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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.

Contents

Abstract	v
1 Introduction	1
1.1 Research Questions	1
1.1.1 Research Question 1	1
1.1.2 Research Question 2	1
1.1.3 Research Question 3	1
1.1.4 Research Question 4	2
1.1.5 Research Question 5	2
1.2 Shortcomings	2
2 Foundations	3
2.1 Genetic Algorithm	3
2.1.1 History	3
2.1.2 Different Hyperparameter	3
2.2 Behavior Tree	5
2.2.1 Usage for GA	5
2.3 Traffic Manager	6
2.3.1 Action Interface	6
2.3.2 Graphics	7
3 Implementation	9
3.1 Map and Starting Scenario	9
3.2 Genetic Algorithm	9
3.2.1 Encoding	10
3.2.2 Rules	10
3.2.3 Cost Function	11
3.3 Behavior Tree	11

4	Hyperparameter Tuning	15
4.1	No Free Lunch Theorem	15
4.2	Start Scenario	15
4.3	Population	15
4.3.1	Suggested hyperparameter from the literature	16
4.3.2	results	18
4.4	Design of Experiment	19
4.4.1	Taguchi Design	21
4.4.2	Selection of a suitable standart orthogonal array	24
4.4.3	Analysing the results	29
5	Evaluation	37
5.1	Comparison with random and default ga Values	37
5.2	Generalization on different start scenarios	37
6	Conclusion	39
6.1	Test	39
	Appendix A.	43
	Bibliography	45

List of Figures

3.1	Used Behaviour Tree	12
4.1	List Settings per Population Size	18
4.2	mean and error bars per population	19
4.3	List of Hyperparamters (Factors) matched to a Code and defined settings (Levels)	23
4.4	$L_{16}(2^{15})$ Taguchi ortohogonal array taken from Roy, 1990	25
4.5	Linear Graph of $L_{16}(2^{15})$ taken from Yang and El-Haik, 2009 .	26
4.6	Rules taken from Roy, 1990	26
4.7	Modified Linear Graph to fit our needs	27
4.8	Building 4 Level columns from 2 Level columns	28
4.9	Final version of used Taguchi orthogonal array	29
4.10	Main Effects	30
4.11	Test of interactions	31
4.12	ANOVA results	32
4.13	Percentage Contribution	33
1	Start scenario 1	43
2	List of results	44

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?

In this thesis,

1.1.2 Research Question 2

Can hypertuning improve the performance of a Genetic Algorithm?

1.1.3 Research Question 3

Can a hypertuned Genetic Algorithm generalize on different start scenarios?

1.1.4 Research Question 4

Is the usage of a Behavior Tree on the Ego vehicle improving the criticality of resulting scenarios?

1.1.5 Research Question 5

Can rules help to improve the performance of a genetic algorithm?

1.2 Shortcomings

This Master Thesis started with the development of the Traffic Manger and thus progress was closely linked. Without a working simulations, no genetic algorithms 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 compations of hyperparamter, so only a handful can be tested. In further chapers, these shortcuts will be explained and their relevancy will be dicussed.

2 Foundations

2.1 Genetic Algorithm

Genetic Algorithms are a popular search algorithm that utilizes the principle of Darwin. They have been used successfully in various areas. Some of their strengths are However we will also look at shortcomings, which mainly evolve around performance. We will have a look at its History and then discussing the most important parameters.

Define a vocabulary

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.

Usage of GA

2.1.1 History

The GA was invented by....

2.1.2 Different Hyperparameter

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

2 Foundations

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 40 was almost always sufficient, and will thus mostly be used.

Pop Size

Pop size will set the number of Individuals of a GA per Generation. The higher the pop size, the bigger the less change of premature converging. It will however also lead to a longer convergin time.

Selection

Selection defines how which individuals are allowed to mate and move into the next generation.

pros and cons
of roulette vs
Tournament

tournament was chosen to be used for this works because of this paper (and also because of pros and cons list)

cite paper

Other ideas are evolve around having a flexible selection system debending on fitness

Crossover

Discuss all used
crossover meth-
ods

Crossover is the mating process.

Mutation

Discuss individ-
ual mutation

Mutation is responsible for introducing new information into the gene pool.

Discuss all used
mutation meth-
ods

4

Other

More to come....

2.2 Behavior Tree

A behavior tree is a decision tree.

insert a good introduction to BT

2.2.1 Usage for GA

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 controll only NPCs and not the EGO vehicle itself, a behaviour tree is used. The behaviour tree is used to controll the EGO vehicle over the action interface provided by the Traffic Manager. This is the same as the Genetic Algorithm is doing.

insert ref to discussion

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.

In a further chapter it will be dicussed if a GA with controll of the EGO (i.e. no BT will be used) lead to better cost.

While the aim of the GA is to find the most optimal solution, considering the vastness of the hyperspace, this is unlikely. Rather, we want to find the "best" local minimas. Considering the contex of Automotive testing, it is not so much of importance to find "the best fail of the ADAS/AD System", rather its important to find "all" fails.

2.3 Traffic Manager

The Genetic Algorithm will control the simulation of a custom developed Traffic Manager. This Traffic Manager was developed closely to fit the needs of the Genetic Algorithm. It, however, is not part of this Thesis and will thus only get a brief introduction. In general, it will simulate traffic starting from a predefined scenario where the positions and types of Vehicles and Pedestrians are given (i.e. actors). It also allows for an Interface for applying actions on all actors in the simulation, which will be discussed in section 2.3.1.

A simulation consists of multiple NPCs and exactly one EGO vehicle. While the NPCs are only controlled by the Traffic Manager (and dadurch also by its action interface), the ego vehicle can be either partly or even completely controlled by an ADAS/AD Function. This function can then be tested inside the simulation on errors.

2.3.1 Action Interface

To interface with the Traffic Manager, actions have to be used. An action will request a certain behaviour from an actor. If no action is set, the actor will behave in a normal manner inside the simulation. An action can be set to at any timestep (for this thesis, the simulation is running with 100 Hz) for any actor. Pedestrians and vehicles however have different actions.

The following list are now 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.

2.3.2 Graphics

During the simulation, usually no graphics engine is used in order to save performance. In order to visualize the results, two options can be chosen. The more lightweight Esmini, as well as Carla, which is using Unreal Engine to render realistic graphics.

3 Implementation

This chapter will explain

All these actions are accessed by the Genetic Algorithm to maximize a given Cost Function.

3.1 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. Changing the scenario will have a great impact on the Genetic Algorithms performance. For time and complexity reasons, it was thus decided to first stick with one scenario and do all hyperparameter testing there. And finally test the performance for a handfull different scenarios.

3.2 Genetic Algorithm

For implementing the Genetic Algorithm, DEAP was chosen. It is a popular tool for accademia .

explain why
pygad was NOT
chosen

cite

cite 3 examples

dejong talks
about dynamic
param and why
its not good

3.2.1 Encoding

When implementing a Genetic Algorithm, it is necessary to implement a Encoding that fits to the problem.

cite what makes
an encoding
good: eg. sim-
plicity,...

Gene

Genes are the building blocks of a GA.

Chromosome

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

generate images

Encoding 1 has the idea that each gene stands for 1 time step. Because multiple actors exist in the simulation, a gene thus needs to be a list of actions. This list always has the length of the number of all actors. This means that crossover can only move all actions of a timestep at once, modifying between actions of the same timestep can only be done using mutation.

Encoding 2 has not only the time step encoded in the position, also the actor ID is encoded. This makes a chromosome now much longer than in the previous encoding, with the equation being: number of timesteps * number of actors. Now crossover has more possibilities.

In the chapter 5 these two chromosome types will be compared.

3.2.2 Rules

Often, actions are not possible if specific requirements are not met. The obvious example is that it is not possible to perform the action Abort-LaneChange if there is no current LaneChange happening. LaneChange during a LaneChange is not possible as well. Also Pedestrians can not CrossRoad shortly in a Row. The hypothesis is that implementing Rules that

don't allow for these behaviours will reduce the searchspace and will thus make GA converge quicker.

be careful,
lanechange after
lanechange or
crossroad after
crossroad might
be possible if
prev did not
happen. Good
to explain

3.2.3 Cost Function

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. Currently 3 different cost functions are tested

Oracles

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

3.3 Behavior Tree

The Behavior Tree will control the ego vehicle

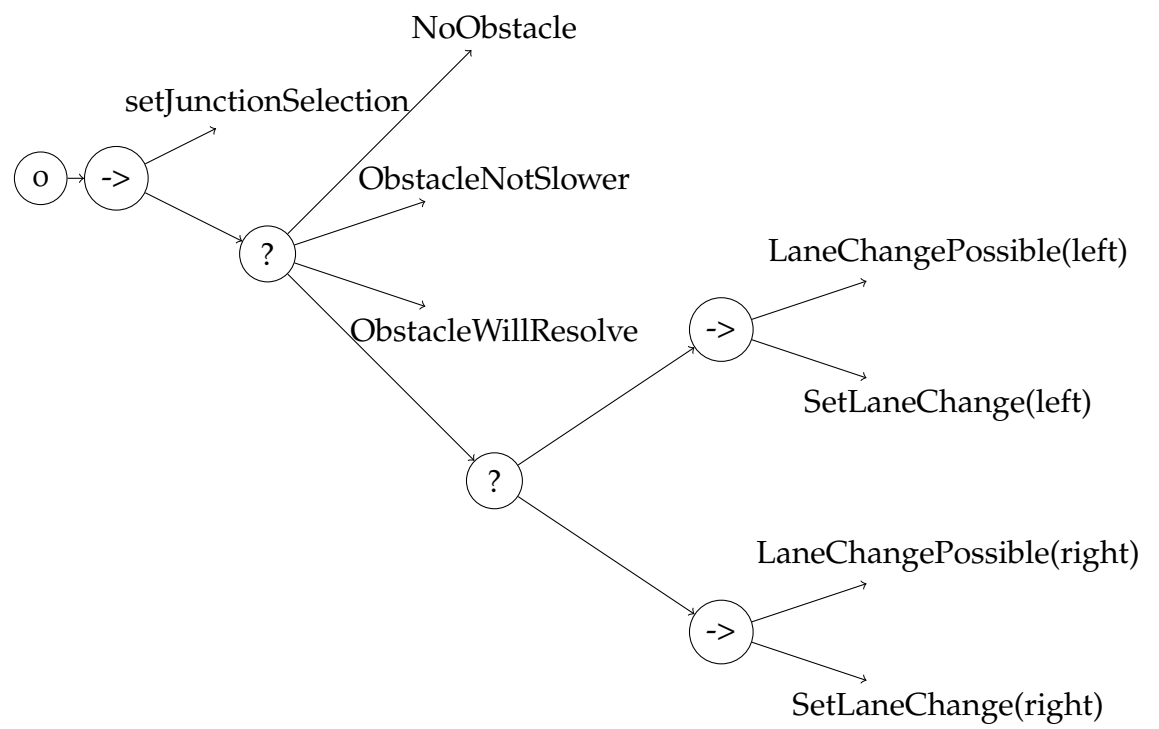
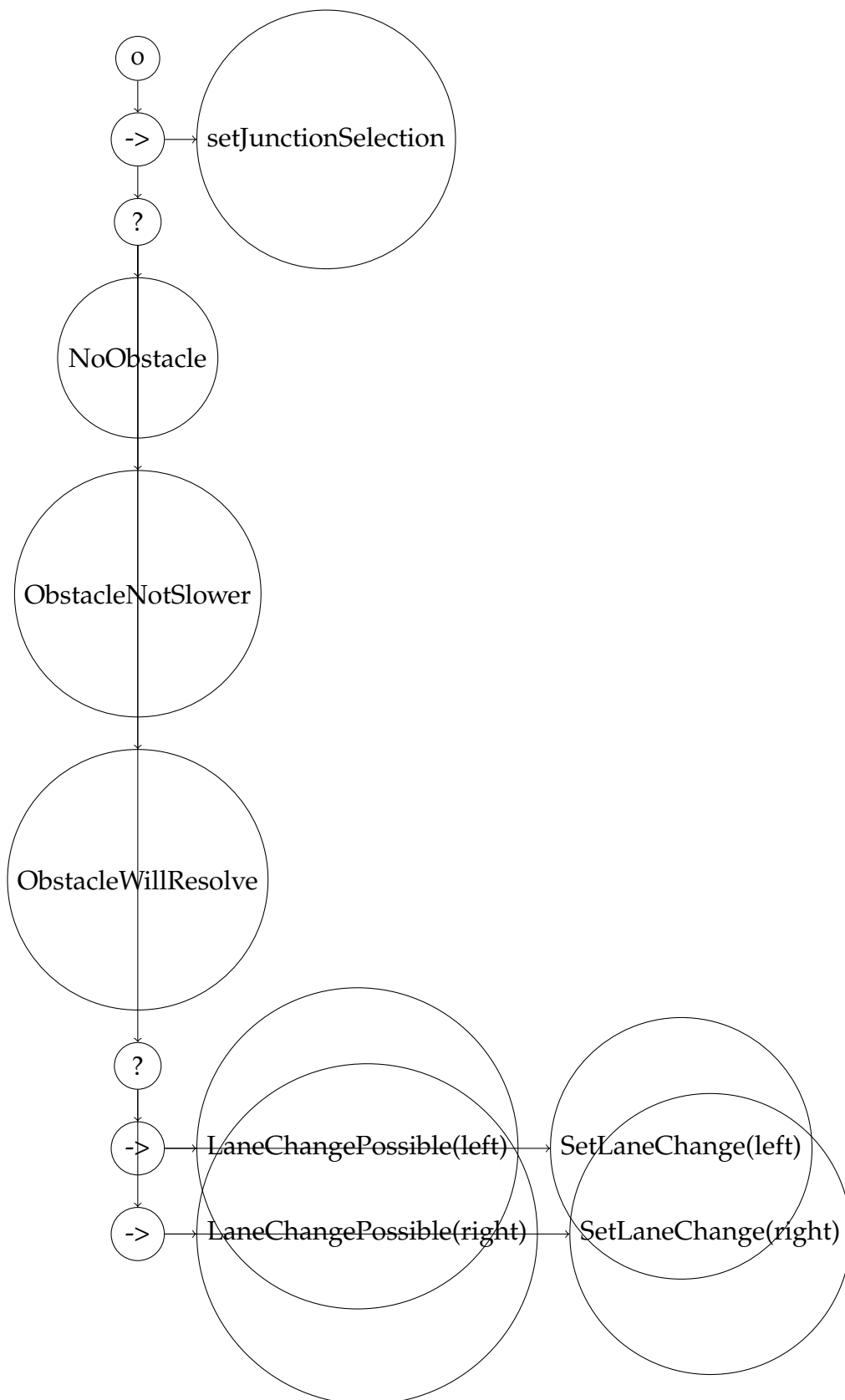


Figure 3.1: Used Behaviour Tree



4 Hyperparameter Tuning

In this chapter, we will incrementally move to an optimized Genetic Algorithm

4.1 No Free Lunch Theorem

No Free Lunch Theorem: The best hyperparameter settings of a Genetic Algorithm are very problem specific. K. De Jong, [2007](#), Dao, Abhary, and Marian, [2016](#)

More ref

4.2 Start Scenario

4.3 Population

The number of Individuals is of high importance to a genetic algorithm, as has been explained in section [2.1](#). Especially considering the limited processing resources available, a suitable population size has to be found. On one hand, a population that is too low 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. Considering these points, the first step of the hyper parameter tuning was to find a suitable population size. In the next chapter [4.4](#), we will aim to improve the hyperparameter using a more robust approach.

In order to test for the best population size, the other hyperparameters have to be assumed using an educated guess. While reviewing the literature,

trends of general settings for genetic algorithms can be found. However Mills, Filliben, and Haines, 2015 highlight the inconsistencies between findings, stating to have "uncovered conflicting opinions and evidence regarding key GA control parameters".

However Grefenstette, 1986 suggests, that "while it is possible to optimize GA control parameters, very good performance can be obtained with a range of GA control parameter settings." This is also complimented by findings from K. De Jong, 2007: "The key insight from such studies is the robustness of EAs with respect to their parameter settings. Getting "in the ball park" is generally sufficient for good EA performance. Stated another way, the EA parameter "sweet spot" is reasonably large and easy to find [18]. As a consequence most EAs today come with a default set of static parameter values that have been found to be quite robust in practice."

Choosing the right selection method is complicated as well, as discussed by K. De Jong, 2007: "One source of difficulty here is that selection pressure is not as easy to "parameterize" as population size. We have a number of families of selection procedures (e.g, tournament selection, truncation selection, fitness-proportional selection, etc.) to choose from and a considerable body of literature analyzing their differences (see, for example, [19] or [15]), but deciding which family to choose or even which member of a parameterized family is still quite difficult, particularly because of the interacting effects with population size [13]."

Looking at the literature might lead to hyperparameters are used that at least sufficient enough, to get an idea which range for population size is suitable. We will now look at different concrete hyperparameter suggestions from the literature.

4.3.1 Suggested hyperparameter from the literature

In an often cited thesis by K. A. De Jong, 1975, the following parameters have been suggested: GA(50, 0.6, 0.001, 1.0, 7, E) These suggested parameters have been used successfully by various different genetic algorithms Grefenstette, 1986.

16

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

Talk about rules (e.g. $1/n$ for mut rate...) - look at: Parameter selection in genetic algorithms

An extensive study by Mills, Filliben, and Haines, 2015 which that took over "over 60 numerical optimization problems." into consideration found that "the most effective level settings found for each factor: population size = 200, selection method = SUS, elite selection percentage = 8%, reboot proportion = 0.4, number of crossover points = 3, mutation rate = adaptive and precision scaling = 1/2 as fine as specified by the user."

Grefenstette, 1986 claim that GA(30, 0.95, 0.01, 1.0, 1, E) and GA(80, 0.45, 0.01, 0.9, 1, P) produced the best results. They also advised against, a mutation rate of over 0.05, suggesting poor performance. 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 state, that "Controversial to existing literature on GA, our computational results reveal that in the case of a dominant set of decision variable the crossover operator does not have a significant impact on the performance measures, whereas high mutation rates are more suitable for GA applications." Other paper also find a relatively high mutation rate useful. Almanee et al., 2021 uses genetic algorithms in a similar domain as this thesis. There, a Population of 50, crossover of 0.8 and mut of 0.2 was used. These used params are the same as the default params from deap (pop = 50 CXPB, MUTPB, NGEN = 0.5, 0.2, 4).

Srinivas and Patnaik, 1994 state, that for a higher population, cross : 0.6, mut: 0.001 and pop: 100 is a good starting point, while a lower population needs higher crossover and mutation rates like this cross: 0.9, mut: 0.01, pop: 30

Fazal et al., 2005 recommends a population size of 50, a scattered crossover function with a crossover probability of 0.5. The used selection function was tournament selection. Elite count was set to 5.

Dao, Abhary, and Marian, 2016 suggests a population size of 200, two point crossover with a crossover probability of 0.7. A Gaussian Mutation Function as well as roulette selection and elite count set to 1.

A population size of 200 and roulette selection is used by Assistant Professor, Amity University, Jaipur, Rajasthan, India et al., 2019. Further, the elite count is set to 10. A heuristic crossover function with a crossover probability of 0.4 is also used.

cite
<https://deap.readthedocs.io/en/latest/>

4.3.2 results

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. Each run will be executed 5 times to get rid of randomness and to make the results more robust. We will run each simulation for 40 Generations.

Comparison of Population Size - mean					
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: 0.2, TS: 2	C	3062	3010	3002	2831
C: 0.6, M: 0.2, 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: 0.2, TS: 2	G	3099	2940	2959	2869
C: 0.8, M: 0.2, TS: 4	H	3058	3005	2794	2809

Figure 4.1: List Settings per Population Size

In figure 4.3.2, 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.

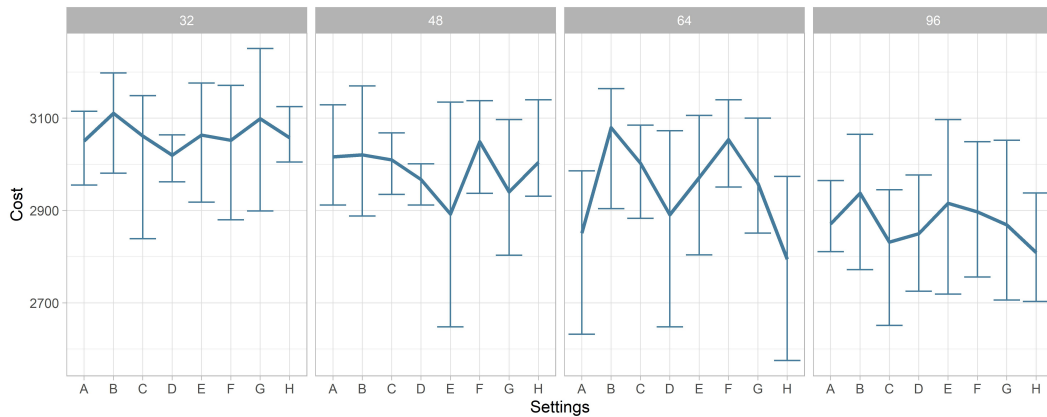


Figure 4.2: mean and error bars per population

A high spread 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 is important to keep the variation low.

4.4 Design of Experiment

Following the conclusion from the previous section 4.3, a population size of 96 will be used. 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.

In order to tune the hyperparameter of the genetic algorithm, various different strategies can be used. Using automated hyperparameter tuning 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 require a high number of runs, which is not feasible.

[find references](#)

4 Hyperparameter Tuning

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, this is a drawback compared to automatic hyperparameter tuning.

"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 4.4.3.

A full factorial design will test over all possible combinations of the manually selected factor levels. Looking at the proposed factors in table 4.4.1, we would require 1024 runs, which is 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 used for estimating higher-order interactions, which are in most cases insignificant.

"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)"

generated by
minitab (or
<https://datatab.net/statistics/calculator/design-of-experiments>)

4.4.1 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.

Using a Taguchi design for evaluating the best hyperparameter has been successfully performed by Dao, Abhary, and Marian, 2016 as well as Assistant Professor, Amity University, Jaipur, Rajasthan, India et al., 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 to 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:

Definition of orthogonal array

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.”

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:

- 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.
- Using the linear graph and interaction table, interactions can be defined.
- 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 4.3. 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 4.4.1, 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 4.4.2. 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.

4.4.2 Selection of a suitable standard 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 $\text{NumberOfLevels} - 1$.
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 4.4.2.

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 ortohogonal 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, 4.4.2 describes the graph which best fits the requirements from table 4.4.1. If no graph with the perfect fit is found, theses 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

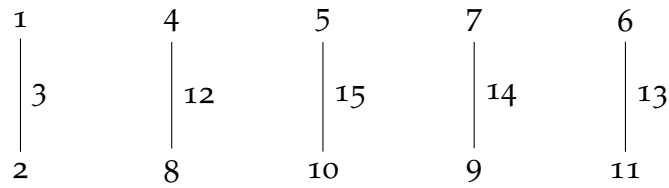


Figure 4.5: Linear Graph of $L_{16}(2^{15})$ taken from Yang and El-Haik, 2009

In a Taguchi linear graph, the nodes as well as the "Lines" 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 4.4.2.

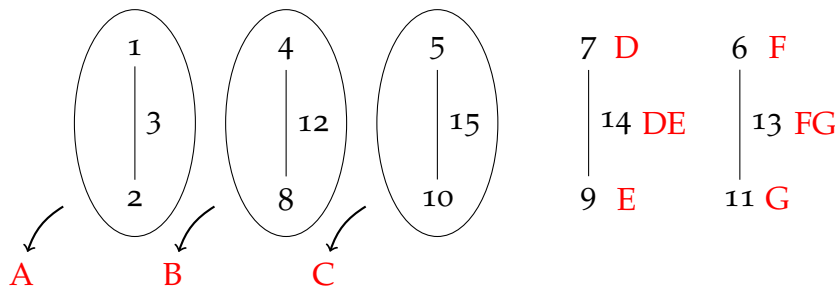


Figure 4.7: Modified Linear Graph to fit our needs

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.

4 Hyperparameter Tuning

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.

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

4.4.3 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 4.4.1. We will repeat every setting 8 times to reduce randomness and gain information about variance. Running the Genetic Algorithm using these 16 different settings each repeated 8 times took 10 days on the two previously described workstations.

ref to section

The results are found in the appendix at 6.1.

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”

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

Example for D

The resulting main-effect charts can be seen here:

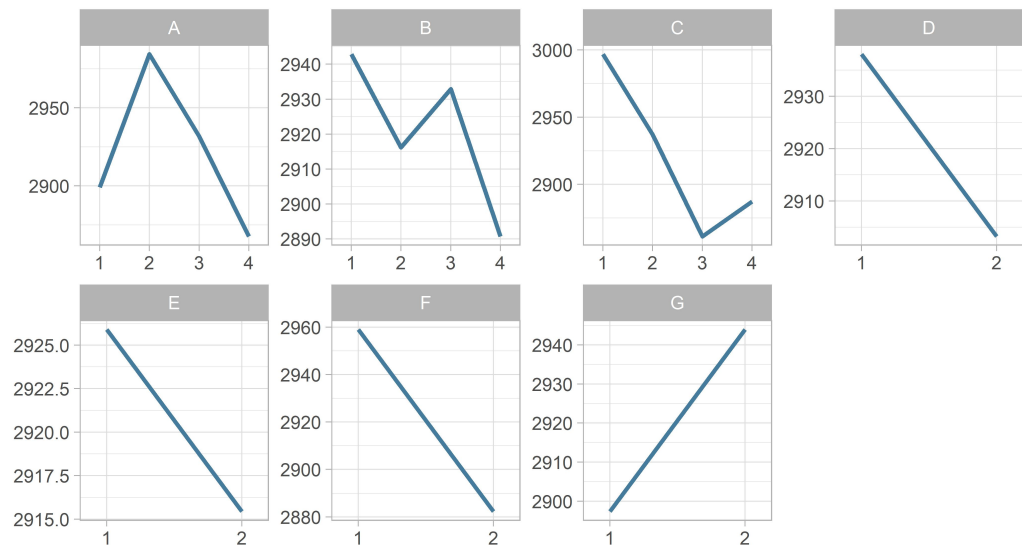


Figure 4.10: Main Effects

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

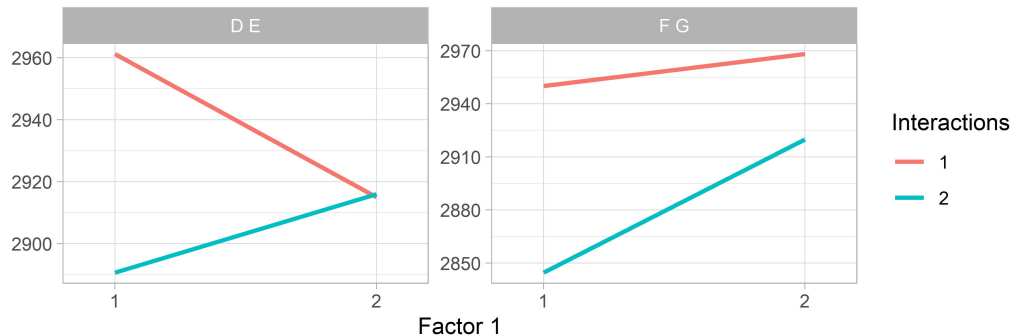


Figure 4.11: Test of interactions

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 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

Summary after reading "Introduction into R"

"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):

$$\begin{aligned} DOF &= totalNumberOfResults - 1 \\ &= numberOfTrials * numberOfRepetitions - 1 \\ &= 16 * 8 - 1 = 127 \end{aligned} \quad (4.2)$$

Calculating ANOVA can be done using R:

```
# pivot the results , so that the table has 8 times the rows
taguchi.combined_pivoted <- taguchi.combined %>% pivot_longer(cols = 2:3)

# run anova analysis
anova <- aov(results ~ factor(A) + factor(B) + factor(C))
summary(anova)
```

This will result in the following table:

Column	DF	Sum Sq	Mean Sq	F value	p value
1	A	3	1000	1000	1000
2	B	3	1000	1000	1000
3	C	3	1000	1000	1000
4	D	1	1000	1000	1000
5	E	1	1000	1000	1000
6	F	1	1000	1000	1000
7	G	1	1000	1000	1000
8	DxE	1	1000	1000	1000
9	FxG	1	1000	1000	1000
Residuals			1000	1000	1000

Figure 4.12: ANOVA results

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 4.4.3

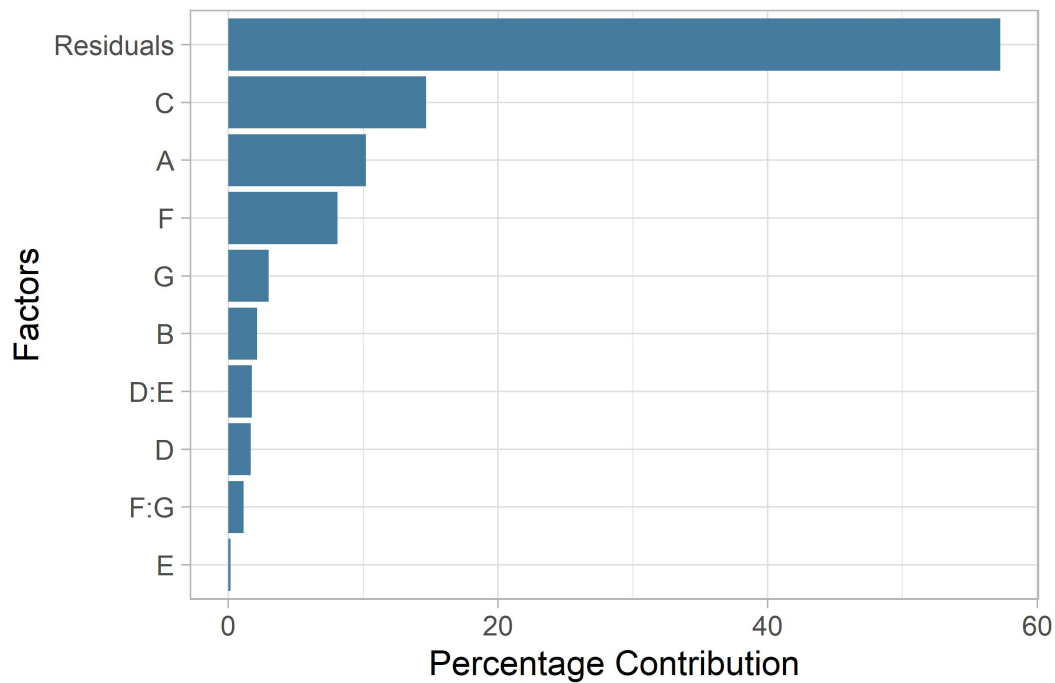


Figure 4.13: Percentage Contribution

Selection of optimal setting

"Further analysis for the significance of this influence is made possible by the ANOVA table in Table 5-16(b), which shows that the interaction $A \times C$ (column 3) is 5.26%, compared to the individual main effects of butter (B) 64.76% and flour (D) 18.4%, and so on."Roy, 1990.

"To reexamine the optimum condition determined only from the factors A2, C1, B2, D1, and E1, we see from Figure 5-6 that AC 11 has a higher value than AC 21. Thus, based on the interaction analysis, the optimum condition must include levels A1 and C1. The new optimum conditions become A1 B2 C1 D1 E1. However, the performance at the new optimum should be compared with the original optimum before the final determination of the interaction effects."Roy, 1990. This means, that If an interaction exist, we 1. look at the best main effect combination 2. check if the interactions align with this combination -> look at Test of interactions 3. if not, compute Y_{opt} ... -> look at page 88 from Roy, 1990. You use the interaction effects only for computing Y_{opt} (although it is also possible to calc it without...)

"For the purpose of analysis, interactions are treated as any other factors; however, their presence is ignored for the preliminary determination of the optimum condition. The relative significance of interactions is obtained from an ANOVA study."Roy, 1990

"The performance at the optimum condition is estimated only from the significant factors. This practice keeps the predicted performance conservative. Therefore, the pooled factors are not included in the estimate."Roy, 1990

If we only look at main effects, we would select: A4, B4, C3, D2, E2, F2, G1 However we select A4, B4, C3, D2, E1, F2, G1 because of important interaction DE. E on the other hand is not significant.

Optimum performance calculation We can also optimum performance when 1. using only main effects or 2. using main effects with applied interaction. Folrumar provided by Roy, 1990.

Better bars

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

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

SN -> proposed by taguchi. "A common approach to analyze such results is to use the average of the trial results for the optimum condition. Unfortunately, average alone does not capture complete information about the variability present."Roy, 1990

"Repetition permits determination of a variance index called the signal-to-noise (S/N) ratio. The greater this value, the smaller the product variance around the target value"Roy, 1990

TODO: 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.

"Advantage of S/N Ratio Over Average To analyze the results of experiments involving multiple runs, use of the S/N ratio over standard analysis (use average of results) is preferred. Analysis using the S/N ratio will offer the following advantages: 1. It provides a guidance to selection of the optimum level based on the least variation around the target and also on the average value closest to the target. 2. It offers objective comparison of two sets of experimental data with respect to variation around the target and the deviation of the average from the target value. Because S/N represents results transformed into a logarithmic scale that linearizes any nonlinear behavior, if present, the assumption of linearity for prediction of optimum performance is validated."Roy, 1990

"On the other hand, for set A, the spread around its average is smaller, but the average itself is quite far from the target. Which one of the two is better?

Based on average value, the product shown by observation B appears to be better. Based on consistency, product A is better. How can one credit A for less variation? How does one compare the distances of the averages from the target? Surely, comparing the averages is one method. Use of the S/N ratio offers an objective way to look at the two characteristics together."Roy, 1990

Not usefull for our purposes... Because df is reduced, run anova without interactions (or maybe without bad main effects). Fazit: S N was tried, however resulting anova showed that no factor was significant. Thus is was not further investigated.

"Effect of S/N Ratio on the Analysis Use of the S/N ratio of the results, instead of the average values, introduces some minor changes in the analysis. 1. Degrees of freedom of the entire experiment is reduced. DOF with S/N ratio = number of trial conditions - 1 (that is, number of repetitions is reduced to 1). Recall that the DOF in the case of the standard analysis is: $\text{DOF} = (\text{number of trials} \times \text{number of repetitions}) - 1$ The S/N ratio calculation is based on data from all observations of a trial condition. The set of S/N ratios can then be considered as trial results without repetitions. Hence the DOF, in the case of S/N, is the number of trials - 1. The rest of the analysis follows the standard procedure."Roy, 1990

5 Evaluation

in this chapter, we evaluate and compare various different settings

5.1 Comparison with random and default ga Values

Compare with Boxplot...

Different Algorithms: 1. Optimized GA 2. Best GA setting from Population
3. Random

5.2 Generalization on different start scenarios

scenario 1: default : 9v 5p scenario 2: 9v 5p scenario 3: 5v 3p scenario 4: 18v
10p

6 Conclusion

6.1 Test

Although lots of shortcomings Results look very vielversprechend. This thesis hopes to have emphasised that this approach has lots of advantages

Appendix

Appendix A.

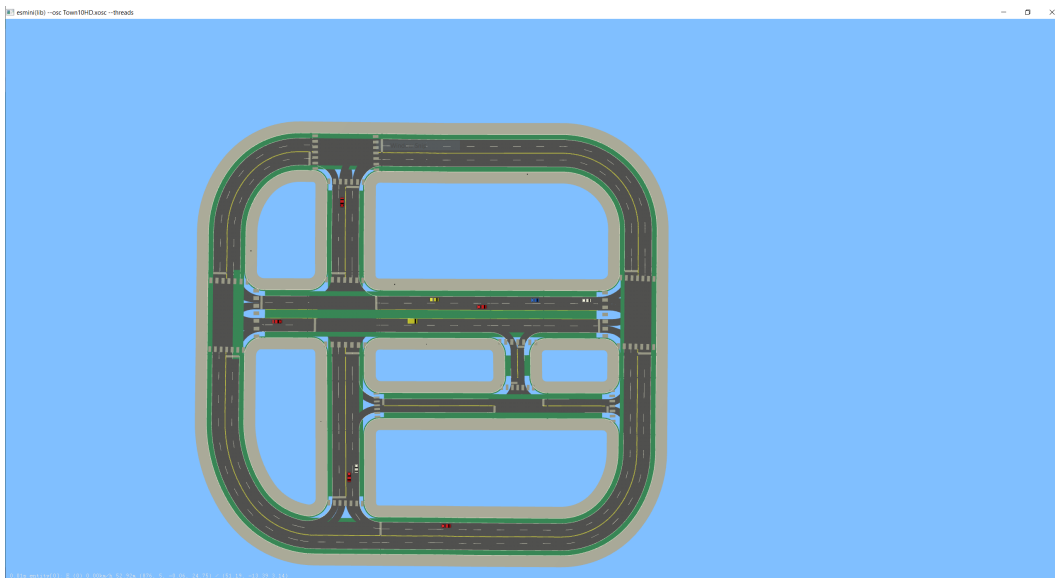


Figure 1: Start scenario 1

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 2: List of results

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