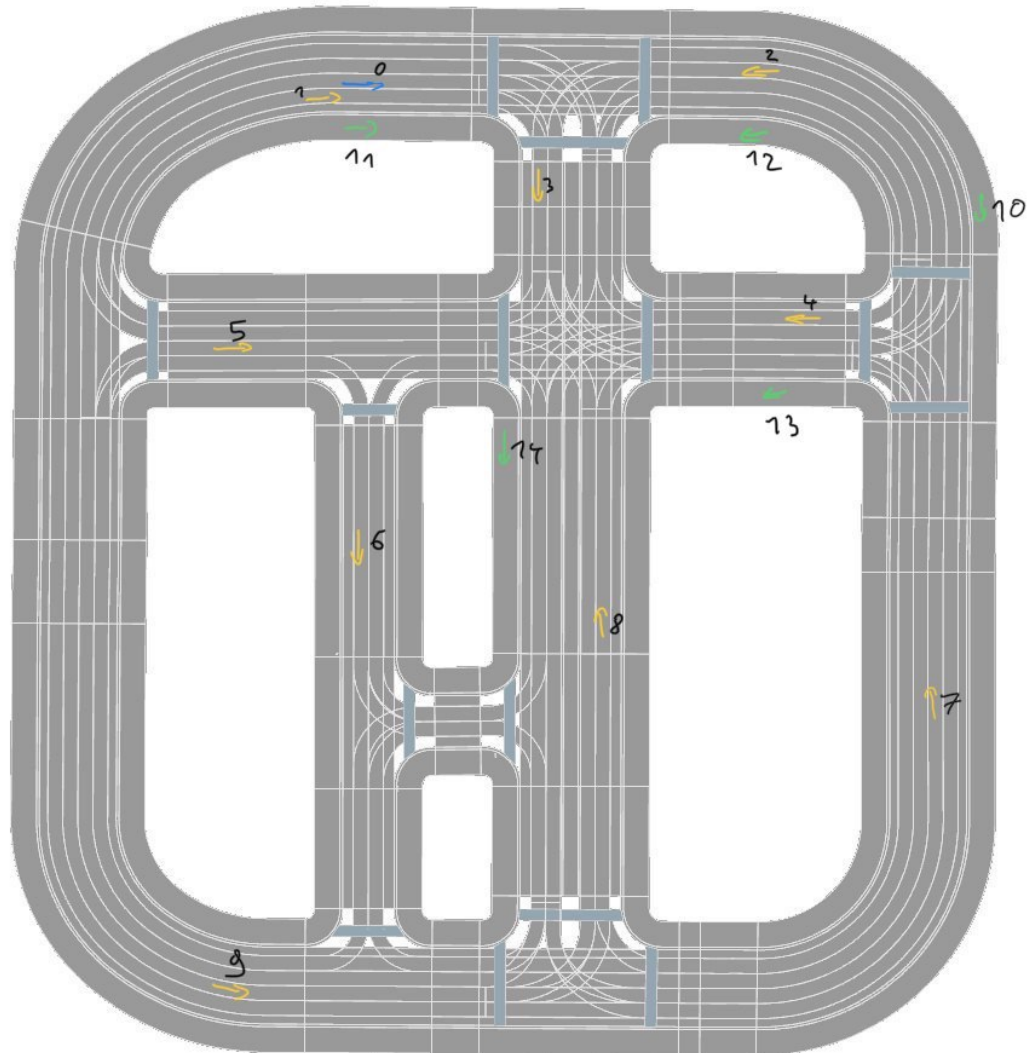


Figure 2: Start scenario 2

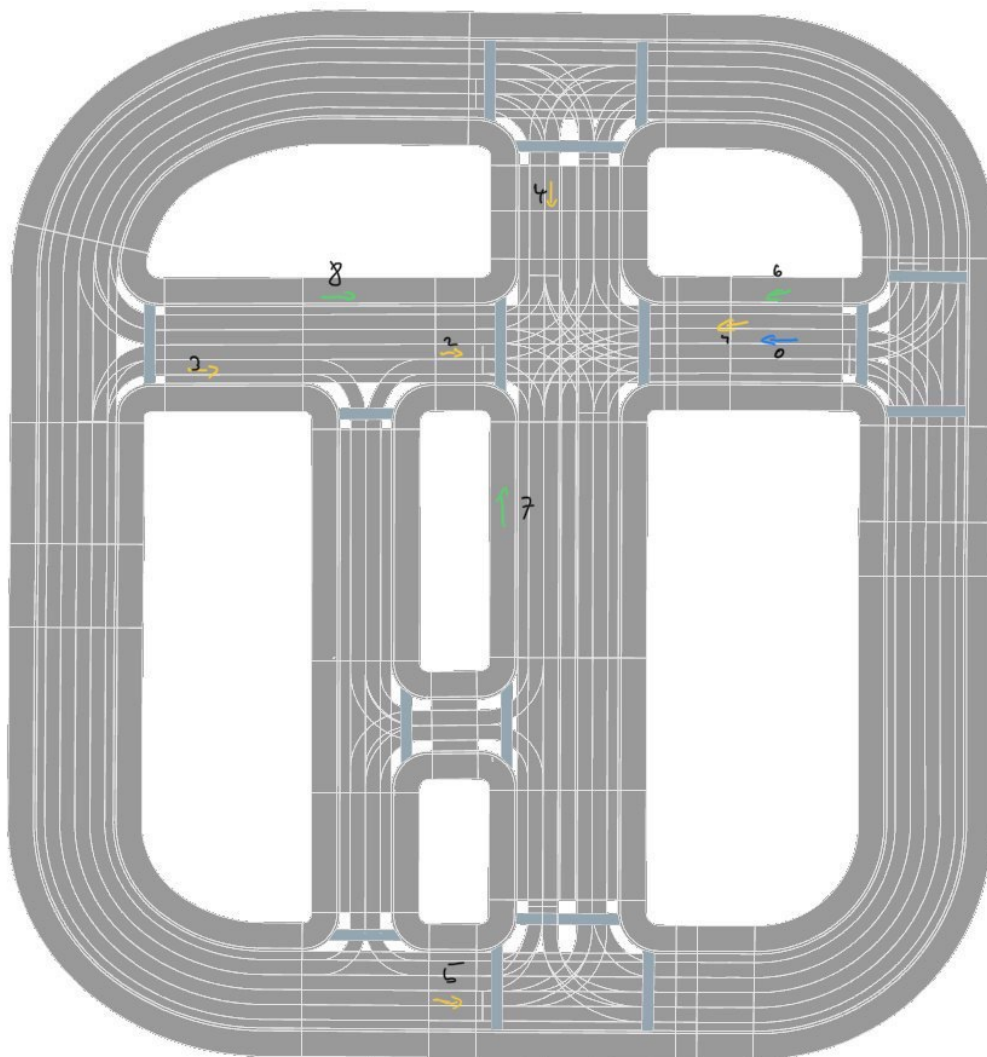


Figure 3: Start scenario 3

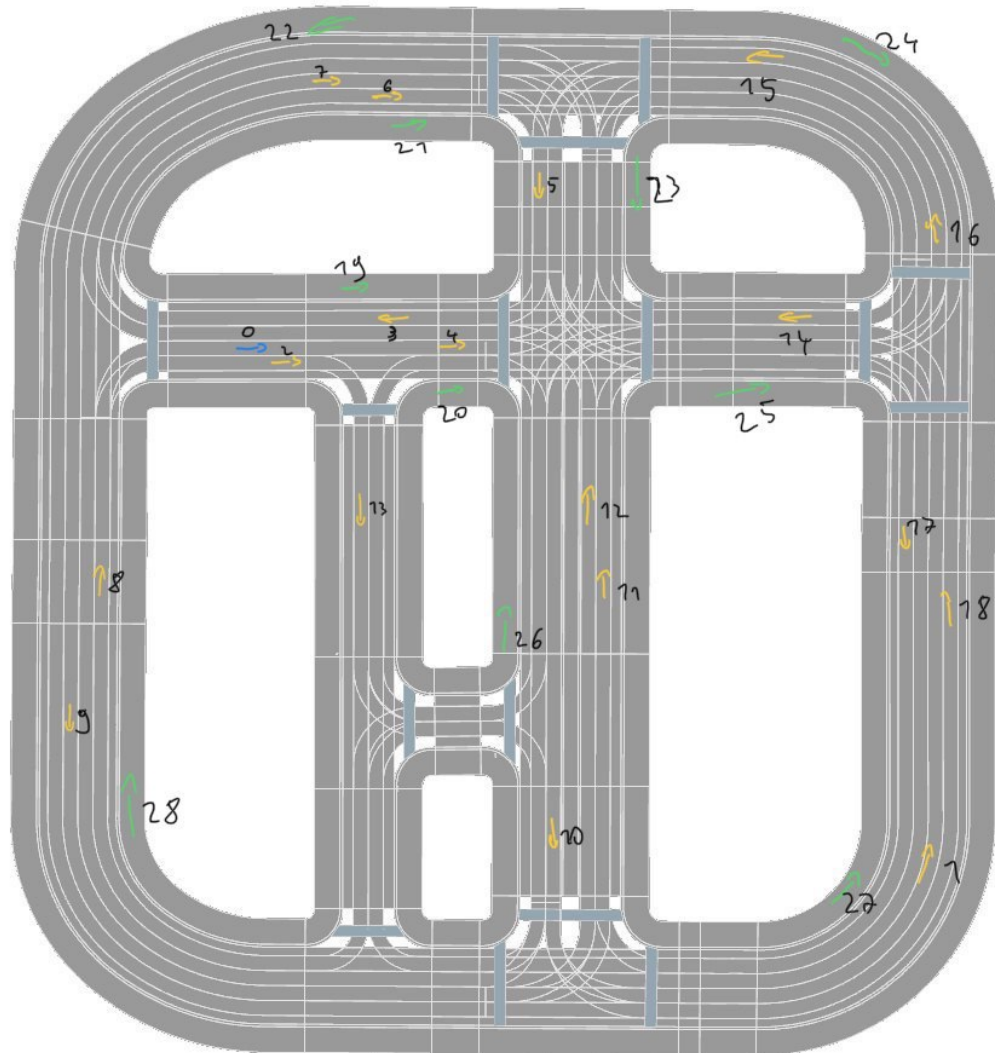


Figure 4: Start scenario 4

## Appendix B.

NO.	rep1	rep2	rep3	rep4	rep5	rep6	rep7	rep8
1	3124	3110	3025	3077	3068	2925	3106	3105
2	2694	2980	3025	2996	3037	2921	3068	2900
3	2638	2711	2624	2856	2623	2832	2904	2778
4	2735	2805	2851	2965	2876	2703	2848	2858
5	3074	2955	3045	3080	3120	2971	2895	2798
6	2974	2979	2929	2941	2952	2936	3139	2953
7	3108	3099	3049	3020	3092	3057	3090	2895
8	2840	2931	2921	2921	2957	2997	2889	2895
9	3007	2995	2983	3009	2847	2996	2734	2927
10	2916	2828	3013	2787	2818	2926	3034	2822
11	3007	2879	3090	3033	2906	2981	3109	3104
12	2946	3016	2790	2917	2904	2983	2898	2606
13	2378	2712	2906	2800	2912	2795	2860	2834
14	2895	2760	2750	2849	2542	2997	2965	2991
15	2842	3065	3050	2779	2862	2923	2955	2892
16	3065	2834	2643	3056	3051	3011	2828	2963

Figure 1: List of results



# Appendix C.

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Insert information of Gene action probabilities





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