Utilising Design of Experiments to tune genetic algorithm crossover, and mutation rates for the Travelling Salesman Problem utilising data from UK logistics firms

by

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A project submitted in partial fulfilment of the award of the degree of
MSc. (Hons) Computing Science
from Staffordshire University

Supervised by Jonathan Westlake
December 2018

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1. Acknowledgments

This study would not have been possible without the support of my wife, Victoria, and my wonderful children Thomas and Charlotte who provided continuous reassurance during my protracted studies. I would also like to acknowledge Jonathan Westlake for his encouragement and advice throughout the dissertation process.

2. Abstract

Logistics is of vital importance to the UK in terms of employment (Barnes 2010) and standard of living (McKinnon, Fernie, Grant, Marchant, Somerville and Sweet 2004) therefore its efficiency can have a major effect on the economy and the wellbeing of the population(McKinnon, Fernie, Grant, Marchant, Somerville and Sweet 2004). One way of improving efficiency is via the optimisation of the routes that are undertaken. A significant proportion of the routes that UK logistics companies undertake are travelling salesman problems (TSP) were a vehicle must visit a number of locations before returning to its point of origin (DFT 2007). TSP problems are NP Complete (Michealevich 1994) (Katayama, Sakamoto, Narihisa 2000) with the number of potential solutions increasing as a factorial of the number of locations to visit (Skiena 2008) for example if a route has to visit ten locations the route could be planned 3,628,800 different ways. Despite this many small and medium companies plan their routes manually and therefore miss the benefits of reduced mileage associated with optimisation (Clarke, Leonardi 2018), this is due to the cost of commercial systems and a lack of trust in the results (Clarke, Leonardi 2018). A potential low cost solution to this problem is a Genetic Algorithm however such algorithms require tuning to their context (Ridge 2007) and no study has been made of the ideal settings for a UK Logistics context. This paper therefore develops a Genetic Algorithm for solving UK TSP problems and then develops a Design of Experiments (DOE) methodology for tuning it (Matthews 2005). In doing so it shows that DOE can be used to effectively tune a Genetic Algorithm; that parameter tuning influences the performance of a Genetic Algorithm (Ridge 2007); that the ideal settings for a Genetic Algorithm depend on the problem size; that the develop algorithm outperforms the original planning and it confirms previous findings that crossover is a major source of the ‘creative power’ (Mitchel 1995 p 38) of a Genetic Algorithm (Hameed, Kanbar 2017) (Grefenstalle, Gopal, Rosmaita, Gucht 1985) (Karapetyan 2010). However, the study contradicted previous findings by Tate and Smith (1993) by showing that mutation played no significant role in the performance of the Genetic Algorithm either directly or via its relationship with crossover, additionally the regression models developed had very poor explanatory power suggesting that un-modelled variable(s) within the Genetic Algorithm may play an important role in solving UK transport TSPs.

1. Introduction

This dissertation uses Design of Experiments (DOE) to tune a genetic algorithm (GA) to solve a subset of UK Logistics Travelling Salesmen Problems (TSP). In doing so it aims to:-

- Develop a GA which can be used for solving TSP problems;
- Illustrate how parameter values influence the performance of GA;
- Understand how parameter values interact to influence the performance of a GA;
- Provide guidance on the optimum levels to set various GA factors for UK Logistics TSPs;
- Provide a methodology for tuning TSP Genetic Algorithms;
- Demonstrate that a GA algorithm will outperform human transport planning.

The study is important because many small and medium size UK Logistics companies distrust the results of optimisation (Clarke, Leonardi 2018) and this will be one of the first to attempt to prove the advantages and while previous studies have examined GA tuning (De Jong 1975) (Greffenstette 1986) (Schaffer, Caruana,Eshelman, Das 1989) (Malhotra, Sing 2011) and the interaction of GA parameters (Lobo 2000) (Chiarandini, Paquete, Preuss, Ridge 2007) Pinel, Danoy, Bouvrey (2011) (De Jong 1975) such studies are rare (Eiben, Smith 2003) and none have been conducted within the context of UK logistics. This is a significant gap as:-

- logistics is vital to the UK economy (Great Britain Transport and the Economy 2010) and many HGV routes are travelling salesman problems;
- the optimum tuning and implementation of GAs has been shown to be context dependent (Dobshaw 2010) (Coffin, Saltzman 2000) and therefore recommendations based on other contexts may not be appropriate;
- many of the test suites used to assess GAs were designed to act as benchmarks for performance rather than practical usage (Rand, Rilo 2005). This is what Hooker has deemed as ‘competitive testing’ (Smit 2012 p 17) and as such they often involve TSP problems which are impractical within UK logistics due to the excessive travelling distance meaning that they would infringe EU driving regulations (Great Britain 2016).

This section has highlighted the key aims of the study and why the study is important. The following section introduces key concepts, these concepts will be further developed in the literature review.

i. The Travelling Sales Man problem and optimisation

The TSP is a combinational optimisation problem which involves finding the shortest tour around a weighted graph which visits each node (city or location)[1] once before returning to its origin this is called a Hamilton Cycle (Tannenbaum 2006), with Figure 1 illustrating two types of TSP:-

- Symmetric - distances between two nodes are the same regardless of travel direction;
- Asymmetric - distances between two nodes depends on the travel direction.

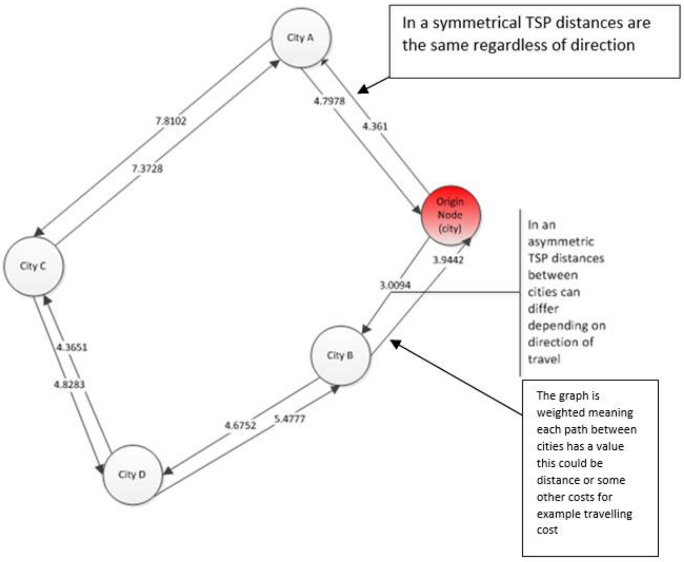

Figure 1 Weighted Graph demonstrating symmetrical and asymmetrical TSP Tours

Although first documented by Euler in 1759[2] the TSPs modern form was introduced in 1948 by the Rand Corporation (Michealevich 1994) (Larranaga, Kuijpers, Murga, Inza, Dizdarevic 1999). TSPs are very common as they apply to any field which involves finding the least cost tour[3] around a weighted graph (Michealevich 1994). For instance it has been applied to circuit

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[1] In the TSP literature the term city is used to represent a node to be visited. This study uses the term location as in real life TSPs there may be many places that need to be visited in the same city.

[2] Euler used the term the Knights Tour Problem (Michealvich 1994 p 209)

[3] The term tour is used within the TSP literature but the terms route or load are used interchangeably in logistics.

board design (Grötschel, Holland 1991), X-ray crystallography (Bland, Shallcross, 1989), and warehouse order picking (Ratliff, Rosenthal 1983) and it has been extended to encompass additional complexity for example the Vehicle Routing Problem which takes into account both distance and vehicle capacity (Mitchell, O'Donoghue, Barnes, McCarville 2003).

The next section describes the difficulty of solving TSP problems and potential solution methods.

ii. Solutions to the TSP

One approach to solving TSPs is to calculate the distance between each node (city, location) and then compute the shortest tour. However, this approach is 'inefficient' (Skiena 2008 p 304) and becomes impossible when the number of nodes becomes large. This is because the number of solutions increases as a factorial of the number of nodes (Figure 2) (Equation 1). This means that the search space is a hypercube of size n! and that TSPs are NP Complete (Michealevich 1994) (Katayama, Sakamoto, Narihisa 2000) meaning that no algorithm can solve them in polynomial time (Can, Beham, Heavey 2008)(Can, Beham, Heavey 2008):-

$$\frac{(n-1)!}{2}$$

EQUATION 1 NUMBER OF POTENTIAL SOLUTIONS TO A STSP PROBLEMS (PANWAR,MITTAL, SINGH 2012 P 2)

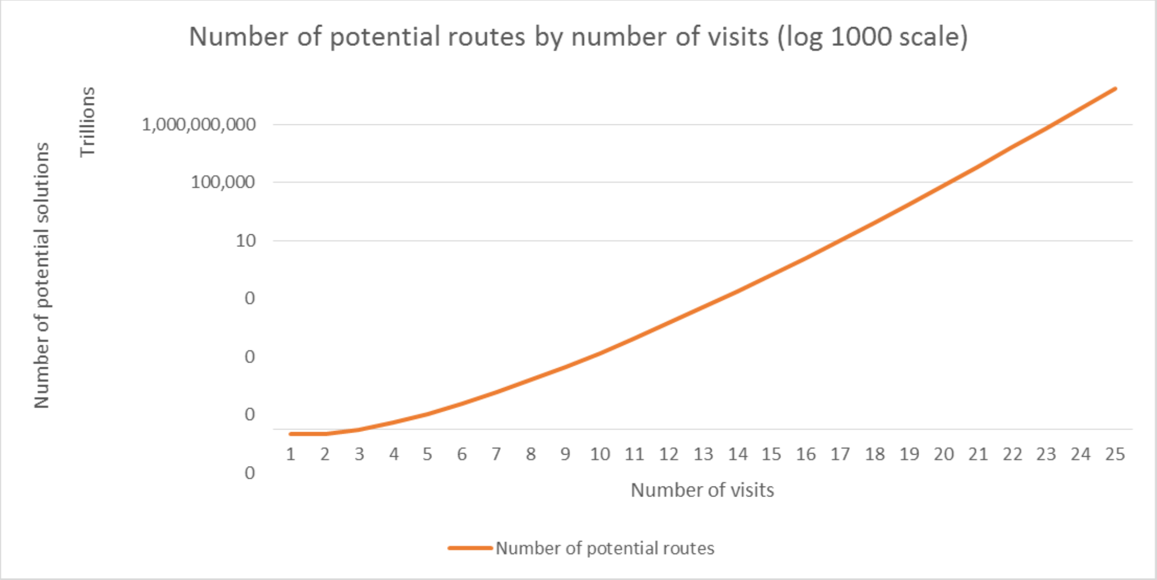

FIGURE 2 GRAPH SHOWING THE INCREASE IN POSIBLE STSB SOLUTIONS (TOURS) AS THE NUMBER OF VISITS (CITIES) INCREASES

Due to their applicability to many situations and their complexity, TSPs are one of the most studied problems in combinatorial mathematics (Jubeir, Almazrooie, Abdullah 2017) with Table 1 illustrating the number of papers published between 2010 and 2017. This focus has led to significant progress with Figure 3 illustrating how the size of the maximum optimally solvable TSP has increased.

Branch and Bound	25
Cutting plane	3
Exact Methods Total	**28**
Heuristics	**107**
Ant Colony	334
Genetic	343
simulated annealing	63
Swarm	90
Bee colony	39
Metaheuristics Total	**869**

TABLE 1 TSP ARTICLES PUBLISHED BETWEEN 2010 AND 2017 IDENTIFIED ON GOOGLE SCHOLAR FOR EACH SOLUTION TYPE

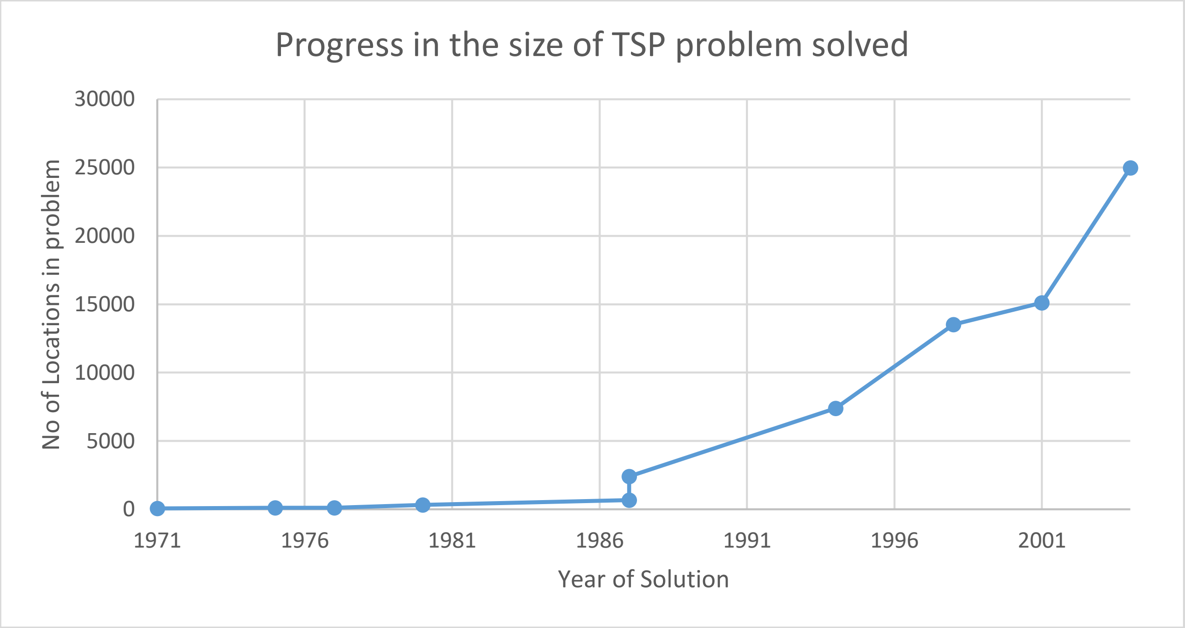

FIGURE 3 GRAPH SHOWING HOW THE MAXIMUM OPTIMALLY SOLVEABLE TSP HAS INCREASED OVERTIME DATA FROM MATH.UWATERLOO (2016)

These improvements have been due to improved algorithms such as Branch & Bound (Jiang,Weise, Lassig, Chiong, Athauda, 2014) and Cutting Plane (Dantzig, Fulkerson, Johnson 1954) which use mathematical techniques to reduce the search space thus allowing an optimum solution to be found quickly (Skiena 2008 p 238).

However, commercial problems are often too large for such methods to solve in acceptable time (Pillac 2012) and industry often needs good not optimal solutions (Pillac 2012). Therefore as the benefits of optimisation are large, industry (DPS) and academia have developed approximate solutions (Table 2).

Approximate TSP approaches can be grouped into:-

- Heuristics (Skiena 2008) – These produce ‘feasible but not necessarily optimum solutions’ in a timely manner (Okediran, Okeyinka, Arulogun, Ganiyu, Alo 2016 p 83). Popular heuristic approaches include the nearest neighbour (Johnson, McGoech 1995) which has a complexity of $O(n^2 Log_2(n))$ (Matai,Mittal, Singh 2012 p 14) and the Christofides algorithms (Bienstock, Goemans, Simchi-Levi, Williamson 1993) which has a complexity of $O(n^3)$ (Matai,Mittal, Singh 2012 p 15) .
- Metaheuristics (Luke 2015) - Currently the most popular area of TSP research (Table 2[4]). A number of methodologies have developed often taking inspiration from nature with GAs being the most popular (Table 2).

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[4] This is not a complete list of meta-heuristics rather it is a list of those meta-heuristics which are most popular according to Google Scholar

Approach	Number of studies	Percentage of total	Notes (if relevant)
Exact Methods			
Cutting Plane	3	0.30%	
Branch and Bound	25	2.49%	
Exact method approaches total	**28**	2.79%	
Heuristics Approaches Total	**107**	10.66%	Many of these papers combine two or more heuristic approaches, whilst others only included heuristic in the title therefore they are grouped into a single heading
Meta-Heuristic Approaches			
Ant Colony Algorithm	334	33.27%	These attempt to find the least cost TSP by mimicing the way that ants navigate the world to find food. When the ant finds 'food' it leaves a path of pheromones on its way back home. Other ants have a certain probability of following these paths (based upon the relative length of that path), if they do they leave their own pheromones making a stronger smell meaning more ants follow it.
Genetic Algorithm	343	34.16%	Explained in next section
Swarm based Algorithms	63	6.27%	These are based on the behaviour of swarms of animals and optimises behavior by the exchange of information between individals (Xuesong Yan, Zhang , Luo,Li, Chen, Liu 2012)
Bee Based Algorithms	90	8.96%	This mimics how bees search for food with different bees doing different roles (scout, employed, and onlooker bees) . This allows the algorithm to search locally using employed bees, scout bees search randomly helping to avoid local optima whilst onlooker bees decide which food source is better (Pathak, Tiwari 2012)
Simulated annualing	39	3.88%	This mimics the annualing process from thermodynamics to find solutions to the TSP (Mu,Wang, Zhao, Sutherland 2016)
Meta-Heuristic Approaches Total	869	86.55%	
Total	1004		

TABLE 2 TABLE SHOWING THE NUMBER OF PAPERS ON VARIOUS APPROACHES TO THE TSP WHICH ARE RETURNED IN A GOOGLESCHOLAR SEARCH FOR ARTICLES 2010 – 2016 WHERE ALL OF THE WORDS APPEAR IN THE TITLE

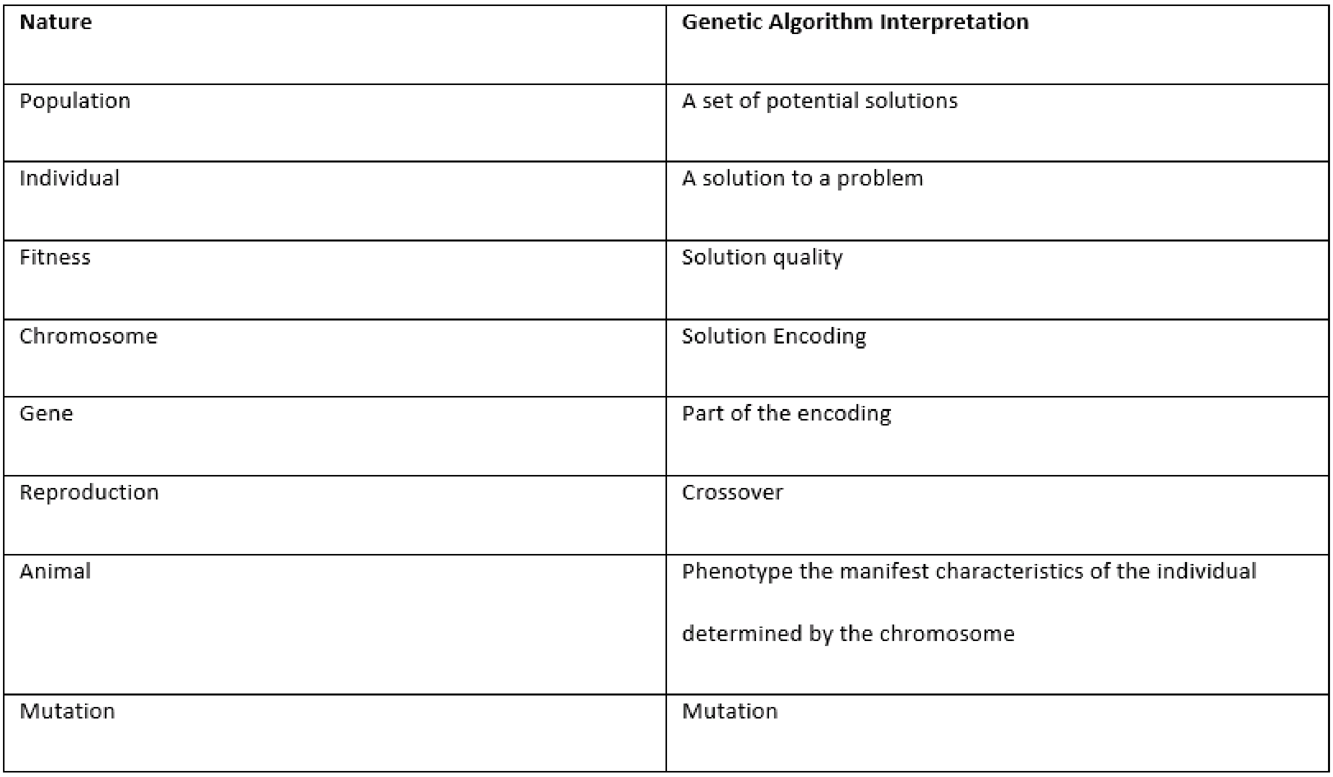
The next section will describe the focus of this study, Genetic Algorithms, in more detail.

iii. Genetic Algorithms

Genetic Algorithms are a scholastic meta-heuristic optimisation technique which are an ‘abstraction of biological evolution’(Mitchell 1995 p 31) applying the principles and language of natural selection (Table 3) (Gutoski 2005) to evolve solutions to a problem iteratively (Malhotra, Singh, Singh 2011). Evolution is a search among innumerable possibilities for solutions which are best adapted to the environment (Mitchell 1995), in mimicking evolution (Table 3) GAs utilise biological techniques such as selection, inheritance and recombination to ‘exploit’ the information encoded in the previous generations of solutions and to explore new areas of the search space via mutation (Mitchell 1995) with ‘natural selection’ (Deep, Adane 2011 p 3) ensuring that favourable traits become increasingly common over generations and unfavourable traits less common (Figure 4). This multi-generational approach is in juxtaposition to other scholastic techniques such as Monte Carlo analysis which are ‘either completely memoryless or utilise only a few…approximation(s) (Gutoski 2005 p 172) and with traditional techniques which concentrate on developing a single solution rather than a population of solutions (Deb 1999 p 302). This population of solutions approach means that GAs can:-

- be parallelised allowing them to take advantage of multiple processors (Haupt, Haupt 2004 p 23)
- be thought as inherently parallel as they investigate a population of solutions at the same time (Mitchell 1995) (Abdoun, Abouchabaka, Tajani 2011) allowing them to study a broader search space than other search algorithms (Haupt, Haupt 2004 p 23).

However, the population of solutions approach can be slower than other algorithms due to the additional processing required to calculate the cost of each potential solution (Haupt, Haupt 2004 p 23).



Nature	**Genetic Algorithm Interpretation**
Population	A set of potential solutions
Individual	A solution to a problem
Fitness	Solution quality
Chromosome	Solution Encoding
Gene	Part of the encoding
Reproduction	Crossover
Animal	Phenotype the manifest characteristics of the individual determined by the chromosome
Mutation	Mutation

TABLE 3 PROCESSES IN NATURE AND THEIR GA REPRESENTATION

Debate exists over what constitutes a GA with some arguing that only implementations that follow the example of Holland's canonical version being true GAs (Michealevich 1994 p 8) however this interpretation has loosened with some interpretations 'being very far away from Holland's intentions' (Kaya, Uyar, Tekin 2011 p 1), this study uses the definition provided by Whitely (1994 p 65):-

> *'any population based model that uses selection and recombination operators to generate new sample points in the search space'*

There are a large number of GA variations for example Hybrid GAs which build in local search algorithms into one or all of the initial population, the crossover operator or the mutation operator (Katayama, Sakamoto, Narihisa 2000) however this study concentrates on the "standard GA" which is shown in Figure 4 with Figure 5 describing how GAs can be used to solve a TSP.

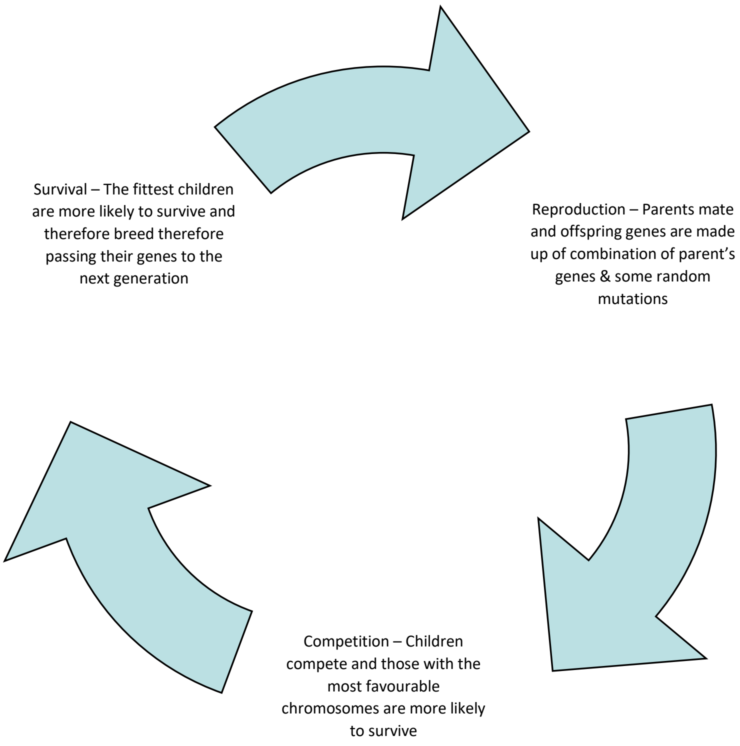


Figure 4 A simplified explanation of a genetic algorithm

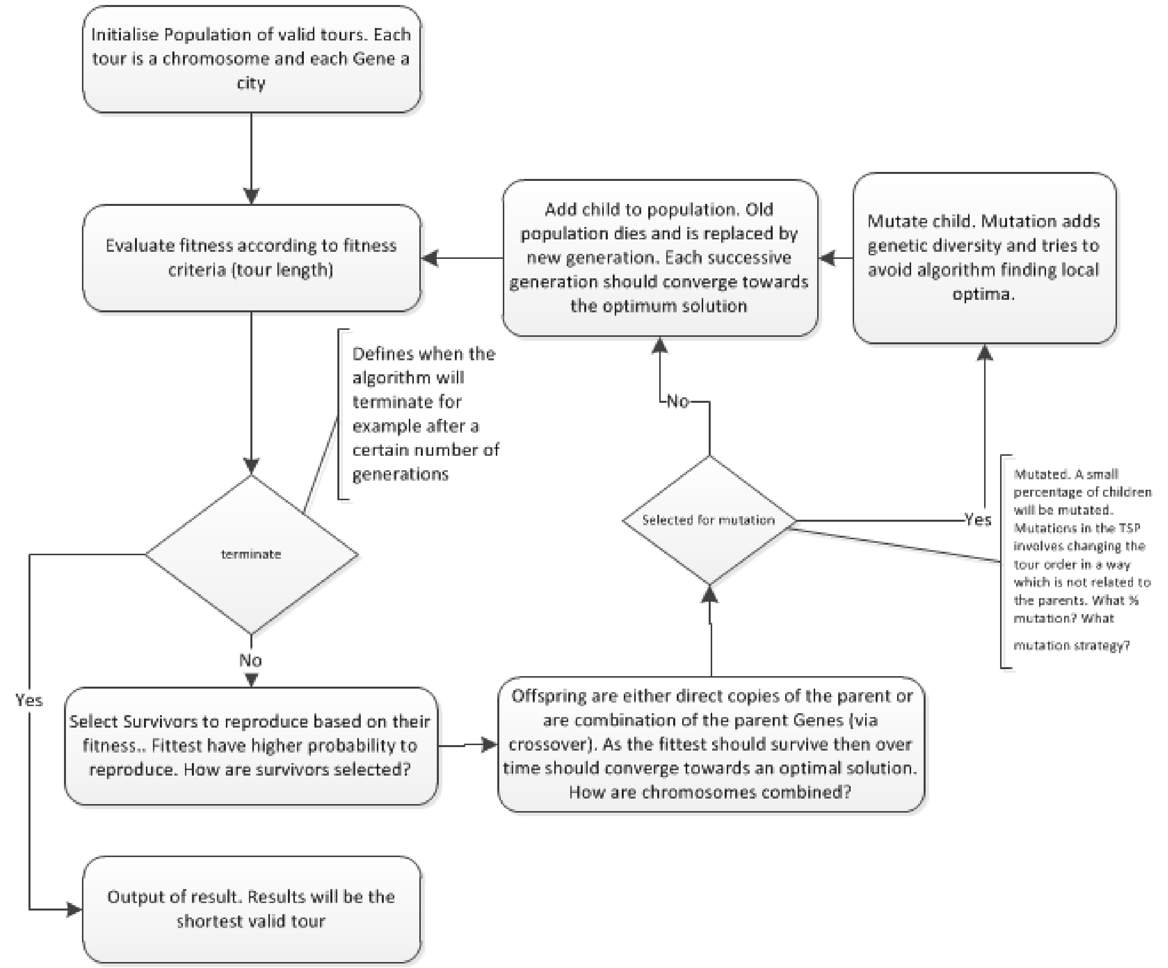


FIGURE 5 GENETIC ALGORITHMS AS APPLIED TO THE TSP. AUTHORS OWN BUT BASED UPON (JACABSON, KAMBER 2015 P 8)

This section described the basic operation of a GA, however, GA approaches diverge significantly in operationalisation (Deep, Adane 2011) these differences will be discussed in the literature review. The next section describes the importance of GA tuning.

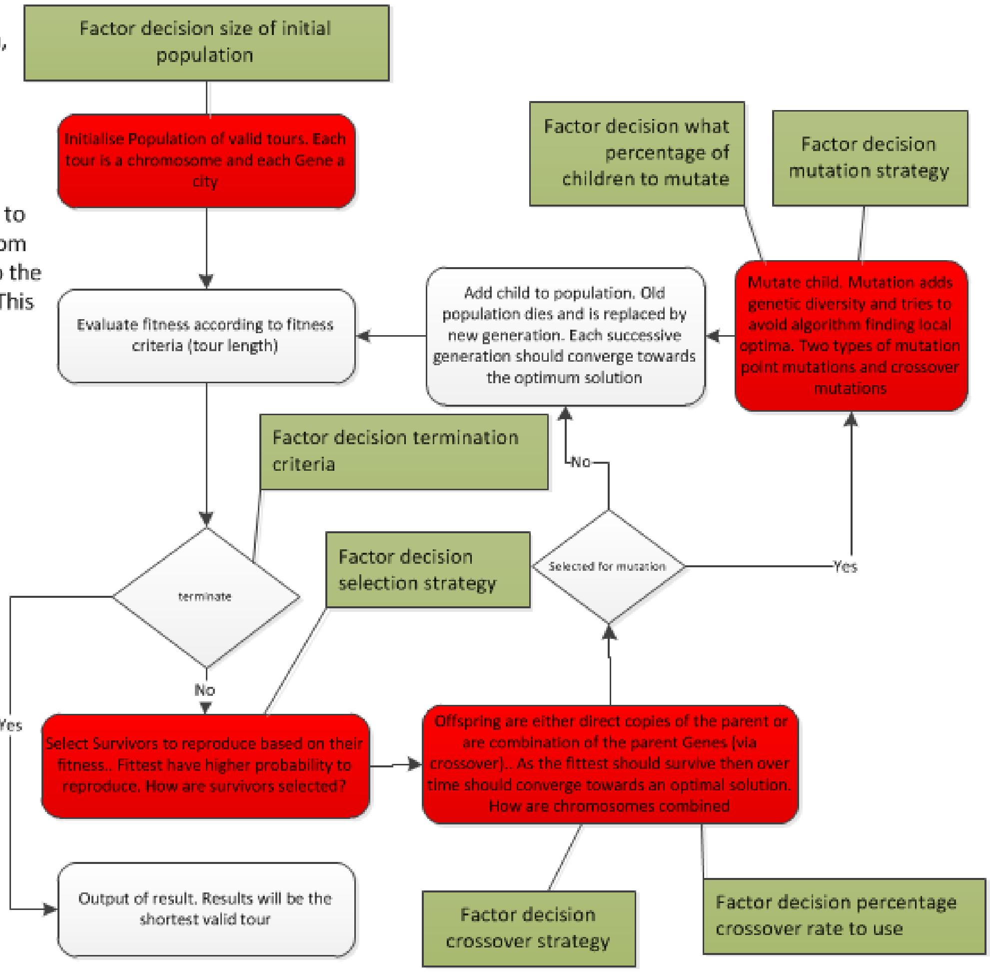
iv. Importance of Tuning

Although studies have shown that GAs have some tolerance to parameter settings (Lobo 2000), the no free lunch theorem of Wolpert, MacReady (1997) states no algorithm will out-perform every algorithm for every problem. However, 'there is a striking gap' between the importance of tuning and the number of studies of GA tuning (Eiben, Smith 2003 p 15).

A difficulty when utilising a GA is deciding which parameters can lead to improved performance (Maturana, Lardeux, Saubion 2009) with Figure 6 identifying factors (in red) which may influence the quality of a GAs TSP solution. The factors that can influence performance have been classified using various terms:-

- Structural (Maturana, Lardeux, Saubion 2009) / Symbolic (Yuan, Gallagher 2007) / Categorical factors (Hutter, Hoos, Stutzle 2007) such as such as the choice of encoding or crossover method;
- Behavioural (Maturana, Lardeux, Saubion 2009), / Numeric (Yuan, Gallagher 2007) such as the probability of mutation or crossover. (Hutter, Hoos, Stutzle 2007)

This paper will use the terms behavioural and structural (Maturana, Lardeux, Saubion 2009) with this study focussing on behavioural factors, however the literature review will investigate behavioural and structural factors as both are important in the design of the GA test bed and because behavioural factors work within the context of the structural factors.



The GAs selection, mutation and crossover setting must allow advantageous features of the trial solutions to be transmitted from one generation to the next generation. This contrasts with solutions such as Monte Carlo Simulation which are often completely memoryless. (Gutowski 2005)

FIGURE 6 ELEMENTS OF A GENETIC ALGORITHM WITH ELEMENTS WHICH MAY REQUIRE TUNING HIGHLIGHTED IN RED

The factors in Figure 6 require tuning (Ridge 2007 p 22) to give the algorithm 'flexibility and robustness' (Fallahi, Amirib, Yaghini 2014 p 497) (Smit 2012). Unfortunately optimum parameters are problem dependent (Fallahi, Amirib, Yaghini 2014) and due to the interaction between parameters, the absolute and relative levels of each parameter must be considered (Fallahi, Amirib, Yaghini 2014). This interaction makes tuning difficult because as the number and levels of parameters increase, potential combinations increase exponentially (Figure 7). However, despite difficulty, identifying good settings is important as incorrect settings can lead to poor performance (Ridge 2007).

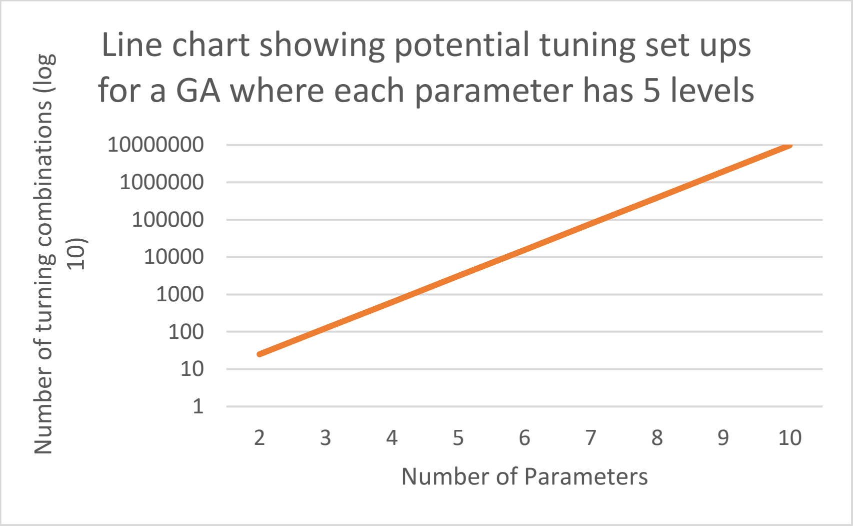


FIGURE 7 LINE CHART SHOWING HOW POTENTIAL TUNING CONFIGURATIONS INCREASES WITH THE INCREASE IN PARAMETERS FOR A GENETIC ALGORITHM WITH 5 LEVELS (LOG 10 SCALE)

Therefore, effective TSP GA use requires an understanding of parameter setting within specific contexts, unfortunately the literature gives little guidance (Luke, Spector 1997) in general and no guidance to the UK logistics industry on how a GA should be tuned. However, the investment of time needed to tune an algorithm is potentially worthwhile as TSPs within UK Logistics are repetitive as although the problem instance changes each day, each instance is similar (Smit 2012 p 27)(DFT 2007).

Thus this paper investigates TSP GA tuning within UK logistics with Figure 8 describing the factors which require tuning. However, feasibility means this study can only investigate the effect of mutation and crossover rates on the TSP solution with the factors being studied at different problem sizes[5].

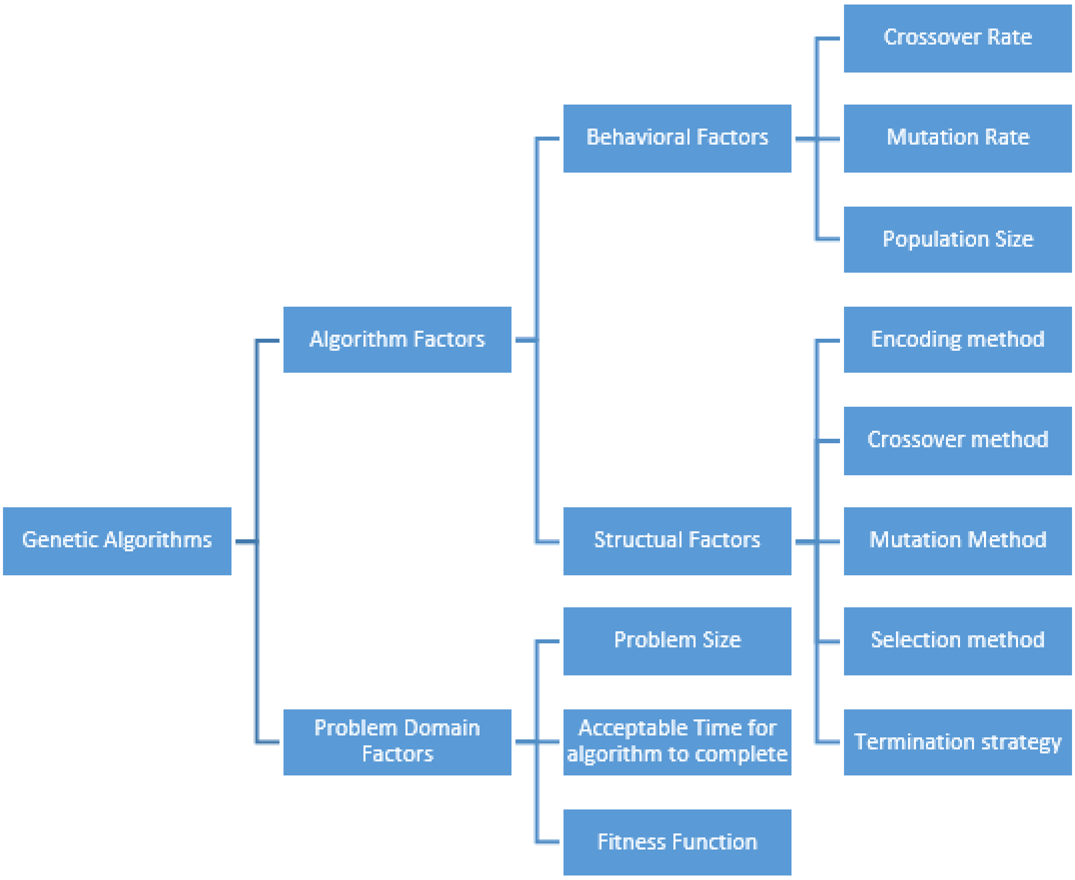


Figure 8 Algorithm and problem specific factors potentially involved in the study adapted from Pongcharoen, Chainate Thapatsuwan (2006 p 215)

v. UK Logistics

This paper studies TSP problems within a subset of UK Logistics. Logistics is:-

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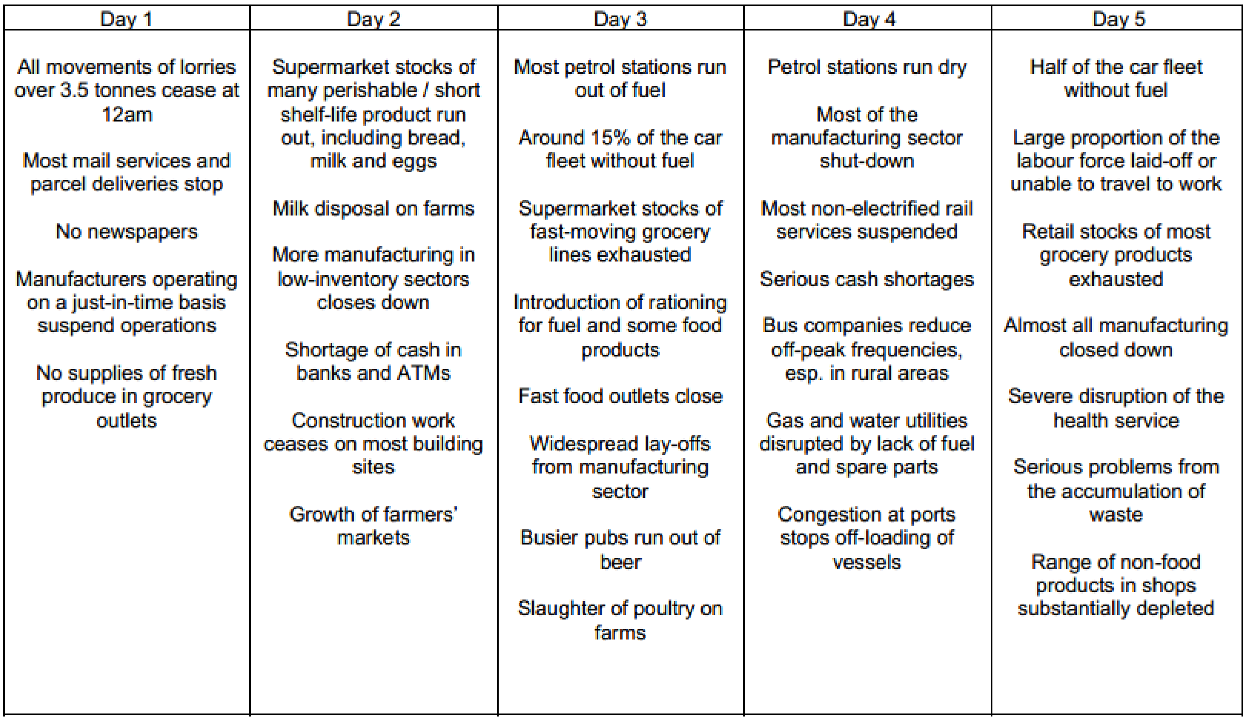
[5] Problem size is the number of stops a vehicle on its route

'The management of the flow of goods between point of origin and point of destination to meet customer and corporate requirements.' (Collins 2018*)*

The subset studied in this paper is the domestic movement of goods by road. This subsector is important for the UK economy employing 220,000 people and moving 68% of all UK freight (Barnes 2010) in doing so it utilises 499500 vehicles travelling 18.6 road KM in 2017 (Great Britain 2018) this importance is illustrated by a dystopian paper by McKinnon, Fernie, Grant, Marchant, Somerville and Sweet (2004) who looked at what would happen if the trucks stopped running and concluded that the chaos in Table 4 would result.



Day 1	Day 2	Day 3	Day 4	Day 5
All movements of lorries over 3.5 tonnes cease at 12am Most mail services and parcel deliveries stop No newspapers Manufacturers operating on a just-in-time basis suspend operations No supplies of fresh produce in grocery outlets	Supermarket stocks of many perishable / short shelf-life product run out, including bread, milk and eggs Milk disposal on farms More manufacturing in low-inventory sectors closes down Shortage of cash in banks and ATMs Construction work ceases on most building sites Growth of farmers' markets	Most petrol stations run out of fuel Around 15% of the car fleet without fuel Supermarket stocks of fast-moving grocery lines exhausted Introduction of rationing for fuel and some food products Fast food outlets close Widespread lay-offs from manufacturing sector Busier pubs run out of beer Slaughter of poultry on farms	Petrol stations run dry Most of the manufacturing sector shut-down Most non-electrified rail services suspended Serious cash shortages Bus companies reduce off-peak frequencies, esp. in rural areas Gas and water utilities disrupted by lack of fuel and spare parts Congestion at ports stops off-loading of vessels	Half of the car fleet without fuel Large proportion of the labour force laid-off or unable to travel to work Retail stocks of most grocery products exhausted Almost all manufacturing closed down Severe disruption of the health service Serious problems from the accumulation of waste Range of non-food products in shops substantially depleted

TABLE 4 PROBABLY EFFECTS OF TRUCK STOPPAGE OVER THE FIRST 5 DAYS (MCKINNON, FERNIE, GRANT, MARCHANT, SOMERVILLE AND SWEET 2004 P 22)[6]

Despite the difficulty of finding the optimum route and the availability of auto-scheduling products such as DPS (DPS 2018), 90% of vehicles used in the case study company are planned manually, this confirms the findings of Clarke, Leonardi (2018) whose case study found that all routes in their sample were manually planned. Such manual planning means that a human may have to assess thousands of potential solutions (Figure 2). Such routing decisions effect firm profitability and environmental impact via:-

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[6] This paper was written by academics for a Road Haulage Industry magazine with the aim of indicating the importance of trucking.

- increased fuel usage due to unnecessary mileage which leads to unnecessary pollution and costs;
- the need for additional vehicles and drivers due to each route taking longer(Clarke, Leonardi 2018)[7].

The issue of suboptimal routes is illustrated in Figure 9 which shows a saving of 3.1 litres of fuel (assuming a 17 tonne vehicle) by selecting the best over the worst route this equates to an:-

- extra £4.02 of cost [8] (Great Britain 2018b)
- extra 8.2 kg of carbon emissions (Commercial Fleet 2018) (Infogram 2018).

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[7] This problem is exasperated by a UK wide driver shortage with 26% of respondents to a recent survey saying that the driver shortage was the largest threat they faced (Moore Stephens 2017)

[8] August 2018 fuel prices

Route No	Tour Route	Tour distance in Miles	Ltrs Used	C02 emisions (kgs)
Route 1	Hartlepool, Middlesborough, Elwick,Wingate, Hartlepool	46.5	23.02266667	60.31939
Route 2	Hartlepool,Middlesborough,Wingate,Elwick,Hartlepool	52.8	26.14186667	68.49169
Route 3	Hartlepool,Wingate,Middlesborough,Elwick,Hartlepool	51.9	25.69626667	67.32422
Route 4	Hartlepool,Wingate,Elwick,Middlesborough,Hartlepool	46.5	23.02266667	60.31939
Route 5	Hartlepool,Elwick,Middlesborough,Wingate,Hartlepool	51.9	25.69626667	67.32422
Route 6	Hartlepool,Elwick,Wingate,Middlesborough,Hartlepool	52.8	26.14186667	68.49169
Best Solution		46.5	**23.02266667**	**60.31939**
Worst Solution		52.8	**26.14186667**	**68.49169**
Difference			**3.1192**	**8.172304**

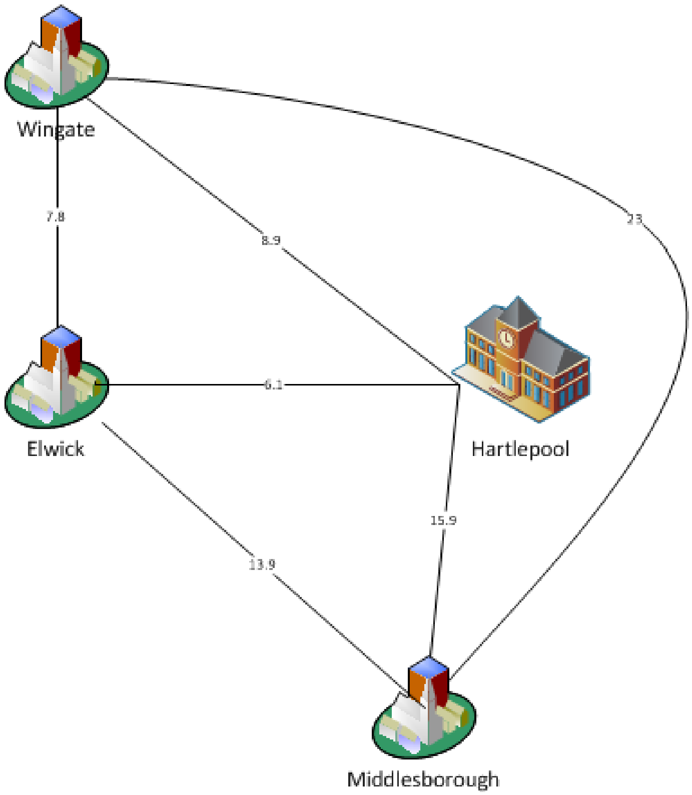

FIGURE 9 ILLUSTRATION OF A FOUR NODE ROUTE[9]

This section has introduced the study domain and gave an overview of the main areas of this study. The next section critically reviews the literature relating to GAs and the TSP and justifies the structural factor choices made in the design of the accompanying GA artefact.

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[9] Emissions details from Commercial Fleet 2018, fuel details from Infogram 2018

2. Literature Review

i. Introduction

The literature relevant to this study can be classified as six overlapping areas (Figure 10). As the literature relating to each is extensive this review will focus on directly relevant studies and those with a high level of citations, furthermore studies which have employed 'knowledge augmented genetic algorithms which utilise problem domain knowledge to augment the genetic algorithm' (Louis, McDonnell 2004) will be excluded. This is because there is no guarantee that assumptions about the problem are correct and because the focus of the study is tuning and not algorithm development. Each of the areas in Figure 10 are discussed.

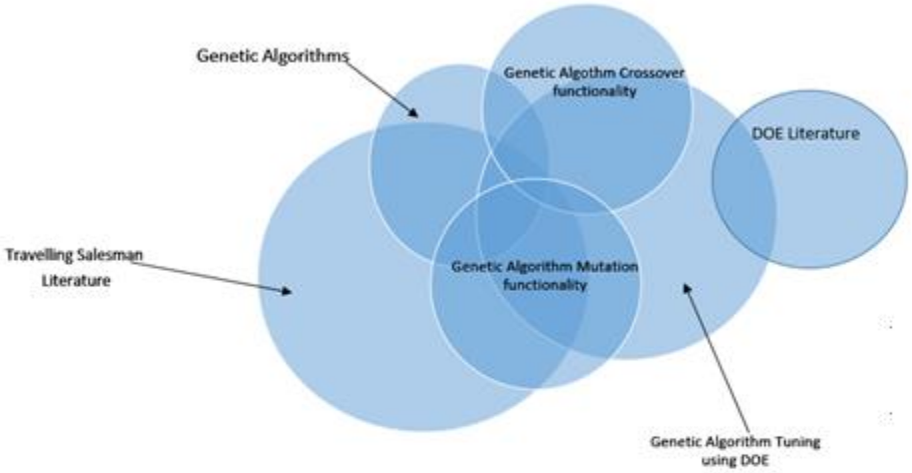
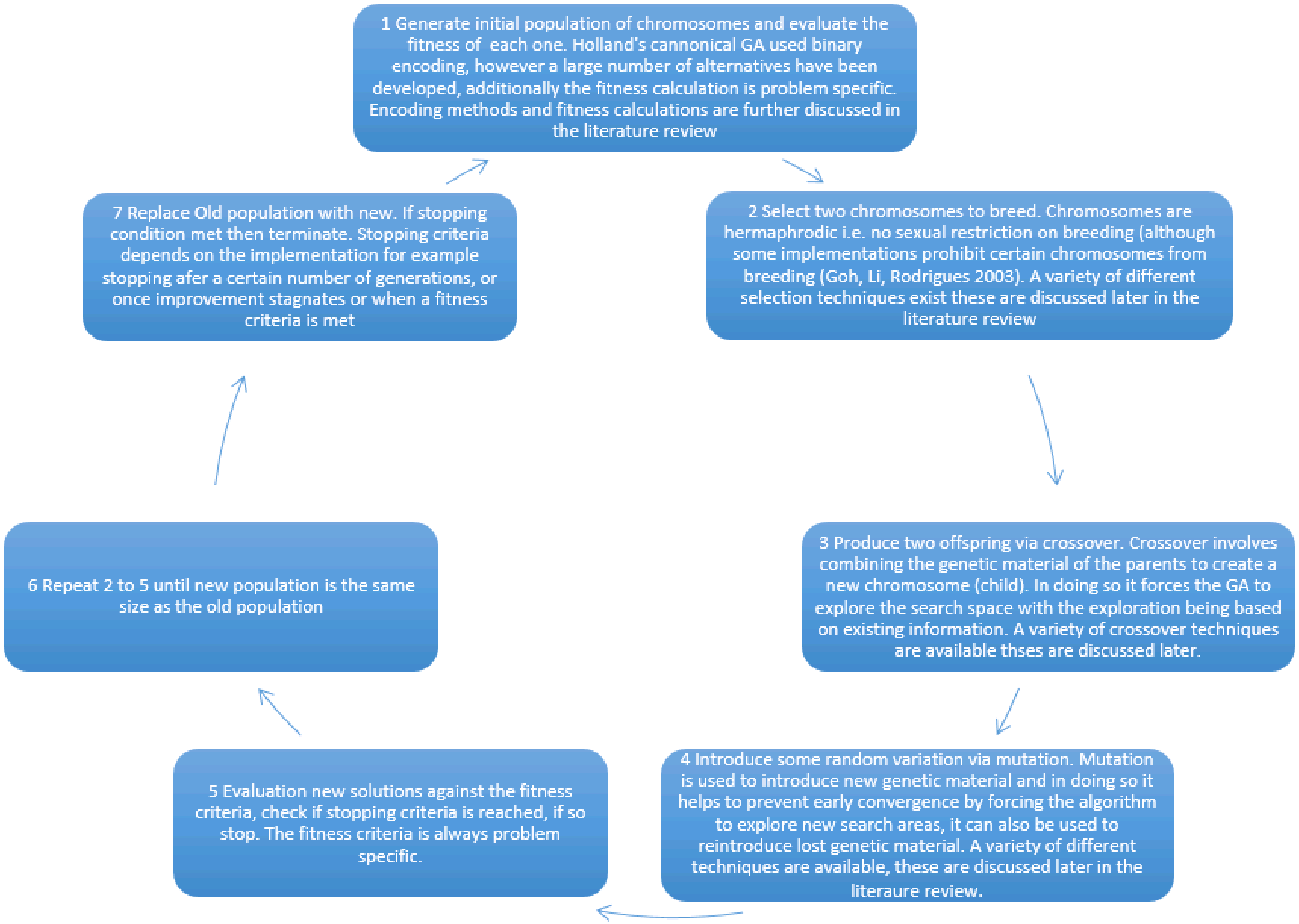


FIGURE 10 VENN DIAGRAM DESCRIBING THE RELEVANT LITERATURE FOR THIS STUDY

ii. Genetic Algorithms and the TSP

Although GA's were developed from Holland's 1975 work 'Adaption in Natural and Artificial Systems' (Katayama, Sakamoto, Narihisi 2000) it was Golberg who introduced the widely accepted interpretation of a GA in 1983 (Figure 11) (Katayama, Sakamoto, Narihisi 2000). While the general process of a GA is widely accepted GA implementations can vary across all structural and behavioural operators (Maturana, Lardeux, Saubion 2009), these variations are due to different encoding methods being more appropriate for some problems and the differing opinions of researchers (Gutowski 2005 p 171).

This section discusses the theoretical basis for how GA’s work, it then analyses the literature relating to developing a GA to solve the TSP before discussing GA tuning.



1 Generate initial population of chromosomes and evaluate the fitness of each one. Holland's cannonical GA used binary encoding, however a large number of alternatives have been developed, additionally the fitness calculation is problem specific. Encoding methods and fitness calculations are further discussed in the literature review

2 Select two chromosomes to breed. Chromosomes are hermaphrodic i.e. no sexual restriction on breeding (although some implementations prohibit certain chromosomes from breeding (Goh, Li, Rodrigues 2003). A variety of different selection techniques exist these are discussed later in the literature review

3 Produce two offspring via crossover. Crossover involves combining the genetic material of the parents to create a new chromosome (child). In doing so it forces the GA to explore the search space with the exploration being based on existing information. A variety of crossover techniques are available thses are discussed later.

4 Introduce some random variation via mutation. Mutation is used to introduce new genetic material and in doing so it helps to prevent early convergence by forcing the algorithm to explore new search areas, it can also be used to reintroduce lost genetic material. A variety of different techniques are available, these are discussed later in the literaure review.

5 Evaluation new solutions against the fitness criteria, check if stopping criteria is reached, if so stop. The fitness criteria is always problem specific.

6 Repeat 2 to 5 until new population is the same size as the old population

7 Replace Old population with new. If stopping condition met then terminate. Stopping criteria depends on the implementation for example stopping afer a certain number of generations, or once improvement stagnates or when a fitness criteria is met

Figure 11 The Generic Genetic Algorithm based upon Gutoski 2005 (p 176) and Malhotra, Singh (2011 p 40)

iii. Theoretical basis for solving a Genetic Algorithm

Although GAs are easy to describe their behaviour is complicated and significant debate exists over how they work (Mitchell 1995). According to Holland (1975) the performance of GAs is based upon the theoretical ideas in Table 5 :-

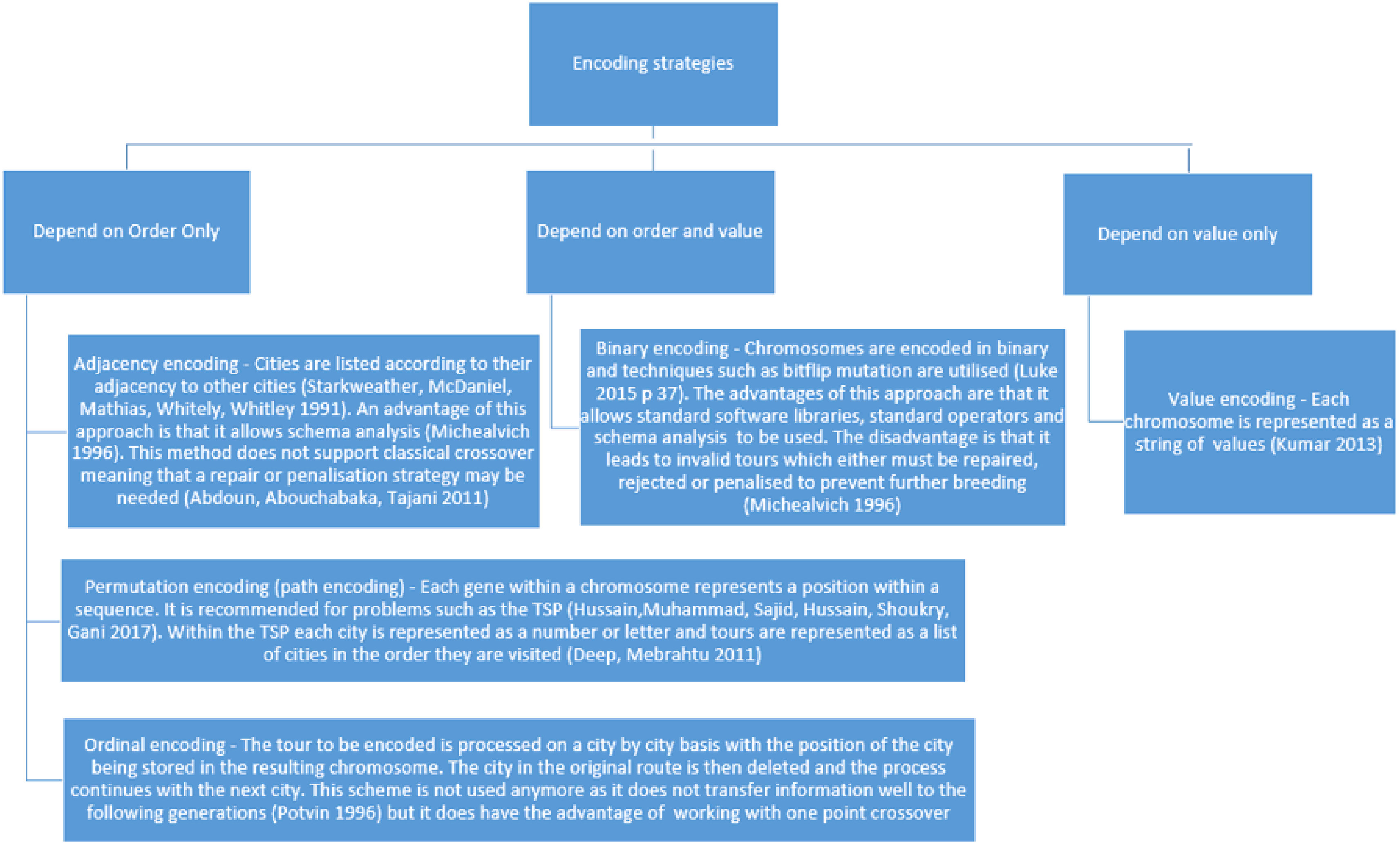
Name	**Description**
Schema theory	A schema is a 'similarity template' (Goldberg 1989 p19) describing a subset of chromosomes with 'one or more things in common' (Man 1996 p 521) (Sawy, Hussein, Zaki, Mousa 2014). Assuming binary chromosome encoding the schema template is made up of 1s, 0s and the 'I don't care meta-symbol' * (Goldberg 1989 p 19). This means that schema *01000 matches two chromosomes 101000 and 001000 therefore it is a 'powerful way of describing similarities between chromosomes (Sawy, Hussein,Zaki, Mousa 2014 p 254) and describing a hyperplane (Whitely 1994 p7) in the search space (Deb 1999 305). Holland defined the following key characteristics of schema as the:- • order – this is the number of fixed positions in the schema • defining length – the distance between the outermost fixed positions in the schema.
Building Block hypothesis	The central point of schema theory is that the selection process biases the sampling towards above average schema (Mitchell 1995) however the recombination and mutation processes destroy some of these schema meaning that it is schema that have a short order and defining length that become the building blocks for solutions. These building blocks are eventually grouped together via the GA to develop 'bigger and better building blocks' (Deb 1999 p 305) causing the GA to 'converge on the optimal solution (Deb 1999 p 305). However, although the idea that crossover works by combining two good building blocks seems theoretically valid it is difficult to prove and this has led to it being challenged by a number of authors (Beyer, Schweffel 2002 p19) and alternative approaches to understanding GA's such as Markov chains have been developed despite this the debate over the workings of GA's remains undecided today (Mitchell 1995) (Luke, Spector 1997).

TABLE 5 HOLLAND'S THEORETICAL BASIS FOR WHY GENETIC ALGORITHMS WORK

This subsection has described the theoretical basis for the working of a GA, the next sections critically analyse the structural and behavioural factors (Maturana, Lardeux, Saubion 2009) of TSP GAs.

iv. Encoding

Within GA's, solutions are represented as chromosomes which are a string of alleles containing all solution information. When using a GA to solve a TSP the chromosome represents a tour and the alleles represent the cities that must be visited. Encoding describes how objects are represented in the chromosome (Kumar 2013). The choice of encoding method is problem dependent (Whitely 1994) and depends upon the fitness function to be assessed (Goldberg 1989) with Koza stating that it is 'the key issue in genetic algorithm(s)… as it can severely limit the window by which the system observes the world' (1992 p 63) this has led to the development of a large number of encoding strategies (Figure 12).



Adjacency encoding - Cities are listed according to their adjacency to other cities (Starkweather, McDaniel, Mathias, Whitely, Whitley 1991). An advantage of this approach is that it allows schema analysis (Michealvich 1996). This method does not support classical crossover meaning that a repair or penalisation strategy may be needed (Abdoun, Abouchabaka, Tajani 2011)

Permutation encoding (path encoding) - Each gene within a chromosome represents a position within a sequence. It is recommended for problems such as the TSP (Hussain,Muhammad, Sajid, Hussain, Shoukry, Gani 2017). Within the TSP each city is represented as a number or letter and tours are represented as a list of cities in the order they are visited (Deep, Mebrahtu 2011)

Ordinal encoding - The tour to be encoded is processed on a city by city basis with the position of the city being stored in the resulting chromosome. The city in the original route is then deleted and the process continues with the next city. This scheme is not used anymore as it does not transfer information well to the following generations (Potvin 1996) but it does have the advantage of working with one point crossover

Binary encoding - Chromosomes are encoded in binary and techniques such as bitflip mutation are utilised (Luke 2015 p 37). The advantages of this approach are that it allows standard software libraries, standard operators and schema analysis to be used. The disadvantage is that it leads to invalid tours which either must be repaired, rejected or penalised to prevent further breeding (Michealvich 1996)

Value encoding - Each chromosome is represented as a string of values (Kumar 2013)

FIGURE 12 GENETIC ALGORITHM ENCODING STRATEGIES BASED UPON KUMAR (2013)

Holland’s canonical GA recommends binary encoding (Luke 2015) with each variable being represented by a 0 or a 1, this approach has been followed by many researchers even though it is ‘difficult and unnatural for many problems’ (Michealevich 1995 p5) with Potvin (1996) pointing out that it was not designed to solve combinatorial problems. The main advantages of binary encoding are that it is generic, meaning it can be adapted to any problem, that its use allows standard GA operators and libraries to be used and it is useful for theoretical studies on how GA’s work (Luke 2015) with Mitchell, O’Donoghue, Barnes, McCarville (2003) utilising this and a repair method to solve TSPs. However, this approach is inappropriate for combination/ordering problems such as the TSP (Hameed, Kanbar 2017) due to:-

1. Difficulty representing solutions as binary strings (Pongcharoen, Chainate and Thapatsuwan 2007)
2. It gives no performance advantages over other encoding strategies as it can create invalid routes, such invalid routes occur because:-
    - A mutation can result in a series of cities which is not a valid tour (Michealevich 1994 p 25) for example a city appearing twice;
    - Some sequences of bits may not represent a valid city for example if we assume 20 cities some 5 bit sequences do not represent any city (Michealevich 1994 p 25) with De Jong (Michealevich 1994 p 6) arguing that binary encoding leads the GA to investigate all ‘combinations of city names…(rather than) all permutations’ therefore as the number of cities increase the permutations are a ‘vanishingly small’ subset of the combinations of names meaning that the GA ‘has been rendered impotent by poor choice of representation’.
3. Invalid routes means that additional resources are needed to either:-
    - repair the invalid routes (Hameed, Kanbar 2017) (Can, Beham, Heavey 2008)(Mitchell, O’Donoghue, Barnes, McCarville 2003)
    - penalise the invalid routes (Can, Beham, Heavey 2008) within the fitness function, however this approach means that time is wasted evaluating and discounting invalid solutions (Michalewicz 1994 p 5) (Sawy, Hussein,Zaki, Mousa 2014).

Therefore whilst GA's were initially hoped to be problem independent there is general agreement that binary encoding is not suited to the TSP (Michealevich 1994 p 210) with research identifying that some problem specific knowledge should be incorporated into the choice of encoding (Michealevich 1994 p 6). As such this study utilises permutation encoding as:-

- it is the natural way of representing the TSP (Deep, Adane 2011) (Hameed, Kanbar 2017) (Potvin 1996) meaning it is now the most common representation used in TSP problems (Larranaga, Kuijpers, Murga, Inza, Dizdarevic 1999)
- the TSP is a 'pure ordering problem' (Potvin 1996 p 349) therefore the information that needs to be held about each city is minimal.

Therefore a tour of:-

Corsham-Gloucester-Bristol-Bath-Corsham

will be encoded as

1-2-3-4-1(each number represents a city)

This section has discussed the encoding strategy and explained the rational for selecting permutation encoding. The next section discusses the initial population and population size.

v. Initial Population & population size

The literature gives little guidance on population size and the type of solutions which should be included within the initial population (Gutowski 2005 p 185). However it has been argued that:-

1. Large initial populations increase the chance of finding the global optimum (Gutoski 2005 p 185) as they provide sufficient domain coverage. However Pinel, Danoy Bouvrey (2011) found that population size played only a small role in GA performance and Malhotra, Singh (2011 p 142) showed that larger populations take longer to find an optimum solution;

2. Diversity should be ensured in the initial population by not allowing duplicate solutions (Luke 2015 p 32) as this means that a population covers more of the search space. However this involves duplicate solutions being discarded leading to additional processing;
3. The initial population should either be spread uniformly over the search space or alternatively concentrated on promising areas if an idea exists about the likely solution (Gutoski 2005 p 185) (Luke 2015 p 32). For example within a TSP a nearest neighbour algorithm (Hameed, Kanbar 2017) could be used to ensure that some good solutions exist in the initial population;
4. Population size should be related to gene length with Goldberg (1989) originally arguing that the population size should increase exponentially with string length, however he later concluded that a linear relationship was sufficient a finding which Greffenstete (1985) agreed with (Richter 2010).

A number of studies have recommended idealised population sizes with these recommendations been based upon either experimentation, meta-genetic algorithms or statistical analysis (Table 6), additionally some studies have dynamically adjusted the population size during the algorithm run (Eiben, Marchioria, Valko 2004). However, as the problems within this study are from logistics and the number of deliveries are in effect restricted by EU driving hours[10] (Great Britain 2016) they are much smaller than the test cases used to make these recommendations therefore as population should relate to problem size (Goldberg 1985) the study follows Schaffer, Caruana, Eshelman and Das (1989) and uses a population of 20 which is at the smaller end of the recommendations.

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[10] EU driving hours restrict the number of hours a driver can work without a break they therefore provide a natural limit to TSB size

Study	Recommended population size	Methodology
De Jong (1975)	50 to 100	Via experimentation
Greffenstette (1986)	40 to 80	Used meta-GA
Freisleben,Hartfelder (1993)	100	Used meta-GA
Schaffer, Caruana, Eshelman, Das (1989)	20 to 30 (online)	Used statistical analysis namely factorial design combined with ANOVA
Petroski, Brownlee, McCall (2005)	76	Used 2_{8-2} fractional factorial as a screening experiment then a response surface design
Haupt, Haupt (2000)	16	Experiment

TABLE 6 TABLE DETAILING THE POPULATION SIZES AND THE METHODOLOGY USED TO MAKE THE RECOMMENDATIONS RECOMMENDED IN THE LITERATURE BASED ON HAUPT, HAUPT (2004 P 129)

The initial population used in this study will be pseudo-randomly generated with no effort being made to base the initial population around specific problem knowledge, furthermore duplicate solutions will be allowed. This decision was made because:-

- A pseudo-random rather than a random population will be used due to the need to prevent invalid solutions in the initial population (Luke 2015 p 32). Such invalid solutions would either need to be discarded (Luke 2015), which leads to unnecessary processing or penalised which reduces the size of the effective population (Gutoski 2005) and wastes processing because the fitness function of routes that will never be selected are calculated (Luke 2015);
- Whilst duplicate solutions reduce the size of the effective population they will be allowed as discounting them increases the processing time and adds programmatic complexity[11];
- While some studies have used tour construction heuristics to create the initial population based on problem knowledge (Greffenstete, Gopal, Rosmaita Gucht 1985) this study has made no effort to bias the initial population as ideas about

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[11] Such functionality would be relatively easy to implement via a HashTable the key would be the route sequence. On crossover and mutation the program would check to see if the route already existed in the hash table and if it did the route would be rejected, if it didn't exist it the route sequence would be added as a new key.

likely optimum solutions are often incorrect (Luke 2015 p 32) and because the study is about the tuning of Genetic Algorithms and introducing another variable into the study adds unnecessary complication.

This subsection has discussed the initial population and has justified the choice of using a pseudo-random population of 20 solutions. The next section discusses parent selection.

vi. Parent Selection

Darwinian Theory (Gutoski 2005) argues that it is the fittest individuals that survive with Mendelian Genetic Inheritance (Michealevich 1994 p 14) explaining how the genes of the fittest individuals are transferred to future generations. GAs utilise this process to select the fittest individuals to breed and pass their genetics to the next generation via their children (Figure 13), this explains how beneficial solution features survive in future generations whilst less beneficial features disappear as parents with less beneficial features are not selected to breed.

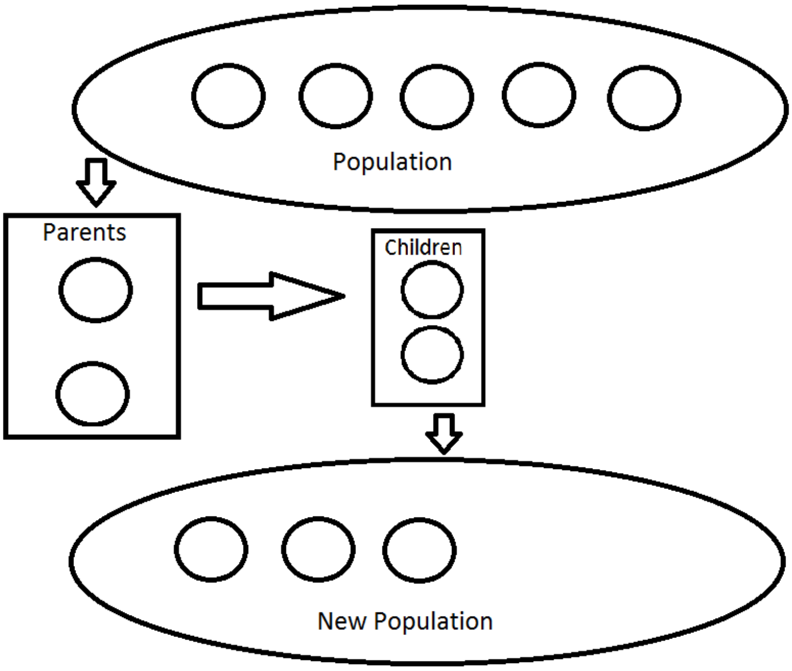
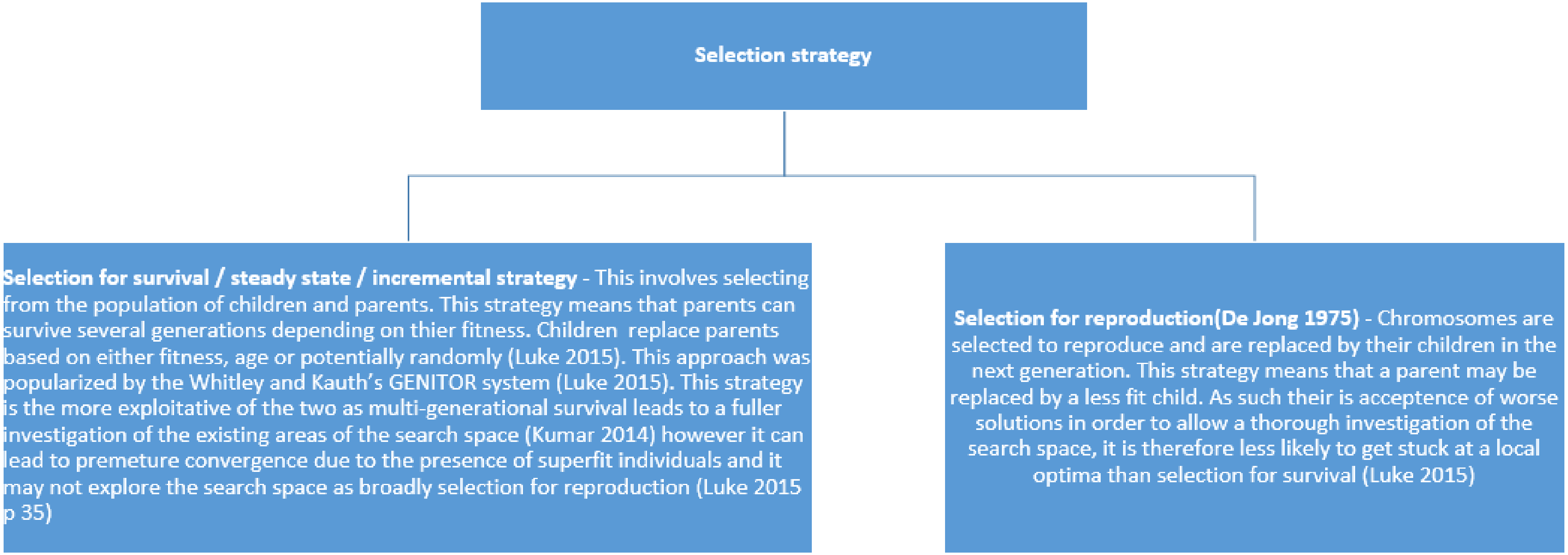


Figure 13 Illustration of the Genetic Algorithm Selection process

The selection operator within a GA therefore has three purposes:-

- Identifying good solutions;
- Making multiple copies of good solutions;
- Removing poor solutions from the population.

Different GA’s implement this logic via opposing strategies (Figure 14):-



Selection strategy

Selection for survival / steady state / incremental strategy - This involves selecting from the population of children and parents. This strategy means that parents can survive several generations depending on thier fitness. Children replace parents based on either fitness, age or potentially randomly (Luke 2015). This approach was popularized by the Whitley and Kauth's GENITOR system (Luke 2015). This strategy is the more exploitative of the two as multi-generational survival leads to a fuller investigation of the existing areas of the search space (Kumar 2014) however it can lead to premeture convergence due to the presence of superfit individuals and it may not explore the search space as broadly selection for reproduction (Luke 2015 p 35)

Selection for reproduction(De Jong 1975) - Chromosomes are selected to reproduce and are replaced by their children in the next generation. This strategy means that a parent may be replaced by a less fit child. As such their is acceptence of worse solutions in order to allow a thorough investigation of the search space, it is therefore less likely to get stuck at a local optima than selection for survival (Luke 2015)

Figure 14 Diagram detailing GA Selection Philosophies based on Richter (2010 p 13)

These strategies dictate how the population changes over time and when considered alongside ‘elitism’, which allows some of the best solutions to survive multiple generations, they form the continuum in Figure 15.

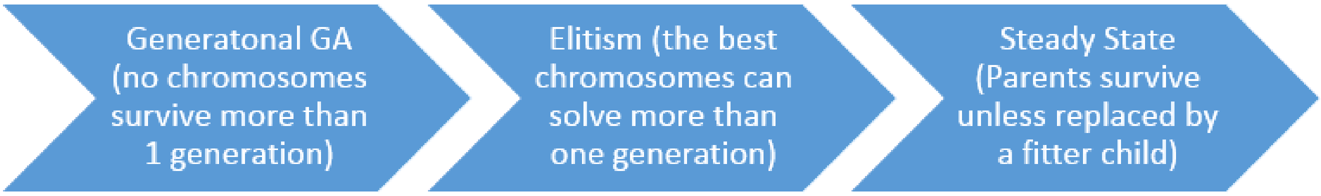
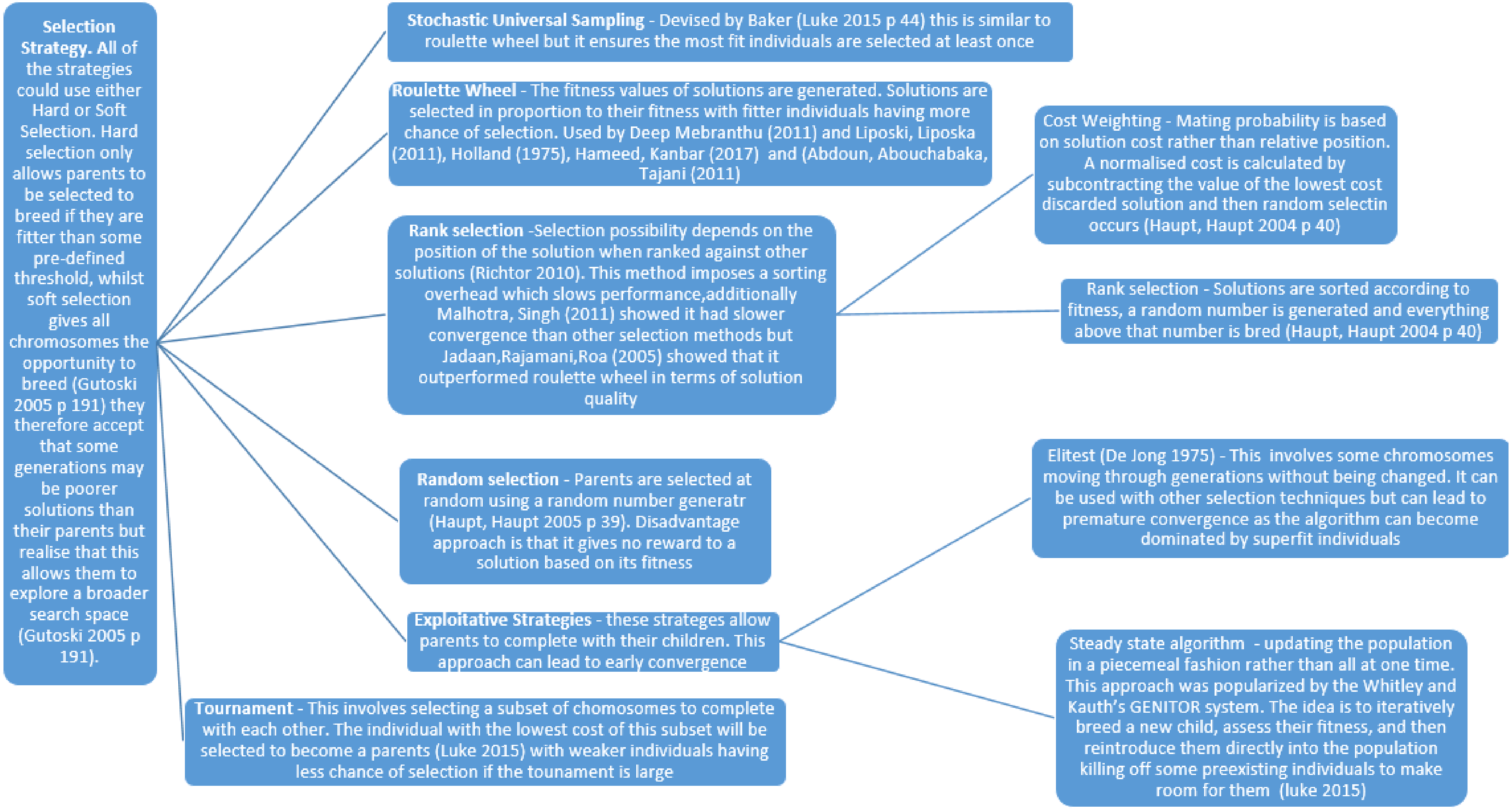


Figure 15 Continuum of Survival Strategies based on Richter (2010 p 13)

However, all population strategies require a selection method to pick solutions to breed and/or survive (Albayrak, Allahverdi 2011). Solutions are selected based upon probability with such probability settings usually being held globally however, some implementations give different chromosomes different probabilities of selection (Smith, Fogarty 1999). Selection performs a vital role in GAs with its purpose being to ‘identify good solutions in the population’ and to ensure the genetics of good solutions survive in future generations (Deb 1999 p 299). As such it is selection which gives evolution its direction (Beyer, Schwefel 2002 p 12) eventually causing the algorithm to converge on a solution via ‘genetic drift’ (Liposki, Liposka 2011 p 1).

A large number of selection methods exist with the ‘most common’ (Deep, Adane 2011) strategies being illustrated in Figure 16. However, despite the importance of selection little study has been made of their effectiveness (Goldberg, Deb 1991 p 70) this is surprising as if selection is too greedy it leads to early convergence due to dominance by fit individuals whilst if it is too random it leads to a meandering search.



Selection Strategy. All of the strategies could use either Hard or Soft Selection. Hard selection only allows parents to be selected to breed if they are fitter than some pre-defined threshold, whilst soft selection gives all chromosomes the opportunity to breed (Gutoski 2005 p 191) they therefore accept that some generations may be poorer solutions than their parents but realise that this allows them to explore a broader search space (Gutoski 2005 p 191).

Stochastic Universal Sampling - Devised by Baker (Luke 2015 p 44) this is similar to roulette wheel but it ensures the most fit individuals are selected at least once

Roulette Wheel - The fitness values of solutions are generated. Solutions are selected in proportion to their fitness with fitter individuals having more chance of selection. Used by Deep Mebranthu (2011) and Liposki, Liposka (2011), Holland (1975), Hameed, Kanbar (2017) and (Abdoun, Abouchabaka, Tajani (2011)

Rank selection -Selection possibility depends on the position of the solution when ranked against other solutions (Richtor 2010). This method imposes a sorting overhead which slows performance,additionally Malhotra, Singh (2011) showed it had slower convergence than other selection methods but Jadaan,Rajamani,Roa (2005) showed that it outperformed roulette wheel in terms of solution quality

Cost Weighting - Mating probability is based on solution cost rather than relative position. A normalised cost is calculated by subcontracting the value of the lowest cost discarded solution and then random selectin occurs (Haupt, Haupt 2004 p 40)

Rank selection - Solutions are sorted according to fitness, a random number is generated and everything above that number is bred (Haupt, Haupt 2004 p 40)

Random selection - Parents are selected at random using a random number generatr (Haupt, Haupt 2005 p 39). Disadvantage approach is that it gives no reward to a solution based on its fitness

Exploitative Strategies - these strateges allow parents to complete with their children. This approach can lead to early convergence

Elitest (De Jong 1975) - This involves some chromosomes moving through generations without being changed. It can be used with other selection techniques but can lead to premature convergence as the algorithm can become dominated by superfit individuals

Steady state algorithm - updating the population in a piecemeal fashion rather than all at one time. This approach was popularized by the Whitley and Kauth's GENITOR system. The idea is to iteratively breed a new child, assess their fitness, and then reintroduce them directly into the population killing off some preexisting individuals to make room for them (luke 2015)

Tournament - This involves selecting a subset of chomosomes to complete with each other. The individual with the lowest cost of this subset will be selected to become a parents (Luke 2015) with weaker individuals having less chance of selection if the tounament is large

FIGURE 16 DIAGRAM DETAILING COMMON SELECTION METHODS USED WITHIN GA'S

This study will utilise the selection for reproduction philosophy due to the need to balance selective pressure with diversity (Michealevich 1994 p 58) combined with tournament selection (Figure 17) as tournament selection:-

- is the most popular selection technique (Luke 2015) (Razali, Geraghty 2011)
- can be calculated in parallel (Goldberg, Deb 1999 p 87).
- can be tuned by increasing the tournament size with larger tournaments increasing the chance that the fittest will be selected (Luke 2015) however large tournaments risk premature convergence due to increased selection pressure leading to reduced diversity (Razali, Geraghty 2011) (Whitely 1989).
- Due to findings by Goldberg & Deb 1991 and by Can, Beham, Heavey (2008) that it was the best performing selection operator.

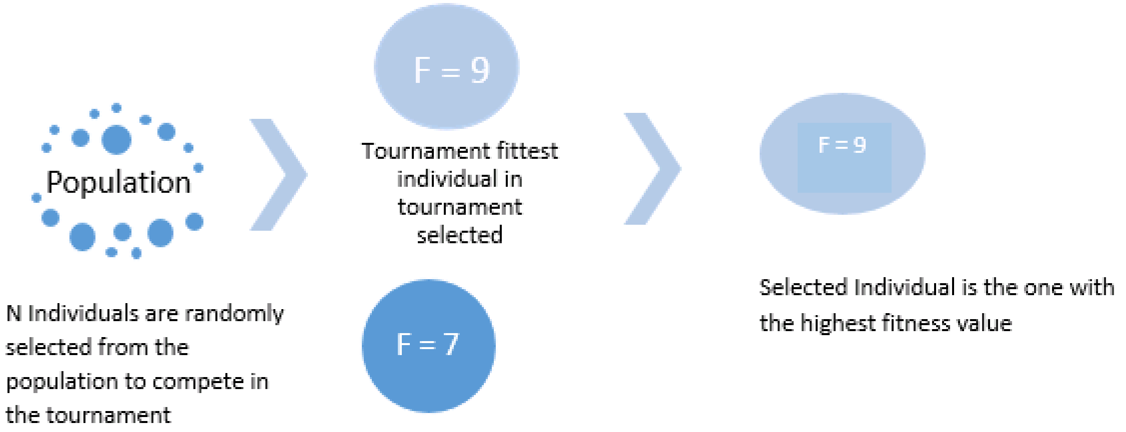


FIGURE 17 FIGURE ILLUSTRATING TOURNAMENT SELECTION

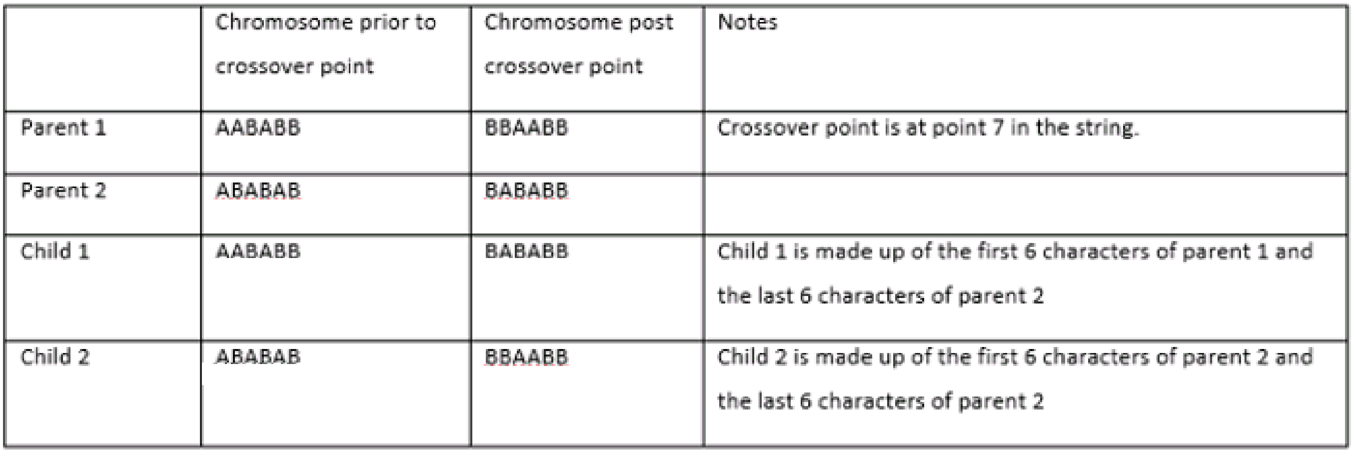
A variety of additional selection parameters / prohibitions have been suggested which could work in conjunction with tournament selection these are:-

- Elitism (Sawy, Hussein,Zaki, Mousa 2014 p 255) this was rejected due to the danger that a super-fit individual would lead to premature convergence;
- 'Implicit' techniques which restrict breeding between groups such as incest-prohibition (Eshelman, Schaffer 1997) and male-female breeding (Richter 2010) (Goh, Lim, Rodrigues 2003) (Sanchez-Velazco, Bullinaria 2003) and 'Explicit' techniques which prevent duplicate (Richter 2010 p 19) chromosomes or remove them (Michealevich 1994 p 58). These potential techniques have been shown to improve genetic algorithm performance by increasing population diversity (Michealevich 1994 p 236) however this study does not utilise these methods due to them increasing complexity and resource needs;
- Birthrate – some GA implementations randomly do not breed selected couples and transfer them to the next generation either unchanged or with mutation this option was rejected as Gutoski (2005 p 194) has argued that the experiments which introduced this parameter had shown little effect.

This section has discussed selection and has justified the use of a selection for reproduction philosophy combined with tournament selection. The literature gives no guidance on the optimal tournament size to use therefore an arbitrary tournament size of four will be utilised. The next section discusses crossover.

vii. Crossover .

The crossover process within a GA is equivalent to biological mating, and it is claimed to be the 'major source of the GAs 'creative power' (Mitchel 1995 p 38) with it playing a vital role in the GA (Hameed, Kanbar 2017) (Grefenstalle, Gopal, Rosmaita, Gucht 1985) (Karapetyan 2010). Crossover is used to explore the search space exploitatively (Kumar 2013) utilising information encoded in parent genes to ensure that child chromosomes are closely related to the parent solutions. Crossover involves creating new child chromosomes made up of substrings of the parent chromosomes with the algorithm selecting point(s) to "crossover" the genes of the parents. This process is illustrated in Figure 18 which utilises a single point crossover where a single point is selected from which parent genes are swapped such an approach can lead to invalid TSP tours (Karapetyan 2010).



	Chromosome prior to crossover point	Chromosome post crossover point	Notes
Parent 1	AABABB	BBAABB	Crossover point is at point 7 in the string.
Parent 2	ABABAB	BABABB	
Child 1	AABABB	BABABB	Child 1 is made up of the first 6 characters of parent 1 and the last 6 characters of parent 2
Child 2	ABABAB	BBAABB	Child 2 is made up of the first 6 characters of parent 2 and the last 6 characters of parent 2

Figure 18 Basic Single point crossover (based on Gutoski 20015 p 176)

Crossover is an effective tool in investigating the search space because:-

1. of ‘building block’ theory (Goldberg 1989) which argues that fit individuals share characteristics (building blocks) with crossover spreading fit building blocks throughout the population;
2. a Gene’s relative position is what makes it valuable i.e. A is valuable as it is next to B but would not be valuable if it was next to G and certain crossover techniques allow relative position retention (Luke 2015 p 40).

The basic crossover process is shown in Figure 19 however, a large number of variations exist with Pongcharoen Chainate, Thapatsuwan (2007) documenting fifteen crossover methods in their literature review.

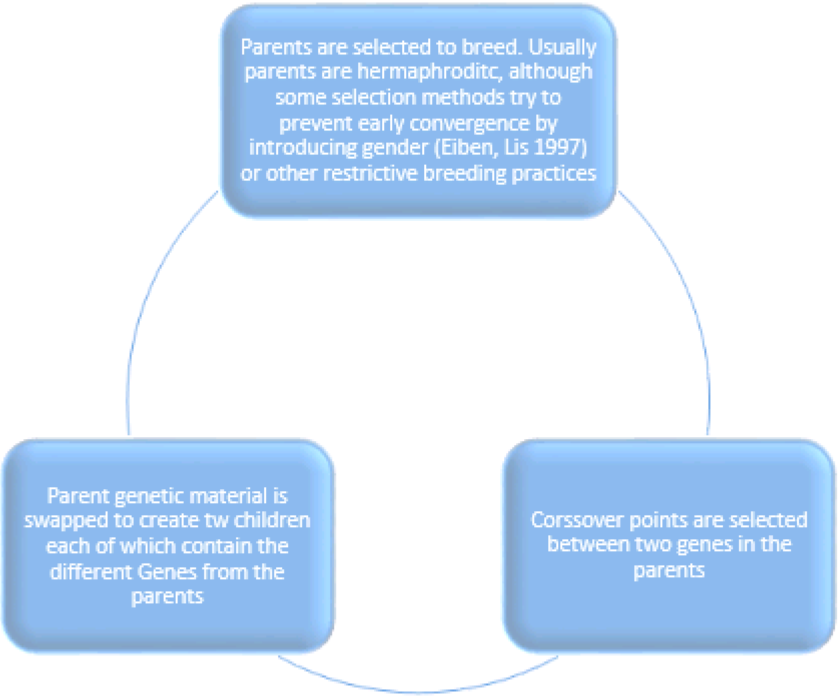


FIGURE 19 DIAGRAM DETAILING A SIMPLIFIED CROSSOVER PROCESS

The actual crossover method utilised depends on the problem to be solved and the encoding strategy (Malhotra, Singh, Singh 2011) therefore as permutation encoding has been selecting only appropriate crossover methods are discussed. The selection of crossover method is important when solving TSP problems as the TSP's hard constraints mean that some crossover approaches create invalid tours were cities are missed or duplicated (Figure 20), various strategies have been developed to cope with this (Figure 21).

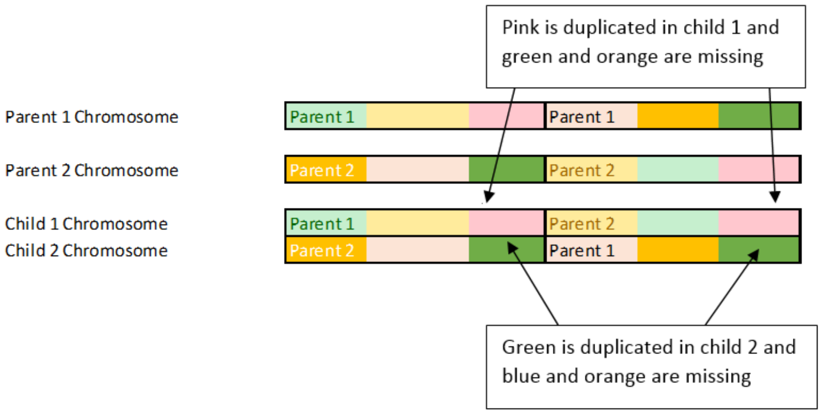
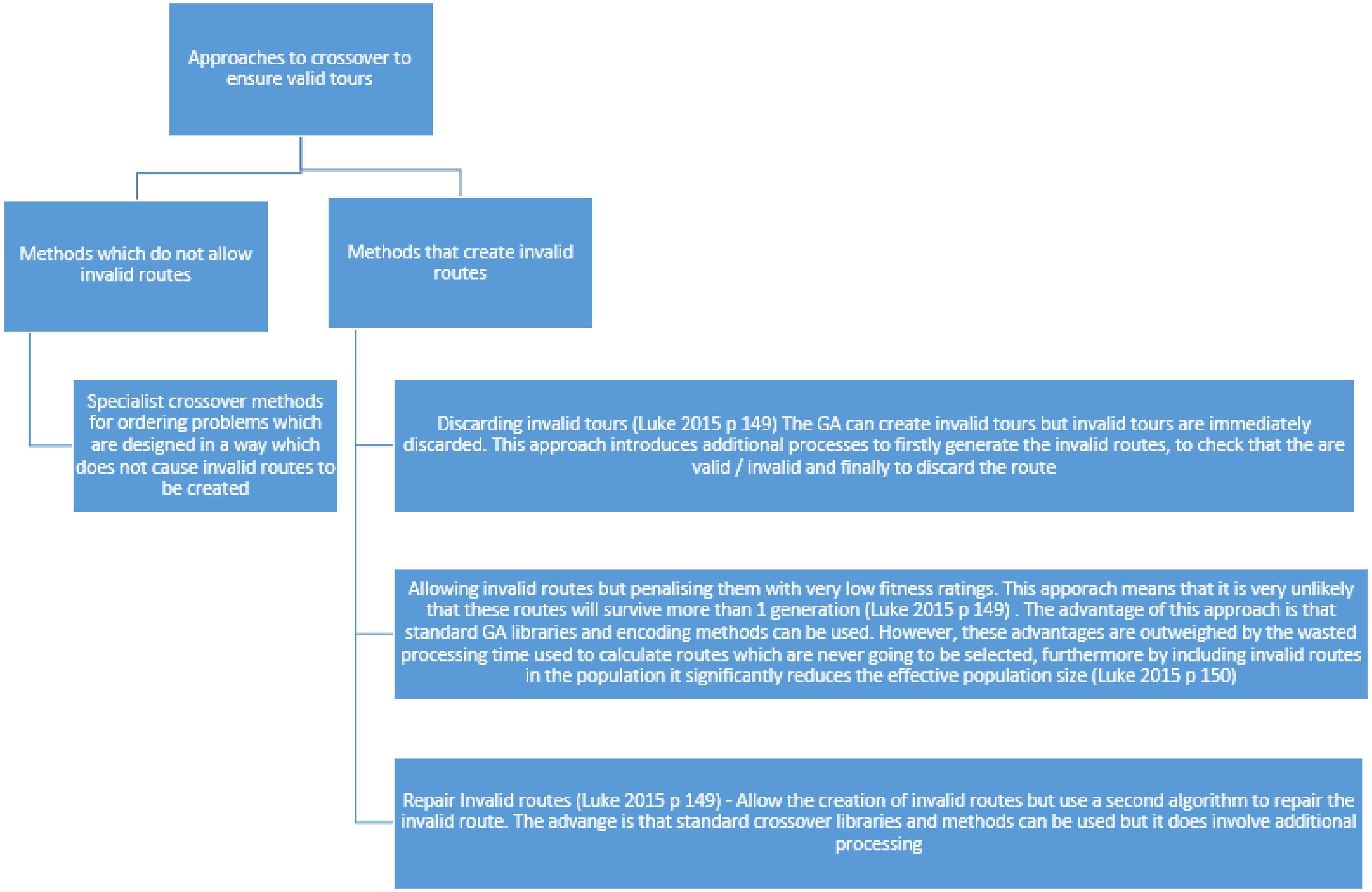


FIGURE 20 DIAGRAM DETAILING A SIMPLIFIED SINGLE POINT CROSSOVER PROCESS WHICH DEMONSTRATES HOW A CROSSOVER METHOD CAN CREATE INVALID TOURS.



Specialist crossover methods for ordering problems which are designed in a way which does not cause invalid routes to be created

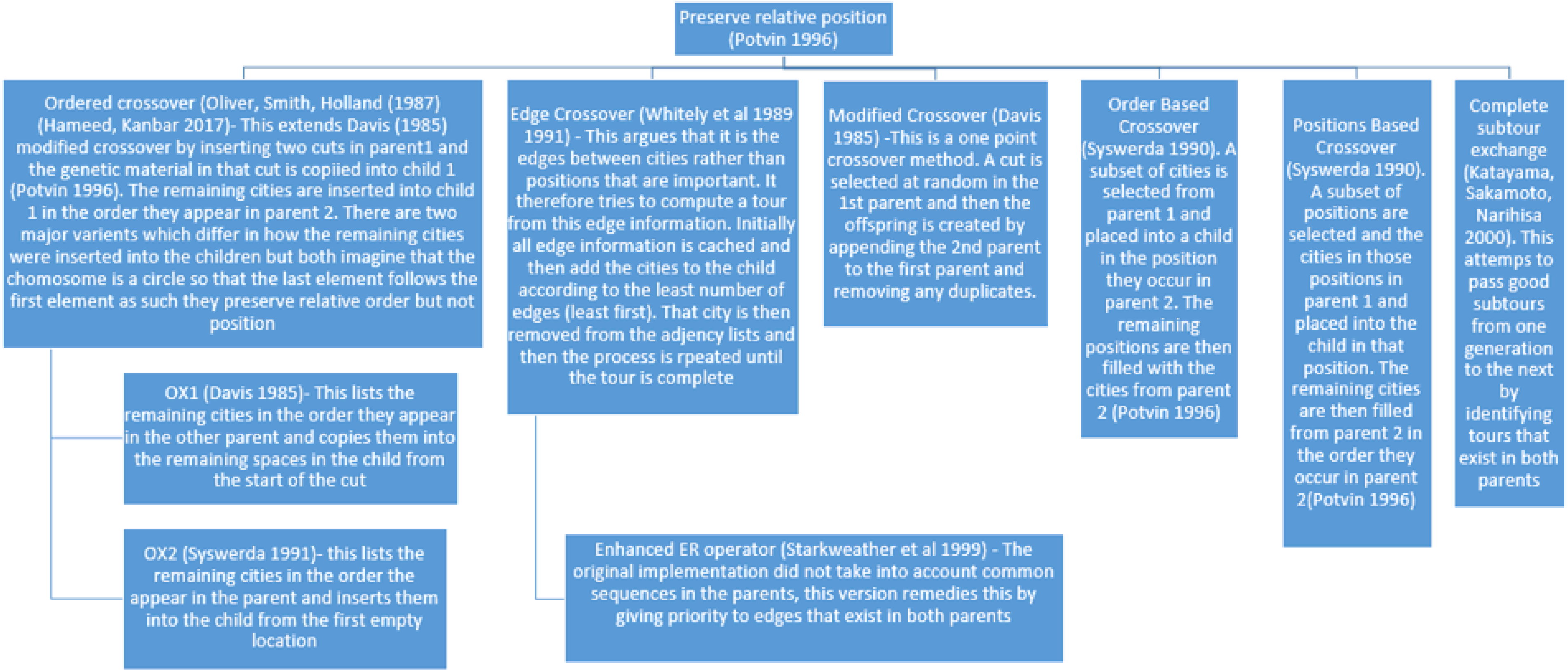
Discarding invalid tours (Luke 2015 p 149) The GA can create invalid tours but invalid tours are immediately discarded. This approach introduces additional processes to firstly generate the invalid routes, to check that the are valid / invalid and finally to discard the route

Allowing invalid routes but penalising them with very low fitness ratings. This apporach means that it is very unlikely that these routes will survive more than 1 generation (Luke 2015 p 149) . The advantage of this approach is that standard GA libraries and encoding methods can be used. However, these advantages are outweighed by the wasted processing time used to calculate routes which are never going to be selected, furthermore by including invalid routes in the population it significantly reduces the effective population size (Luke 2015 p 150)

Repair Invalid routes (Luke 2015 p 149) - Allow the creation of invalid routes but use a second algorithm to repair the invalid route. The advange is that standard crossover libraries and methods can be used but it does involve additional processing

FIGURE 21 DIAGRAM DETAILING THE STRATEGIES WHICH ARE AVAILABLE TO PREVENT OR MANAGE INVALID TOURS CREATED BY THE CROSSOVER PROCESS

This study follows the recommendation of Deep, Adane (2011) and uses a method which does not create invalid tours as this removes the need to waste resources calculating and discarding, repairing or penalising invalid routes. Figure 22 and Figure 23 classify and detail a number of crossover methods which do not create invalid TSP routes.



Preserve relative position (Potvin 1996)

Ordered crossover (Oliver, Smith, Holland (1987) (Hameed, Kanbar 2017)- This extends Davis (1985) modified crossover by inserting two cuts in parent1 and the genetic material in that cut is copiied into child 1 (Potvin 1996). The remaining cities are inserted into child 1 in the order they appear in parent 2. There are two major varients which differ in how the remaining cities were inserted into the children but both imagine that the chomosome is a circle so that the last element follows the first element as such they preserve relative order but not position

OX1 (Davis 1985)- This lists the remaining cities in the order they appear in the other parent and copies them into the remaining spaces in the child from the start of the cut

OX2 (Syswerda 1991)- this lists the remaining cities in the order the appear in the parent and inserts them into the child from the first empty location

Edge Crossover (Whitely et al 1989 1991) - This argues that it is the edges between cities rather than positions that are important. It therefore tries to compute a tour from this edge information. Initially all edge information is cached and then add the cities to the child according to the least number of edges (least first). That city is then removed from the adjency lists and then the process is rpeated until the tour is complete

Enhanced ER operator (Starkweather et al 1999) - The original implementation did not take into account common sequences in the parents, this version remedies this by giving priority to edges that exist in both parents

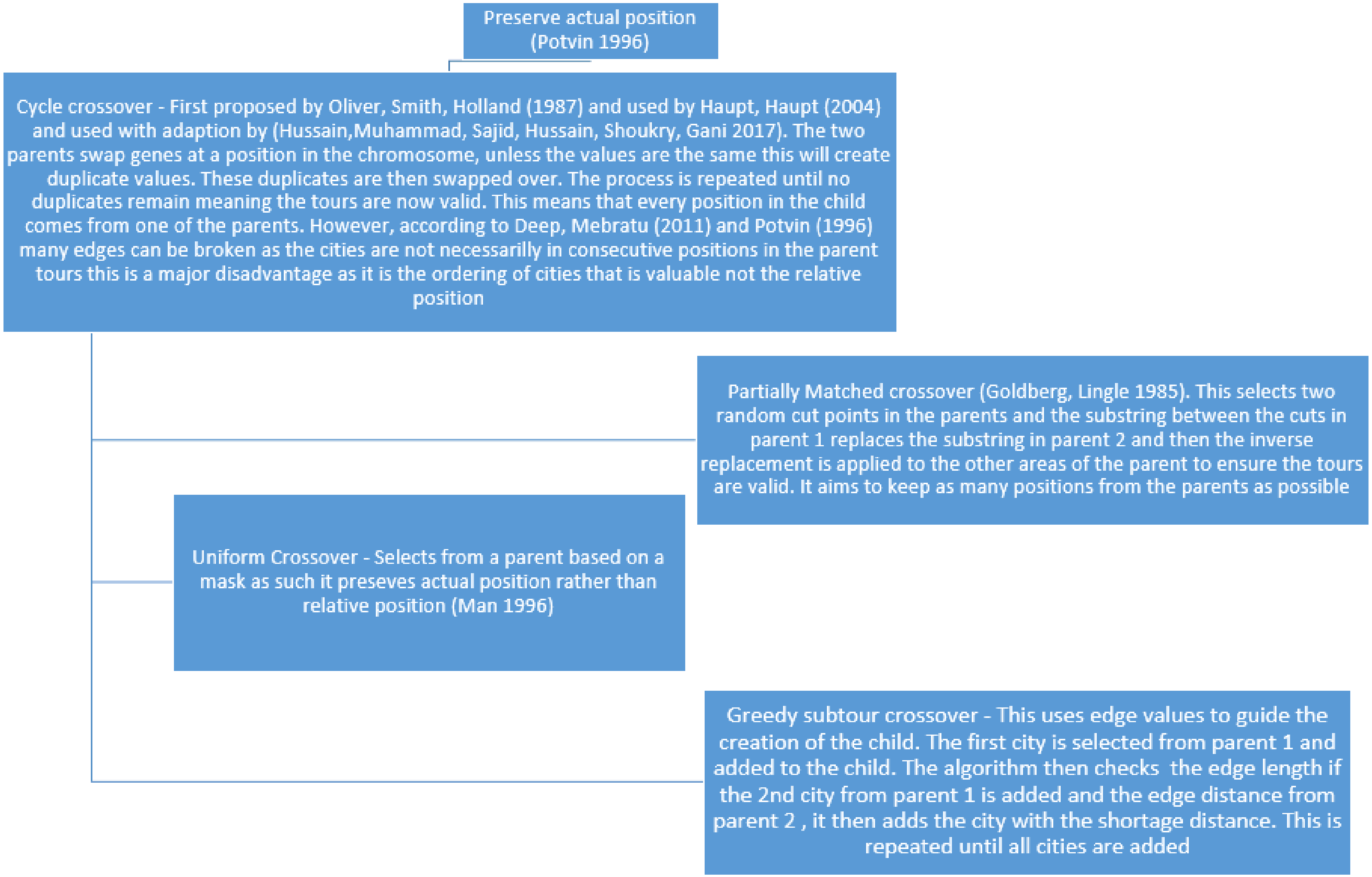
Modified Crossover (Davis 1985) -This is a one point crossover method. A cut is selected at random in the 1st parent and then the offspring is created by appending the 2nd parent to the first parent and removing any duplicates.

Order Based Crossover (Syswerda 1990). A subset of cities is selected from parent 1 and placed into a child in the position they occur in parent 2. The remaining positions are then filled with the cities from parent 2 (Potvin 1996)

Positions Based Crossover (Syswerda 1990). A subset of positions are selected and the cities in those positions in parent 1 and placed into the child in that position. The remaining cities are then filled from parent 2 in the order they occur in parent 2(Potvin 1996)

Complete subtour exchange (Katayama, Sakamoto, Narihisa 2000). This attemps to pass good subtours from one generation to the next by identifying tours that exist in both parents

FIGURE 22 DIAGRAM CLASSIFYING APPROPRIATE TSP CROSSOVER STRATEGIES WHICH PRESERVE RELATIVE POSITIONS BASED UPON DEEP, ADANE (2011)



Preserve actual position (Potvin 1996)

Cycle crossover - First proposed by Oliver, Smith, Holland (1987) and used by Haupt, Haupt (2004) and used with adaption by (Hussain,Muhammad, Sajid, Hussain, Shoukry, Gani 2017). The two parents swap genes at a position in the chromosome, unless the values are the same this will create duplicate values. These duplicates are then swapped over. The process is repeated until no duplicates remain meaning the tours are now valid. This means that every position in the child comes from one of the parents. However, according to Deep, Mebratu (2011) and Potvin (1996) many edges can be broken as the cities are not necessarilly in consecutive positions in the parent tours this is a major disadvantage as it is the ordering of cities that is valuable not the relative position

Partially Matched crossover (Goldberg, Lingle 1985). This selects two random cut points in the parents and the substring between the cuts in parent 1 replaces the substring in parent 2 and then the inverse replacement is applied to the other areas of the parent to ensure the tours are valid. It aims to keep as many positions from the parents as possible

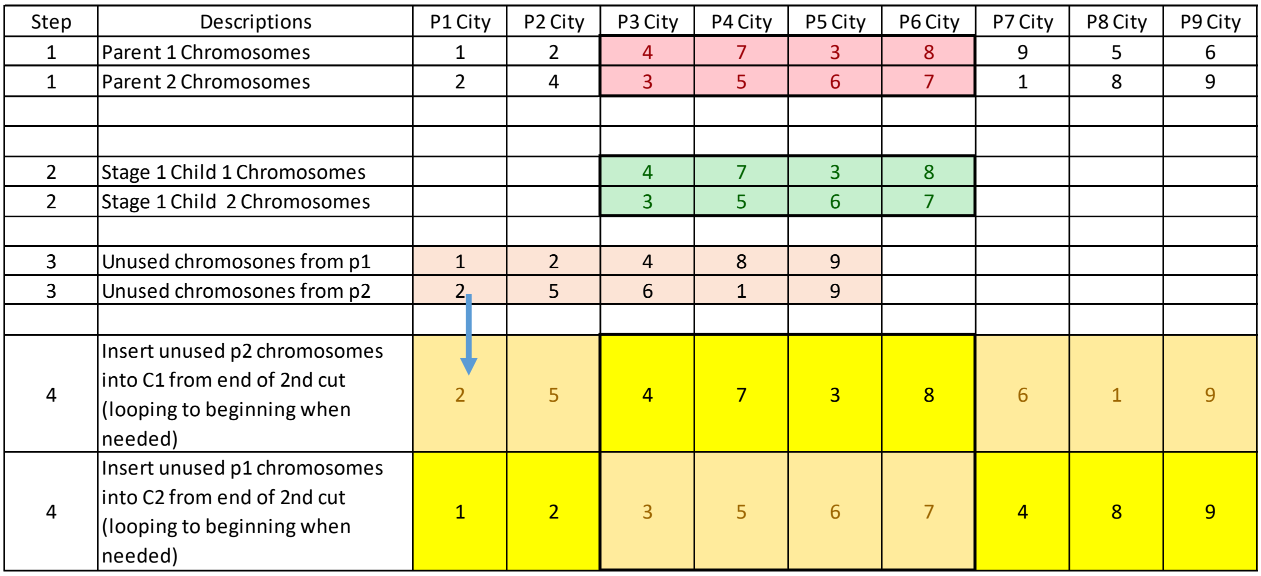
Uniform Crossover - Selects from a parent based on a mask as such it preseves actual position rather than relative position (Man 1996)

Greedy subtour crossover - This uses edge values to guide the creation of the child. The first city is selected from parent 1 and added to the child. The algorithm then checks the edge length if the 2nd city from parent 1 is added and the edge distance from parent 2 , it then adds the city with the shortage distance. This is repeated until all cities are added

FIGURE 23 DIAGRAM CLASSIFYING APPROPRIATE TSP CROSSOVER STRATEGIES WHICH PRESERVE POSITION BASED UPON DEEP, ADANE (2011B)

Within a TSP it is city order rather than position (Michealevich 1994 p 218) (Starkweather, McDaniel, Mathias, Whitely, Whitely 1991) (Oliver, Smith, Holland 1987) which is important therefore a crossover method that preserves order should be selected. This study utilises OX2 crossover (Figure 24) as this:

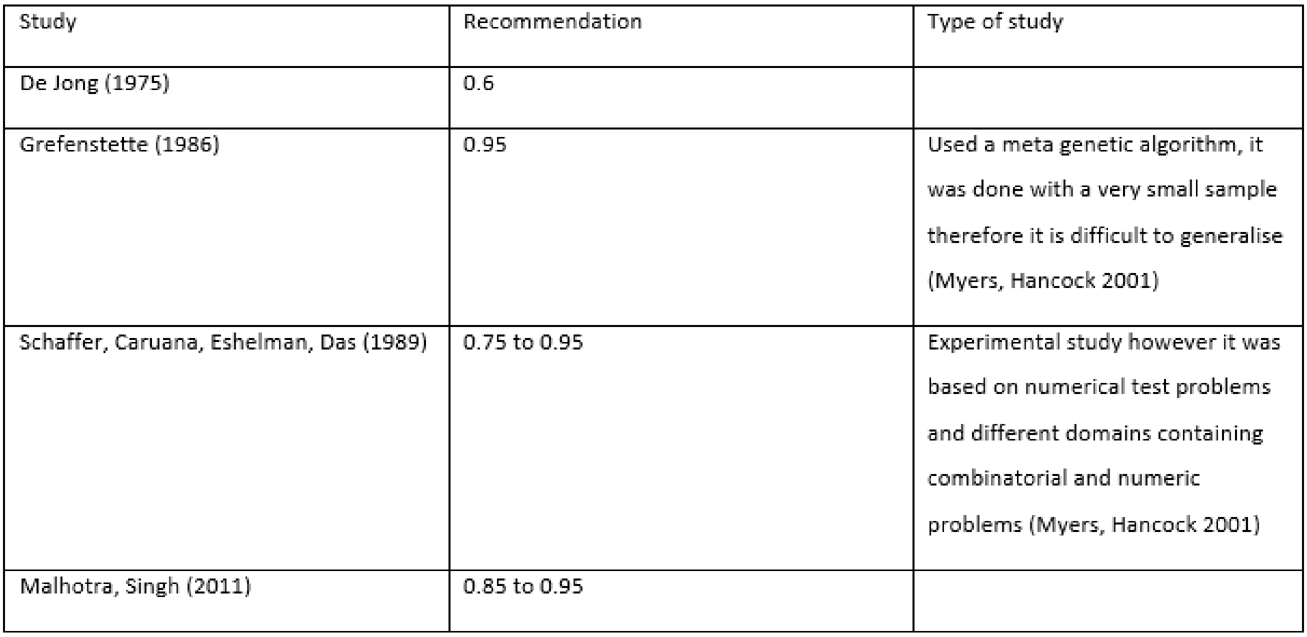
- preserves the order of cities (Michealevich 1994 p 218);
- It is a two point crossover method and therefore avoids the problems of one point crossover where the heads and tails of the tour are swapped too frequently and some combinations may be impossible due to make up of the initial population (Man 1996 p 523)
- Deep, Adane (2011) found it to be the best method with a study by Oliver (Michealevich 1994 p 218) finding that it outperformed PMX by 11% and CX by 15%. However, in contrast Larranaga, Kuijpers, Murga, Inza, Dizdarevic (1999) found that despite good performance it was outperformed by OX1 and Edge Recombination in most of the problems they studied.



Step	Descriptions	P1 City	P2 City	P3 City	P4 City	P5 City	P6 City	P7 City	P8 City	P9 City
1	Parent 1 Chromosomes	1	2	4	7	3	8	9	5	6
1	Parent 2 Chromosomes	2	4	3	5	6	7	1	8	9
2	Stage 1 Child 1 Chromosomes			4	7	3	8			
2	Stage 1 Child 2 Chromosomes			3	5	6	7			
3	Unused chromosomes from p1	1	2	4	8	9				
3	Unused chromosomes from p2	2	5	6	1	9				
4	Insert unused p2 chromosomes into C1 from end of 2nd cut (looping to beginning when needed)	2	5	4	7	3	8	6	1	9
4	Insert unused p1 chromosomes into C2 from end of 2nd cut (looping to beginning when needed)	1	2	3	5	6	7	4	8	9

FIGURE 24 EXAMPLE OF OX2 CROSSOVER METHOD

This study aims to find the optimum crossover rate for a TSP algorithm within a UK logistics context. A number of previous studies of optimum crossover rate have been undertaken (Table 7) with most GA implementations recommending a high chance of crossover (Goldberg, Korb, Deb 1989) as a low crossover rate can lead to early convergence (Malhotra, Singh, Singh 2011 p 142) with Table 8 describing the hypotheses to be tested.



Study	Recommendation	Type of study
De Jong (1975)	0.6	
Grefenstette (1986)	0.95	Used a meta genetic algorithm, it was done with a very small sample therefore it is difficult to generalise (Myers, Hancock 2001)
Schaffer, Caruana, Eshelman, Das (1989)	0.75 to 0.95	Experimental study however it was based on numerical test problems and different domains containing combinatorial and numeric problems (Myers, Hancock 2001)
Malhotra, Singh (2011)	0.85 to 0.95	

TABLE 7 TABLE DETAILING CROSSOVER RATES WHICH HAVE BEEN RECOMMENDED IN THE LITERATURE (EIBEN, HINTERDING, MICHALEWICZ 1999)

C1_H0	Crossover level does not have a significant effect on the response variable
C1_H1	Crossover level does not have a significant effect on the response variable

TABLE 8 TABLE DETAILING THE CROSSOVER HYPOTHESES TO BE TESTED

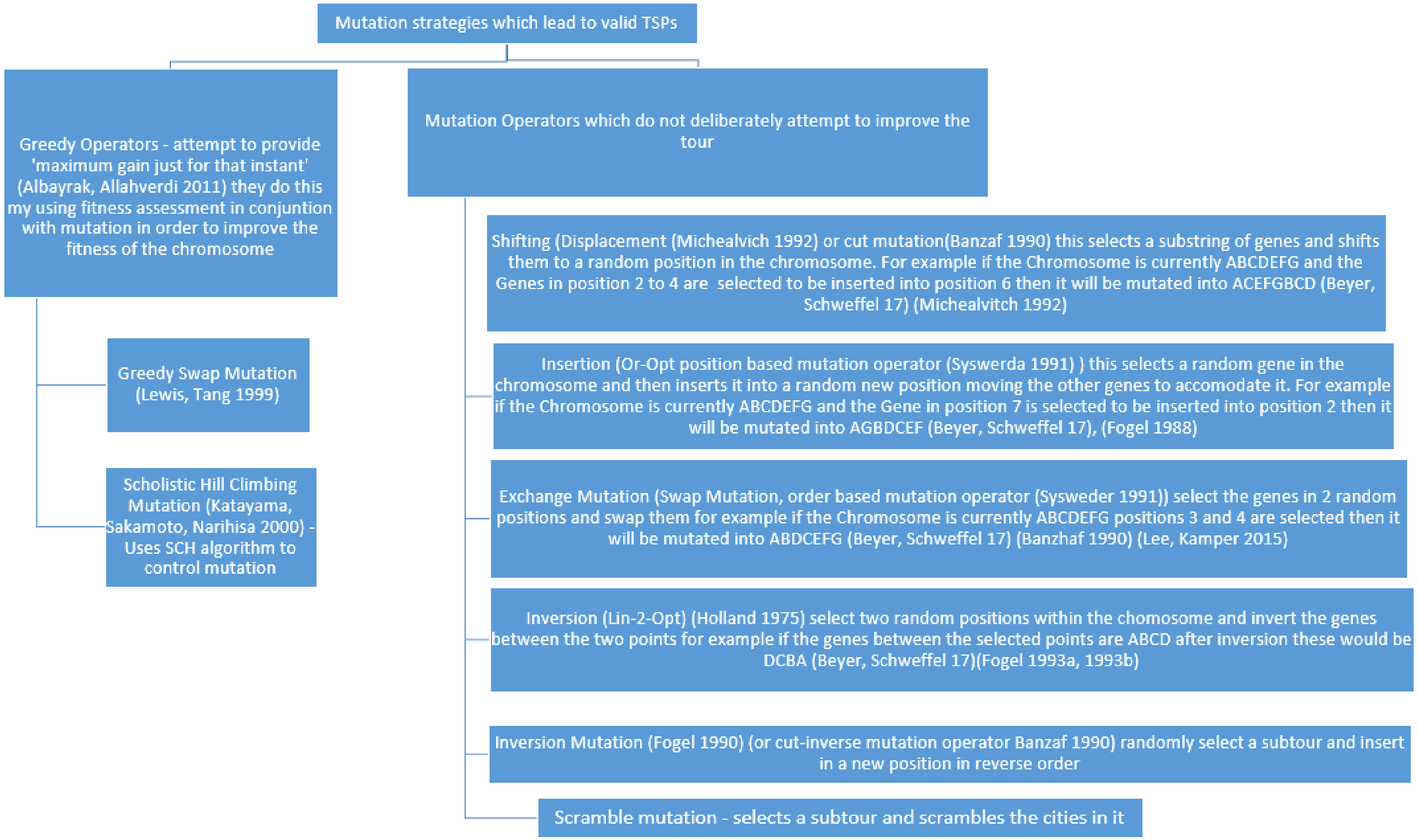
This section has discussed the literature relating to crossover, has justified the choice of crossover method and has developed two hypotheses to test. The next section discusses mutation.

viii. Mutation

A mutation is a characteristic of an organism which is not inherited from its parents, such mutations can be neutral, harmful or advantageous with natural selection meaning that advantageous mutations are passed onto future generations via reproduction. Within a genetic algorithm, mutation involves introducing some feature to a child which the parents do not have and as such it is an exploratory operator (Malhotra, Singh, Singh 2011 p 141) forcing the algorithm to explore new areas of the search space (Gutowski 2005), additionally it:-

- Restores lost genetic material. This is necessary as valuable genetic material contained in non-selected chromosomes is lost (Deep, Adane 2011) (Mitchell 1995). However, this is less of a problem in a TSP GA as by definition valid tours must visit every city;
- Prevents premature convergence to local optima (Albayrak, Allahverdi 2011, Gutowski 2005), this can be a problem when highly fit individuals breed many similar offspring early in 'evolution time' (Malhotra, Singh, Singh 2011 p 141).

Pongcharoen Chainate, Thapatsuwan (2007) reviewed 11 different mutation operators. However as pointed out by Beyer, Schweffel (2002) the choice of mutation method is problem dependent and due to TSP's hard constraints (Luke 2015) and the encoding method selected, many standard GA approaches such as bit mutation (Holland 1975), are inappropriate and therefore repair strategies such as GENOCOP III (Sawy, Hussein,Zaki, Mousa 2014 p 254) or specialised mutation methods must be used (Deep, Adane 2011) (Figure 25).



Mutation strategies which lead to valid TSPs

Greedy Operators - attempt to provide 'maximum gain just for that instant' (Albayrak, Allahverdi 2011) they do this my using fitness assessment in conjuntion with mutation in order to improve the fitness of the chromosome

Greedy Swap Mutation (Lewis, Tang 1999)

Scholistic Hill Climbing Mutation (Katayama, Sakamoto, Narihisa 2000) - Uses SCH algorithm to control mutation

Mutation Operators which do not deliberately attempt to improve the tour

Shifting (Displacement (Michealvich 1992) or cut mutation(Banzaf 1990) this selects a substring of genes and shifts them to a random position in the chromosome. For example if the Chromosome is currently ABCDEFG and the Genes in position 2 to 4 are selected to be inserted into position 6 then it will be mutated into ACEFGBCD (Beyer, Schweffel 17) (Michealvitch 1992)

Insertion (Or-Opt position based mutation operator (Syswerda 1991)) this selects a random gene in the chromosome and then inserts it into a random new position moving the other genes to accomodate it. For example if the Chromosome is currently ABCDEFG and the Gene in position 7 is selected to be inserted into position 2 then it will be mutated into AGBDCEF (Beyer, Schweffel 17), (Fogel 1988)

Exchange Mutation (Swap Mutation, order based mutation operator (Sysweder 1991)) select the genes in 2 random positions and swap them for example if the Chromosome is currently ABCDEFG positions 3 and 4 are selected then it will be mutated into ABDCEFG (Beyer, Schweffel 17) (Banzhaf 1990) (Lee, Kamper 2015)

Inversion (Lin-2-Opt) (Holland 1975) select two random positions within the chomosome and invert the genes between the two points for example if the genes between the selected points are ABCD after inversion these would be DCBA (Beyer, Schweffel 17)(Fogel 1993a, 1993b)

Inversion Mutation (Fogel 1990) (or cut-inverse mutation operator Banzaf 1990) randomly select a subtour and insert in a new position in reverse order

Scramble mutation - selects a subtour and scrambles the cities in it

Figure 25 Diagram describing and classifying some popular mutation methods

This study follows the approach of Banzhaf (1990) and utilises exchange mutation (Figure 26) as it is simple to implement and preserves city adjacency, the alternative strategy of using a greedy approach was discounted due to their tendency to become stuck at local optima (Albayrak, Allahverdi 2011) and because of the recommendation of Beyer, Schweffel (2002) that mutation should be unbiased and should not be guided by fitness criteria.

	City in Position 1	**City in Position 2**	**City in Position 3**	**City in Position 4**	**City in Position 5**	**City in Position 6**	**City in Position 7**	**City in Position 8**	**City in Position 9**	**City in Position 10**
Pre Mutation	A	B	C	D	E	F	G	H	I	J
Post Mutation	A	B	C	J	E	F	G	H	I	D

FIGURE 26 DIAGRAM DEMONSTRATING EXCHANGE MUTATION

It is generally accepted that mutation is an important ancillary operator within GAs (Gutoski 2005) with most research indicating that low mutation probability is optimum (Table 9).

Study	Recommendation	Methodology
De Jong (1975)	0.001	Experimentation
Grefenstette (1986)	0.01	Meta GA
Schaffer, Caruana, Eshelman, Das (1989)	0.005, 0.01	Used statistical analysis namely factorial design combined with ANOVA
Petroski, Brownlee, McCall (2005)	0.092	Used 2^{8-2} fractional factorial as a screening experiment then a response surface design
Haupt, Haupt 2000	5 to 20% (Haupt, Haupt 129)	Experimentation

TABLE 9 TABLE DESCRIBING THE MUTATION LEVELS RECOMMENDED IN THE LITERATURE AND THE METHODS USED BY THE STUDY

However, any mutation decisions seem to be based on 'intuition' (Gutowski 2005 p 165) with relatively few studies examining the effects of different mutation levels (Rexhepi,Maxhuni, Diki 2013) and how they interact with other parameters (Rexhepi, Maxhuni, Dika 2013) (Fallahi, Amirib, Yaghini 2014) leading to hypotheses M1 and M2 (Table 10). Low mutation rates are usually favoured (Rexhepi,Maxhuni, Diki 2013) as the intelligence built into selection and crossover should come to a desired solution faster than random mutations (Gutowski 2005) with Malhotra, Singh (2011 p 143) stating that ‘mutation is an artificial and forced method of … changing a value…(it) should be avoided as far as possible’. Whilst it is generally accepted that mutation plays an important role this has been challenged by Pinel, Danoy Bouvrey (2011) who found mutation size played only a small role and by Rexhepi, Maxhuni, Dika (2013) who found that whilst mutation played a valuable role when initial populations are small, its importance decreases as the population size increases. In juxtaposition the central role of crossover has been challenged by authors who have argued that naïve mutation only evolution may work just as well as combined crossover and mutation approaches (Czarn, MacNish, Vijayan, Turlach, Gupta 2004) (Schaffer,Caruana, Eshalman, Das 1989) whilst studies such as those by Shaffer and Eshelman (1991) and Tate and Smith (1993) have shown that mutation plays a larger role than previously thought leading to hypothesis M3 (Table 10).

M1_H0	No significant interaction exists between crossover and mutation
M1_H1	Significant interaction exists between crossover and mutation
M2_H0	The relationship between mutation rate and crossover rate is not non-linear
M2_H1	The relationship between mutation rate and crossover rate is non-linear
M3_H0	Mutation does not have a significant direct effect on the response variable
M3_H1	Mutation does have a significant direct effect on the response variable

TABLE 10 TABLE DESCRIBING THE MUTATION HYPOTHESES TO BE TESTED

This section has discussed the literature relating to mutation, has justified the choice of mutation method and has developed three hypotheses to test (Table 10). The next section discusses stopping criteria.

ix. Stopping criteria

GAs run until a stopping criteria is met for example, a predefined level of fitness, a number of generations or a number of generations without improvement. As TSP problems are NP hard no algorithm can solve them in polynomial time (Can, Beham, Heavey 2008) and therefore it is not possible to tell if an optimal solution has been found. Therefore this study will utilise dual stopping criteria:-

- The algorithm will stop after a pre-determined number of generations. This approach is common in TSP GAs (Haupt, Haupt 2004) with Rexhepi, Maxhuni, Dika (2013) GA stopping after 5000 generations this seems extreme and will take unnecessary computation time, therefore the findings of Razali, Geraghty (2011) will be used who found that when using tournament selection solutions converged for 10 city problems at 20 generations and 30 city problems at 50 generations. As UK logistics problems are usually smaller than 10 cities 20 generations will be utilised.
- The algorithm will stop if no improvement has been found in ten consecutive generations, this is to prevent unnecessary processing.

This section has discussed stopping criteria and justified the stopping criteria to be used. The next section discusses the fitness assessment.

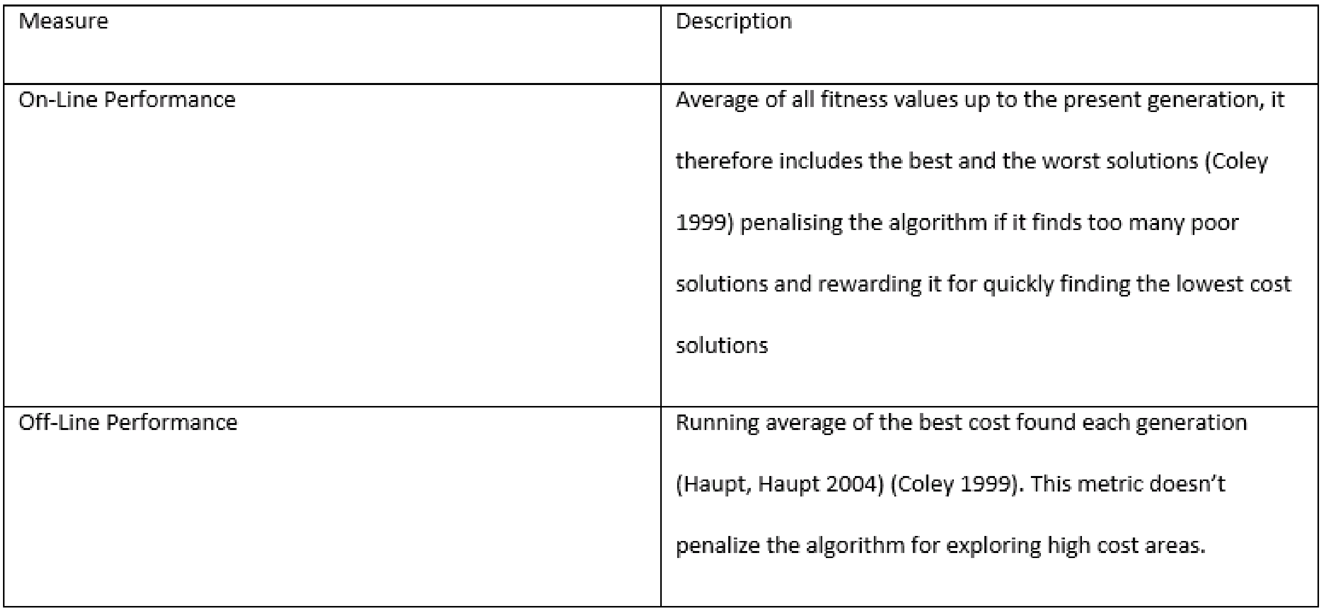
x. Solution Fitness Assessment

The fitness assessment of a GA solution is problem dependent (Whitely 1994). Within a Euclidean TSP the fitness criteria is the total Euclidian distance of the tour (Katayama, Sakamoto, Narihisa 2000) with the shortest valid TSP tour being the fittest. As only valid routes will be created no penalisation of invalid routes will be necessary.

This section has discussed the assessment of a TSP solutions fitness, the next section discusses GA assessment.

xi. GA Assessment

In order to tune an algorithm a measure of the desired performance must be developed, despite this no accepted method of judging the relationship between parameter values and performance of a GA exists (Czarn, MacNish, Vijayan, Turlach, Gupta 2004). When assessing algorithm performance two performance categories are usually assessed – solution quality and speed (Smit 2012) (Eiden, Smith (2003) with Smit (2012) adding robustness which is the ability of the algorithm to perform consistently despite changes to the problem, the random seeds or the parameter settings to this duopoly. This study is a univariate study (Chiarandini, Paquete, Preuss, Ridge 2007) concentrating on solution quality. Various measures of solution quality have been suggested for example Eiden, Smith (2003) suggested Mean Best Fitness as an appropriate measure. However, solution quality measurement has been heavily influenced by DeJong's 1975 work (Haupt, Haupt 2004) which defined the measures in Table 11.



Measure	Description
On-Line Performance	Average of all fitness values up to the present generation, it therefore includes the best and the worst solutions (Coley 1999) penalising the algorithm if it finds too many poor solutions and rewarding it for quickly finding the lowest cost solutions
Off-Line Performance	Running average of the best cost found each generation (Haupt, Haupt 2004) (Coley 1999). This metric doesn't penalize the algorithm for exploring high cost areas.

Table 11 DeJong's Measures of solution Quality

When developing an assessment measure it is important to consider algorithm usage for example in a time critical environment were only one solution is enacted it is only the best solutions that are relevant (Smit 2012). Therefore, this study utilises off-line performance as its measure as the algorithm should not be penalised for conducting a thorough investigation of the search space, and within logistics only one solution will be enacted, additionally this approach means that its results are comparable to others in the literature.

Additionally for a GA to be useful within commercial operations it must be able to outperform human planners (Clarke, Leonardi 2018) as such the best solution in the final generation will be compared to the original planning to test hypothesis stated in Table 12.

G1_H0	There is no difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning
G1_H1	There is a difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning

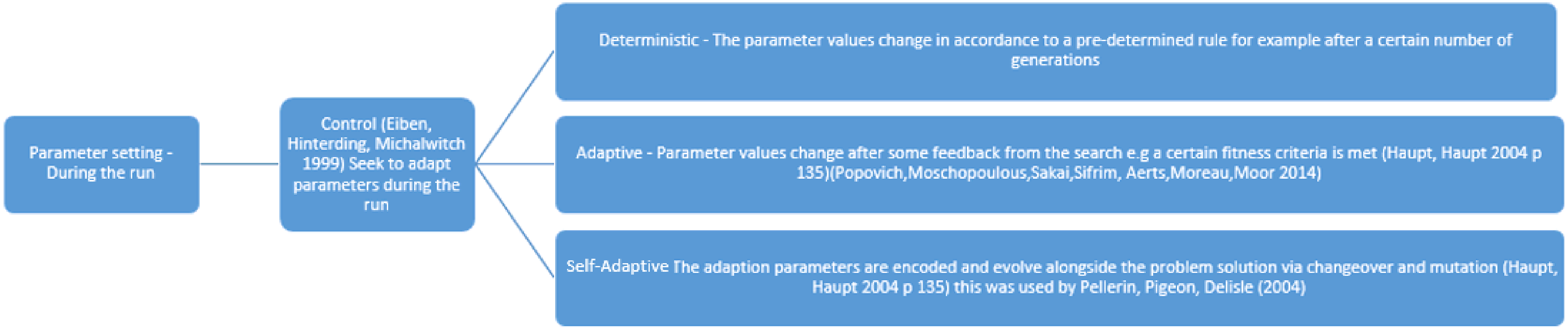
TABLE 12 GA PERFORMANCE V ORIGINAL PLANNING HYPOTHESES

This section has discussed the literature related to GA assessment, has justified its choice of assessment method ad developed two hypotheses to test, the next section discusses GA tuning.

xii. Tuning a Genetic Algorithm

The no free lunch theorem (Wolpert, Macready 1997) argues that no algorithm is perfect for every problem, this can be extended to say that no GA parameter setting is ideal for every scenario, this leads to hypotheses T1 and T3 which aim to test whether the size of the TSP problem influences the optimum settings for mutation and crossover whilst T2 tests if parameter settings make a significant difference to algorithm performance (Table 14). Additionally tuning can be for different purposes. For example Angelova, Pencheva (2011) used tuning to improve convergence time whilst De Jong (1975) used it to improve performance. Due to the combined effect of TSP GAs being used multiple times and the performance improvement associated with GA tuning, the investment of time that is needed to tune a GA is worthwhile (Smit 2012). This has led to a large number of studies seeking to develop idealised settings for the key genetic algorithm parameters however significant debate exists on the best settings (Rexhepi,Maxhuni, Diki 2013). The first such study was conducted by De Jong in 1975 (Haupt, Haupt 2004 p 2018) who performed experimental analysis on a test suit of problems and his findings have become the standard settings for GAs

(Haupt, Haupt 2004). However, despite De Jong’s (1975) settings becoming the standard their applicability to other situations in general and UK TSP problems in particular is debatable as many of the studies which utilise them had small sample sizes (Myers, Hancock 2001) or focussed on large problem sets (Hussain,Muhammad, Sajid, Hussain, Shoukry, Gani 2017) from test suites such as the TSPLIB (Reinelt 1991) which due to driver time constraints (Great Britain 2016) are not feasible within UK logistics. Since De Jong’s ground breaking 1975 study no standard approach for tuning GAs has developed (Whitely 1996 p 66) instead researchers and practitioners have developed a raft of methodologies these have classified by Eiben, Hintarding and Michealwicz (1999) into techniques which tune the parameters before the run and those which are conducted during the run (Pinel, Danoy, Bouvrey 2011) with Figure 27 and Figure 28 detailing this taxonomy and the approaches within it.



Parameter setting - During the run

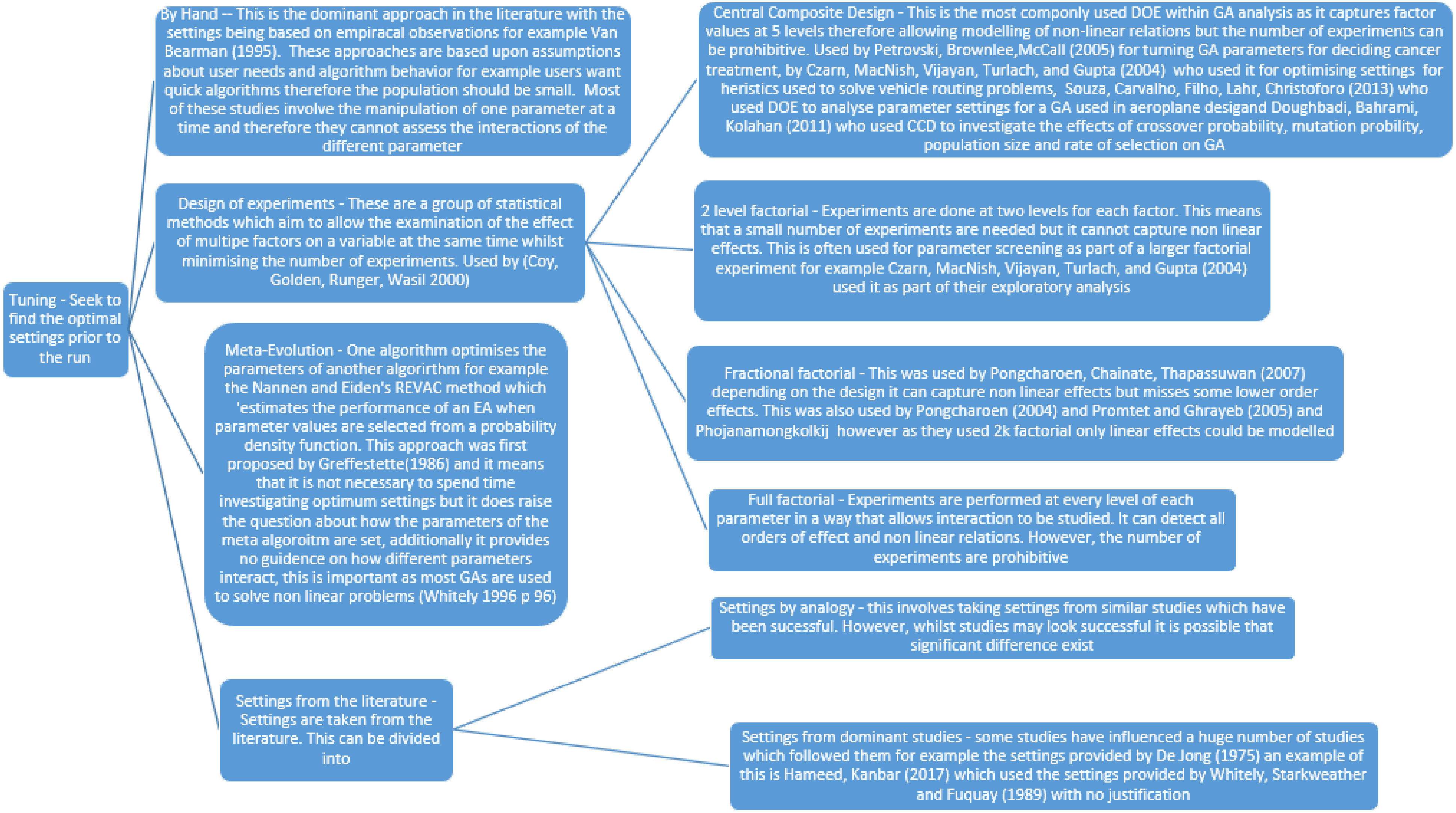
Control (Eiben, Hinterding, Michalwitch 1999) Seek to adapt parameters during the run

Deterministic - The parameter values change in accordance to a pre-determined rule for example after a certain number of generations

Adaptive - Parameter values change after some feedback from the search e.g a certain fitness criteria is met (Haupt, Haupt 2004 p 135)(Popovich,Moschopoulous,Sakai,Sifrim, Aerts,Moreau,Moor 2014)

Self-Adaptive The adaption parameters are encoded and evolve alongside the problem solution via changeover and mutation (Haupt, Haupt 2004 p 135) this was used by Pellerin, Pigeon, Delisle (2004)

FIGURE 27 A TAXONOMY OF PARAMETER TUNING METHODS PART A BASED UPON IDEAS IN EIBEN, HINTARDING AND MICHEALWICZ (1999)



Tuning - Seek to find the optimal settings prior to the run

By Hand – This is the dominant approach in the literature with the settings being based on empiracal observations for example Van Bearman (1995). These approaches are based upon assumptions about user needs and algorithm behavior for example users want quick algorithms therefore the population should be small. Most of these studies involve the manipulation of one parameter at a time and therefore they cannot assess the interactions of the different parameter

Design of experiments - These are a group of statistical methods which aim to allow the examination of the effect of multipe factors on a variable at the same time whilst minimising the number of experiments. Used by (Coy, Golden, Runger, Wasil 2000)

Central Composite Design - This is the most componly used DOE within GA analysis as it captures factor values at 5 levels therefore allowing modelling of non-linear relations but the number of experiments can be prohibitive. Used by Petrovski, Brownlee,McCall (2005) for turning GA parameters for deciding cancer treatment, by Czarn, MacNish, Vijayan, Turlach, and Gupta (2004) who used it for optimising settings for heristics used to solve vehicle routing problems, Souza, Carvalho, Filho, Lahr, Christoforo (2013) who used DOE to analyse parameter settings for a GA used in aeroplane desigand Doughbadi, Bahrami, Kolahan (2011) who used CCD to investigate the effects of crossover probability, mutation probility, population size and rate of selection on GA

2 level factorial - Experiments are done at two levels for each factor. This means that a small number of experiments are needed but it cannot capture non linear effects. This is often used for parameter screening as part of a larger factorial experiment for example Czarn, MacNish, Vijayan, Turlach, and Gupta (2004) used it as part of their exploratory analysis

Fractional factorial - This was used by Pongcharoen, Chainate, Thapassuwan (2007) depending on the design it can capture non linear effects but misses some lower order effects. This was also used by Pongcharoen (2004) and Promtet and Ghrayeb (2005) and Phojanamongkolkij however as they used 2k factorial only linear effects could be modelled

Full factorial - Experiments are performed at every level of each parameter in a way that allows interaction to be studied. It can detect all orders of effect and non linear relations. However, the number of experiments are prohibitive

Meta-Evolution - One algorithm optimises the parameters of another algorirthm for example the Nannen and Eiden's REVAC method which 'estimates the performance of an EA when parameter values are selected from a probability density function. This approach was first proposed by Greffestette(1986) and it means that it is not necessary to spend time investigating optimum settings but it does raise the question about how the parameters of the meta algoroitm are set, additionally it provides no guidence on how different parameters interact, this is important as most GAs are used to solve non linear problems (Whitely 1996 p 96)

Settings from the literature - Settings are taken from the literature. This can be divided into

Settings by analogy - this involves taking settings from similar studies which have been sucessful. However, whilst studies may look successful it is possible that significant difference exist

Settings from dominant studies - some studies have influenced a huge number of studies which followed them for example the settings provided by De Jong (1975) an example of this is Hameed, Kanbar (2017) which used the settings provided by Whitely, Starkweather and Fuquay (1989) with no justification

Figure 28 A taxonomy of parameter tuning methods part B based upon ideas in Eiben, Hintarding and Michealwicz (1999)

This research will utilise a DOE approach to find the optimal settings for a UK logistics TSP. This approach was selected partly due to weaknesses in alternative techniques:-

- Parameter-less algorithms (Nadi, Khader 2011) require knowledge on how parameters should adapt during runtime and most do not consider parameter interaction (Fallahi, Amirib, Yoghini 2014 p 497);
- setting parameters based on the literature were rejected as these offer little new knowledge and those settings may not be appropriate to the context of UK logistics;
- setting a parameter by hand, recording and then analysing the result - rejected as this does not allow the interaction of parameters to be analysed, this is an important consideration due to the potential of non-linear relationships between parameters (Ridge 2007) (Rexhepi, Maxhuni, Dika 2013) (Fallahi, Amirib, Yaghini 2014);
- Meta-genetic Algorithm (Myers, Hancock 2001)(Luke 2015 p 54) (Brain, Addicote 2010) to tune the TSP - rejected as such approaches just move the issue of parameter tuning to the meta-GA.

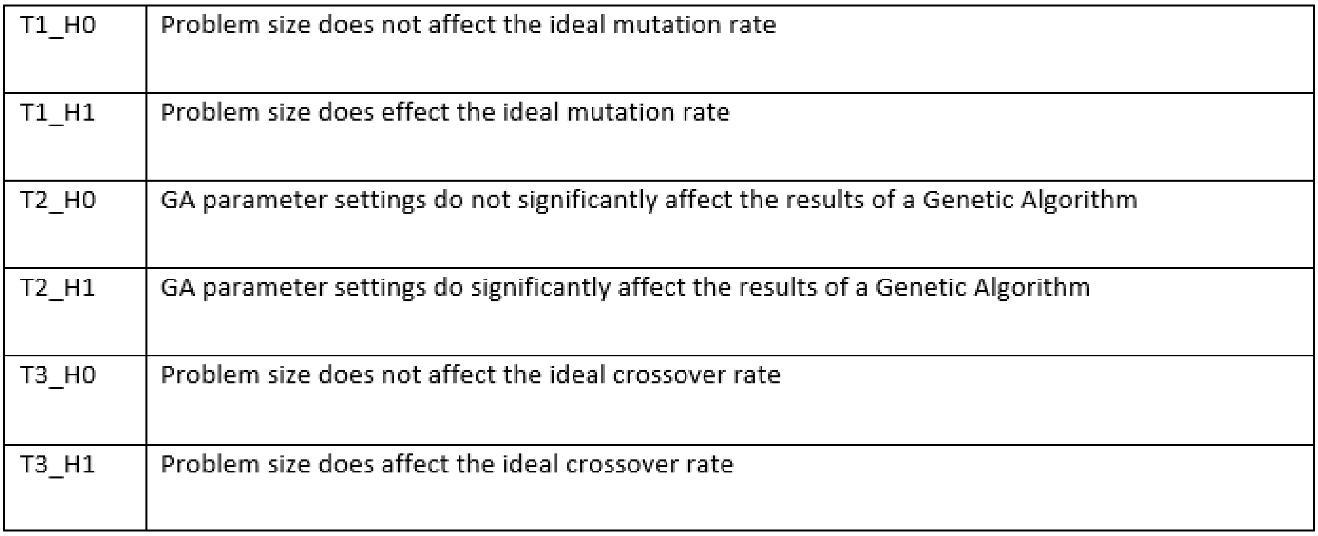
In addition DOE has significant strengths:-

- DOE tests multiple variables at the same time - this means that it is quicker and It can detect non-linear relationships in any direction if either a CCC or full factorial designs are is utilised (Matthews 2005)
- It forces the experimenter to organise their thoughts and to design the experimental plan prior to performing the analysis as such it allows the development of a structured time efficient and repeatable way of conducting experiments and therefore it can be copied by future research (Pinel, Danoy, Bouvrey 2011). This may help to remedy the finding of Aytug, Khouja, Vergara (2003) reported in Pongcharoen, Chainate and Thapatsuwan (2006) that of the 110 GA research papers that they reviewed most lacked well designed experiments.
- It has been used in a number of areas including the tuning of algorithms (Table 13) however many of those studies didn’t study parameter settings in a GA TSP and those that did were not UK based TSPs. This gives this approach the selected approach the advantage of originality.

Study	Parameters Approach	Operators Studied	Approach	Issues
Pongcharoen Chainate, Thapatsuwan (2007)	population size probabilities of crossover and mutation operators including crossover and mutation operators MOPand mechanism		one-ninth fractional factorial experimental design is embedded within a full Latin Square	Fractional design meant that many lower order interactions cannot be measured furthermore only linear effects can be measured. The problem studied is a tour round Thialand such distances are not possible within a UK TSP due to EU Driving hours
COY, Golden, Runger, Wasil (2000)	Did not study GAs studied Ant Colony optimisation. However used DOE methods	Studied heuristics	Used 2 level factorial combined with a fractional factorial with centre points	Not a study of GAs. Did not use star points so cannot fully model non linear relationships (can only indicate)
Ridge (2007)	Did not study GAs studied Ant Colony optimisation. However used DOE methods	Studied Ant Colony Optimisation	Used 2 level factorial combined with a fractional factorial with centre points	Not a GA study

TABLE 13 TABLE DETAILING STUDIES WHICH HAVE USED DOE APPROACHES FOR THE TUNING OF ALGORITHMS

The process of tuning will allow the following hypotheses to be tested:-



T1_H0	Problem size does not affect the ideal mutation rate
T1_H1	Problem size does effect the ideal mutation rate
T2_H0	GA parameter settings do not significantly affect the results of a Genetic Algorithm
T2_H1	GA parameter settings do significantly affect the results of a Genetic Algorithm
T3_H0	Problem size does not affect the ideal crossover rate
T3_H1	Problem size does affect the ideal crossover rate

TABLE 14 TUNING RELATED HYPOTHESES

This section has discussed the methods used within the literature to tune genetic algorithm and justifies the choice of DOE.

xiii. Conclusion

This section has critically reviewed the literature relating to genetic algorithms, the TSP and tuning whilst also identifying a number of hypotheses to test. The literature is large and disparate with a huge number of different structural methods

(Maturana, Lardeux, Saubion 2009) existing therefore the review is limited to the most popular methods. In reviewing the literature this section has identified the behavioural and structural factors (Maturana, Lardeux, Saubion 2009) which influence GA performance and defined the approach the artefact will use for example the crossover and mutation methods. It has also developed a number of hypotheses to test.

The next section details the research method utilised by this paper and the design of the artefact, in doing so it builds upon the findings of the literature review.

3. Research Method

i. Choice of Epistemological approach

This study takes a post-positivist approach (Creswell 2003 p 7) to knowledge believing that in the case of GA tuning there is a single objective reality, and this reality is independent of the researcher. As such it will use repeatable statistical methods to conduct empirical research utilising the developed program as an experiment, analyse the findings and provide guidance to practitioners on the tuning of GAs.

ii. Type of study

Dawson (2009 p 7) classifies computer and information system research into several types. This study exists at the intersection of development, research and problem solving categories of research (Figure 29).

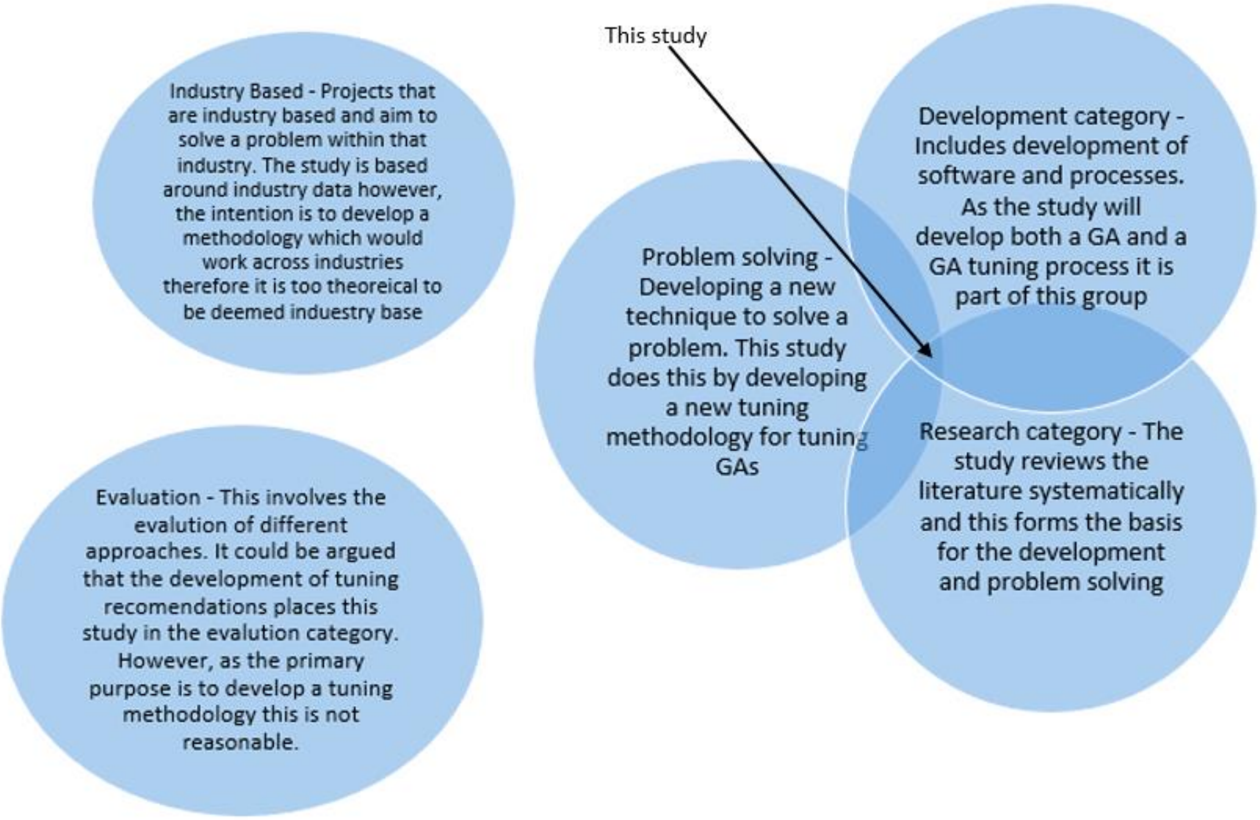


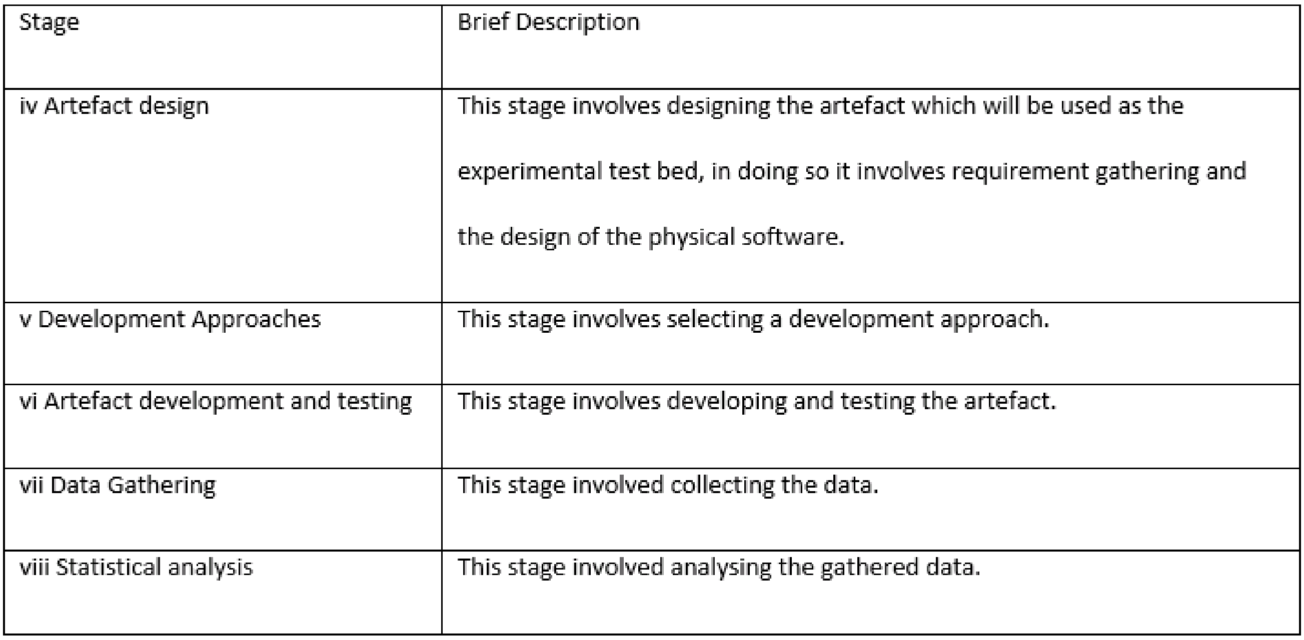
FIGURE 29 POSITION OF THE STUDY WITHIN DAWSON'S 2005 RESEARCH TAXONOMY

The study takes an experimental approach with it utilising a program which has been designed to enable the manipulation of GA parameters and the analysis of the results of these parameters. An experimental approach was selected because of the:-

- lack of ‘theoretical guidelines’ (Chiarandi, Paquete, Preuss, Ridge 2007 p 1) on the workings of GAs this means experimentation is needed to help develop such guidelines. This study does this via the manipulation of variables to detect cause and effect relationships with the use of a DOE approach allowing the investigation of each factor independently and in interaction with other variables at different factor levels;
- need to test existing theories quantitatively using statistical methods and to develop new models based on the findings.

iii. Overview of methodology

The project methodology is made up of the stages detailed in Table 15:-



Stage	Brief Description
iv Artefact design	This stage involves designing the artefact which will be used as the experimental test bed, in doing so it involves requirement gathering and the design of the physical software.
v Development Approaches	This stage involves selecting a development approach.
vi Artefact development and testing	This stage involves developing and testing the artefact.
vii Data Gathering	This stage involved collecting the data.
viii Statistical analysis	This stage involved analysing the gathered data.

Table 15 Research methodology stages

Each of these areas are discussed in detail in the following sections.

iv. Artefact Design

Essential to the analysis was the development of a computer program which allowed the analysis of the effect of parameter levels on GA performance. Due to developer skillset, support for object orientated programming, its support for the MVC design pattern and the large amount of reference material and useful software libraries the software was developed in Java using the JSF framework, HTML, Primefaces, Bootstrap CSS, Glassfish server and MySQL.

Requirements gathering

Requirements were gathered utilising a variety of different techniques:-

- Behavioural and structural (Maturana, Lardeux, Saubion 2009) algorithm requirements such as the ability to vary parameter rates and the operation of a GA were gathered from the literature, these are discussed in the literature review;
- User Interface requirements, non-functional requirements and requirements which are not directly related to the algorithm where gathered via brain storming and the analysis of similar systems such DPS (2008) this resulted in brainstorming documents similar to Figure 30.

Ability to create location (city)

Ability to add location to route (tour)

Ability to add analyse a route (tour) multiple times with different settings

Ability to add multiple routes (tours) to a run. Allows multiple TSP problems to be solved with one run of the algorithm

Ability to record address details including latitudes / longitude

Ability to add via selectOne box

Ability to set parameters at the process level. (Originally was going to be at the run level but on analysis this identified that numerous identical runs would need to be created therefore to avoid this work process functionality was added. This enables a run to be added to a process with analysis results being stored against the process ID and parameter settings being stored against the processID

Results to be stored against runID, routeID and processID

The program will take a long time to run therefore run asynchronously and email user when results are ready

Ability to download results in CSV format

Validation to ensure that the location (city does not exist)

Validation to ensure that a location is added to a route (tour) once only

Should distance to be calculated from Lat or Long or from Google API. Number of calls made Google restrictive therefore calculate from latitude and longitude

Results to include best solution per generation for each route(tour), descriptive statistics for each generation for each (route)

FIGURE 30 AN ILLUSTRATIVE EXAMPLE OF BRAINSTORMING PROCESS

Requirement gathering was iterative as new requirements were discovered in the literature, and during the software development process. On completion of initial brainstorming requirements were built into a use case diagram, this underwent several iterations as functionality was identified with the final diagram being shown in Figure 31

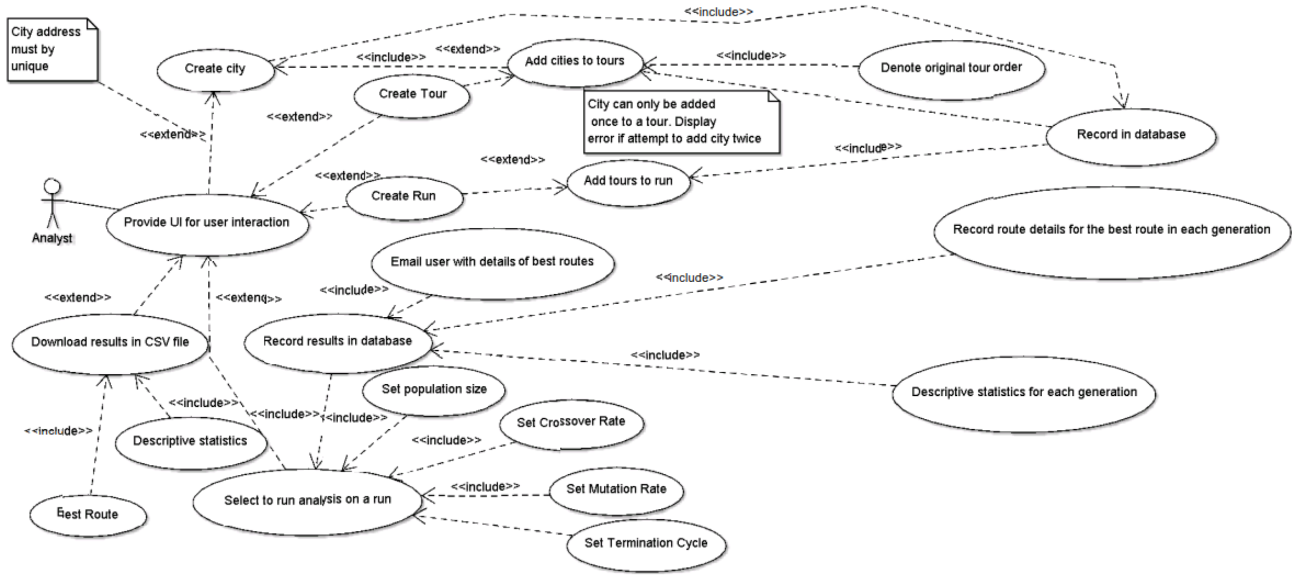


FIGURE 31 USE CASE DIAGRAM FOR THE GENETIC ALGORITHM

These requirements where analysed, grouped into areas (Figure 32) and user stories were developed. The user stories were used to develop the content view (Holt 2009) of the system this was used iteratively to guide the development, and were supplemented as further information was gleaned.

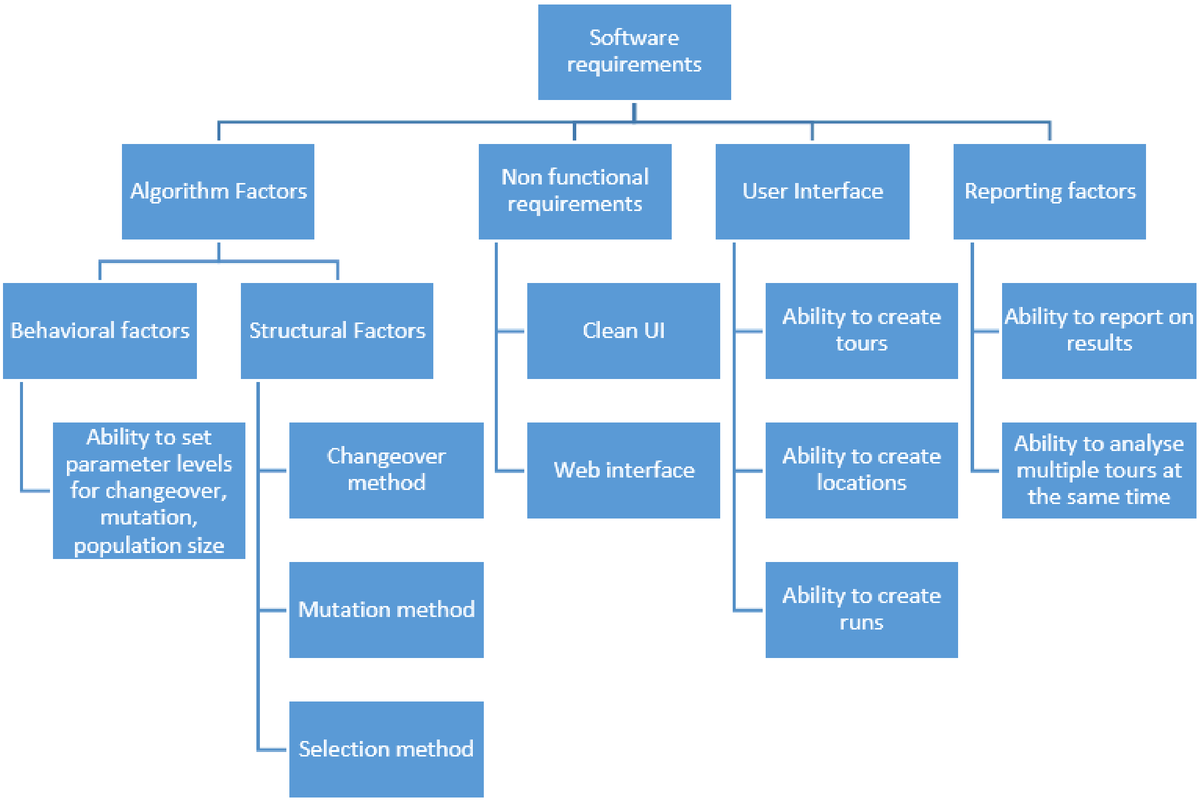
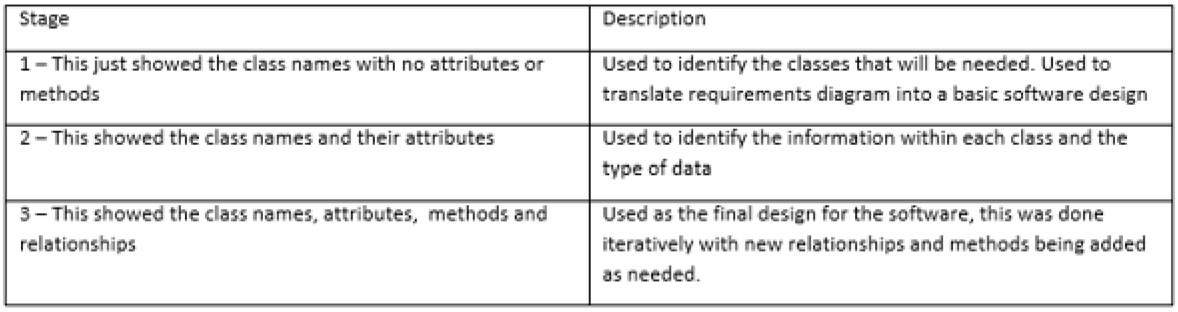


FIGURE 32 DIAGRAM DETAILING THE DIFFERENT CLASSES OF REQUIREMENTS THAT NEED TO BE MET BY THE ARTIFACT

The next sections detail the software design via a series of UML diagrams. It is important to note that these are the final version of the diagrams in reality several iterations of each were developed through the design for example the Class diagram developed via the stages shown in Table 16.



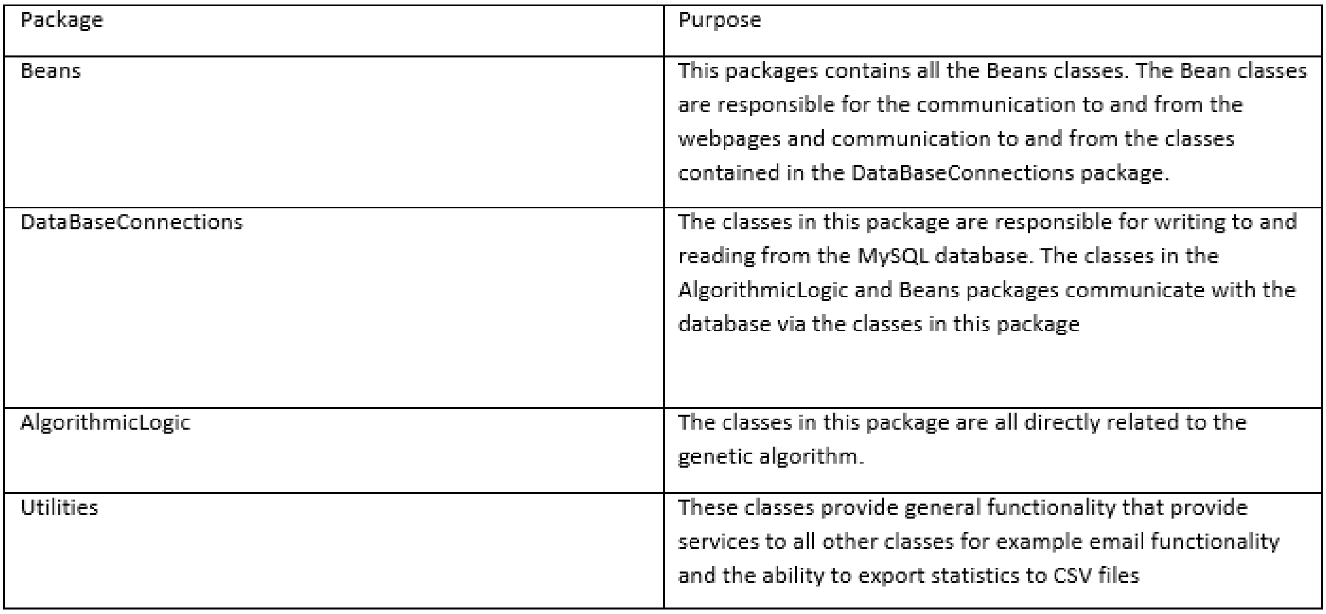
Stage	Description
1 – This just showed the class names with no attributes or methods	Used to identify the classes that will be needed. Used to translate requirements diagram into a basic software design
2 – This showed the class names and their attributes	Used to identify the information within each class and the type of data
3 – This showed the class names, attributes, methods and relationships	Used as the final design for the software, this was done iteratively with new relationships and methods being added as needed.

TABLE 16 TABLE DETAILING THE DIFFERENT ITERATIONS OF THE CLASS DIAGRAM

Software Architecture

This subsection describes the design of the software. As described in Table 16 the design process was iterative therefore this section only describes the final versions of the documents, furthermore as many classes follow similar designs[12] only illustrative examples are shown[13].

To improve code readability and to provide access protection (Pilone, Pitman 2005) classes with similar purposes where organised into packages. Packages were identified by performing clustering analysis with classes which perform similar functions being grouped together, the packages in Table 17 were identified leading to the development of the package diagram in Figure 33.



Package	Purpose
Beans	This packages contains all the Beans classes. The Bean classes are responsible for the communication to and from the webpages and communication to and from the classes contained in the DataBaseConnections package.
DataBaseConnections	The classes in this package are responsible for writing to and reading from the MySQL database. The classes in the AlgorithmicLogic and Beans packages communicate with the database via the classes in this package
AlgorithmicLogic	The classes in this package are all directly related to the genetic algorithm.
Utilities	These classes provide general functionality that provide services to all other classes for example email functionality and the ability to export statistics to CSV files

TABLE 17 PACKAGES IN THE TSP ARTEFACT

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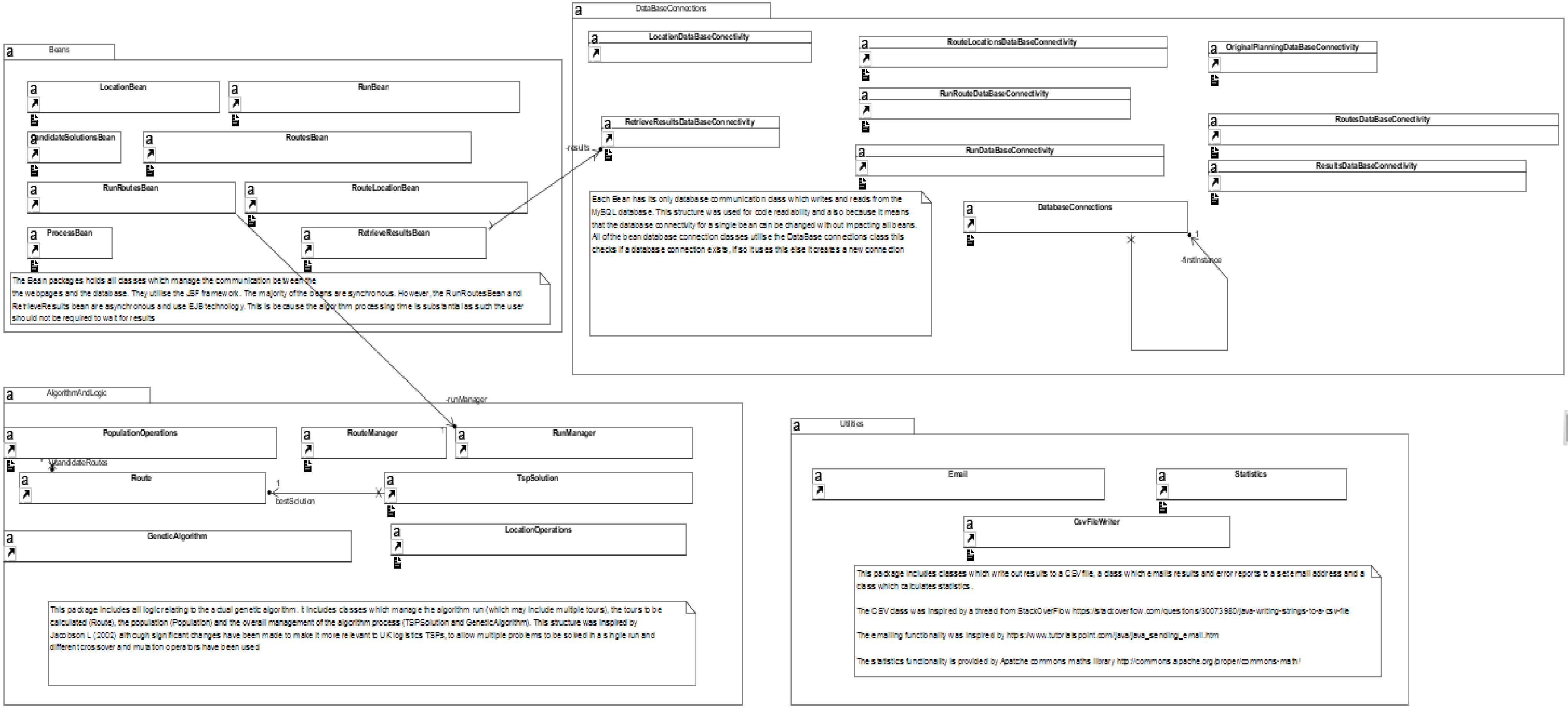
[12] This was done to reduce the coding time and to increase maintainability of the code

[13] for example most Beans use the same technique to connect to the webpage and to the database



The Bean packages holds all classes which manage the communication between the the webpages and the database. They utilise the JSF framework. The majority of the beans are synchronous. However, the RunRoutesBean and RetrieveResults bean are asynchronous and use EJB technology. This is because the algorithm processing time is substantial as such the user should not be required to wait for results

Each Bean has its only database communication class which writes and reads from the MySQL database. This structure was used for code readability and also because it means that the database connectivity for a single bean can be changed without impacting all beans. All of the bean database connection classes utilise the DataBase connections class this checks if a database connection exists, if so it uses this else it creates a new connection

This package includes all logic relating to the actual genetic algorithm. It includes classes which manage the algorithm run (which may include multiple tours), the tours to be calculated (Route), the population (Population) and the overall management of the algorithm process (TSPSolution and GeneticAlgorithm). This structure was inspired by Jacobson L (2002) although significant changes have been made to make it more relevant to UK logistics TSPs, to allow multiple problems to be solved in a single run and different crossover and mutation operators have been used

This package includes classes which write out results to a CSV file, a class which emails results and error reports to a set email address and a class which calculates statistics.

The CSV class was inspired by a thread from StackOverFlow https://stackoverflow.com/questions/30073980/java-writing-strings-to-a-csv-file

The emailing functionality was inspired by https://www.tutorialspoint.com/java/java_sending_email.htm

The statistics functionality is provided by Apache commons maths library http://commons.apache.org/proper/commons-math/

FIGURE 33 PACKAGE DIAGRAM OF THE TSP GENETIC ALGORITHM ARTEFACT INCLUDING HIGH LEVEL CLASS INFORMATION

The high level class information shown in Figure 33 was expanded to give the content and information views (Holt 2009) of the system via the class diagram Figure 34 this illustrates salient features shown in Table 18.

Feature	Purpose
A user can assign a large number of TSP routes to a runBean	This was done so that a user can analyse a large number of TSP routes within a single experimental run this means that unlike many experiments the artefact can be used to analyse a broad base of problems at the same time thus saving significant experimentation time.
A runBean can be used multiple times with each use been assigned a process number	This was done to save experimental time as it meant that the same run could be analysed multiple times without the need for duplication and additional work, this was vital as DOE involves using different parameter settings over the same data multiple times.
All beans share the same basic design e.g. how they connect to the database	This was done so that system development was easier as each bean followed a similar pattern meaning that developer speed improved through the process and learnings from each bean could be applied to the other beans.
Separation of layers	The software is developed using multiple tiers with separation existing between display, business logic, database connectivity and the database. This separation was used as it helps in the development of readable code and it means that it is possible to make changes to one layer without other layers being affected therefore making development easier.

TABLE 18 SALIENT ARTEFACT DESIGN FEATURES

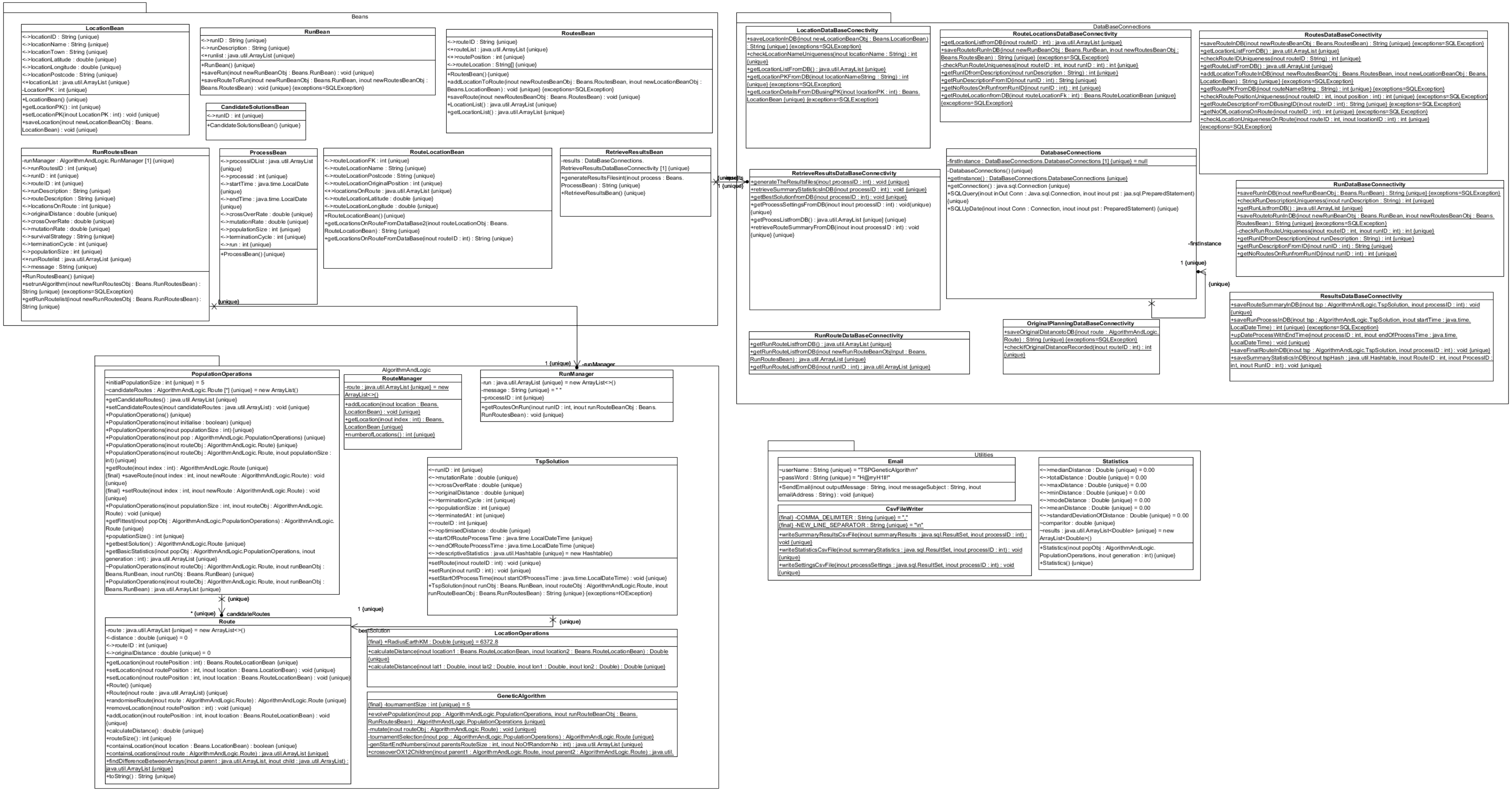


FIGURE 34 DETAILED CLASS DIAGRAM FOR THE TSP GENETIC ALGORITHM ARTEFACT

A class diagram gives a static view of software (Holt 2009), however to give data persistence it is written to a database. The data that needs to be stored was gathered via brainstorming and literature review, this information was:-

- grouped into database tables and then the information in each table was put into columns taking care to identify primary keys;
- Relationships between tables and the appropriate foreign keys were identified;
- Normalisation analysis was performed to ensure that the data was properly structured this resulted in the database design in Figure 35.

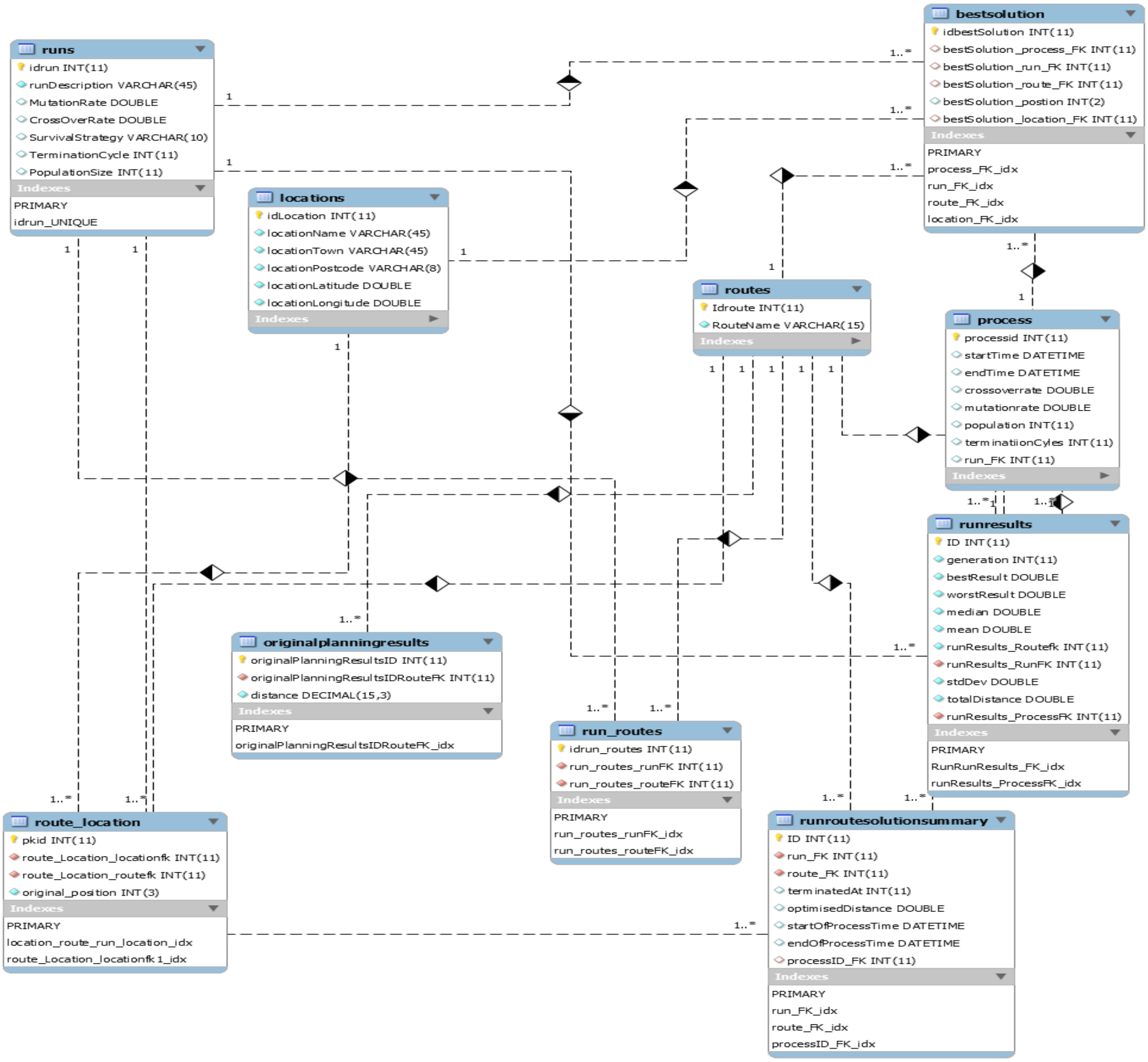


FIGURE 35 ENTITY RELATIONSHIP DIAGRAM SHOWING THE DATABASE DESIGN FOR THE TSP ALGORITHM

Figure 34 and Figure 35 give a static view of the software and database (Holt 2009). However, programs are not static therefore the following section uses activity diagrams to show the behavioural view of the system and sequence diagrams to show the process instance view in doing so they show how classes interact to deliver use cases. Due to the large amount of functionality within the software only illustrative examples are included.

Adding a location to the database

All masterfile records are added using the same process. This section uses the location masterfile to illustrate the addition of a new location to the system. A mock-up of the screen is shown in Figure 36 and the process is illustrated in the use case script in Figure 37, the sequence diagrams in Figure 38 and Figure 39 and the activity diagram in Figure 40.

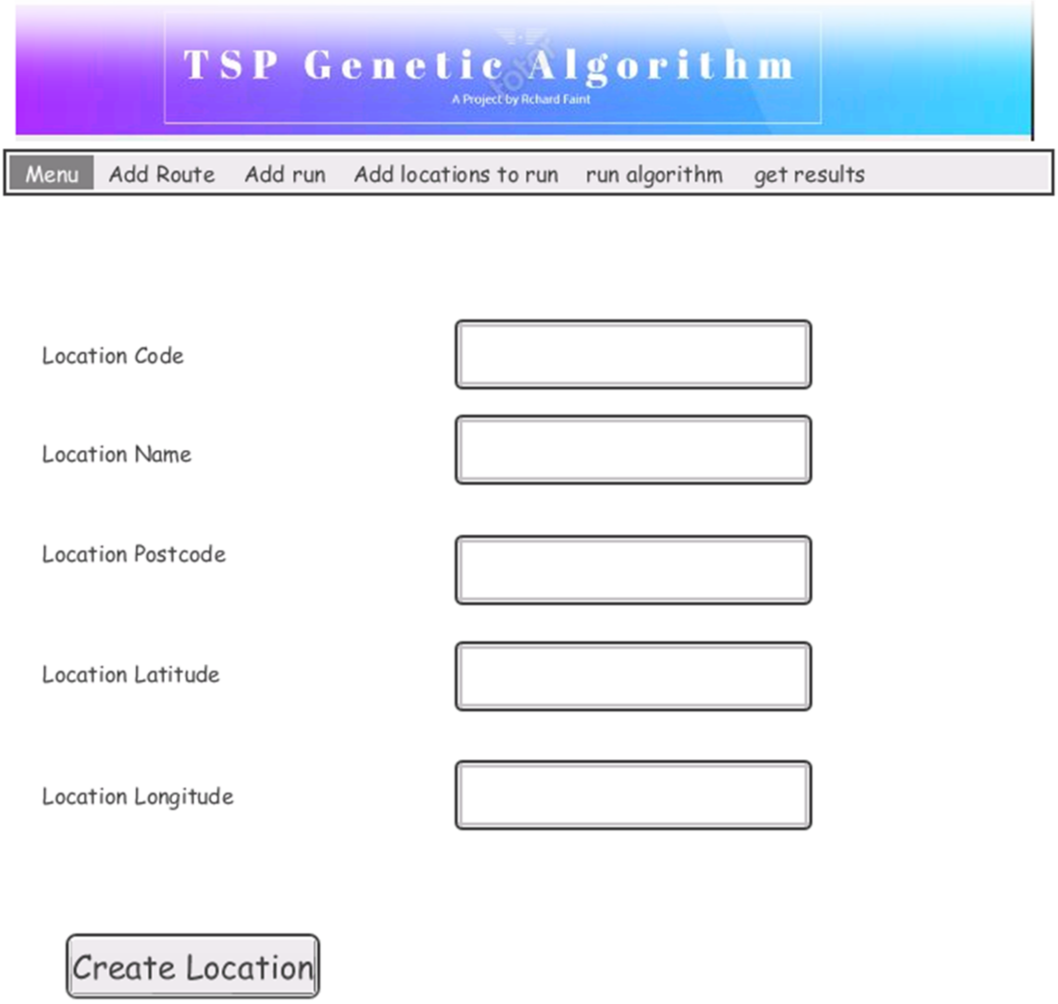
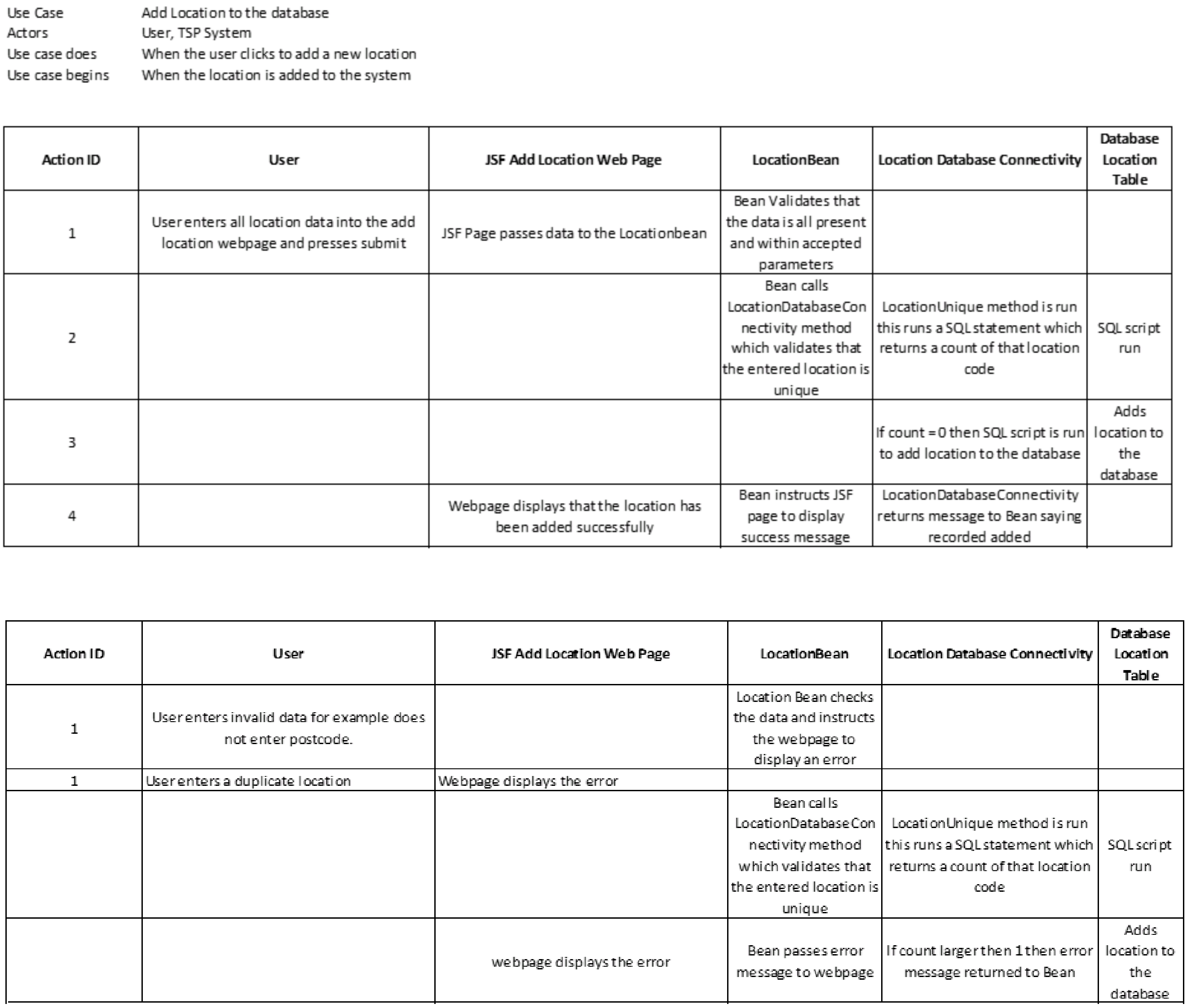


FIGURE 36 MOCK-UP OF THE CREATE LOCATION SCREEN IN THE TSP GENETIC ALGORITHM ARTEFACT

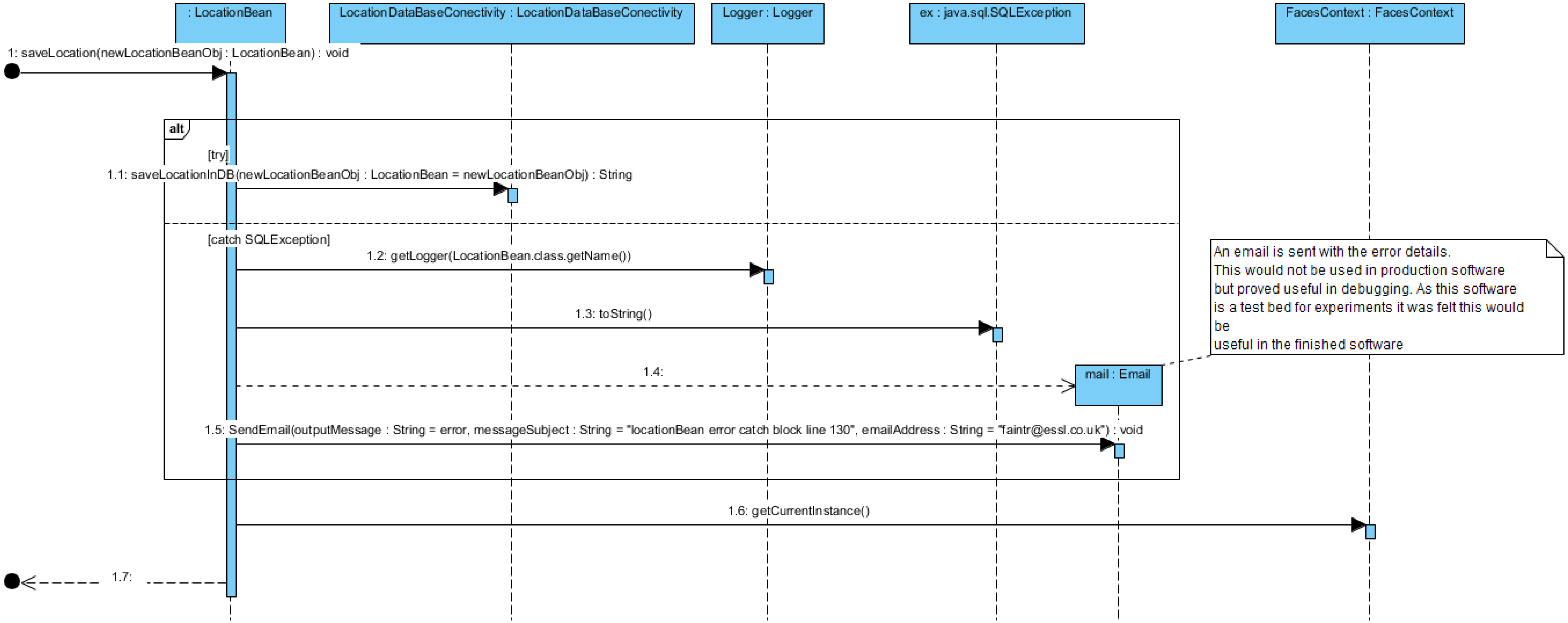


Use Case	Add Location to the database
Actors	User, TSP System
Use case does	When the user clicks to add a new location
Use case begins	When the location is added to the system

Action ID	User	JSF Add Location Web Page	LocationBean	Location Database Connectivity	Database Location Table
1	User enters all location data into the add location webpage and presses submit	JSF Page passes data to the Locationbean	Bean Validates that the data is all present and within accepted parameters		
2			Bean calls LocationDatabaseConnectivity method which validates that the entered location is unique	LocationUnique method is run this runs a SQL statement which returns a count of that location code	SQL script run
3				If count = 0 then SQL script is run to add location to the database	Adds location to the database
4		Webpage displays that the location has been added successfully	Bean instructs JSF page to display success message	LocationDatabaseConnectivity returns message to Bean saying recorded added	

Action ID	User	JSF Add Location Web Page	LocationBean	Location Database Connectivity	Database Location Table
1	User enters invalid data for example does not enter postcode.		Location Bean checks the data and instructs the webpage to display an error		
1	User enters a duplicate location	Webpage displays the error			
			Bean calls LocationDatabaseConnectivity method which validates that the entered location is unique	LocationUnique method is run this runs a SQL statement which returns a count of that location code	SQL script run
		webpage displays the error	Bean passes error message to webpage	If count larger then 1 then error message returned to Bean	Adds location to the database

FIGURE 37 USE CASE SCRIPT FOR ADDING A LOCATION TO THE DATABASE – STANDARD AND ALTERNATIVE USE CASES



An email is sent with the error details.
This would not be used in production software
but proved useful in debugging. As this software
is a test bed for experiments it was felt this would
be
useful in the finished software

FIGURE 38 SEQUENCE DIAGRAM FOR ADDING A LOCATION

For simplicity Figure 38 does not show how the locationDatabaseConnectivityObject gets a connection to the database, this process is shown in Figure 39 with the software checking if any connections are available and using them, else a new connection is created[14].

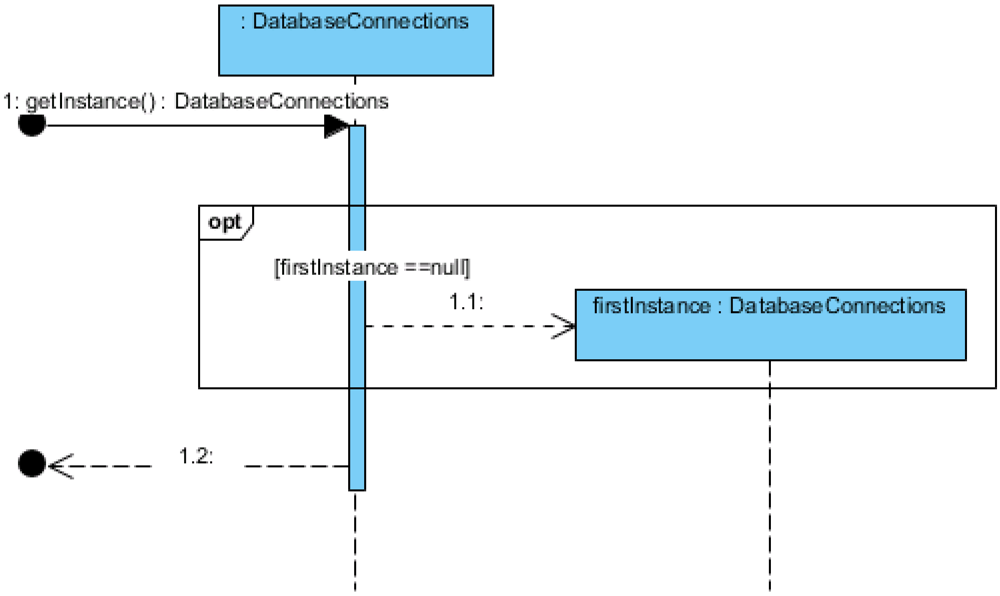


FIGURE 39 SEQUENCE DIAGRAM FOR GETTING A NEW DATABASE CONNECTION

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[14] One bug that was discovered during tested was that the software was opening up thousands of new database connections therefore a new closeDataBase function was added. As this was discovered in testing it does not appear on the design UMLs.

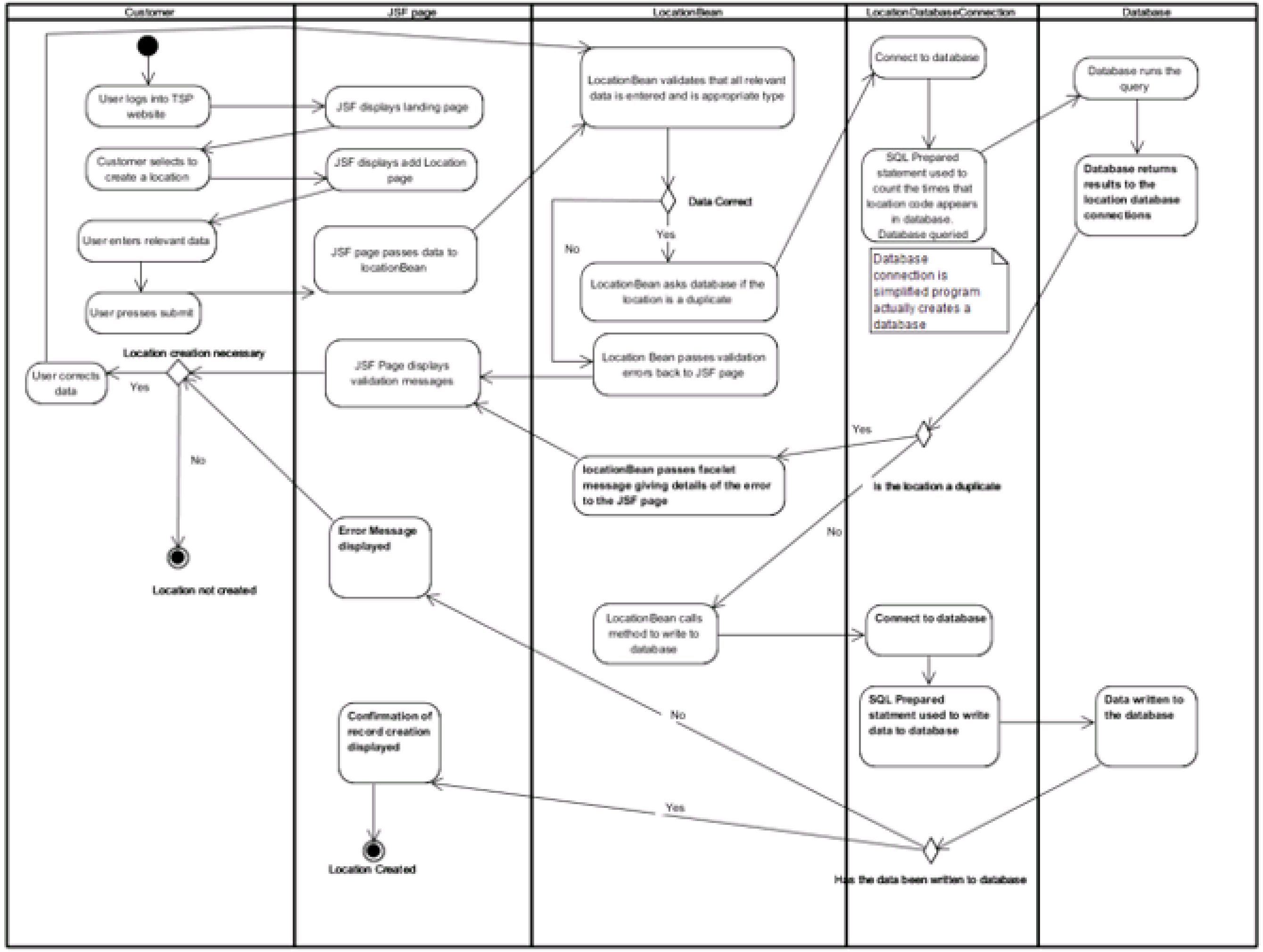


Figure 40 Activity diagram showing how a database is added to the TSP Genetic Algorithm system

Genetic Algorithm Process

The Genetic Algorithm process forms the core of the system. This process is described in UML diagrams which follow. Due to the complexity of the process it is broken down over a number of activity and sequence diagrams with their roles described in Table 19.

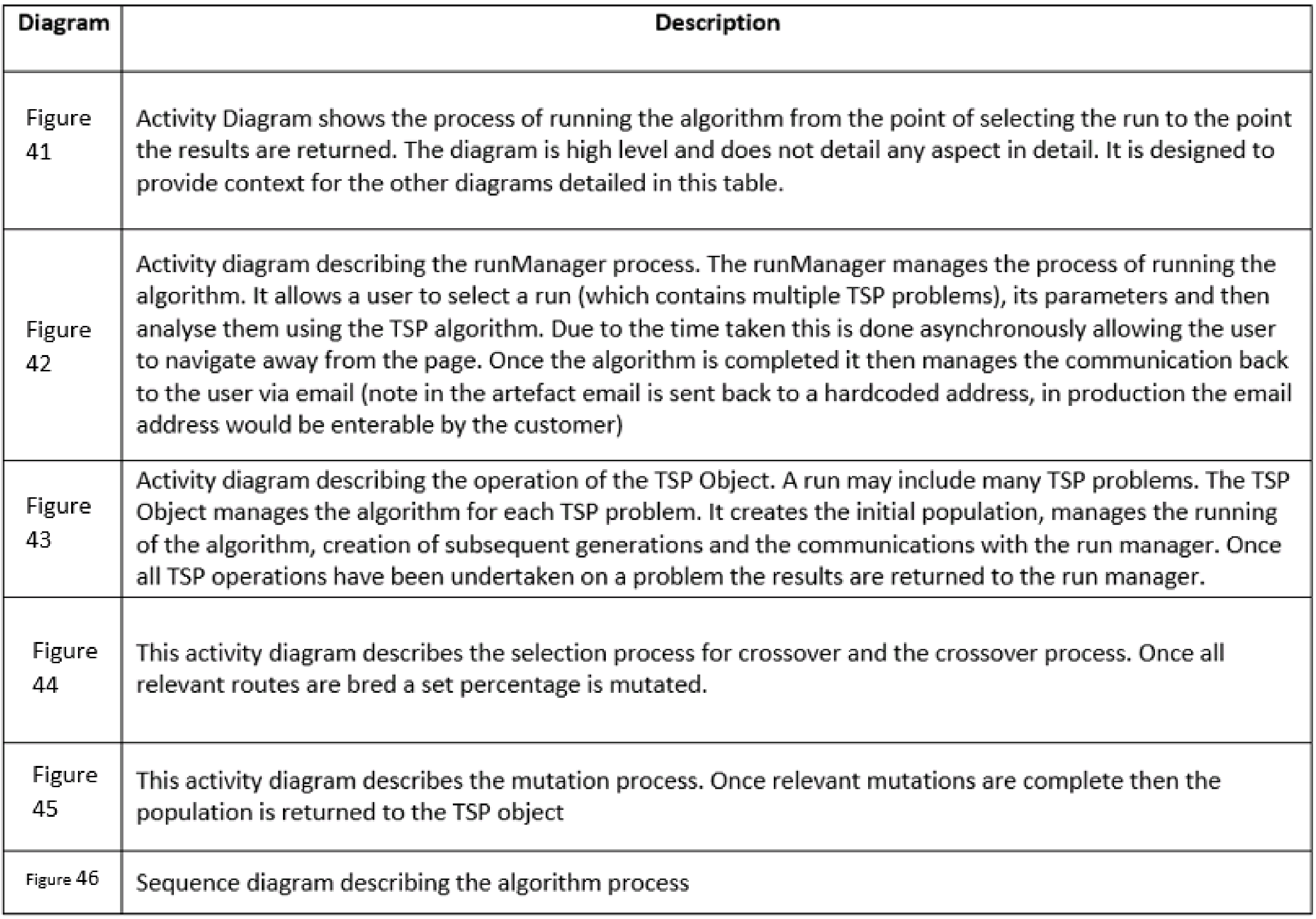


Diagram	Description
Figure 41	Activity Diagram shows the process of running the algorithm from the point of selecting the run to the point the results are returned. The diagram is high level and does not detail any aspect in detail. It is designed to provide context for the other diagrams detailed in this table.
Figure 42	Activity diagram describing the runManager process. The runManager manages the process of running the algorithm. It allows a user to select a run (which contains multiple TSP problems), its parameters and then analyse them using the TSP algorithm. Due to the time taken this is done asynchronously allowing the user to navigate away from the page. Once the algorithm is completed it then manages the communication back to the user via email (note in the artefact email is sent back to a hardcoded address, in production the email address would be enterable by the customer)
Figure 43	Activity diagram describing the operation of the TSP Object. A run may include many TSP problems. The TSP Object manages the algorithm for each TSP problem. It creates the initial population, manages the running of the algorithm, creation of subsequent generations and the communications with the run manager. Once all TSP operations have been undertaken on a problem the results are returned to the run manager.
Figure 44	This activity diagram describes the selection process for crossover and the crossover process. Once all relevant routes are bred a set percentage is mutated.
Figure 45	This activity diagram describes the mutation process. Once relevant mutations are complete then the population is returned to the TSP object
Figure 46	Sequence diagram describing the algorithm process

TABLE 19 TABLE DESCRIBING THE UML DIAGRAMS WHICH DESCRIBE THE GENETIC ALGORITHM PROCESS

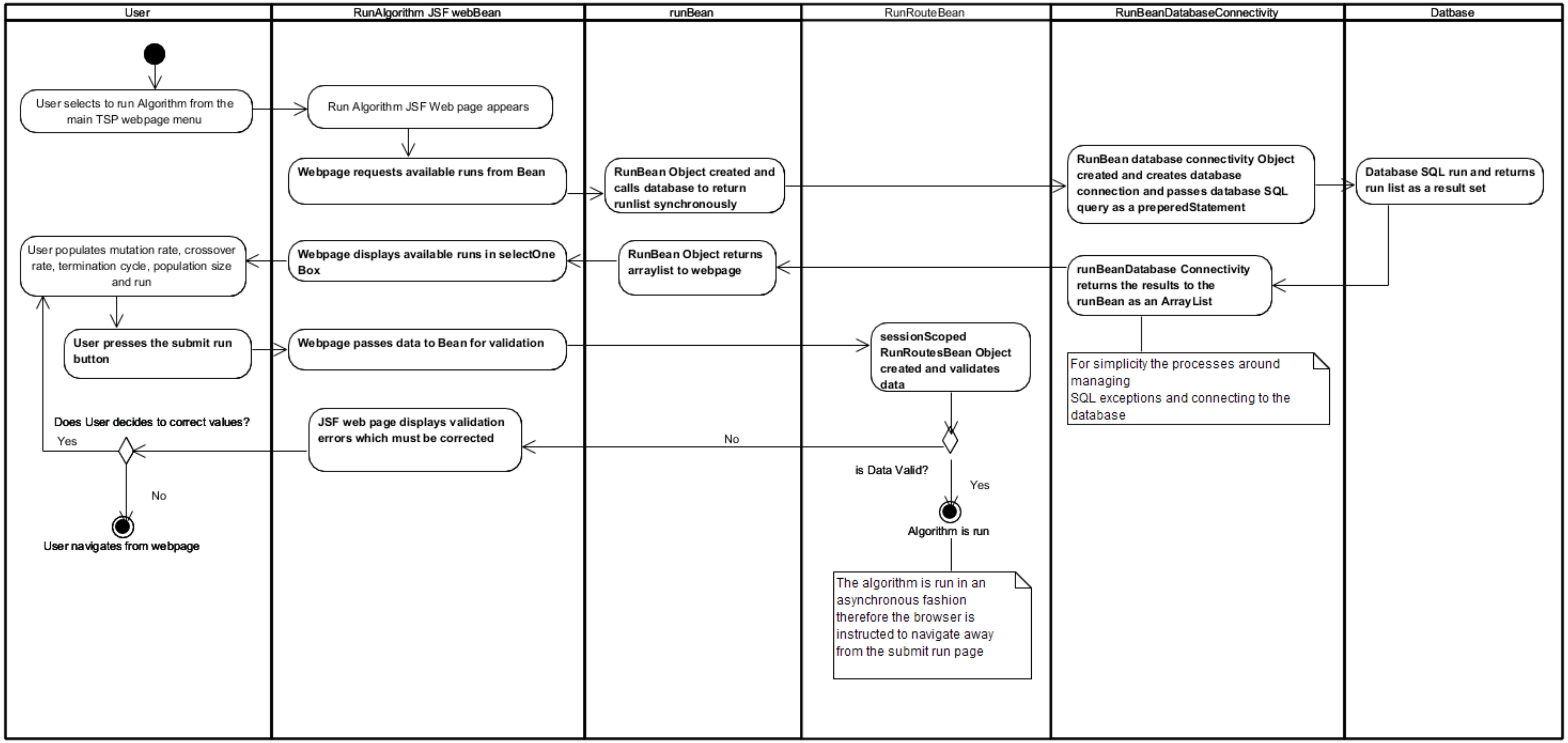


FIGURE 41 ACTIVITY DIAGRAM DESCRIBING THE ALGORITHM PROCESS AT A HIGH LEVEL

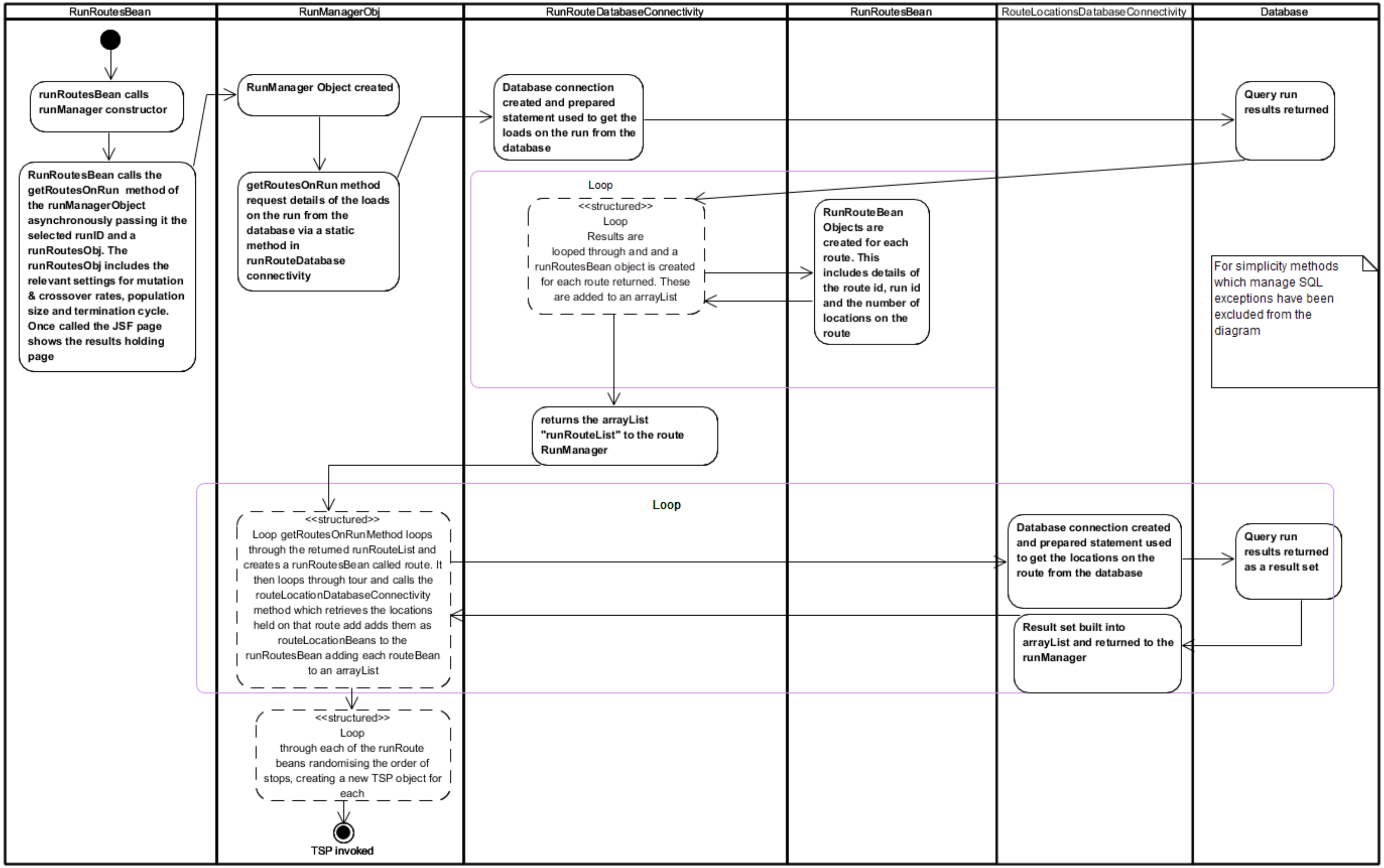


FIGURE 42 ACTIVITY DIAGRAM DESCRIBING THE RUN MANAGER PROCESS

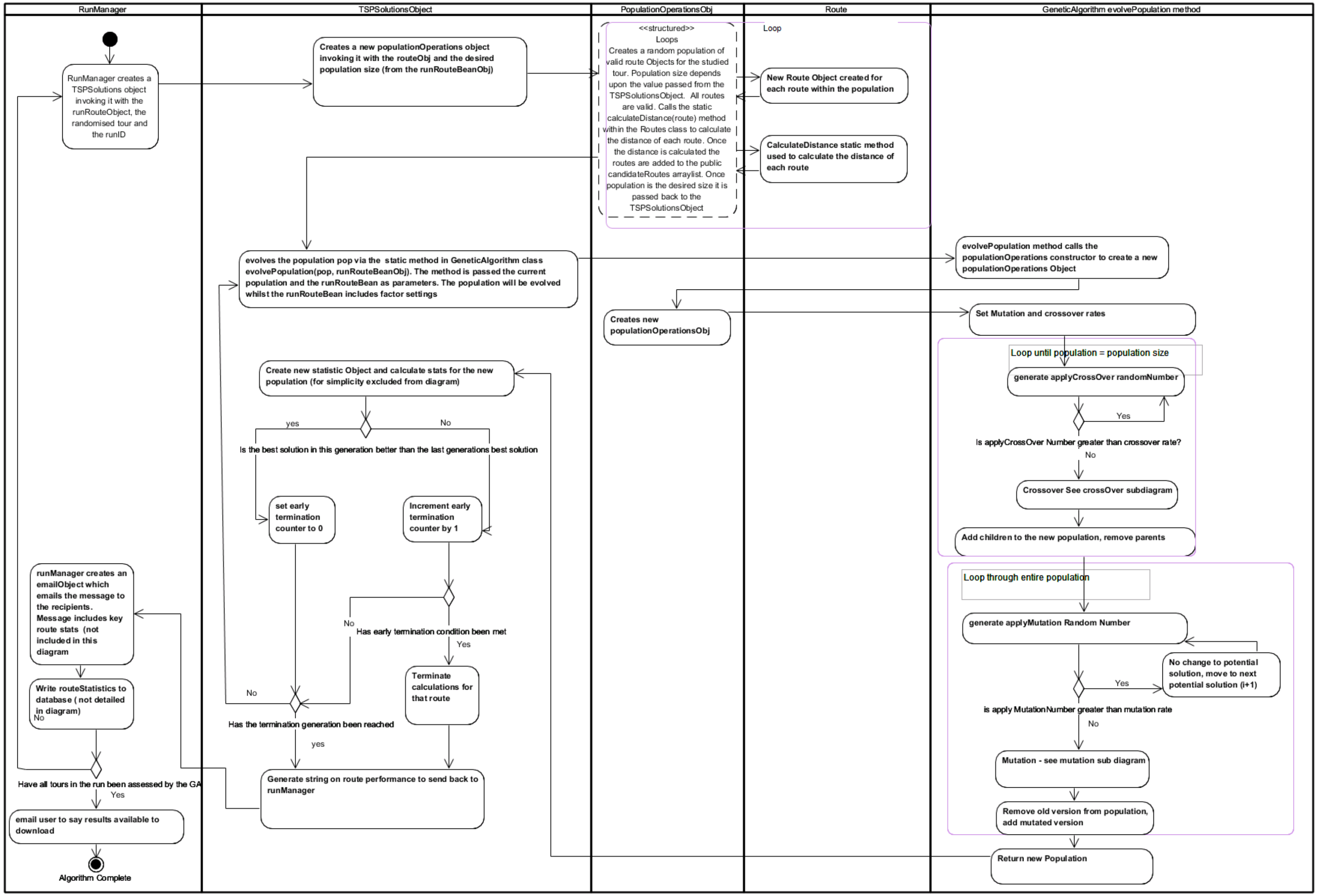


FIGURE 43 GENETIC ALGORITHM TSP OBJECT

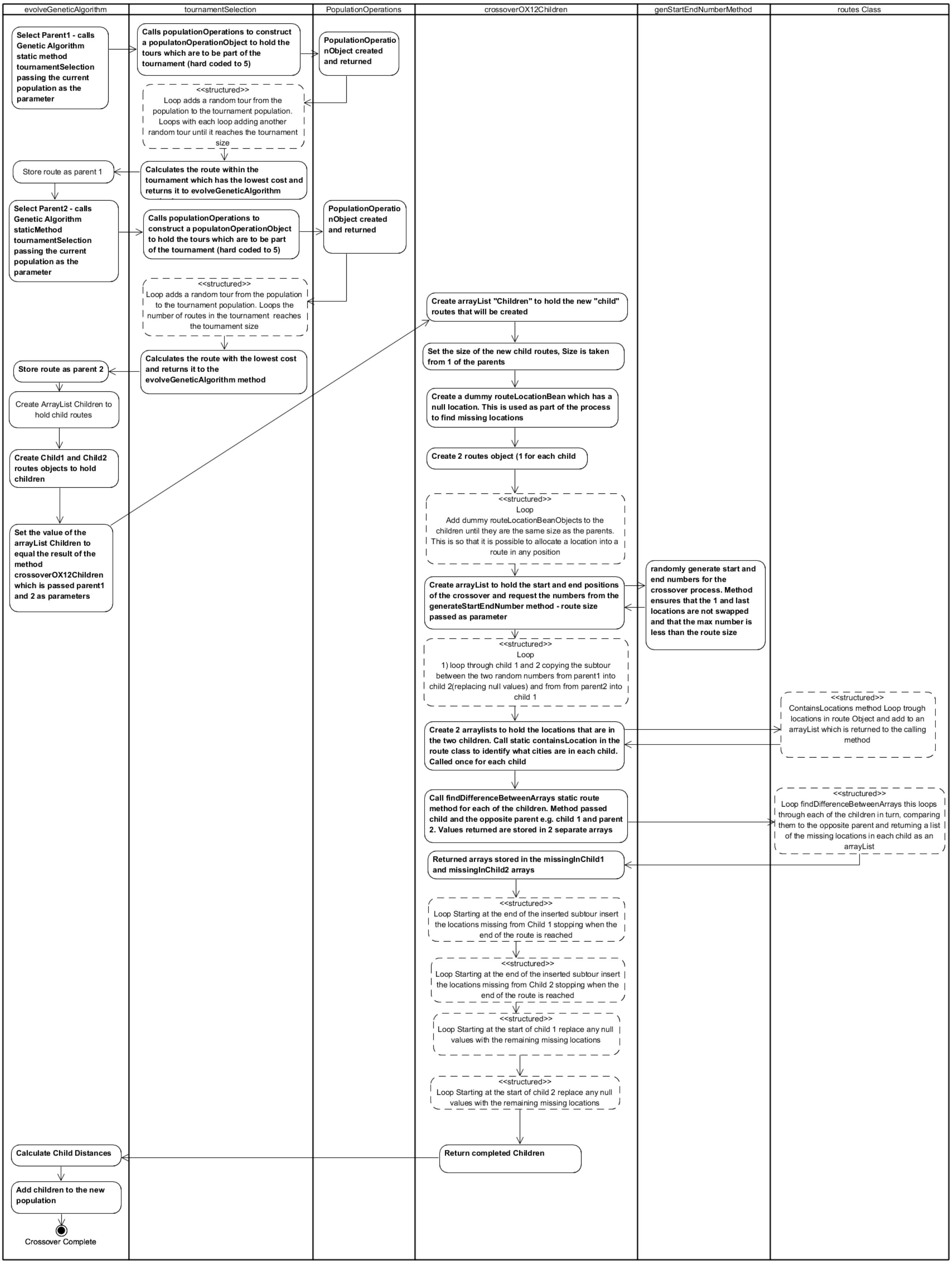


FIGURE 44 ACTIVITY DIAGRAM SHOWING THE SELECTION AND CROSSOVER PROCESS

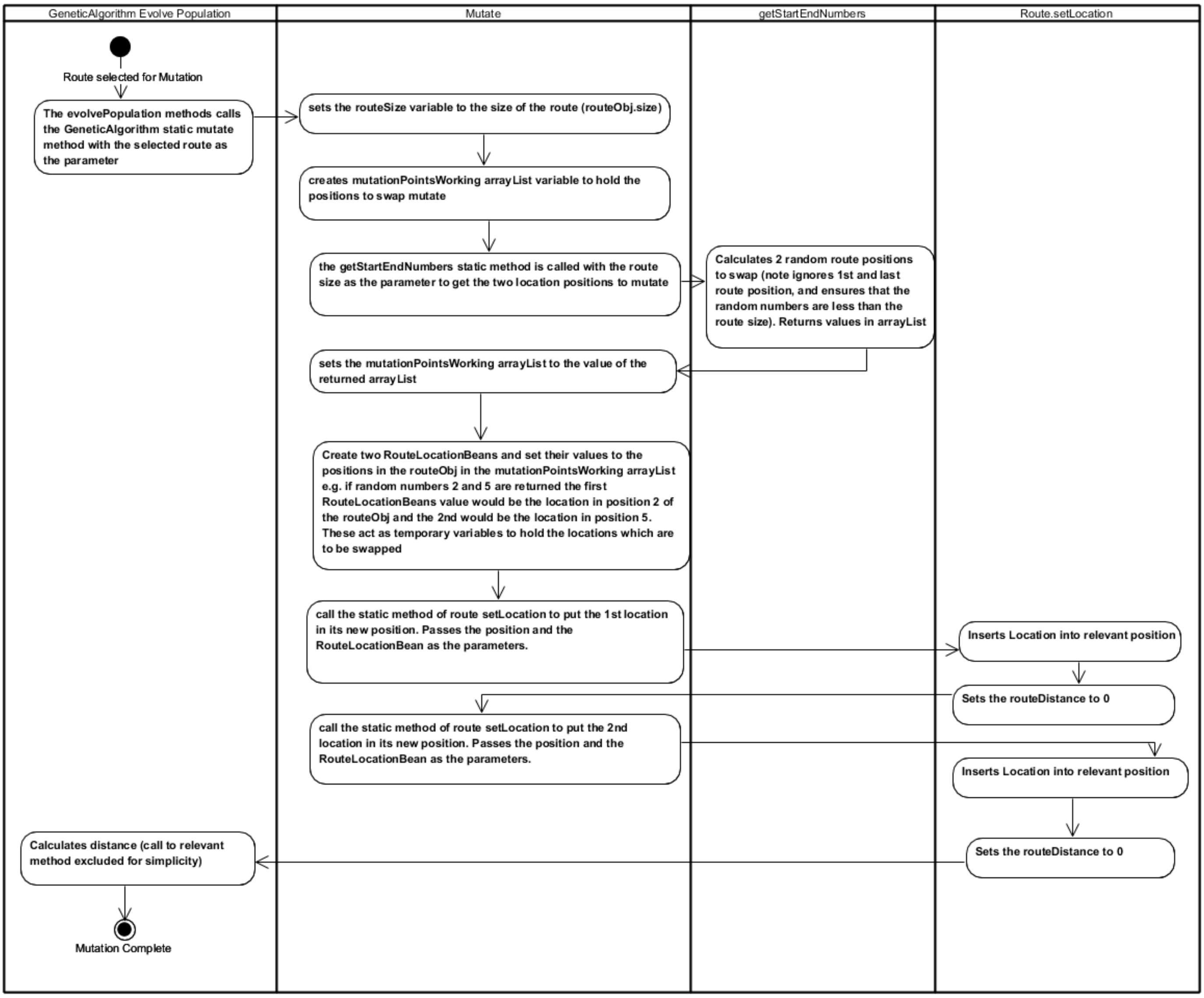


FIGURE 45 ACTIVITY DIAGRAM DESCRIBING THE MUTATION PROCESS

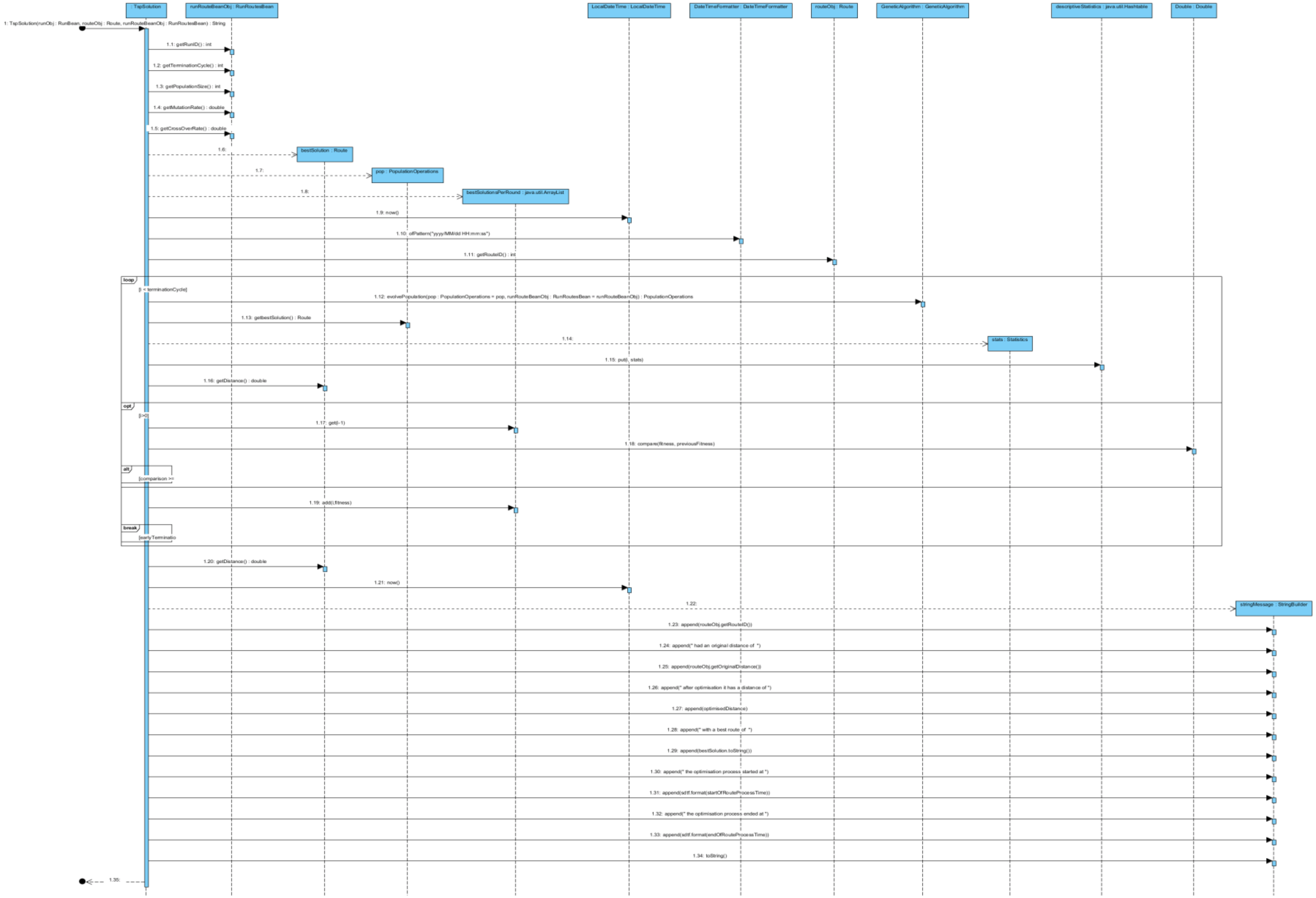


Figure 46 Sequence diagram detailing the algorithm process

v. Development approach

An Agile development philosophy was utilised and user stories were built into a detailed product backlog which was then broken into short sprints. Each sprint contained a number of tasks with Figure 47 illustrating the sprint process for adding a location to the database. Once the sprint was complete the software was tested and corrected before moving onto the next development. This meant that issues were identified and fixed whilst the code was fresh in the developers mind (Ambler nnnn) and that the design could easily be changed during the development process if new requirements were identified (Ambler nnnn).

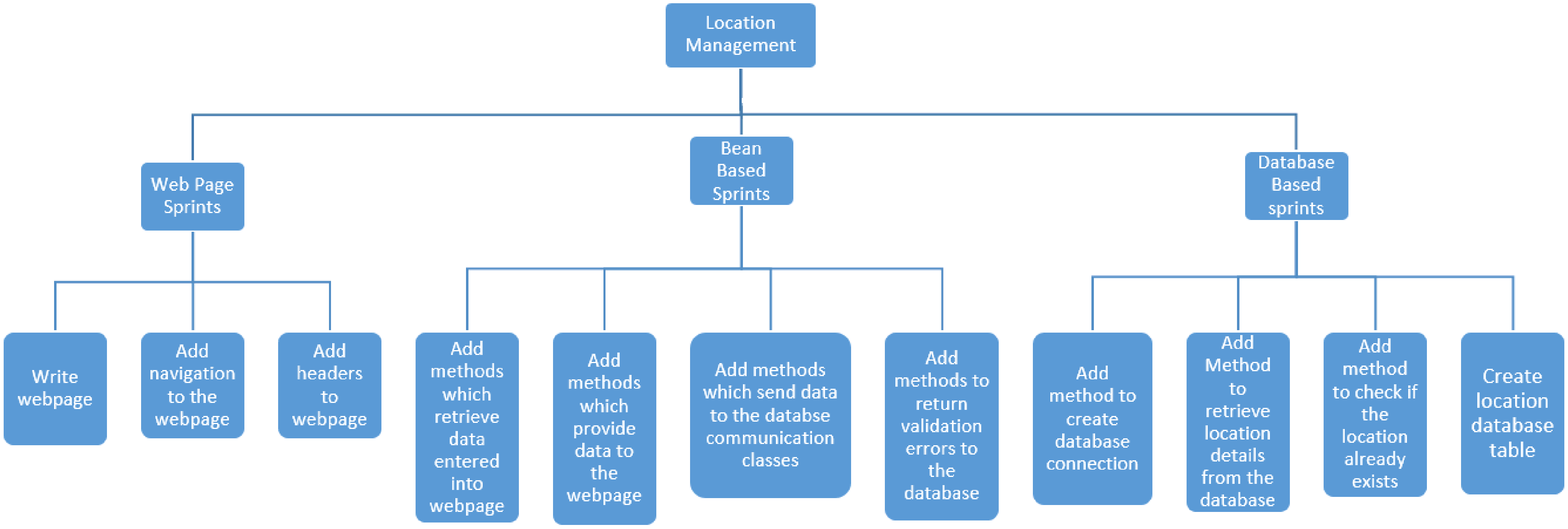


FIGURE 47 DIAGRAM ILLUSTRATING THE SPRINT PROCESS USED

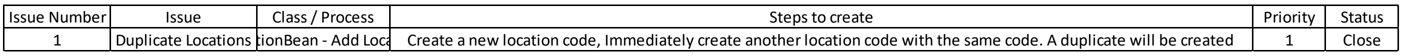
vi. Artefact Development and testing

As the software is only going to be used for this paper an automated test strategy was not appropriate and therefore a manual incremental testing approach was used, this testing strategy and process is described in Table 20.

Test Type	How tested
Unit Test	Each function was tested individually immediately on code completion to assess if was working, this enabled:- • Quick identification of issues meaning that they could be fixed whilst the code was fresh in the lines. • Learnings gained from the discovered bugs could be used in the development of the next user story. This was vital as many classes followed similar design patterns. The relevant tests were identified from the user stories. The tests defined the actions that needed to be tested and the response needed for example one test was to prevent a duplicate location being created therefore the test involved checking that this was not possible.
Integration testing part 1	The system was developed in a Bean specific way this meant that all logic relating to the locationBean was completed before any work on any other functionality was started. Once all locationBean work was completed the lifecycle of a locationBean was tested e.g. creation of a locationBean from new information and retrieval of location information from the database and subsequent creation of locationBeans. This approach meant that learnings gained from each Beans development influenced the development of the next Bean.
Integration testing part 2	Part 1 focussed on the testing vertically i.e. all functionality around a specific bean and ignored interaction between Beans. Integration testing 2 focussed on testing the interaction between Beans and between Beans and the GA.
System Test	This involved using realistic data gained from the sample company to run through the lifecycle of the system to check that the system worked as a whole this involved checking that masterfile creation worked and the algorithm performed as expected.
Volume testing	This involved sending a significant volume of routes through the GA program to assess if the system was capable of managing the required volume of data.

TABLE 20 TESTING STRATEGY

Once identified bugs were entered onto a spreadsheet with the steps to recreate, were prioritised and resolved in priority order (Figure 48).



Issue Number	Issue	Class / Process	Steps to create	Priority	Status
1	Duplicate Locations	tionBean - Add Loca	Create a new location code, Immediately create another location code with the same code. A duplicate will be created	1	Close

FIGURE 48 SAMPLE ENTRY FROM ISSUE LIST

vii. Data Gathering

The study considered contacting a large number of UK logistics companies to take part. However, investigation showed that this was impractical due to data access issues caused by commercial sensitivities and GDPR (Great Britain 2018c), furthermore despite searches no appropriate publically available datasets were available[15]. As such it was decided that only routes from a single company would be utilised. The company was selected due to convenience in that they were the only one that agreed to share data as long as the data was anonymous, this is a drawback as the possibility exists that their data is not representative of the industry as a whole.

To assess how representative the company data is the sample was compared against publically available summary statistics. In the sample week the case study company completed 11037 deliveries across 6641 delivery routes giving an average number of stops of 1.82 per route this is significantly less stops than the average stops per route of 5.68 found by a 2007 study of the food and drink haulage industry (FBP 2007) this difference is due to the high proportion of full load work done by the company[16]. Of the routes in the sample 5306 were TSP tours[17]

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[15] This may be due to commercial sensitivities, additionally a Google Scholar search identified that no academic papers have been published on this sector in the last 4 years.

[16] Full load work is where the volume to be delivered to a single location is the same as the capacity of the truck meaning that the vehicle can only complete one stop before reloading at base

[17] The difference is because a number of the routes involved multiple collection locations and some vehicles did not return to their point of origin.

Number of stops	Frequency	Pencentage	Number of potential combinations
3	4141	78.04%	1
4	616	11.61%	2
5	235	4.43%	6
6	135	2.54%	24
7	75	1.41%	120
8	55	1.04%	720
9	20	0.38%	5040
10	12	0.23%	40320
11	9	0.17%	362880
12	5	0.09%	3628800
13	2	0.04%	39916800
14	1	0.02%	479001600
	5306		

TABLE 21 FREQUENCY TABLE FOR THE SAMPLE DATA[18]

The frequency table in Table 21 identifies that many of the routes are not suitable for GA analysis due to the small number of potential combinations therefore all routes with less than 8 stops will be excluded (Table 22),

Number of stops	Frequency	Pencentage
8	55	52.88%
9	20	19.23%
10	12	11.54%
11	9	8.65%
12	5	4.81%
13	2	1.92%
14	1	0.96%
	104	

TABLE 22 FREQUENCY TABLE FOR THE SAMPLE DATA 8 STOPS AND OVER[19]

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[18] As the first location and last location on these routes are fixed then potential combination calculation excludes these two stops

[19] As the first location and last location on these routes are fixed then potential combination calculation excludes these two stops

The sample data in Table 22 gives an average stops per delivery route of 9.02 this is more than the mean of 5.68 found by DFT (2007). However, it is in line with a 2004 DFT study into pallet distribution which found that on average pallet network vehicles performed 9 stops per day, this similarity is unsurprising as pallet networks perform TSP routing as all vehicles return to the depot each night and because they perform multiple deliveries on the same vehicle, as such we can have some confidence that the data selected is at least partly representative[20].

Due to time constraints it is not possible to analyse all of these routes therefore a stratified sample will be taken with the data being stratified by route length. To identify the relevant strata exploratory cluster analysis was undertaken this identified the following strata 8 – 9, 10 – 11 and 12 to 14 with test subjects being taken from each stratum in proportion to their presence in the population.

A stratified sampling approach was selected as:-

- Previous studies have indicated that problem size (tour length) may influence the optimal parameters (Mason, Gunst, Hess 2003) therefore the use of a stratified sample will ensure a representative sample is taken;
- Variability within subgroups is likely to be less than variability within the population as a whole meaning the technique has high statistical precision meaning that a smaller sample size is possible saving significant time (Matthews 2005)

Within DOE statistical power derives from the replication of experiments (Matthews 2005), however to enable generalisation the sample used for the experiment should still be representative of the population. The use of proportional stratification ensures that the sample is partly representative however it is still important to ensure that an adequate sample size it selected. Matthews (2005) details sample size calculations for when the population standard deviation is known and the population is normally distributed, however these details are not known and therefore a convenience sample of 20% of routes will be selected from the population.

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[20] As the raw data for the DFT studies are not available it is not possible to performing any statistical analysis to confirm that the mean values are the same for both samples therefore we cannot be confident that the sample is truly representative.

viii. Statistical Analysis

The research utilised a DOE approach. DOE is a formal repeatable scholastic framework of statistical methods which provide organisation for the design and analysis of experiments (Souza, Carvalho, Filho, Lahr, Christoforo 2013) (Dobslaw 2010) and provides tools to understand situations where there is a response that varies as a function of one or many factors (Matthews 2005). Figure 49 details the factors and response variables within a GA, this study seeks to understand the effect of mutation rate and crossover rate and problem size on off-Line performance. Figure 49 illustrates that other factors affect the response variable therefore to ensure that we gain an understanding of the relevant variables blocking was utilised with the levels of non-studied factors being kept constant across experiment runs. A 'nuisance factor' within the analysis (Matthews 2005 p 117) is the TSPs random initial population as this cannot be kept constant and may influence the results causing issues with the findings. A blocking (Matthews 2005) approach was considered but this would have involved using a non-random initial population for each TSP problem adding significant complexity and meaning that the studied program was not a true GA therefore the effect of the initial random population and other sources of 'statistical noise' (Matthews 2005 p 112) was monitored by replicating the experiment and analysing the pooled results (Matthews 2005 p 112) this was deemed appropriate as the random nature of the initial population means that it should not introduce inherent bias (Matthews 2005).

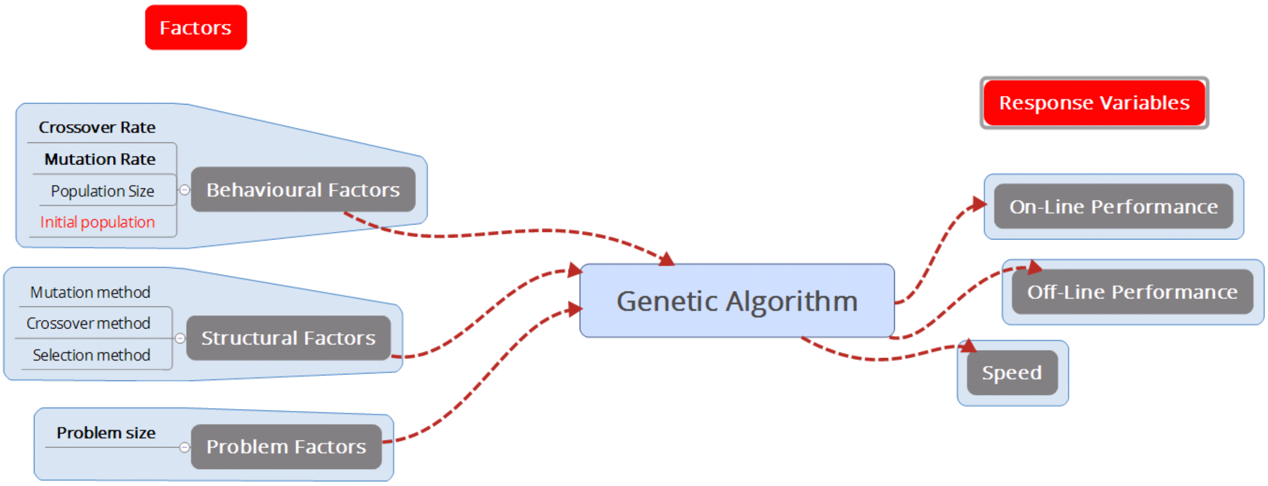


FIGURE 49 FACTORS AND RESPONSES WITHIN A GENETIC ALGORITHM

All experiment designs within the DOE framework were considered but due to the need to model variable interaction a two level experiment which examines the effects of the factors on the response variable at high and low values was inappropriate as they cannot detect nonlinear relationships and previous studies by Shaffer, Caruana, Eshelman and Das (1999) and Pinel, Danoy, Bouvrey (2011) have discovered such relationships[21], whilst a full factorial experiment which tests all factors at all levels was not feasible as the continuous nature of the variables meant that a huge number of experiments would be necessary (Chiarandini, Paquete, Preuss, Ridge 2007). The methodology selected is similar to that used by Coy, Golden, Runger, Wasil (2000), Souza, Carvalho, Filho, Lahr, Christoforo (2013) and Doughbadi, Bahrami, Kolahan (2011) and it involves the use of a response surface form of DOE called CCD, this design was selected because it is:-

- the 'most popular design when there are a large number of parameters,(and) it gives equal precision in all directions' due to its rotatable nature (Doughbadi, Bahrami, Kolahan 2011)
- it provides high quality predictions over the entire search space as it tests variables at 5 levels, additionally unlike 2 level factorial and some fractional factorial designs (Matthews 2005 p 442) it allows the identification of nonlinear relationships in any direction (Montgomery 2005).

The steps involved in this methodology are as follows:-

---

[21] It is generally recommended that a 2 level experiment is conducted first so as to identify profitable areas of study, before a multi-level experiment is undertaken. However, the short time scales and the guidance provided by the literature on profitable areas of study meant this was not feasible or necessary.

Stage	Description
1 Select sample of problems	Problems were selected at random from each strata of problem size
2 Identify high and low levels for each parameter	Parameters and their range were identified in the literature (Coy, Golden, Runger, Wasil 2000) and were used to guide the selection of centre, and axial point (Table 24). The choice of levels was difficult as if settings are too close the analysis can miss important interactions, if they are incorrectly positioned the experiment may lose rotateability and may result in unfeasible values (Montgomery 2005) for example a negative mutation rate.
3 Develop experiment schedule	A CCD experiment schedule was developed in Minitab this detailed the experiments that needed to be undertaken avoided confounding where two variables are at the same level at the same time (Montgomery 2005). Although DOE allows the use of star points in the design (Matthews 2005) these were not utilised as the low possibility of mutation led to star points being placed at unfeasible negative levels. The order of experimentation was randomised this meant that:- • any unobserved variables were randomly and uniformly distributed (Matthews 2005 p 111) and therefore did not inherently bias the experiments; • probability theory could be utilised therefore giving a solid foundation for statistical analysis (Matthews 2005) (Appendix One – Experiment Time Table)
4 Experimentation	The sample data was run through the artefact according to the CCD experimental schedule and the results of the experiment were extracted from the database using SQL. The experiments were grouped into homogenous blocks with none studied factors such as population size kept constant between runs. Replication was used to identify statistical noise and to increase the degrees of freedom. The number of replications needed was difficult to calculate as it depends on error in the process and the size of the smallest variable effect therefore following Matthews (2005) advice that the majority of the advantages of replication come with the first few replications each run was replicated ten times this enables the identification of statistical noise, allows the quantification of uncertainty (Matthews 2005 p 112), allows the analysis to identify smaller effects and maintains orthogonality (Matthews 2005)
5 Analysis	The results of the sample runs were analysed utilising CCD Response Surface Analysis and regression (Petrovski, Brownlee,McCall 2005) (Matthews 2005). The running average of the best individual in each generation (Haupt, Haupt 2004) (Coley 1999) was assessed as the response variable with crossover and mutation rates being the studied factors. This allowed the development of a model of how factors influenced the response variable and to ascertain whether the developed null hypotheses could be rejected. This null hypotheses will be rejected when $p<0.001$ this high required confidence level is used due to the dangers of alpha errors where the null hypothesis is rejected when it should have been accepted this error is more serious than the opposite beta error due to the danger of making major decisions based upon a study with a large amount of risk (Matthews 2005). Further analysis was conducted for the large and small routes in the sample therefore allowing investigation of whether problem size effects optimal settings for the studied parameters

TABLE 23 STEPS IN THE EXPERIMENTAL METHODOLOGY

Level	Description	Number in experiment	Values
Centre Points	These are the levels at the centre for the factor, this means that they are set half way between the high and low values for the factors.	30 in cube and 30 in axial	These are derived from cube points with mutation rate being 0.05575 and crossover 0.725
Cube Points	These are points which would be within a cube formed by a 2 level DOE experiments	40	Values were taken from the literature with the high level for crossover being set at 0.85 and the low point being 0.60 and mutation being set at 0.0195 and 0.092. The selection of these points was partly taken to ensure all axial points are feasible
Axial Points	These are outside of the designs high and low limits	40	These are at equal distance from the centre and are outside of the cube. They are set at 0.54823 and 0.901777 for crossover and 0.004485 and 0.107015 for mutation

TABLE 24 AXIAL, CUBE AND CENTRE POINT SETTINGS FOR DOE EXPERIMENTS

ix. Methodology Limitations

All experiments suffer from limitations this study suffers from the following methodological limitations:-

- The sample is a convenience sample and may not be representative of the UK transport industry as a whole, additionally the transport industry must also take into account factors such as vehicle capacity, fixed booking times and multiple collections and deliveries these have been ignored within this analysis;
- The number of replications was limited due to the time available and therefore some smaller effects may have been missed;
- The experimental program is one implementation of a GA, the recommended settings may therefore only apply to this implementation;
- The study does not deal with issues around the randomness in a GA for example the random initial population and these may be a cause of some of the variation in the results (Czarn, MacNish, Vijayan, Turlach, Gupta 2004).

4. Research findings and Data Analysis

i. Introduction

This chapter uses DOE to tune a GA whilst answering the research questions and testing the developed hypotheses (Table 25). The findings of the study are presented under the major headings of Data Collection, Reliability and Statistical Appropriateness, Descriptive Statistics and Hypothesis testing.

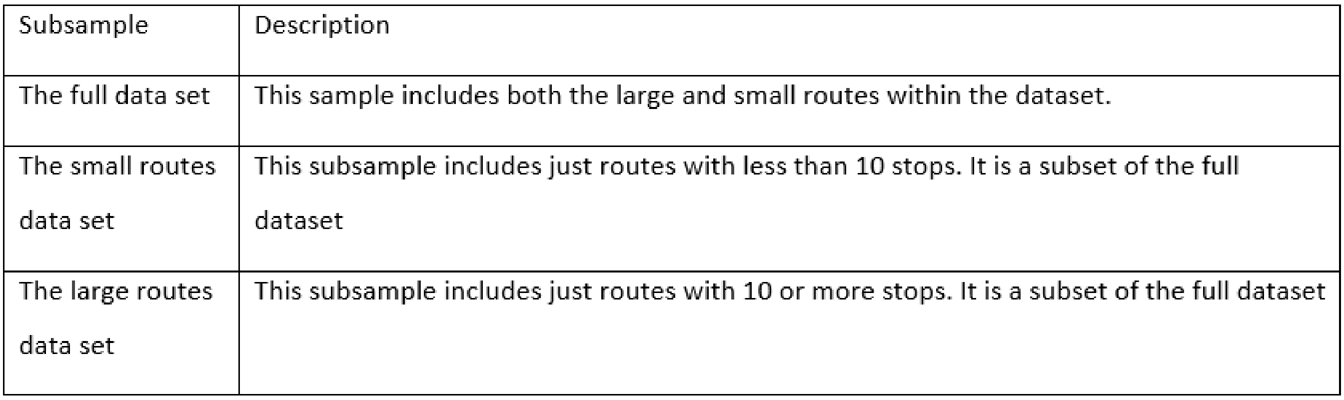
Hypothesis ID	Hypothesis
C1_H0	Crossover level does not have a significant effect on the response variable
C1_H1	Crossover level does have a significant effect on the response variable
M1_H0	No significant interaction exists between crossover and mutation levels
M1_H1	Significant interaction exists between crossover and mutation levels
M2_H0	The relationship between mutation rate and crossover is not non-linear
M2_H1	The relationship between mutation rate and crossover is non-linear
M3_H0	Mutation Level does not have a significant effect on the response variable
M3_H1	Mutation Level does have a significant effect on the response variable
T1_H0	Problem size does not effect the optimum mutation rate
T1_H1	Problem size does effect the optimum mutation rate
T2_H0	Genetic algorithm parameter settings for crossover and mutation do significantly affect the results of a Genetic Algorithm
T2_H1	Genetic algorithm parameter settings for crossover and mutation do not significantly affect the results of a Genetic Algorithm
T3_H0	Problem size does not affect the ideal crossover rate
T3_H1	Problem size does affect the ideal crossover rate
G1_H0	There is no difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning
G1_H1	There is a difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning

TABLE 25 HYPOTHESES TO BE TESTED

ii. Data Collection

Data was collected from the supplier company database using SQL. The data was extracted into a spreadsheet and TSP routes were identified using the sampling techniques described in the research method chapter. The routes were analysed and those with missing data were excluded. Consideration was given on how to manage routes with missing data, as data may be missing for reasons which bias the analysis. However, the missing data was non mandatory in the company’s system and did not seem to follow a pattern therefore the assumption was made that it was missed as a time saving measure and does not introduce ambiguity into any inferences (Papageorgiou, Grant, Takkenberg, Mokhles 2018).

The appropriate number of routes within each stratum were randomly selected this minimised the possibility of inherent bias being introduced. Additionally the data was stratified for analysis purposes with each route being categorised as large (10 stops or over) or small (under 10 stops)[22] (Table 26), this approach was taken so that it will be possible to identify if differences exist between the optimal settings for each strata and the relationships between the parameters for each strata.



Subsample	Description
The full data set	This sample includes both the large and small routes within the dataset.
The small routes data set	This subsample includes just routes with less than 10 stops. It is a subset of the full dataset
The large routes data set	This subsample includes just routes with 10 or more stops. It is a subset of the full dataset

TABLE 26 SAMPLES TO BE ANALYSED

iii. Reliability and statistical appropriateness

Normality Tests

Normality test – All Results

Before statistical analysis is undertaken the research must assess if the proposed techniques are appropriate. This study intends to use parametric statistics; these assume the normal distribution and their use with data which does not follow the normal distribution can lead to Type I and II errors[23] (Matthews 2005) (Hinton, Brownlow, McMurray, Cozens 2008). To assess if the response variable follows the normal distribution the Kolmogorov-Smirnov test[24] (Matthews 2005)(Minitab 2018) was used to analyse the results of the DOE experiments for three datasets (Figure 50, Figure 51, Figure 52).

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[22] The research method chapter identified 3 strata however the number of routes in the strata were small meaning that they could not be analysed individually therefore for analysis a two strata was utilised.

[23] A type I error is when a null hypothesis is rejected incorrectly, a type II error is when the null hypothesis is accepted when it should have been rejected (Matthews 2005)

[24] The Kolmogorov-Smirnov test compares the actual distribution of scores with the normal distribution (Hinton, Brownlow, McMurray, Cozens 2008) by testing the null hypothesis that variables are not normally distributed with significance scores > 0.01 signifying a normal distribution.

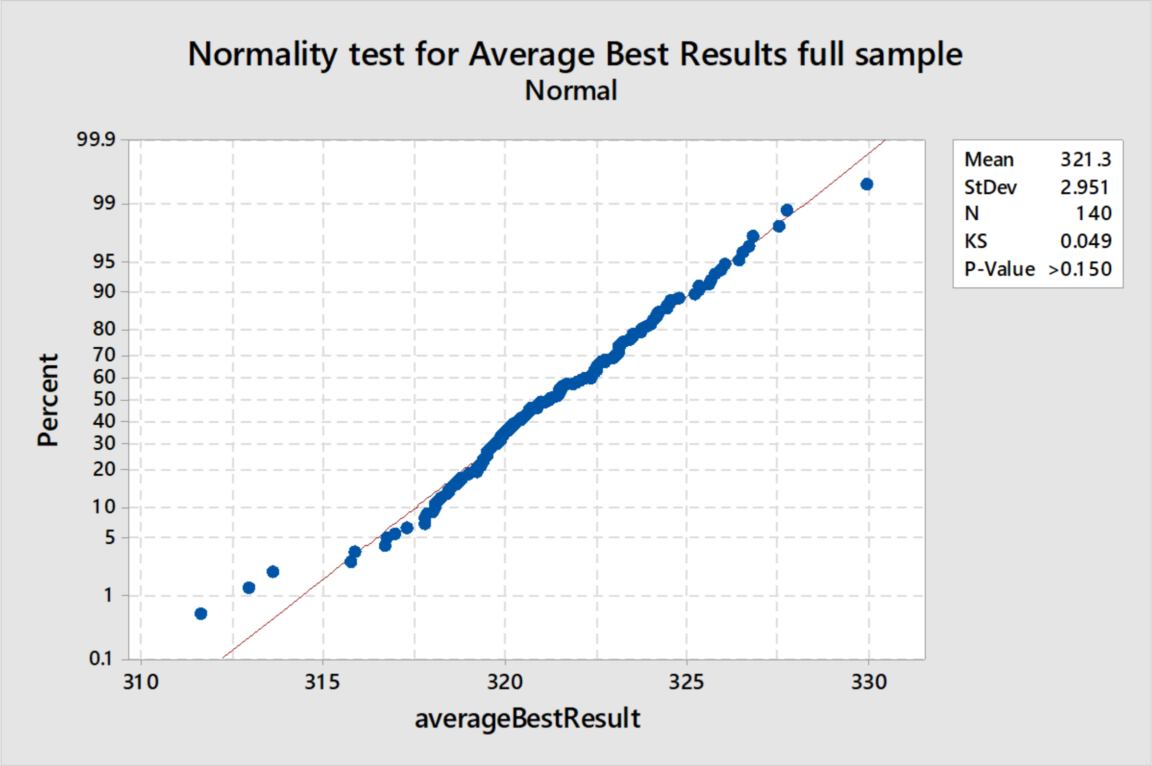

FIGURE 50 KOLMOGOROV-SMIRNOV NORMALITY TEST FOR THE FULL SAMPLE

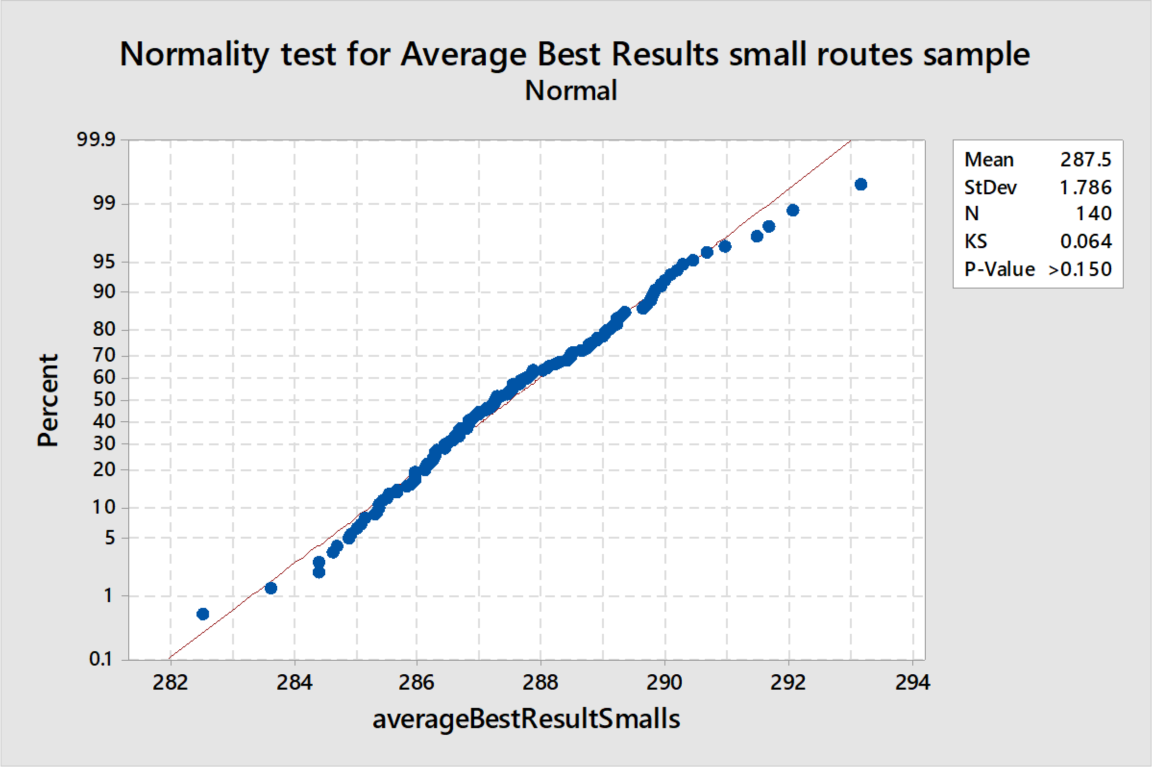

FIGURE 51 KOLMOGOROV-SMIRNOV NORMALITY TEST FOR THE SMALL ROUTES IN THE SAMPLE

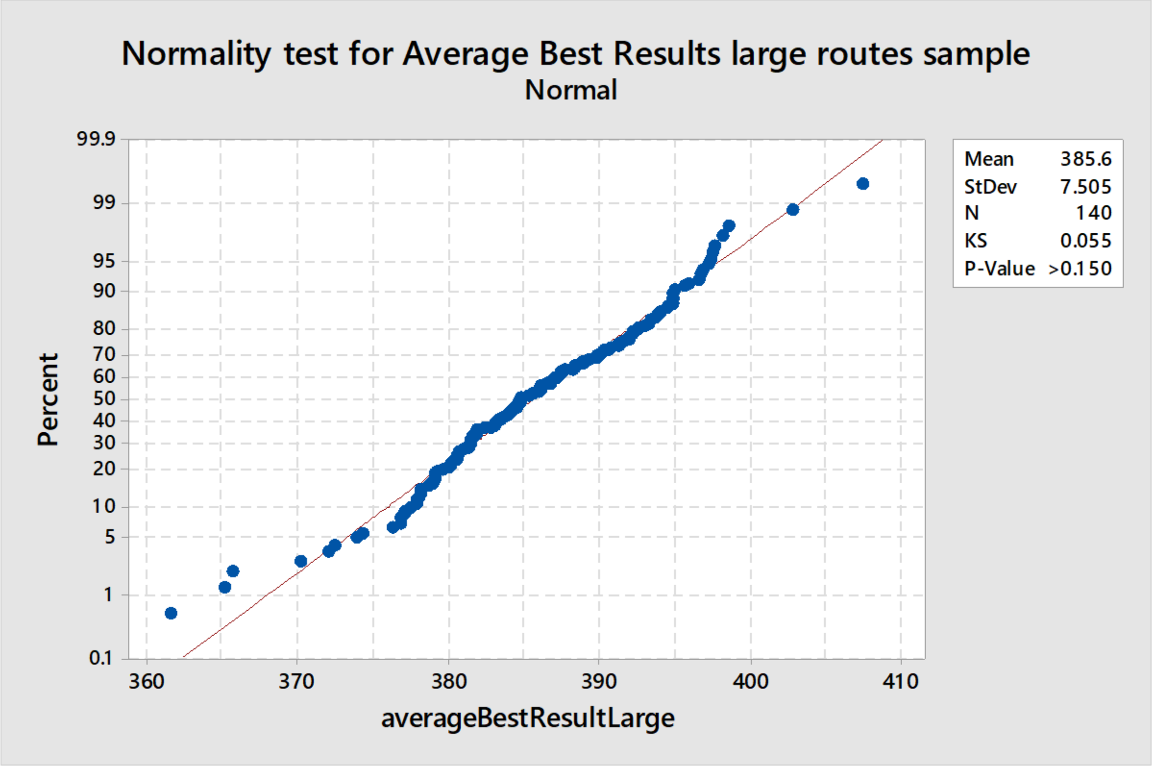

FIGURE 52 KOLMOGOROV-SMIRNOV NORMALITY TEST FOR LARGE ROUTES IN THE SAMPLE

The test shown in Figure 50, Figure 51 and Figure 52 show that the response variable is normally distributed as p>0.01 meaning that parametric statistics can be used and the data will not need to be transformed using techniques such as Box-Cox (Minitab 2018).

Outlier Tests

The data was checked for outliers which are cases which have ‘exceptionally high or low values’ (Janssens, Wijnen, Pelsmacker, Kenhove 2008 p 141), these may be a sign of data entry error (Hinton, Brownlow, McMurray, Cozens 2008) for example, the incorrect input of parameters or results. Such outliers can significantly influence the analysis. Outliers were identified by performing the Grubbs statistical test for all samples (Table 27). This identified no outliers ($p>0.001$)[25].

Sample	N	Mean	StdDev	Min	Max	G	P
Full sample	140	321.33	2.95	311.94	329.94	3.29	0.111
Large Routes	140	385.62	7.5	361.62	407.35	3.2	0.16
Small Routes	140	287.5	1.79	282.49	293.16	3.17	0.178

TABLE 27 GRUBBS OUTLIER TEST FOR THE FULL SAMPLE, LARGE ROUTES IN THE SAMPLE AND SMALL ROUTES IN THE SAMPLE

One purpose of the study is to identify optimal settings for a GA in the given context and to test if changing the parameter settings has a significant effect on the response variable. As such DOE was used to compare the response variable with all categories of experimental settings for example, high mutation and low crossover. Therefore, we need to assess for outliers in the response variable within each category for each sample. To do this each of the experiments was assigned a category based on the crossover and mutation rate for that experiment and the Grubbs test was repeated with it identifying no outliers (Figure 53, Figure 54, Figure 55) for any combined subset & parameter setting category.

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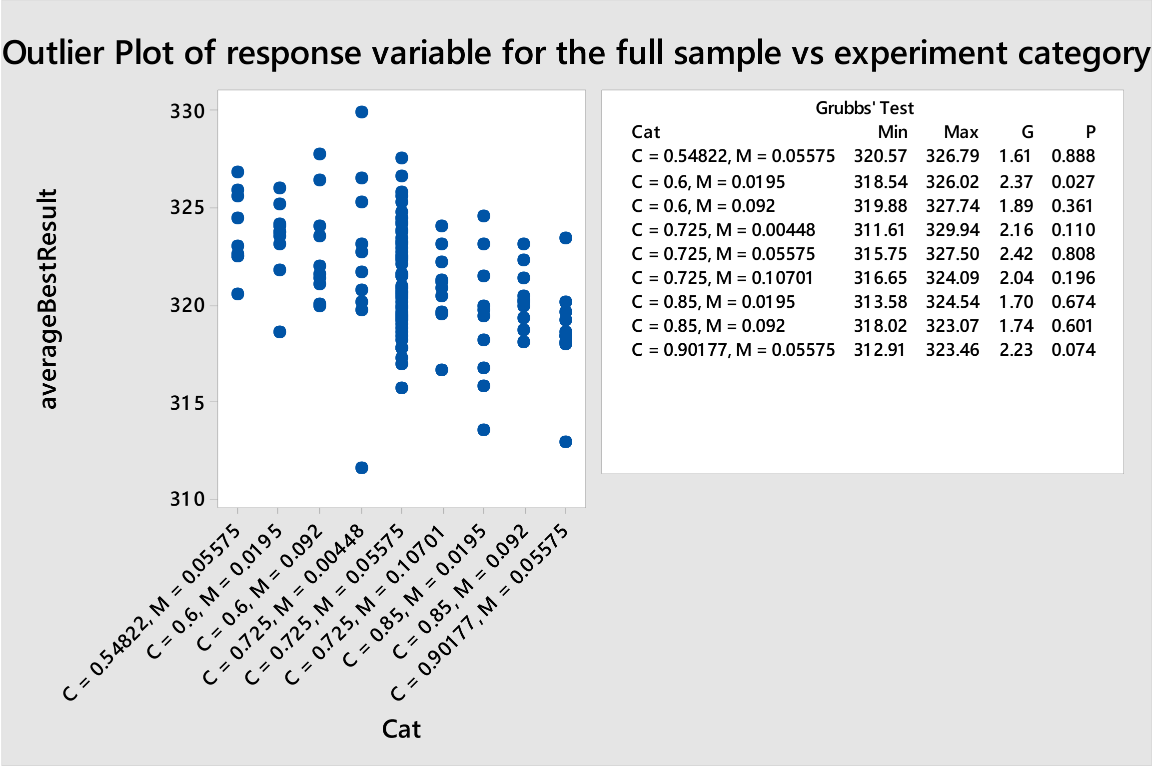
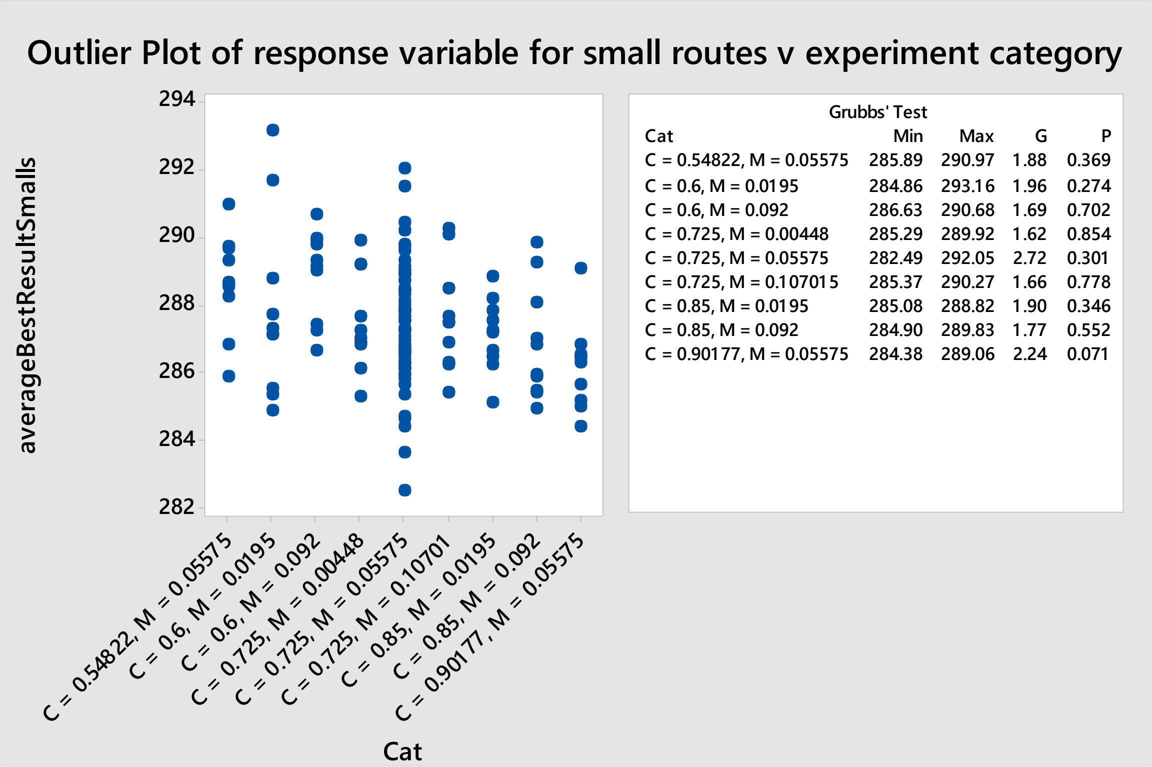
[25] If an outlier had been found the data would have been checked and judgement about the removal of the outlier would have been made. If removed the test would have been repeated to identify other outliers as the Grubbs test only identifies the most extreme outlier. Once all outliers had been removed normality tests would be repeated.



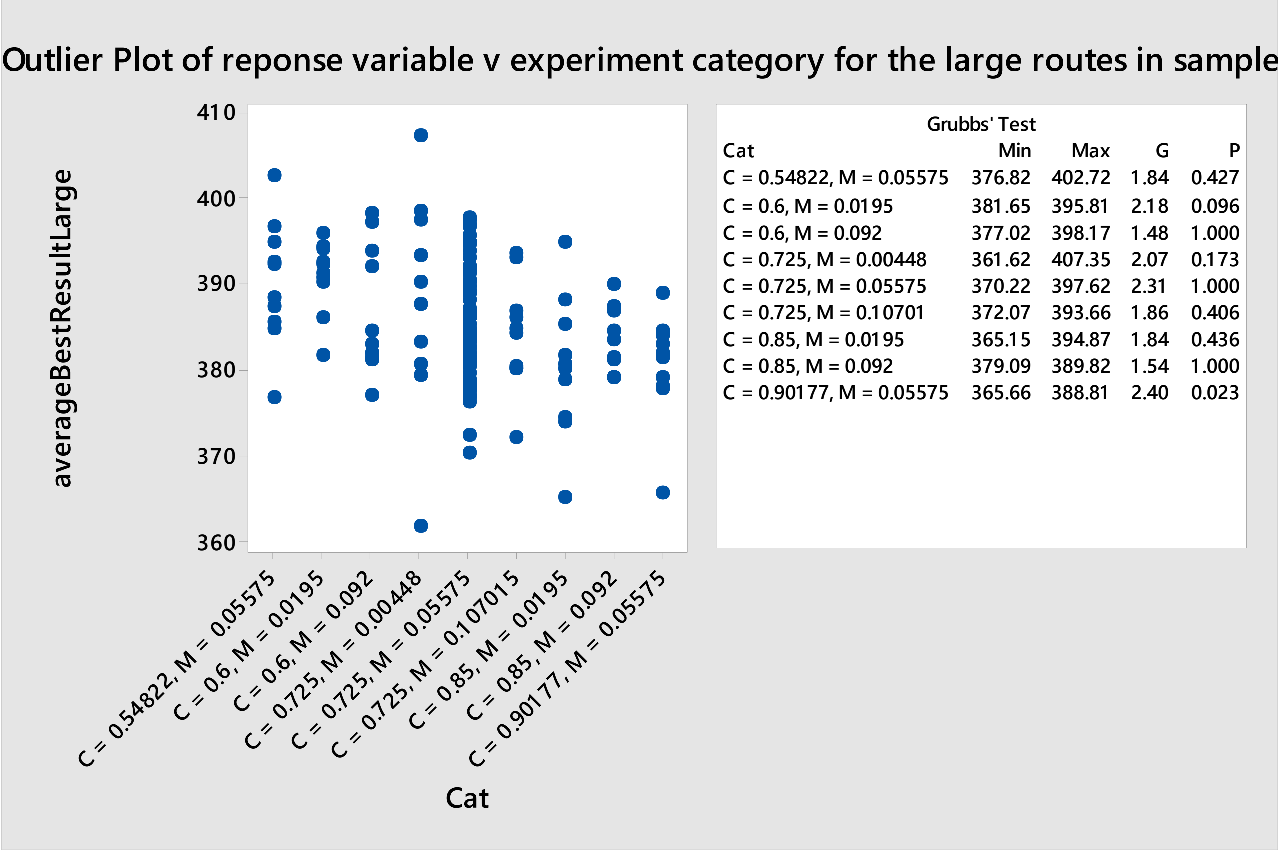
Cat	Min	Max	G	P
C = 0.54822, M = 0.05575	320.57	326.79	1.61	0.888
C = 0.6, M = 0.0195	318.54	326.02	2.37	0.027
C = 0.6, M = 0.092	319.88	327.74	1.89	0.361
C = 0.725, M = 0.00448	311.61	329.94	2.16	0.110
C = 0.725, M = 0.05575	315.75	327.50	2.42	0.808
C = 0.725, M = 0.10701	316.65	324.09	2.04	0.196
C = 0.85, M = 0.0195	313.58	324.54	1.70	0.674
C = 0.85, M = 0.092	318.02	323.07	1.74	0.601
C = 0.90177, M = 0.05575	312.91	323.46	2.23	0.074

FIGURE 53 GRUBBS TEST FOR THE AVERAGE BEST RESULT RESPONSE VARIABLE BY EXPERIMENT TYPE FOR THE FULL SAMPLE



Cat	Min	Max	G	P
C = 0.54822, M = 0.05575	285.89	290.97	1.88	0.369
C = 0.6, M = 0.0195	284.86	293.16	1.96	0.274
C = 0.6, M = 0.092	286.63	290.68	1.69	0.702
C = 0.725, M = 0.00448	285.29	289.92	1.62	0.854
C = 0.725, M = 0.05575	282.49	292.05	2.72	0.301
C = 0.725, M = 0.107015	285.37	290.27	1.66	0.778
C = 0.85, M = 0.0195	285.08	288.82	1.90	0.346
C = 0.85, M = 0.092	284.90	289.83	1.77	0.552
C = 0.90177, M = 0.05575	284.38	289.06	2.24	0.071

FIGURE 54 GRUBBS TEST FOR THE AVERAGE BEST RESULT RESPONSE VARIABLE BY EXPERIMENT TYPE FOR THE SMALL ROUTES IN SAMPLE



Grubbs' Test

Cat	Min	Max	G	P
C = 0.54822, M = 0.05575	376.82	402.72	1.84	0.427
C = 0.6, M = 0.0195	381.65	395.81	2.18	0.096
C = 0.6, M = 0.092	377.02	398.17	1.48	1.000
C = 0.725, M = 0.00448	361.62	407.35	2.07	0.173
C = 0.725, M = 0.05575	370.22	397.62	2.31	1.000
C = 0.725, M = 0.10701	372.07	393.66	1.86	0.406
C = 0.85, M = 0.0195	365.15	394.87	1.84	0.436
C = 0.85, M = 0.092	379.09	389.82	1.54	1.000
C = 0.90177, M = 0.05575	365.66	388.81	2.40	0.023

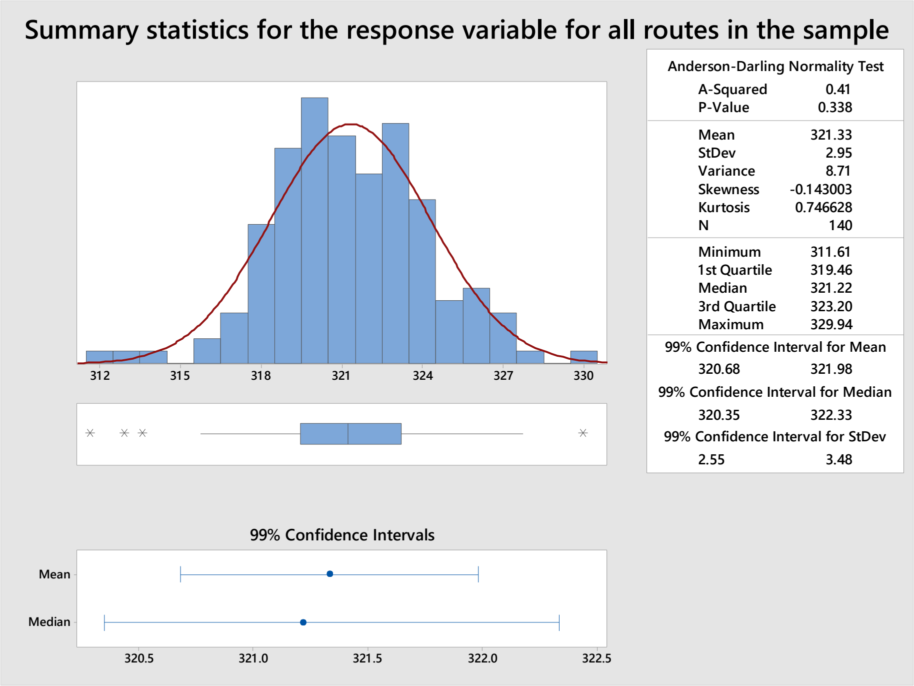
FIGURE 55 GRUBBS TEST FOR THE AVERAGE BEST RESULT RESPONSE VARIABLE BY EXPERIMENT TYPE FOR THE LARGE ROUTES IN SAMPLE

iv. Descriptive Statistics

Response Variable

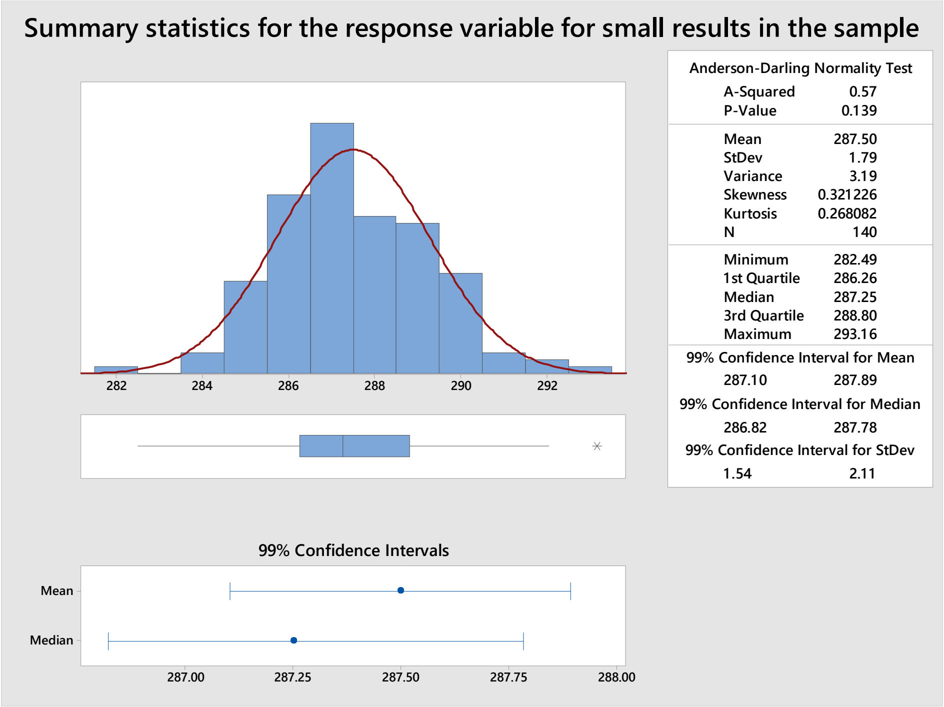
To gain an understanding of the response variable and to understand potential profitable areas of investigation descriptive statistics analysis was undertaken on the three subsets:-

Figure 56 details the descriptive statistics for the response variable across all experiment types for the full sample. It indicates that the results are normally distributed with low levels of kurtosis and skewness, additionally it shows that the range of mean solutions was only 18 miles with a low level of standard deviation (2.95 miles). The small range and low level of standard deviation suggests that with the small route sizes typical in UK logistics parameter settings may make little difference, this analysis was repeated for small and large routes with similar results (Figure 57, Figure 58).


Summary statistics for the response variable for all routes in the sample

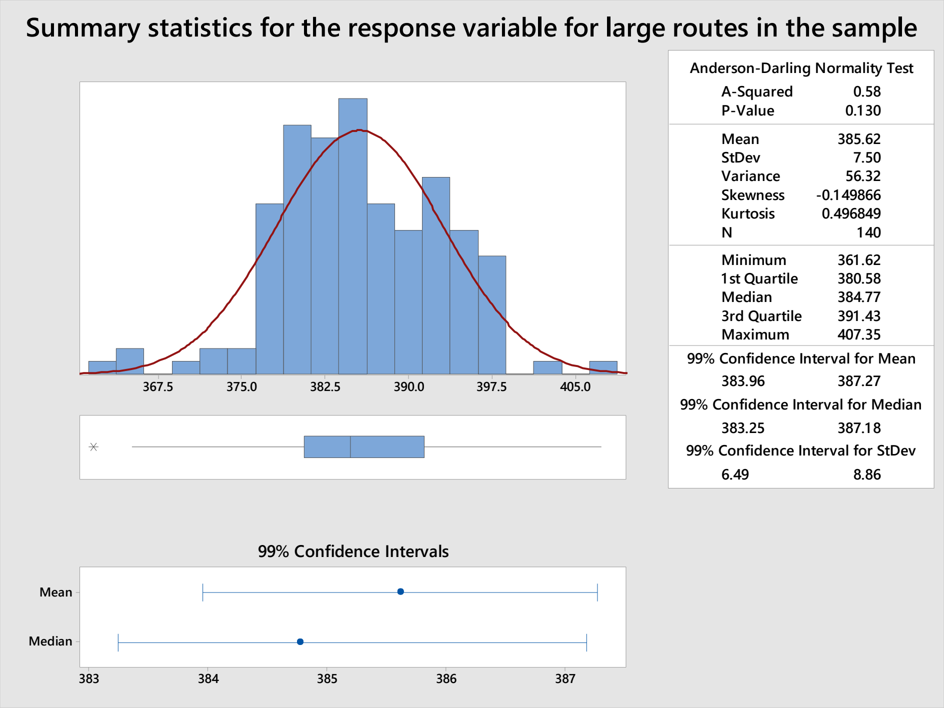
Anderson-Darling Normality Test	
A-Squared	0.41
P-Value	0.338
Mean	321.33
StDev	2.95
Variance	8.71
Skewness	-0.143003
Kurtosis	0.746628
N	140
Minimum	311.61
1st Quartile	319.46
Median	321.22
3rd Quartile	323.20
Maximum	329.94
99% Confidence Interval for Mean	
320.68	321.98
99% Confidence Interval for Median	
320.35	322.33
99% Confidence Interval for StDev	
2.55	3.48

FIGURE 56 DESCRIPTIVE STATISTICS FOR RESPONSE VARIABLE FOR ALL ROUTES IN THE SAMPLE


Summary statistics for the response variable for small results in the sample

Anderson-Darling Normality Test	
A-Squared	0.57
P-Value	0.139
Mean	287.50
StDev	1.79
Variance	3.19
Skewness	0.321226
Kurtosis	0.268082
N	140
Minimum	282.49
1st Quartile	286.26
Median	287.25
3rd Quartile	288.80
Maximum	293.16
99% Confidence Interval for Mean	
287.10	287.89
99% Confidence Interval for Median	
286.82	287.78
99% Confidence Interval for StDev	
1.54	2.11

FIGURE 57 DESCRIPTIVE STATISTICS FOR RESPONSE VARIABLE FOR SMALL ROUTES IN THE SAMPLE



Anderson-Darling Normality Test	
A-Squared	0.58
P-Value	0.130
Mean	385.62
StDev	7.50
Variance	56.32
Skewness	-0.149866
Kurtosis	0.496849
N	140
Minimum	361.62
1st Quartile	380.58
Median	384.77
3rd Quartile	391.43
Maximum	407.35
99% Confidence Interval for Mean	
383.96	387.27
99% Confidence Interval for Median	
383.25	387.18
99% Confidence Interval for StDev	
6.49	8.86

FIGURE 58 DESCRIPTIVE STATISTICS FOR RESPONSE VARIABLE FOR LARGE ROUTES IN THE SAMPLE

Algorithm Process

To gain understanding of the artefact and the operation of the algorithm over multiple generations a number of time series graphs of the experimental results by generation were produced with Table 28 explaining the time series graphs.

Description	Figure	Purpose
Variation of the response variable for each generation for the whole sample	Figure 59	Used to identify the change in the response variable over each generation for the full sample.
Each experimental category for the full sample.	Figure 60	Used to identify the change in the response variable over each generation for the full sample by each category. This approach was used to try and identify differences between parameter settings, if a potential difference was identified it would be subject to statistical analysis.
Each experimental category for the small route sample.	Figure 61	Used to identify the change in the response variable over each generation for the small route subset by each category. This approach was used to try and identify differences between parameter settings and to try and ascertain differences between the operation of the algorithm on different route sizes. If a potential difference was identified it would be subject to statistical analysis.
Each experimental category for the small route sample.	Figure 62	Used to identify the change in the response variable over each generation for the large route subset by each category. This approach was used to try and identify differences between parameter settings and to try and ascertain differences between the operation of the algorithm on different route sizes. If a potential difference was identified it would be subject to statistical analysis.

TABLE 28 EXPLANATION OF THE VARIOUS TIME SERIES GRAPHS AND THEIR PURPOSE

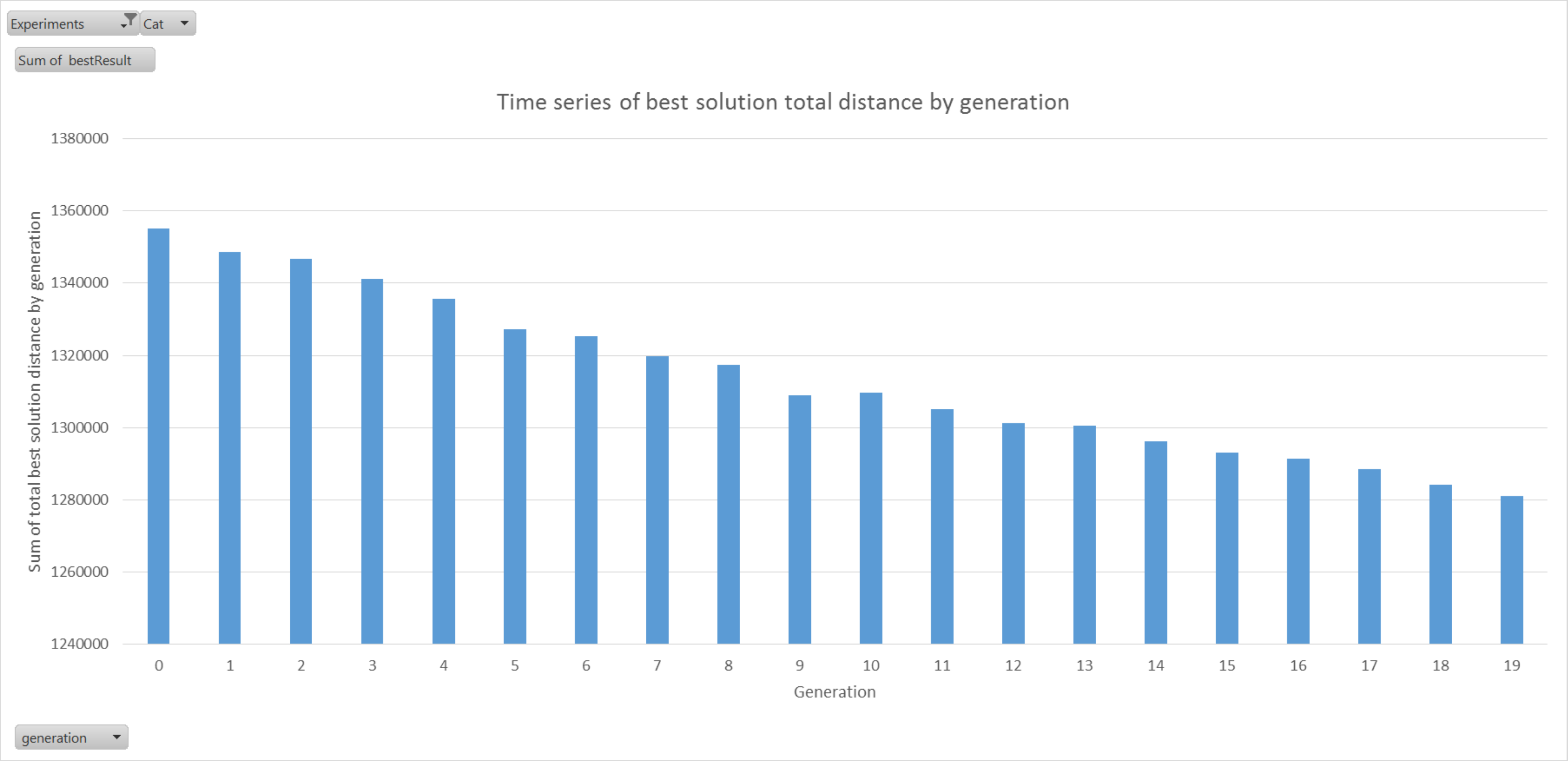


FIGURE 59 TIME SERIES GRAPH OF THE TOTAL DISTANCE OF THE BEST SOLUTION FOR ALL ROUTES AND EXPERIMENTS

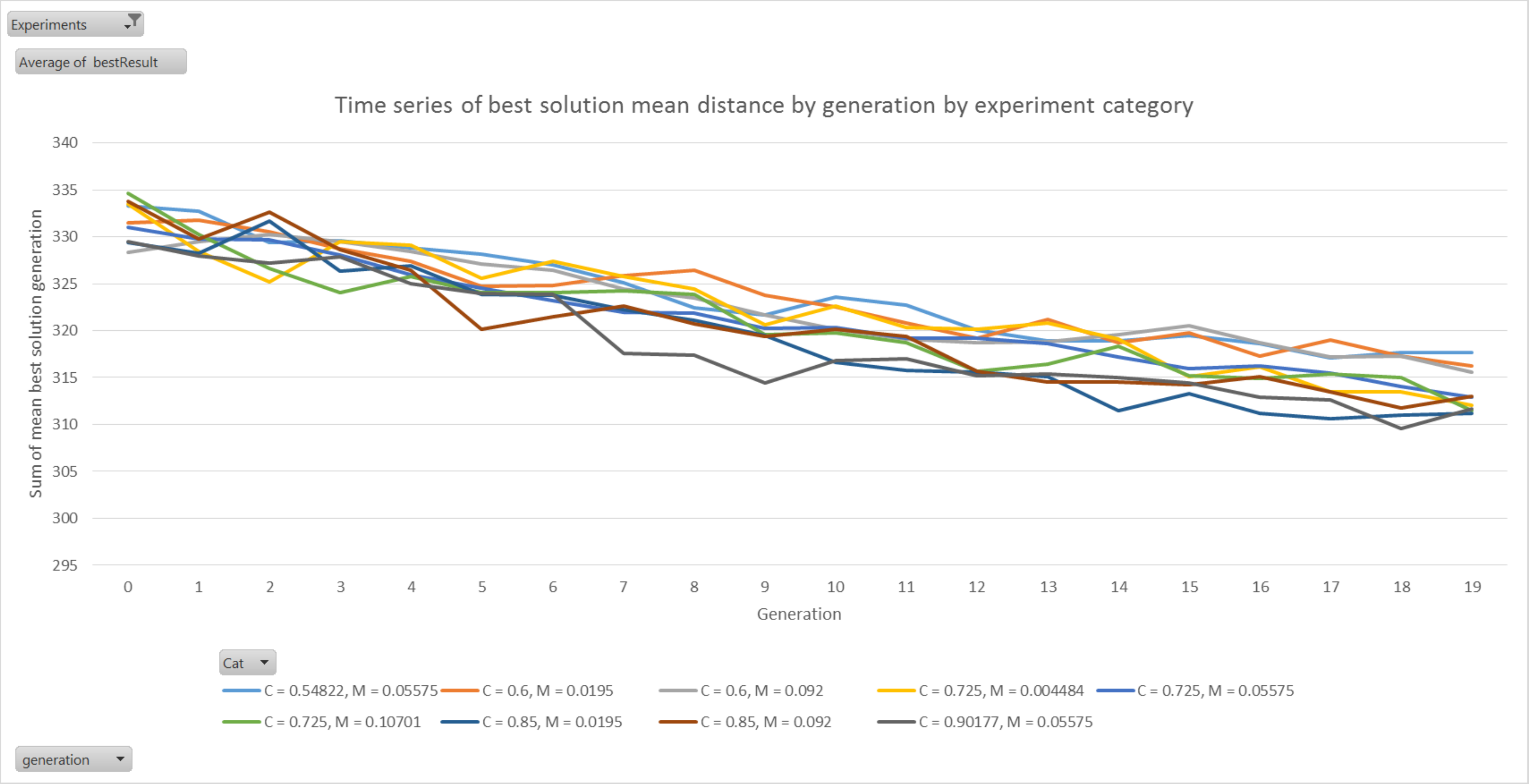


FIGURE 60 TIME SERIES GRAPH SHOWING OF MEAN BEST SOLUTION BY GENERATION FOR EACH EXPERIMENT CATEGORY

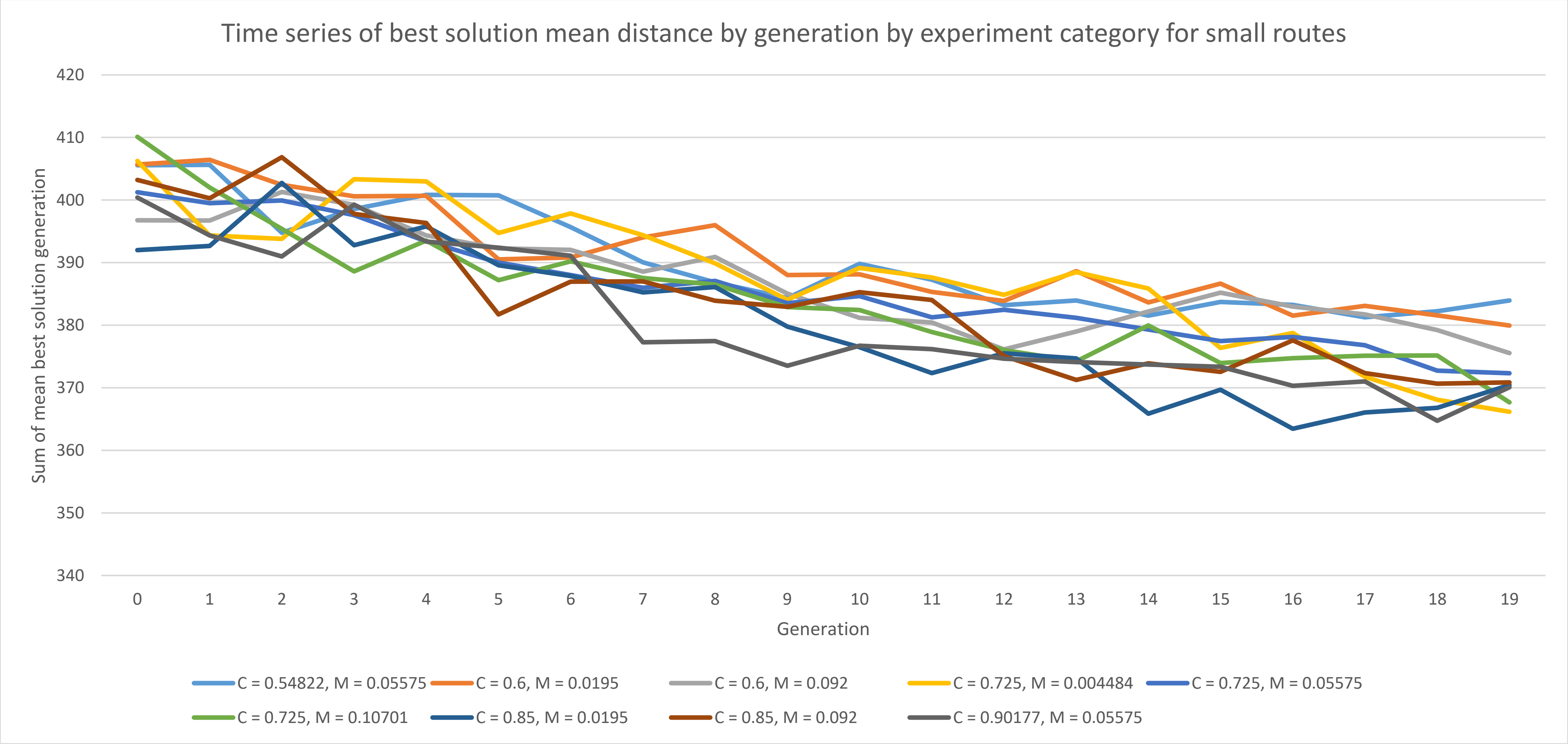


Figure 61 time series graph showing of mean best solution by generation for each experiment category for small routes

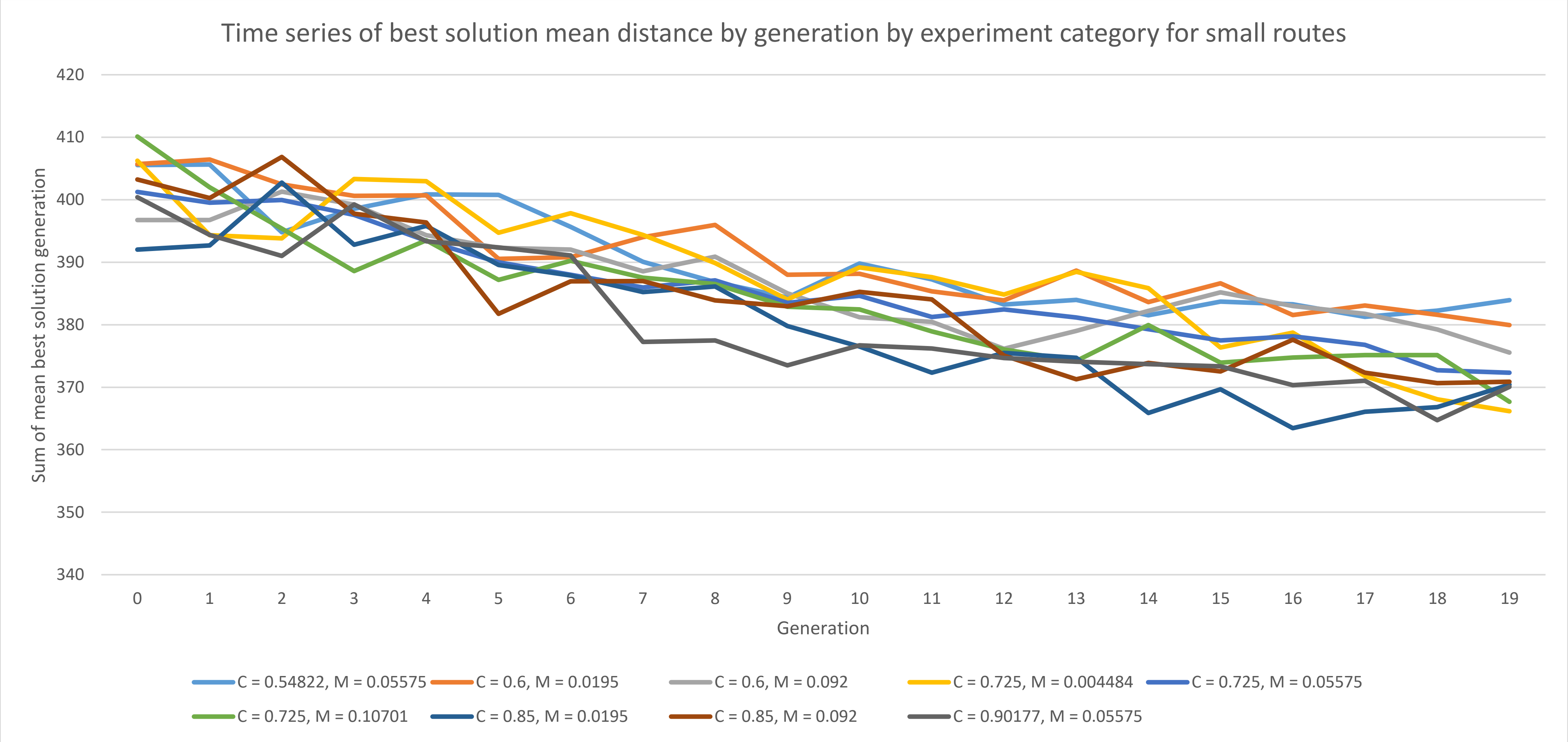


Figure 62 time series graph showing of mean best solution by generation for each experiment category for large routes

The time series graphs indicate that:-

- Improvement occurs throughout the generations of the GA when realistic route sizes are considered showing that selection forces convergence on a solution via ‘genetic drift’ (Liposki, Liposka 2011 p 1);
- Whilst the pooled graph indicates almost constant improvement, when the data is subdivided by experiment setting category it is clear that generation decline is relatively common suggesting that further research is needed on the use of elitism;
- There may to be more variation in best solutions between generations when the routes are larger, this is logical as the larger the number of stops the larger the number of combinations.
-

i. Genetic Algorithm Tuning and hypothesis testing

Introduction

The literature review identified a number of hypotheses to be tested (Table 29), this section and its subsections will detail these hypotheses and utilise statistical tests to reject or accept the null hypotheses. The null hypothesis will be rejected if a significance level of 0.05 is met.

Hypothesis ID	Hypothesis
C1_H0	Crossover level does not have a significant effect on the response variable
C1_H1	Crossover level does have a significant effect on the response variable
M1_H0	No significant interaction exists between crossover and mutation levels
M1_H1	Significant interaction exists between crossover and mutation levels
M2_H0	The relationship between mutation rate and crossover is not non-linear
M2_H1	The relationship between mutation rate and crossover is non-linear
M3_H0	Mutation Level does not have a significant effect on the response variable
M3_H1	Mutation Level does have a significant effect on the response variable
T1_H0	Problem size does not effect the optimum mutation rate
T1_H1	Problem size does effect the optimum mutation rate
T2_H0	Genetic algorithm parameter settings for crossover and mutation do significantly affect the results of a Genetic Algorithm
T2_H1	Genetic algorithm parameter settings for crossover and mutation do not significantly affect the results of a Genetic Algorithm
T3_H0	Problem size does not affect the ideal crossover rate
T3_H1	Problem size does affect the ideal crossover rate
G1_H0	There is no difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning
G1_H1	There is a difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning

TABLE 29 HYPOTHESES TO BE TESTED

Performance of the GA versus the original human planning

When assessing whether it is worthwhile using a GA in an operational context it is important to understand if the GA can outperform human planning due to the intelligence built into the algorithm. To answer this a comparison was undertaken between the original planning and the best solution for each route (Table 30). The analysis visually shows large improvements over the original planning regardless of settings for most routes, this is in contrast to Clarke, Leonardi (2018) who found no improvements in the use of commercial optimisation software over manual planning for their sample company[26].

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[26] The generalisations from Clarke, Leonardi (2018) to this study are limited as we do not know how the algorithms were tuned, additionally as the software is a commercial products we do not know what algorithmic technique(s) they utilise

Route	C = 0.548223, M = 0.05575	C = 0.6, M = 0.0195	C = 0.6, M = 0.092	C = 0.725, M = 0.004484	C = 0.725, M = 0.05575	C = 0.725, M = 0.107015	C = 0.85, M = 0.0195	C = 0.85, M = 0.092	C = 0.90177, M = 0.05575	Grand Total
large	**-2.17%**	**-1.11%**	**0.06%**	**2.56%**	**0.92%**	**2.16%**	**1.42%**	**1.31%**	**1.52%**	**0.81%**
2659	1.75%	0.96%	0.03%	3.11%	2.71%	1.31%	1.00%	4.12%	0.55%	2.07%
2827	-10.98%	-5.86%	-1.93%	-0.62%	-1.80%	-3.61%	0.57%	-0.06%	-0.39%	-2.39%
2845	-25.04%	-18.56%	-23.77%	-14.05%	-18.43%	-15.27%	-19.72%	-22.33%	-18.20%	-19.10%
3251	0.24%	-0.32%	5.39%	7.46%	4.62%	7.43%	4.39%	6.04%	3.38%	4.40%
3619	-13.58%	-10.64%	-13.64%	-14.35%	-14.03%	-14.27%	-8.20%	-15.62%	-9.84%	-13.14%
3651	6.56%	6.70%	6.44%	7.70%	8.18%	7.46%	8.57%	8.38%	9.27%	7.88%
4161	18.92%	19.73%	18.36%	20.27%	19.41%	18.98%	19.80%	21.42%	19.99%	19.57%
4210	-7.14%	-5.60%	-5.33%	-5.10%	-3.67%	-5.39%	-4.50%	-4.49%	-4.01%	-4.54%
4514	-32.91%	-22.94%	-37.50%	-31.71%	-36.91%	-27.35%	-29.80%	-36.38%	-25.62%	-33.21%
5488	4.19%	0.25%	1.09%	2.16%	1.06%	1.54%	2.80%	2.16%	6.65%	1.98%
small	**19.76%**	**19.77%**	**19.40%**	**19.52%**	**20.10%**	**20.02%**	**20.53%**	**19.82%**	**20.30%**	**19.98%**
1031	40.35%	41.57%	40.80%	40.66%	40.91%	42.48%	41.61%	40.22%	40.59%	40.98%
1234	4.68%	3.85%	3.04%	5.33%	3.81%	3.32%	5.26%	4.51%	3.37%	4.01%
2084	20.11%	17.86%	17.94%	18.71%	20.47%	17.54%	20.19%	19.24%	20.36%	19.63%
2649	-0.19%	-0.41%	-0.58%	-0.09%	0.11%	-0.74%	-0.05%	-0.25%	-0.03%	-0.12%
2654	-5.39%	-4.13%	-8.76%	-4.63%	-2.47%	-3.31%	-2.19%	-4.12%	-1.13%	-3.45%
2657	10.56%	10.76%	10.52%	10.52%	10.70%	10.82%	10.92%	10.74%	10.73%	10.70%
2665	3.65%	3.57%	3.59%	3.05%	3.69%	3.06%	3.73%	3.82%	3.63%	3.59%
2667	2.78%	2.48%	2.09%	0.07%	2.57%	3.45%	2.51%	3.03%	3.74%	2.55%
2670	13.92%	12.88%	13.29%	13.20%	13.46%	13.23%	13.53%	14.00%	13.69%	13.47%
2804	2.61%	2.49%	2.39%	2.54%	2.49%	2.36%	2.58%	2.56%	2.39%	2.49%
2815	5.22%	6.16%	5.59%	4.81%	5.71%	5.20%	6.58%	6.25%	6.38%	5.75%
2825	40.16%	40.19%	40.12%	40.25%	40.30%	40.29%	40.25%	40.02%	40.27%	40.24%
2831	3.12%	-0.92%	2.83%	2.60%	2.23%	3.00%	4.27%	4.34%	3.33%	2.57%
2832	0.88%	1.10%	1.18%	1.11%	1.24%	1.13%	1.54%	1.19%	1.41%	1.22%
2844	7.36%	7.04%	7.43%	7.66%	8.66%	7.43%	7.66%	9.14%	9.45%	8.23%
2900	1.25%	1.97%	1.00%	1.67%	1.35%	1.72%	1.93%	2.78%	1.92%	1.60%
3021	37.81%	37.95%	38.54%	38.60%	38.52%	38.97%	39.34%	39.07%	39.06%	38.61%
3948	5.37%	4.72%	2.94%	4.10%	3.85%	4.96%	5.71%	7.25%	5.53%	4.56%
8801	21.51%	22.51%	22.13%	21.42%	21.99%	22.37%	22.50%	21.19%	22.48%	22.01%
Grand Total	**56.38%**	**56.57%**	**56.66%**	**57.14%**	**57.03%**	**57.23%**	**57.26%**	**57.01%**	**57.20%**	**56.98%**

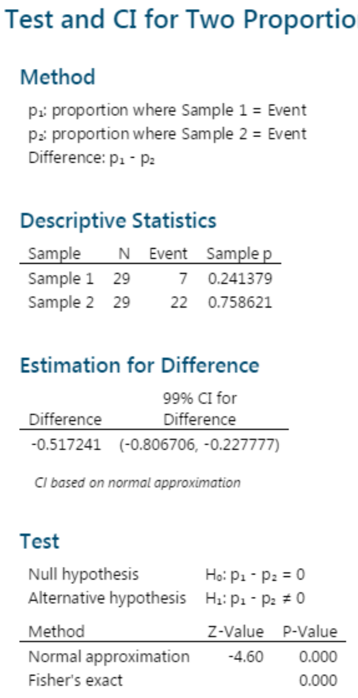
TABLE 30 TABLE SHOWING THE PERCENTAGE DISTANCE REDUCTION BETWEEN ORIGINAL PLANNING RESULT FOR EACH ROUTE AND THE BEST SOLUTION IN THE FINAL GENERATIONS FOR EACH EXPERIMENT [27]

---

[27] Numbers in red indicates that the route generated was on worse than the manual planning

Despite Table 30 indicating that the GA may outperform human planning to understand whether we can generalise these results and reject the null hypothesis that '*There is no difference in the proportion of routes which were shorter using the Genetic Algorithm v manual planning'* statistical testing must be undertaken to ascertain if results to be generalised to the population as a while.

To test if the null can be rejected a proportions test was undertaken comparing the proportion of routes which were planned more effectively by the algorithm with the proportion were human planning was better (Figure 63). As the p value for Fishers exact is less than 0.01 we can declare that the two proportions are different and can conclude that the Genetic algorithm outperforms human planning. However, Table 30 does indicate that the best solution the GA found was consistently worse than the original solution for a number of routes on further investigation these usually had 10 or more stops, unfortunately the reason for this is out of the scope of this study but it could be that these are regular routes which the planners have improved via experience or it could be due to the operation of the algorithm.



```
Test and CI for Two Proportions

 Method
  p₁: proportion where Sample 1 = Event
  p₂: proportion where Sample 2 = Event
  Difference: p₁ - p₂

 Descriptive Statistics
  Sample      N   Event   Sample p
  Sample 1   29       7   0.241379
  Sample 2   29      22   0.758621

 Estimation for Difference
                     99% CI for
  Difference         Difference
  -0.517241   (-0.806706, -0.227777)

   CI based on normal approximation

 Test
  Null hypothesis          H₀: p₁ - p₂ = 0
  Alternative hypothesis   H₁: p₁ - p₂ ≠ 0

  Method                 Z-Value   P-Value
  Normal approximation     -4.60     0.000
  Fisher's exact                     0.000
```

FIGURE 63 PROPORTIONS DIFFERENCE TEST MANUAL PLANNING (SAMPLE 1) V GENETIC ALGORITHM (SAMPLE 2)

The roles of crossover and mutation in a genetic algorithm

Entire Sample

It is the general consensus that it is crossover which is 'major source of the GA's creative power (Mitchel 1995 p 38) (Hameed, Kanbar 2017) (Grefenstalle, Gopal, Rosmaita, Gucht 1985) (Karapetyan 2010). However, this has been challenged by Czarn, MacNish, Vijayan, Turlach, Gupta (2004) and Schaffer,Caruana, Eshalman, Das (1989) who argued that mutation only GA's may work just as well as combined crossover analysis. These opinions led to the hypotheses in Table 31:-

Hypothesis ID	Hypothesis
C1_H0	Crossover level does not have a significant effect on the response variable
C1_H1	Crossover level does have a significant effect on the response variable
M1_H0	No significant interaction exists between crossover and mutation levels
M1_H1	Significant interaction exists between crossover and mutation levels
M2_H0	The relationship between mutation rate and crossover is not non-linear
M2_H1	The relationship between mutation rate and crossover is non-linear
M3_H0	Mutation Level does not have a significant effect on the response variable
M3_H1	Mutation Level does have a significant effect on the response variable

TABLE 31 HYPOTHESES RELATING TO THE ROLES OF CROSSOVER AND MUTATION

To answer these hypotheses a response surface regression analysis was performed on the full sample. The analysis showed that crossover rate had the largest impact on the response variable and that this was the only statistically significant interaction of the modelled variables, this is shown in the Pareto chart in Figure 64 with the length of the bars showing the strength of the interaction and the dotted line at 2.613 indicating the line of statistical significance.

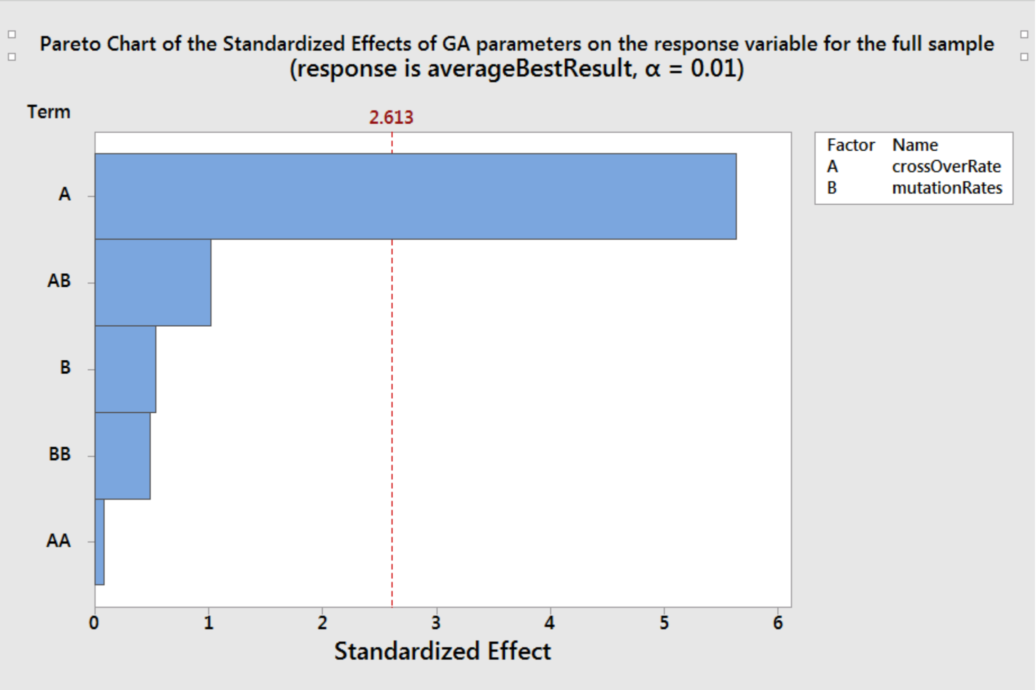


FIGURE 64 PARETO CHART OF THE STANDARDISED EFFECTS OF PARAMETER SETTINGS ON THE FULL SAMPLE

The findings in Figure 64 are expanded in the analysis in Figure 65 this confirms that only crossover rate has a statistically significant effect on the response variable and that the interaction between crossover and mutation rate is not significant (p>0.935) this means that:-

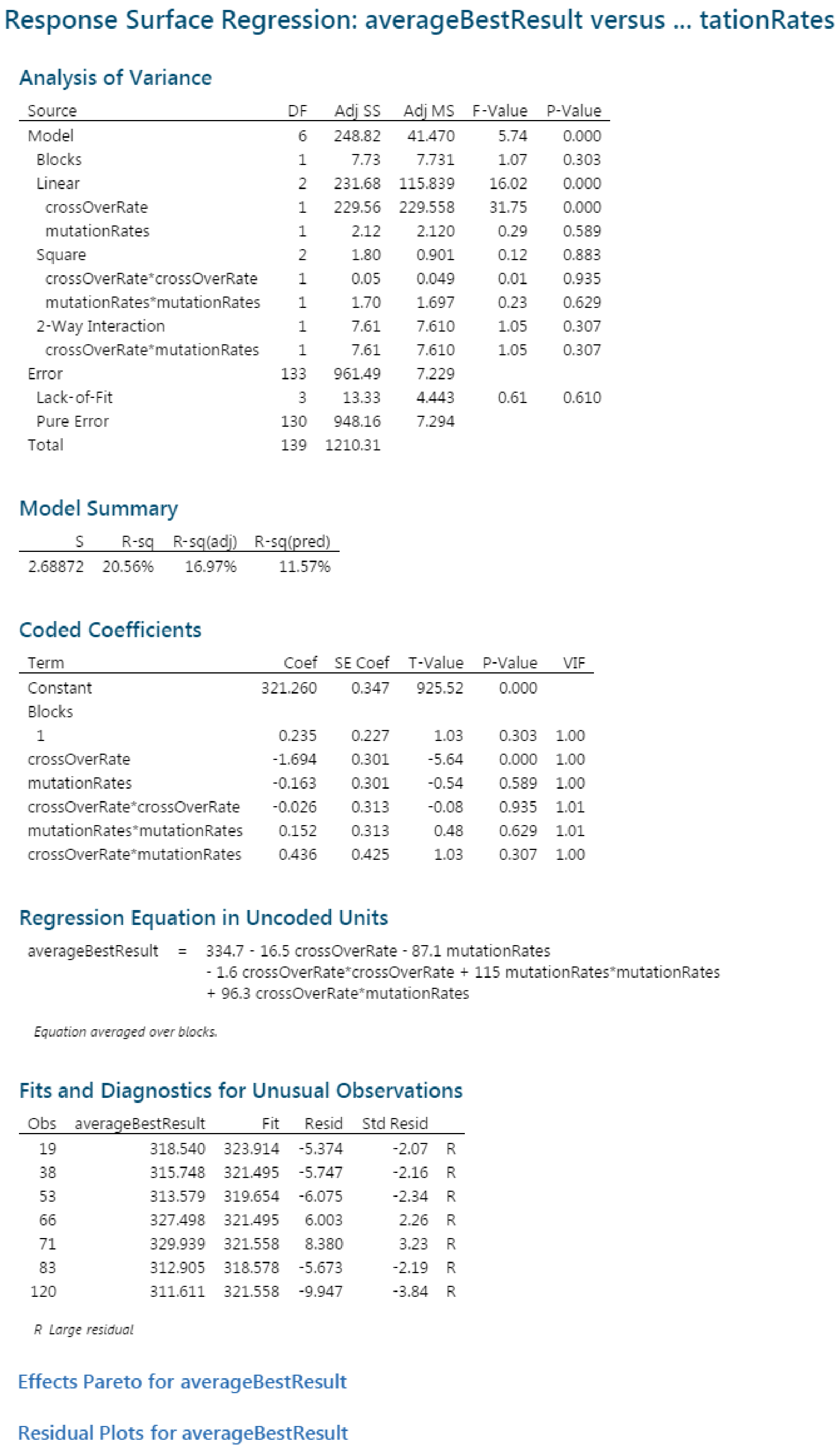
- we cannot reject the null hypothesis M1_H0 that there is no significant interaction between the crossover rate and the mutation rate;
- We cannot reject the null hypothesis M2_H0 that the relationship between crossover and mutation rate is not non-linear as the squared terms value is not significant;
- We cannot reject the null hypothesis that M3_H0 that mutation does not have a significant effect on the response variable;
- We can reject the null hypothesis C1_H0 as crossover does have a significant effect on the response variable.

The developed regression model was checked to ensure that the techniques used were appropriate[28] (Figure 66) but despite appropriateness the regression model has little explanatory power with its R2 value showing that it explained just 20.56% of response variable behaviour suggesting that non-modelled variables may play a large role in the performance of the GA, therefore a further regression model was developed using only the statistically significant terms this was a marginally better fit but still left a large amount of unexplained variance (Appendix Two – Crossover Only Regression Model, Figure 70).

Despite poor explanatory performance the model enables the production of the response surface diagrams in Figure 67 which can be used for tuning the GA. The diagram indicates that the best results would be gained by using a crossover rate of 0.9 and a mutation rate of almost 0.00 these recommendations correspond to the findings of Malhotra, Singh (2011) who proposed a crossover range of 0.85 to 0.95, and Schaffer, Caruana, Eshelman, Das (1989) who proposed arrange of 0.75 to 0.95 and with findings that a very low mutation rate is best (Malhotra, Singh 2011). The identification of optimal settings confirms that a DOE approach can be utilised to tune a GA whilst further endorses the critical role of crossover (Hameed, Kanbar 2017) (Grefentalle, Gopal, Rosmaita, Gucht 1985) (Karapetyan 2010).

---

[28] The residuals are randomly distributed and have constant variance (residuals versus fit plot Figure 66), are normally distributed as they follow a straight line on the normal probability plot (Figure 66) and do not follow a pattern (residuals versus order Figure 66)



Response Surface Regression: averageBestResult versus ... tationRates

Analysis of Variance

```
Source                          DF   Adj SS   Adj MS  F-Value  P-Value
Model                            6   248.82   41.470     5.74    0.000
  Blocks                         1     7.73    7.731     1.07    0.303
  Linear                         2   231.68  115.839    16.02    0.000
    crossOverRate                1   229.56  229.558    31.75    0.000
    mutationRates                1     2.12    2.120     0.29    0.589
  Square                         2     1.80    0.901     0.12    0.883
    crossOverRate*crossOverRate  1     0.05    0.049     0.01    0.935
    mutationRates*mutationRates  1     1.70    1.697     0.23    0.629
  2-Way Interaction              1     7.61    7.610     1.05    0.307
    crossOverRate*mutationRates  1     7.61    7.610     1.05    0.307
Error                          133   961.49    7.229
  Lack-of-Fit                    3    13.33    4.443     0.61    0.610
  Pure Error                   130   948.16    7.294
Total                          139  1210.31
```

Model Summary

```
      S    R-sq  R-sq(adj)  R-sq(pred)
2.68872  20.56%     16.97%      11.57%
```

Coded Coefficients

```
Term                            Coef  SE Coef  T-Value  P-Value   VIF
Constant                     321.260    0.347   925.52    0.000
Blocks
  1                            0.235    0.227     1.03    0.303  1.00
crossOverRate                 -1.694    0.301    -5.64    0.000  1.00
mutationRates                 -0.163    0.301    -0.54    0.589  1.00
crossOverRate*crossOverRate   -0.026    0.313    -0.08    0.935  1.01
mutationRates*mutationRates    0.152    0.313     0.48    0.629  1.01
crossOverRate*mutationRates    0.436    0.425     1.03    0.307  1.00
```

Regression Equation in Uncoded Units

```
averageBestResult  =  334.7 - 16.5 crossOverRate - 87.1 mutationRates
                      - 1.6 crossOverRate*crossOverRate + 115 mutationRates*mutationRates
                      + 96.3 crossOverRate*mutationRates
```

Equation averaged over blocks.

Fits and Diagnostics for Unusual Observations

```
Obs  averageBestResult      Fit   Resid  Std Resid
 19            318.540  323.914  -5.374      -2.07  R
 38            315.748  321.495  -5.747      -2.16  R
 53            313.579  319.654  -6.075      -2.34  R
 66            327.498  321.495   6.003       2.26  R
 71            329.939  321.558   8.380       3.23  R
 83            312.905  318.578  -5.673      -2.19  R
120            311.611  321.558  -9.947      -3.84  R
```

R Large residual

Effects Pareto for averageBestResult

Residual Plots for averageBestResult

FIGURE 65 RESULTS OF THE RESPONSE SURFACE REGRESSION ANALYSIS FOR THE FULL SAMPLE

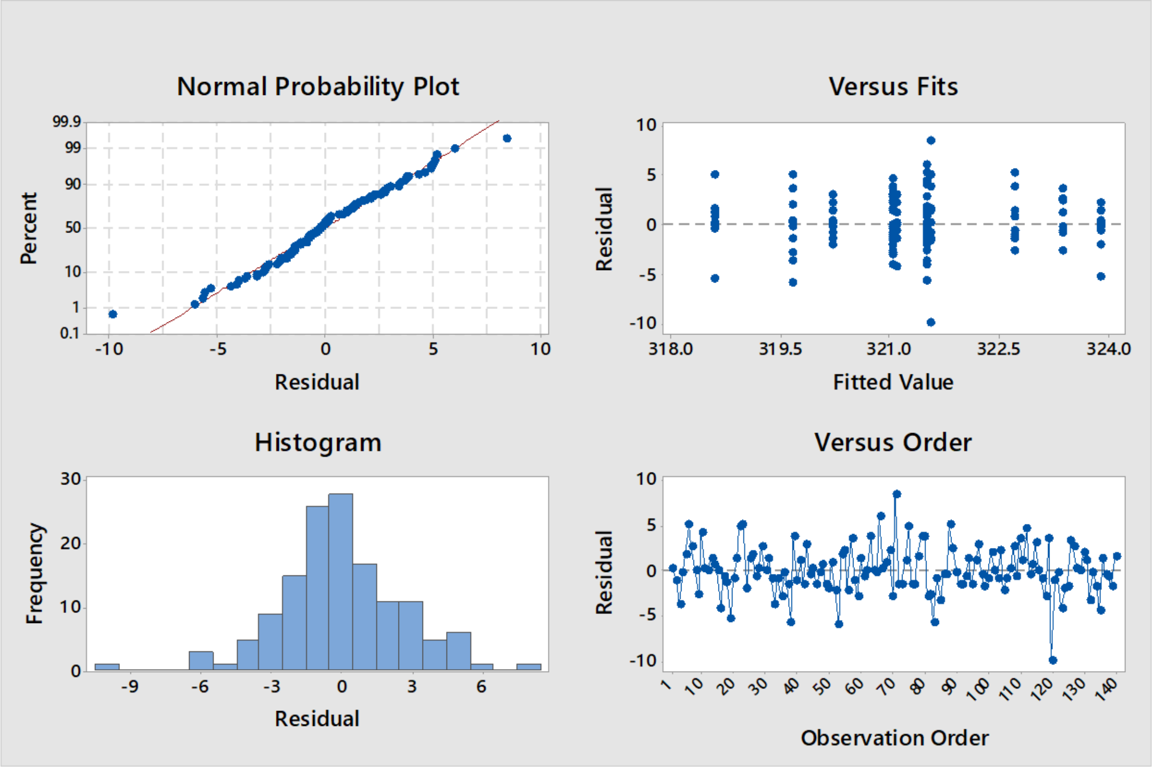


FIGURE 66 RESIDUALS PLOT AND ANALYSIS

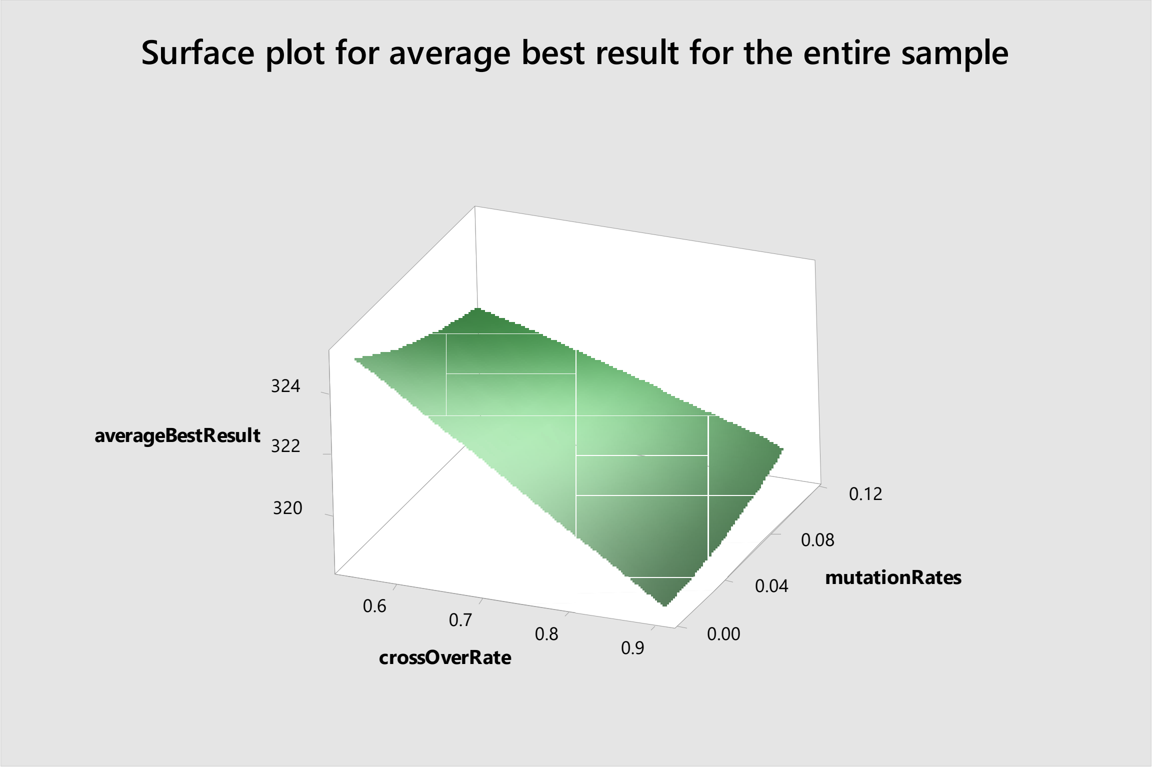


FIGURE 67 RESPONSE SURFACE PLOT OF THE RESPONSE FACTOR FOR THE ENTIRE SAMPLE

Subsamples

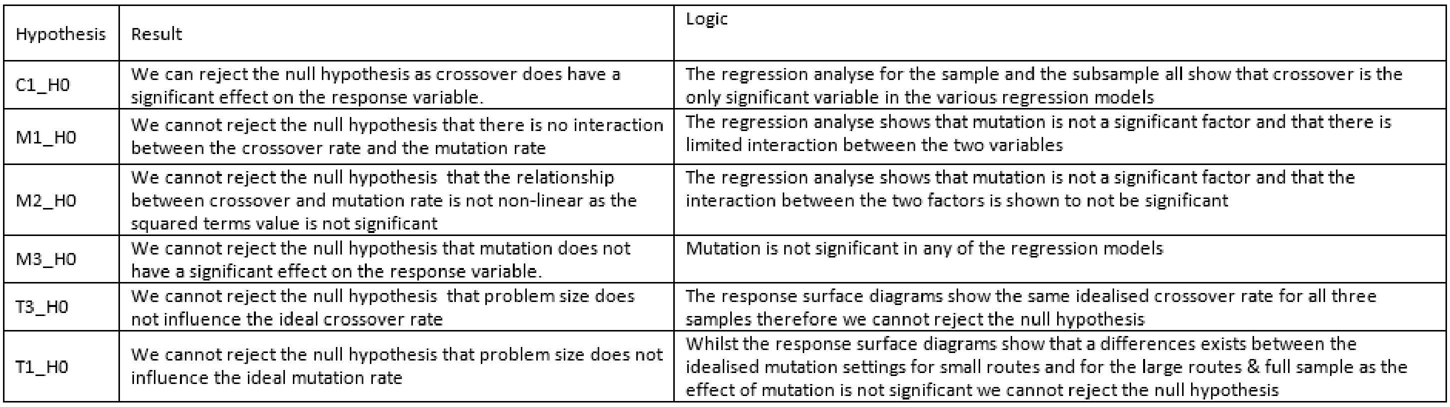
The possibility exists that the relationships between crossover, mutation and the response variable and the optimal settings differ for problems of different sizes and that hypotheses which were not true for the entire sample may be true for sub-samples of small or large routes. To test this separate analyses were performed for the small and large routes in the sample, the results of these analyses show that:-

- Crossover is the only significant modelled factor in explaining the response variable for both small (appendix three - Figure 73) and large routes (appendix four - Figure 78) therefore a crossover only models were developed (Figure 76, Figure 81).
- The developed regression models are a poor explanation of the response variable with the full regression model for small routes explaining just 12.99% of the response (R2), with the crossover only model only explaining 10.1% (adjusted R squared)(appendix three - Figure 73). Similar results were found for the larger routes with the regression model explaining only 14.80% of the response (R2) with the crossover only regression model only explaining 11.14% of the response (adjusted R squared)(appendix four - Figure 78), furthermore all of the models had poor predictive quality;
- The response surface diagrams indicates that for small routes the ideal crossover rate is 0.9 and mutation rate is 0.12 (appendix three - Figure 75) this differs from the idealised settings of 0.9 crossover and almost 0.00 mutation found for both the full sample and the large routes subsample (appendix four - Figure 80). The difference between the ideal settings for a TSP Genetic Algorithm for routes of different sizes show that the ideal settings depend at least partly on problem size[29] and that DOE is an appropriate method for identifying such differences;

This section has developed regression models which explain how the response variable react to parameter changes and has identified idealised settings for routes of different sizes. In doing so it has allowed the testing of the hypotheses in Table 32.

---

[29] The effect of mutation is not significant



Hypothesis	Result	Logic
C1_H0	We can reject the null hypothesis as crossover does have a significant effect on the response variable.	The regression analyse for the sample and the subsample all show that crossover is the only significant variable in the various regression models
M1_H0	We cannot reject the null hypothesis that there is no interaction between the crossover rate and the mutation rate	The regression analyse shows that mutation is not a significant factor and that there is limited interaction between the two variables
M2_H0	We cannot reject the null hypothesis that the relationship between crossover and mutation rate is not non-linear as the squared terms value is not significant	The regression analyse shows that mutation is not a significant factor and that the interaction between the two factors is shown to not be significant
M3_H0	We cannot reject the null hypothesis that mutation does not have a significant effect on the response variable.	Mutation is not significant in any of the regression models
T3_H0	We cannot reject the null hypothesis that problem size does not influence the ideal crossover rate	The response surface diagrams show the same idealised crossover rate for all three samples therefore we cannot reject the null hypothesis
T1_H0	We cannot reject the null hypothesis that problem size does not influence the ideal mutation rate	Whilst the response surface diagrams show that a differences exists between the idealised mutation settings for small routes and for the large routes & full sample as the effect of mutation is not significant we cannot reject the null hypothesis

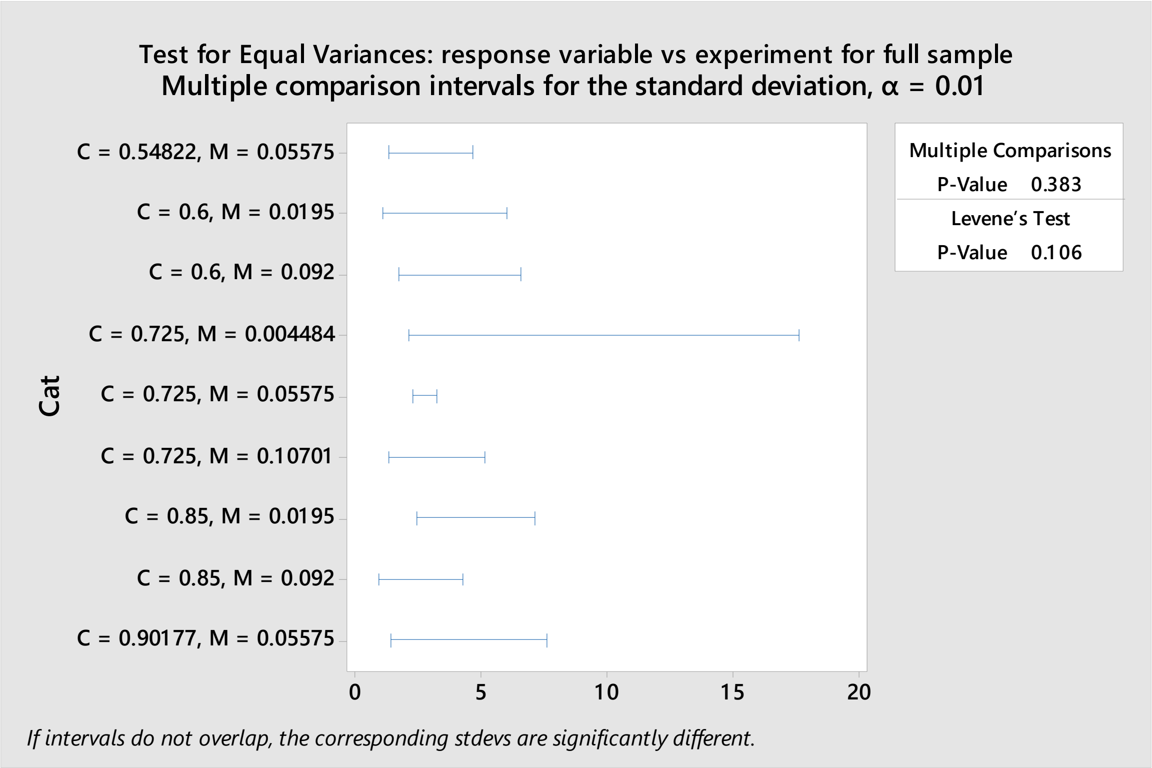
TABLE 32 SUMMARY OF HYPOTHESIS RESULTS FOR THIS SECTION

Genetic Algorithm Parameter Settings significantly affect the response variable

Hypothesis T2_H0 is the null hypothesis that genetic algorithm parameter settings for crossover and mutation do not significantly affect the results of a Genetic Algorithm. To test this hypothesis one way analysis of variance was utilised to assess whether the mean results gathered at each combination of mutation and crossover rate were significantly different. As one way analysis of variance assumes equal variances Levene's test was performed. This identified that the data was suitable for one way Anova analysis utilising Tukey's method $(p>0.01)$[30](Minitab 2018) (Figure 68)

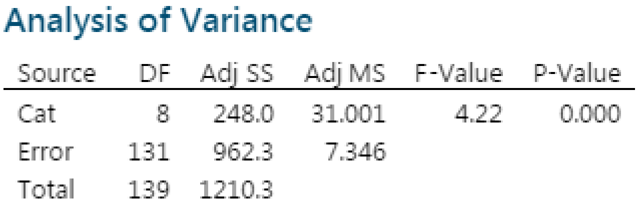
---

[30] Levenes' test is a statistical test which assesses if two samples or subsets have equal variance, it tests the null hypothesis that none of the samples have statistically different variance therefore a p value of over 0.001 would mean that there are differences in the variances of the subgroups or samples.



If intervals do not overlap, the corresponding stdevs are significantly different.

FIGURE 68 LEVENE'S TEST FOR EQUAL VARIANCES FOR THE FULL SAMPLE



Analysis of Variance

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Cat	8	248.0	31.001	4.22	0.000
Error	131	962.3	7.346		
Total	139	1210.3			

FIGURE 69 ONE WAY ANOVA UTILISING TUKEY'S METHOD FOR THE FULL SAMPLE

As the p value in Figure 69 is less than 0.001 we can reject the null hypothesis T2_H0 therefore parameter settings do influence the results of a genetic algorithm meaning that tuning can make a difference. However, Figure 69 does not identify which parameter settings cause different results. This is remedied by Table 33 which identifies that whilst the means are not equal there are significant overlaps between the parameter settings with the only significant differences being between ID1 and ID2 and ID9 and between ID8 and ID1 and ID2.

Grouping Information Using the Tukey Method and 95% Confidence

ID	Cat	N	Mean	StDev	99% CI	Grouping		
1	C = 0.54822, M = 0.05575	10	323.648	1.953	(321.407, 325.888)	A		
2	C = 0.6, M = 0.0195	10	323.379	2.039	(321.138, 325.619)	A		
3	C = 0.6, M = 0.092	10	322.747	2.642	(320.507, 324.987)	A	B	
4	C = 0.725, M = 0.00448	10	322.15	4.88	(319.91, 324.39)	A	B	C
5	C = 0.725, M = 0.05575	60	321.26	2.58	(320.345, 322.175)	A	B	C
6	C = 0.725, M = 0.10701	10	320.885	2.076	(318.645, 323.126)	A	B	C
7	C = 0.85, M = 0.0195	10	319.25	3.33	(317.01, 321.49)	A	B	C
8	C = 0.85, M = 0.092	10	320.36	1.557	(318.120, 322.600)		B	C
9	C = 0.90177, M = 0.05575	10	318.675	2.59	(316.435, 320.915)			C

Pooled StDev = 2.71031

Means that do not share a letter are significantly different.

TABLE 33 GROUPING INFORMATION USING TUKEY'S METHOD FOR THE FULL SAMPLE

This analysis was repeated for:-

- small routes - the results were similar P<0.05 with difference existing between groups which have crossover values at the extreme of the DOE design (see Appendix five – Do parameter settings affect the response variable for small routes)
- large routes - as Levene's test showed that variances between the means were not equal, meaning that Welch's Anova test was used. This identified that experiment settings do affect the response variable but it was not able to identify which groups were different (Appendix Six – Do parameter settings affect the response variable for large routes)

This section has analysed whether parameter settings significantly affect the response variable with it identifying that they do for the full sample and the sub samples therefore the null hypothesis T2_H0 can be rejected. However the differences between the results are small (range of 318.675 to 324.648 between the best and worst solutions which is a difference of 5.973 or 1.8%) suggesting the importance of tuning for the smaller TSP problems which are typical within a TSP may have been overstated and potentially disproving Smit (2012) who found that tuning was worthwhile when the algorithms were used to solve the same types of problems frequently.

ii. Summary

This section has confirmed that DOE can be utilised to tune a GA by demonstrating how it can be used for finding idealised settings for samples of various route sizes. In doing so it has developed and documented a repeatable methodology which can be used by other researchers or practitioners to tune their GAs. As a result of the experimentation process it has been discovered that mutation does not play a statistically significant role in the workings of the developed Genetic Algorithm either directly (M3_H0) or via interaction with crossover (M1_H0, M2_H0) when used to solve realistically sized UK TSPs. This is in conflict with the findings of Rexhepi, Maxhuni, Dika (2013) who found that mutation played an important role when initial populations are small and Shaffer and Eshelman (1991) and Tate and Smith (1993) who all found that mutation plays a larger role than usually thought and with Shaffer, Caruana, Eshelman and Das (1999) and Pinel, Danoy, Bouvrey (2011) who found a non-linear relationship between mutation and crossover. In doing so it agrees with the findings of Hameed, Kanbar (2017) Grefenstalle, Gopal, Rosmaita, Gucht (1985) and (Karapetyan 2010) who found that it was crossover which gives the Genetic Algorithm its 'creative power' (Mitchel 1995 p 38).

However, whilst the study provided valuable information on the working and tuning of a Genetic Algorithm and showed that a GA can outperform human planning (G1_H0) the effect of the tuning, although significant, was small suggesting that tuning may not be necessary for the small route sizes typical in UK logistics and that companies could use the values recommended in the literature. Furthermore the developed regression models had very poor explanatory power, this suggests that an un-modelled variable may exert significant influence over the workings of the GA. Without conducting additional experimentation it is not possible to state which variable this is however deduction suggests that it is the initial random population as this was the only non-modelled variable which was not held constant. Such a finding, if confirmed, would contradict Pinel, Danoy, Bouvrey's (2011) who argued that the initial population played only a small role in GA performance. The potential large influence of the initial population on the performance of the algorithm is possibly because the small route size means that a higher proportion of good building blocks exist in the initial population than in studies which use larger TSP problems. This means that crossover and mutation play smaller role.

The next section outlines the contributions of the research, highlights the limitations and makes recommendations for future research.

5. Conclusions

iii. Contributions

Table 34 details the research aims of this study, the section of the contributions subsection they are discussed in and gives an overview of the success of the study in meeting that aim, each aim is then discussed in the relevant section.

No.	Aim	Section Heading	Aim achieved?
1	Develop a GA which can be used for solving TSP problems	Algorithm tuning methodology	Yes, a Genetic algorithm was developed which is capable of solving TSP problems
2	Illustrate how parameter values influence the performance of GA	Algorithm tuning methodology	The study has demonstrated that it is crossover which is the major studied parameter in GA performance (Figure 66) and that a high level of crossover is ideal (Figure 68)
3	Understand how parameter values interact to influence the performance of a GA	Relationships between parameters	The study found no significant linear or nonlinear interaction between crossover and mutation (Figure 66).
4	Provide guidance on the optimum levels to set various GA factors for UK Logistics TSPs	Algorithm tuning methodology	The study found that a high level of crossover (90%) is ideal regardless of the TSP problem size (Figure 68)
5	Provide a methodology for tuning TSP Genetic Algorithms	Algorithm tuning methodology	The study has demonstrated and developed a DOE method for tuning a GA.
6	Demonstrate that a GA algorithm will outperform human transport planning.	Performance of GA v human planning	The developed algorithm outperformed original human planning.

TABLE 34 STUDY AIMS

The study has achieved all of its aims, the following sections summarise the study contributions.

Algorithm tuning methodology

This study has developed a Genetic Algorithm for solving TSP problems and a DOE based methodology for tuning a GA. The developed GA has tested and tuned by the developed methodology using data from a sample UK logistics company. In doing so it has shown that DOE is an appropriate approach for tuning a GA, therefore confirming the findings of Ridge (2007) and Coy, Golden, Runger, Wasil (2000), as it allowed the identification of:-

- optimum parameter settings for various TSP problem sizes with it discovering that a very high rate of crossover of 0.90 is appropriate for routes of all studied sizes, whilst mutation plays no significant role (Figure 65, Figure 73, Figure 78), this recommended rate of crossover is much higher than De Jong's 1975 recommendation of 0.60 (Luke 2015);
- a repeatable experiment design with clear guidelines;
- interaction between the various parameters in a time efficient way (Figure 65, Figure 73, Figure 78).

The identification of DOE as a valid and appropriate method of GA tuning is a valuable contribution as it is repeatable by other researchers, is time efficient and it forces the experimenter to use a well-designed experiment, with the lack of a well-defined repeatable experimental strategy being a major problem within previous parameter tuning experiments (Pongcharoen, Chainate, Thapatsuwan 2006).

Performance of GA v human planning

The analysis showed that GAs consistently outperform human planning for the relatively small TSP problems typical in UK logistics (Figure 63) (FBP 2007). Therefore a relatively simplistic GA can outperform human planning, this is an important finding as no previous study has compared human planning of a UK logistics TSP with a GA and whilst route optimisation is used by many large logistics providers it is often too expensive for small to medium enterprises (Clarke, Leonardi 2018).

Importance of tuning

The analysis identified that whilst tuning does improve performance the improvements are not huge (Figure 56, Figure 57, Figure 58) suggesting that the expense of tuning a GA for UK logistics TSP problems may not be necessary and that companies could use the values in the literature as such it is counter to the findings of Smit (2012) that the investment in tuning is worthwhile for repeating problems.

Relationships between parameters

The study confirmed the findings of Hameed, Kanbar (2017) Grefenstalle, Gopal, Rosmaita, Gucht (1985) and (Karapetyan 2010) that it is crossover that plays the central role within a GA but found that mutation played no significant role in determining the response variable either directly or via interaction with crossover (Figure 65, Figure 73, Figure 78) therefore contradicting the findings of Shaffer, Caruana, Eshelman and Das (1999), Pinel, Danoy, Bouvrey (2011), Shaffer, Eshelman (1991) and Tate. Smith (1993).

Context

This is the first GA TSP study which has examined UK logistics TSPs this is a valuable contribution due to the importance of the logistics industry (Table 4) and the juxtaposition of the small route sizes typical in this industry with the test suites usually used to tune TSP GA which would be impossible in reality due to driver time constraints (Great Britain 2016).

iv. Limitations

This study suffers from a number of limitations, these are:-

- The sample routes come from a single company and although these have been compared to publically available statistics it is not possible to be certain that they are representative;
- The study makes justifiable judgements on which techniques of encoding, crossover , mutation and selection should be used, if other judgements had been made the results may be different;
- The study only models the effect of two parameters, furthermore the regression models built around these factors have poor explanatory value suggesting that non modelled factors may be more important (Figure 65, Figure 73, Figure 78).

v. Recommendations for future research

A number of the findings of this study could lead to fruitful research these potential research areas are-

- The causal models left a huge amount of variation unexplained therefore further research is needed to identify the cause of this variance with the likely cause being the initial population. If the initial population is found to be a major explanatory factor in the value of response variable it would contradict research which has argued that population plays only a small role (Pinel, Danoy, Bouvrey’s 2011);

- The study found differences in response for small and large routes therefore confirming the findings of Mason, Gunst, Hess (2003), however some UK courier company routes are significantly larger than those carried out by logistics companies (Clarke, Leonardi 2018) as such it would be interesting to extend the stratification from small and large to very large and ascertaining if this changes the idealised settings;

vi. Reflections

On study commencement, the large number of different implementations of the factors was not understood and this meant that it was hard to give each factor the required coverage. Whilst the research questions were answered, the poor explanatory power of the regression models is concerning and I wish I had developed a way to control for the initial population as I suspect this is the nuisance variable. In terms of artefact design I should have designed a way to upload the experimental settings into the artefact and then automatically run each experiment as this would have saved significant time allowing more experiments to be undertaken therefore giving the analysis more statistical power.

6. Appendices

i. Appendix One – Experiment Time Table

Standard Order	RunOrder	PT Type	Blocks	crossOverRate	mutationRate
15	1	1	1	0.6	0.0195
105	2	0	1	0.725	0.05575
72	3	1	1	0.85	0.0195
113	4	1	1	0.6	0.0195
119	5	0	1	0.725	0.05575
45	6	1	1	0.6	0.092
131	7	0	1	0.725	0.05575
34	8	0	1	0.725	0.05575
115	9	1	1	0.6	0.092
6	10	0	1	0.725	0.05575
16	11	1	1	0.85	0.0195
61	12	0	1	0.725	0.05575
77	13	0	1	0.725	0.05575
73	14	1	1	0.6	0.092
117	15	0	1	0.725	0.05575
91	16	0	1	0.725	0.05575
75	17	0	1	0.725	0.05575
129	18	1	1	0.6	0.092
1	19	1	1	0.6	0.0195
130	20	1	1	0.85	0.092
43	21	1	1	0.6	0.0195
128	22	1	1	0.85	0.0195
35	23	0	1	0.725	0.05575
29	24	1	1	0.6	0.0195
132	25	0	1	0.725	0.05575
19	26	0	1	0.725	0.05575
31	27	1	1	0.6	0.092
127	28	1	1	0.6	0.0195
5	29	0	1	0.725	0.05575
88	30	1	1	0.85	0.092
102	31	1	1	0.85	0.092
133	32	0	1	0.725	0.05575
103	33	0	1	0.725	0.05575
71	34	1	1	0.6	0.0195
101	35	1	1	0.6	0.092
85	36	1	1	0.6	0.0195
59	37	1	1	0.6	0.092
89	38	0	1	0.725	0.05575
17	39	1	1	0.6	0.092
3	40	1	1	0.6	0.092
104	41	0	1	0.725	0.05575

Standard Order	RunOrder	PT Type	Blocks	crossOverRate	mutationRate
60	42	1	1	0.85	0.092
116	43	1	1	0.85	0.092
57	44	1	1	0.6	0.0195
100	45	1	1	0.85	0.0195
47	46	0	1	0.725	0.05575
86	47	1	1	0.85	0.0195
62	48	0	1	0.725	0.05575
44	49	1	1	0.85	0.0195
63	50	0	1	0.725	0.05575
90	51	0	1	0.725	0.05575
118	52	0	1	0.725	0.05575
58	53	1	1	0.85	0.0195
2	54	1	1	0.85	0.0195
46	55	1	1	0.85	0.092
74	56	1	1	0.85	0.092
114	57	1	1	0.85	0.0195
76	58	0	1	0.725	0.05575
30	59	1	1	0.85	0.0195
87	60	1	1	0.6	0.092
48	61	0	1	0.725	0.05575
18	62	1	1	0.85	0.092
20	63	0	1	0.725	0.05575
21	64	0	1	0.725	0.05575
4	65	1	1	0.85	0.092
33	66	0	1	0.725	0.05575
32	67	1	1	0.85	0.092
49	68	0	1	0.725	0.05575
99	69	1	1	0.6	0.0195
7	70	0	1	0.725	0.05575
122	71	-1	2	0.725	0.004484758
11	72	-1	2	0.725	0.107015242
84	73	0	2	0.725	0.05575
135	74	-1	2	0.901776695	0.05575
107	75	-1	2	0.901776695	0.05575
69	76	0	2	0.725	0.05575
67	77	-1	2	0.725	0.107015242
52	78	-1	2	0.725	0.004484758
111	79	0	2	0.725	0.05575
94	80	-1	2	0.725	0.004484758

Standard Order	RunOrder	PT Type	Blocks	crossOverRate	mutationRate
92	81	-1	2	0.548223305	0.05575
42	82	0	2	0.725	0.05575
37	83	-1	2	0.901776695	0.05575
120	84	-1	2	0.548223305	0.05575
97	85	0	2	0.725	0.05575
106	86	-1	2	0.548223305	0.05575
124	87	0	2	0.725	0.05575
38	88	-1	2	0.725	0.004484758
96	89	0	2	0.725	0.05575
25	90	-1	2	0.725	0.107015242
136	91	-1	2	0.725	0.004484758
41	92	0	2	0.725	0.05575
65	93	-1	2	0.901776695	0.05575
82	94	0	2	0.725	0.05575
125	95	0	2	0.725	0.05575
64	96	-1	2	0.548223305	0.05575
83	97	0	2	0.725	0.05575
112	98	0	2	0.725	0.05575
56	99	0	2	0.725	0.05575
8	100	-1	2	0.548223305	0.05575
13	101	0	2	0.725	0.05575
28	102	0	2	0.725	0.05575
10	103	-1	2	0.725	0.004484758
22	104	-1	2	0.548223305	0.05575
26	105	0	2	0.725	0.05575
78	106	-1	2	0.548223305	0.05575
137	107	-1	2	0.725	0.107015242
140	108	0	2	0.725	0.05575
53	109	-1	2	0.725	0.107015242
36	110	-1	2	0.548223305	0.05575
109	111	-1	2	0.725	0.107015242
110	112	0	2	0.725	0.05575
12	113	0	2	0.725	0.05575
79	114	-1	2	0.901776695	0.05575
39	115	-1	2	0.725	0.107015242
95	116	-1	2	0.725	0.107015242
98	117	0	2	0.725	0.05575
14	118	0	2	0.725	0.05575
126	119	0	2	0.725	0.05575

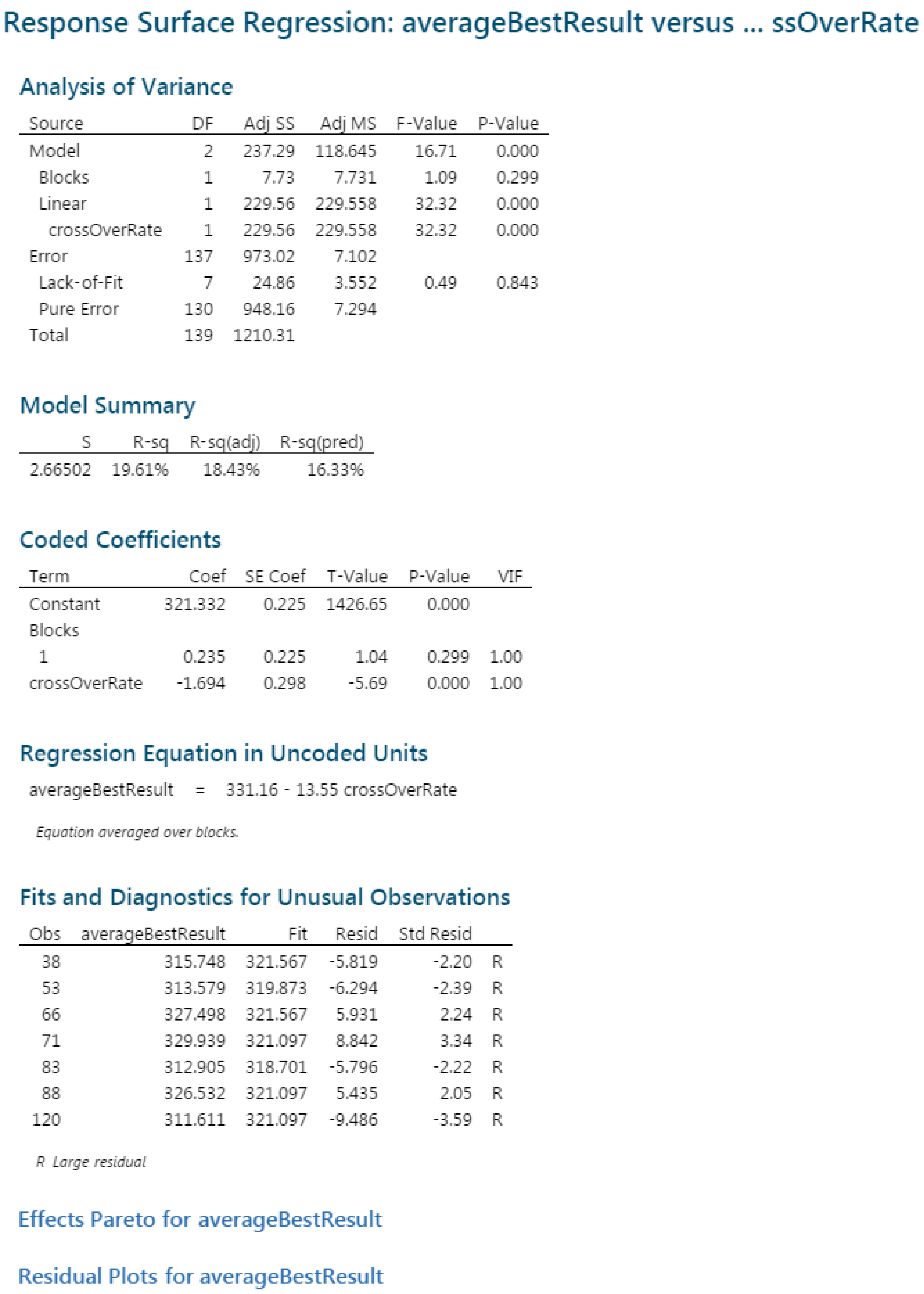
Standard Order	RunOrder	PT Type	Blocks	crossOverRate	mutationRate
24	120	-1	2	0.725	0.004484758
55	121	0	2	0.725	0.05575
93	122	-1	2	0.901776695	0.05575
70	123	0	2	0.725	0.05575
68	124	0	2	0.725	0.05575
54	125	0	2	0.725	0.05575
40	126	0	2	0.725	0.05575
50	127	-1	2	0.548223305	0.05575
80	128	-1	2	0.725	0.004484758
23	129	-1	2	0.901776695	0.05575
123	130	-1	2	0.725	0.107015242
108	131	-1	2	0.725	0.004484758
27	132	0	2	0.725	0.05575
121	133	-1	2	0.901776695	0.05575
138	134	0	2	0.725	0.05575
81	135	-1	2	0.725	0.107015242
139	136	0	2	0.725	0.05575
9	137	-1	2	0.901776695	0.05575
134	138	-1	2	0.548223305	0.05575
66	139	-1	2	0.725	0.004484758
51	140	-1	2	0.901776695	0.05575

Key

- Standard Order – This is the order of the experimental runs before they are randomised
- Run Order – This is the order that of the experimental runs after randomisation
- PtType – 1 is a corner point, 0 centre point, -1 is an axial
- Blocks – A categorical value which can be used to explain variations in response variable not caused by the studied factors
- mutationRate – the values for the likelihood of mutation
- crossOverRate – the values for the likelihood of crossover

ii. Appendix Two – Crossover Only Regression Model

When developing regression models it is important to remove non-significant terms from the model (Matthews 2005), therefore the analysis was repeated using just crossover as a factor. This generated the analysis in Figure 70 as the model has fewer terms it has a lower squared value but it has a higher adjusted R2 value than the previous model, it also has a higher predictive R2 value indicating that it is better at predicting the response for new experiments. The model is again a poor fit for the data suggesting that an un-modelled factor is having a significant effect. Figure 71 confirms this analysis is suitable for the data.



Response Surface Regression: averageBestResult versus ... ssOverRate

Analysis of Variance

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Model	2	237.29	118.645	16.71	0.000
Blocks	1	7.73	7.731	1.09	0.299
Linear	1	229.56	229.558	32.32	0.000
crossOverRate	1	229.56	229.558	32.32	0.000
Error	137	973.02	7.102		
Lack-of-Fit	7	24.86	3.552	0.49	0.843
Pure Error	130	948.16	7.294		
Total	139	1210.31			

Model Summary

S	R-sq	R-sq(adj)	R-sq(pred)
2.66502	19.61%	18.43%	16.33%

Coded Coefficients

Term	Coef	SE Coef	T-Value	P-Value	VIF
Constant	321.332	0.225	1426.65	0.000	
Blocks					
1	0.235	0.225	1.04	0.299	1.00
crossOverRate	-1.694	0.298	-5.69	0.000	1.00

Regression Equation in Uncoded Units

averageBestResult = 331.16 - 13.55 crossOverRate

Equation averaged over blocks.

Fits and Diagnostics for Unusual Observations

Obs	averageBestResult	Fit	Resid	Std Resid	
38	315.748	321.567	-5.819	-2.20	R
53	313.579	319.873	-6.294	-2.39	R
66	327.498	321.567	5.931	2.24	R
71	329.939	321.097	8.842	3.34	R
83	312.905	318.701	-5.796	-2.22	R
88	326.532	321.097	5.435	2.05	R
120	311.611	321.097	-9.486	-3.59	R

R Large residual

Effects Pareto for averageBestResult

Residual Plots for averageBestResult

FIGURE 70 REGRESSION ANALYSIS FOR CROSSOVER ONLY MODEL FOR THE FILL SAMPLE

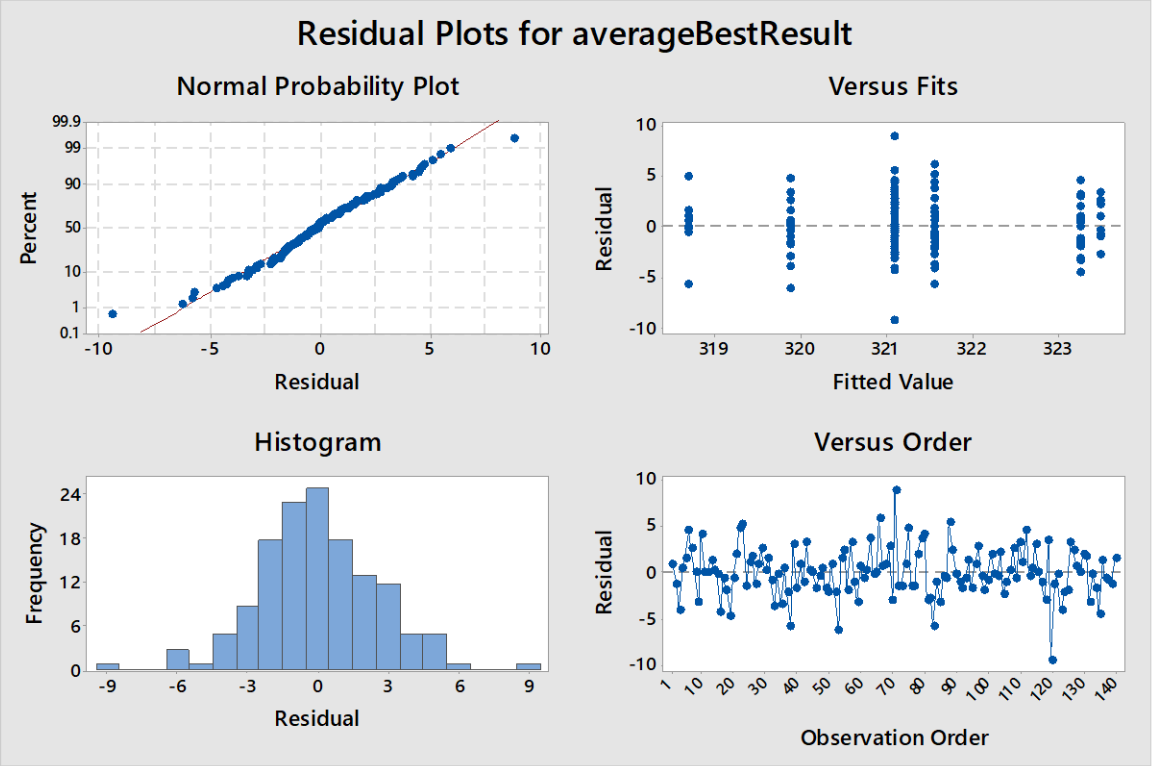


FIGURE 71 RESIDUALS PLOT AND ANALYSIS FOR CROSSOVER ONLY MODEL

iii. Appendix Three – DOE Analysis of small routes in the sample

Figure 72 shows that for small routes only crossover is a statistically significant factor in explaining the response variable.

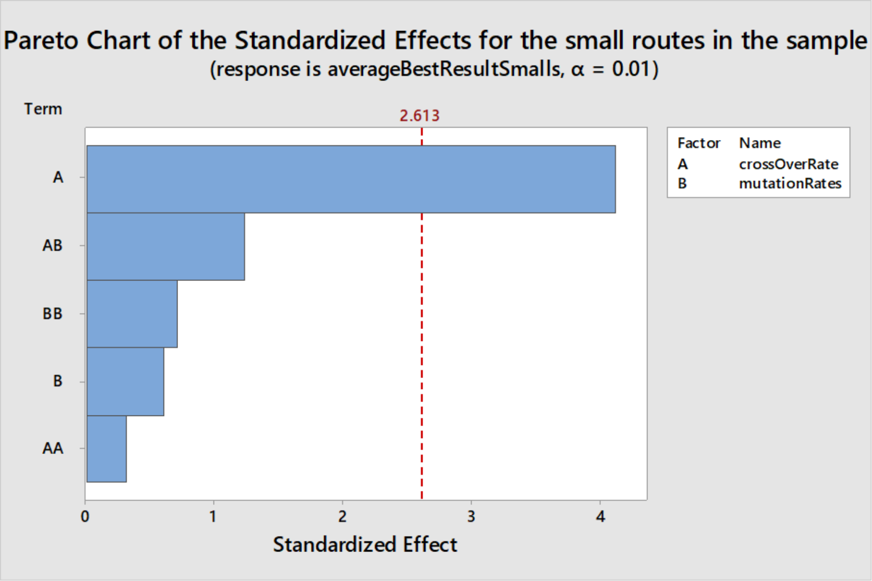
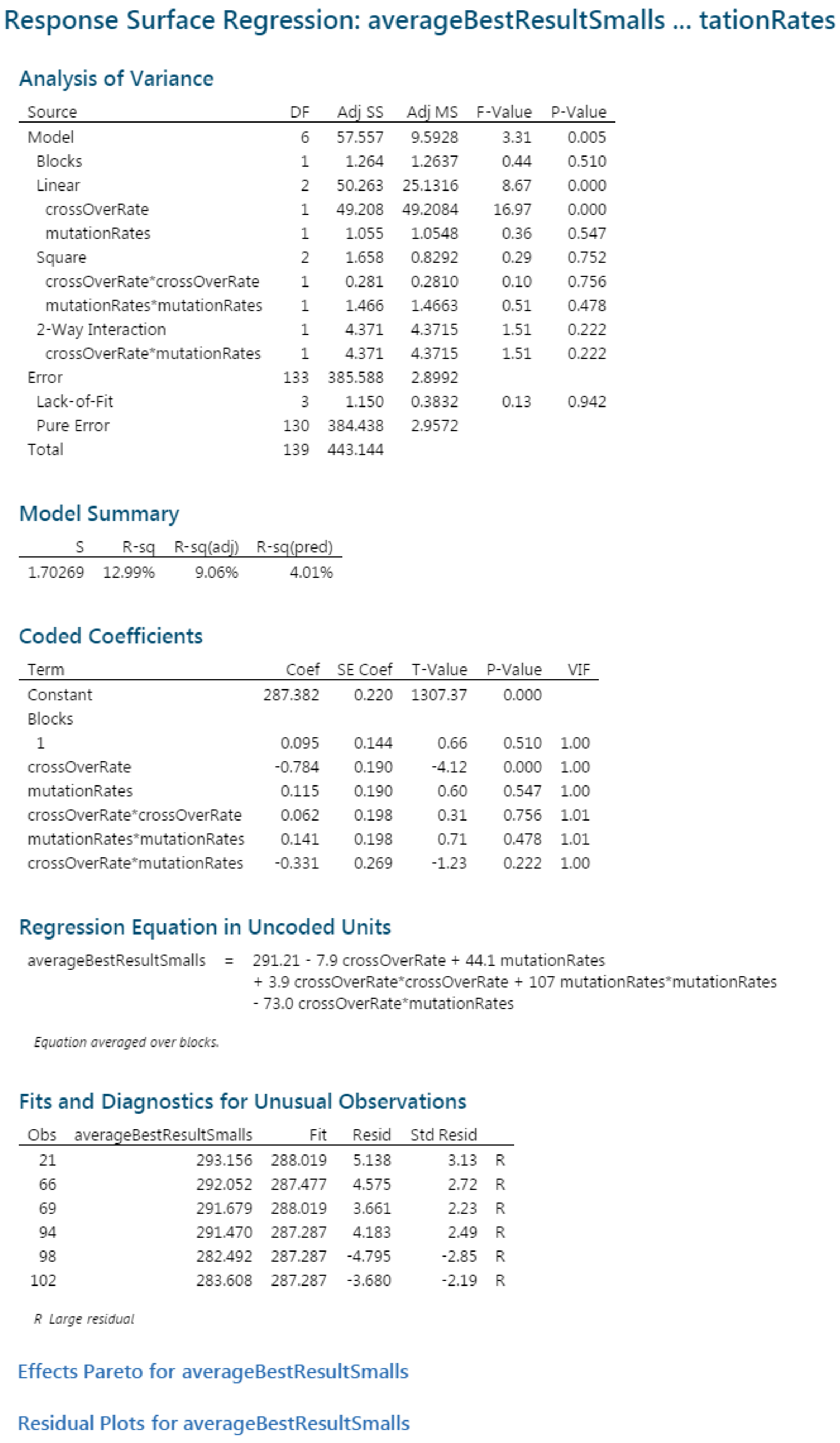


FIGURE 72 PARETO CHART OF THE STANDARDISED EFFECTS OF PARAMETER SETTINGS ON THE SMALL ROUTES ON THE SAMPLE



```
Response Surface Regression: averageBestResultSmalls ... tationRates

Analysis of Variance

Source                          DF   Adj SS    Adj MS  F-Value  P-Value
Model                            6   57.557    9.5928     3.31    0.005
  Blocks                         1    1.264    1.2637     0.44    0.510
  Linear                         2   50.263   25.1316     8.67    0.000
    crossOverRate                1   49.208   49.2084    16.97    0.000
    mutationRates                1    1.055    1.0548     0.36    0.547
  Square                         2    1.658    0.8292     0.29    0.752
    crossOverRate*crossOverRate  1    0.281    0.2810     0.10    0.756
    mutationRates*mutationRates  1    1.466    1.4663     0.51    0.478
  2-Way Interaction              1    4.371    4.3715     1.51    0.222
    crossOverRate*mutationRates  1    4.371    4.3715     1.51    0.222
Error                          133  385.588    2.8992
  Lack-of-Fit                    3    1.150    0.3832     0.13    0.942
  Pure Error                   130  384.438    2.9572
Total                          139  443.144

Model Summary

      S    R-sq  R-sq(adj)  R-sq(pred)
1.70269  12.99%      9.06%       4.01%

Coded Coefficients

Term                            Coef  SE Coef  T-Value  P-Value   VIF
Constant                     287.382    0.220  1307.37    0.000
Blocks
 1                             0.095    0.144     0.66    0.510  1.00
crossOverRate                 -0.784    0.190    -4.12    0.000  1.00
mutationRates                  0.115    0.190     0.60    0.547  1.00
crossOverRate*crossOverRate    0.062    0.198     0.31    0.756  1.01
mutationRates*mutationRates    0.141    0.198     0.71    0.478  1.01
crossOverRate*mutationRates   -0.331    0.269    -1.23    0.222  1.00

Regression Equation in Uncoded Units

averageBestResultSmalls  =  291.21 - 7.9 crossOverRate + 44.1 mutationRates
                            + 3.9 crossOverRate*crossOverRate + 107 mutationRates*mutationRates
                            - 73.0 crossOverRate*mutationRates

  Equation averaged over blocks.

Fits and Diagnostics for Unusual Observations

Obs  averageBestResultSmalls      Fit   Resid  Std Resid
 21                  293.156  288.019   5.138       3.13  R
 66                  292.052  287.477   4.575       2.72  R
 69                  291.679  288.019   3.661       2.23  R
 94                  291.470  287.287   4.183       2.49  R
 98                  282.492  287.287  -4.795      -2.85  R
102                  283.608  287.287  -3.680      -2.19  R

  R  Large residual

Effects Pareto for averageBestResultSmalls

Residual Plots for averageBestResultSmalls
```

FIGURE 73 RESULTS OF THE RESPONSE SURFACE REGRESSION ANALYSIS FOR THE SMALL ROUTES IN THE SAMPLE

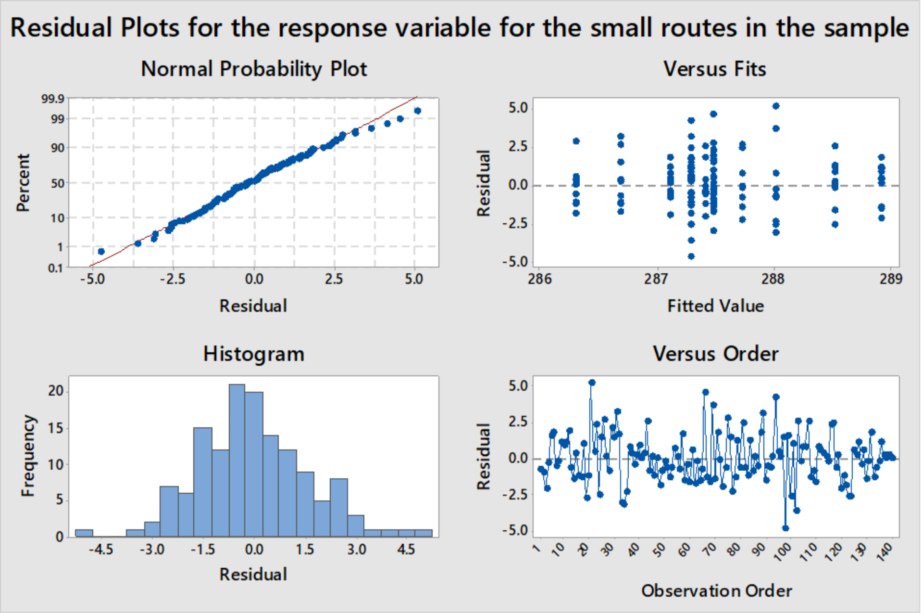


FIGURE 74 RESIDUAL PLOTS FOR THE SMALL ROUTES IN THE SAMPLE

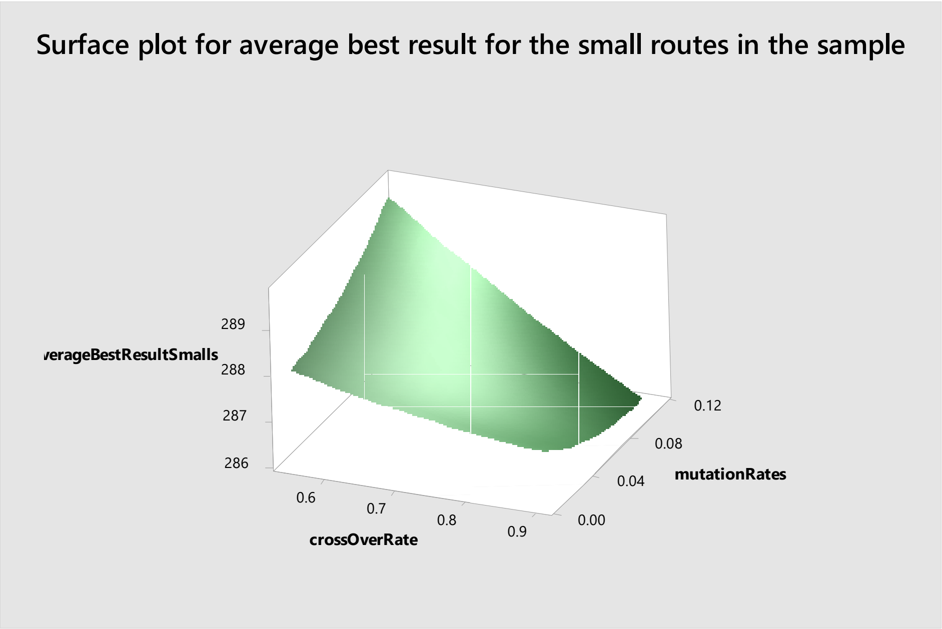
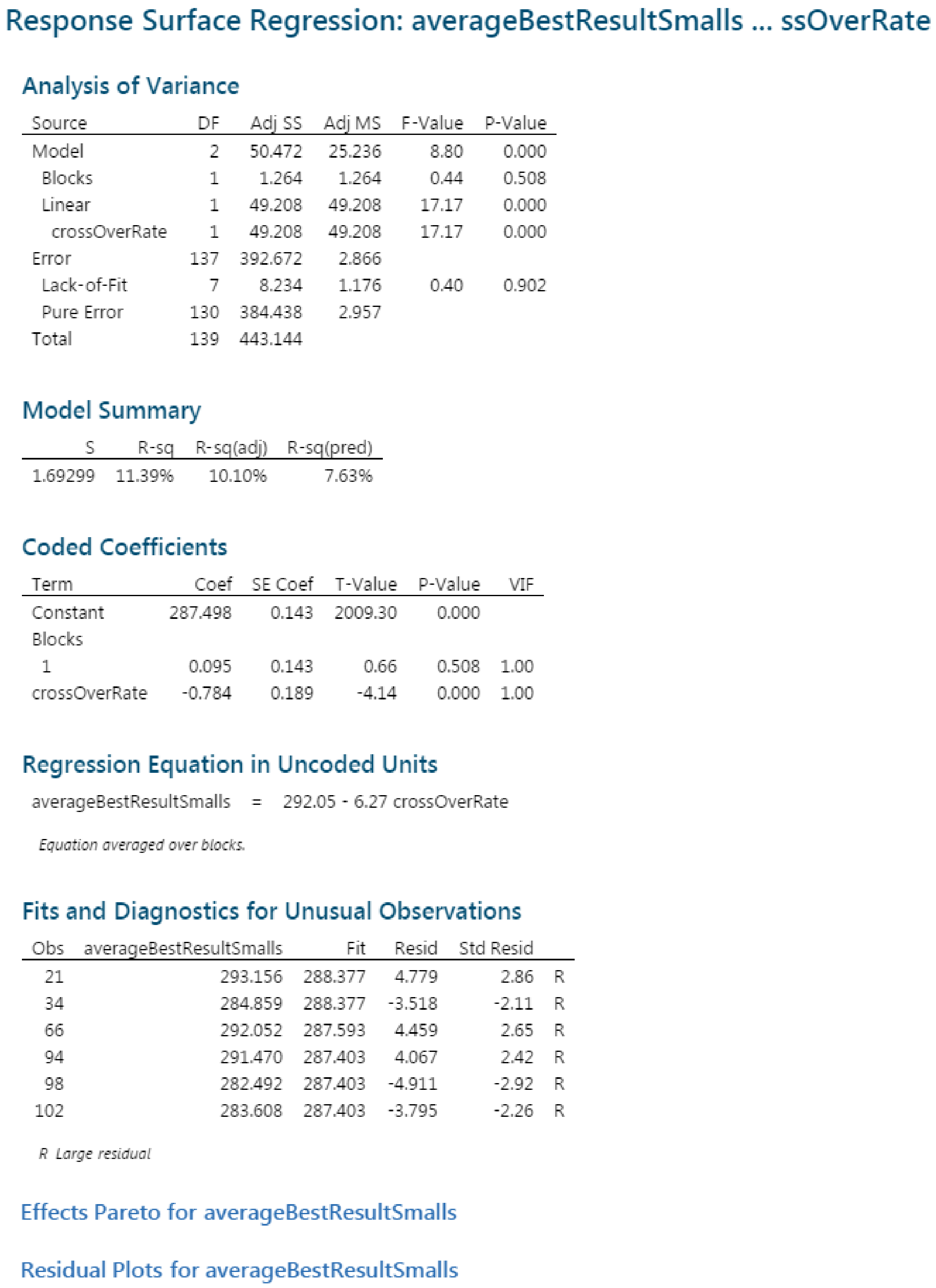


FIGURE 75 SURFACE PLOT FOR THE RESPONSE VARIABLE FOR THE SMALL ROUTES IN THE SAMPLE



Response Surface Regression: averageBestResultSmalls ... ssOverRate

Analysis of Variance

```
Source             DF   Adj SS   Adj MS  F-Value  P-Value
Model               2   50.472   25.236     8.80    0.000
  Blocks            1    1.264    1.264     0.44    0.508
  Linear            1   49.208   49.208    17.17    0.000
    crossOverRate   1   49.208   49.208    17.17    0.000
Error             137  392.672    2.866
  Lack-of-Fit       7    8.234    1.176     0.40    0.902
  Pure Error      130  384.438    2.957
Total             139  443.144
```

Model Summary

```
      S    R-sq  R-sq(adj)  R-sq(pred)
1.69299  11.39%     10.10%       7.63%
```

Coded Coefficients

```
Term              Coef  SE Coef  T-Value  P-Value   VIF
Constant       287.498    0.143  2009.30    0.000
Blocks
  1              0.095    0.143     0.66    0.508  1.00
crossOverRate   -0.784    0.189    -4.14    0.000  1.00
```

Regression Equation in Uncoded Units

```
averageBestResultSmalls  =  292.05 - 6.27 crossOverRate
```

Equation averaged over blocks.

Fits and Diagnostics for Unusual Observations

```
Obs  averageBestResultSmalls      Fit   Resid  Std Resid
 21                  293.156  288.377   4.779       2.86  R
 34                  284.859  288.377  -3.518      -2.11  R
 66                  292.052  287.593   4.459       2.65  R
 94                  291.470  287.403   4.067       2.42  R
 98                  282.492  287.403  -4.911      -2.92  R
102                  283.608  287.403  -3.795      -2.26  R
```

R Large residual

Effects Pareto for averageBestResultSmalls

Residual Plots for averageBestResultSmalls

FIGURE 76 RESULTS OF THE CROSSOVER ONLY RESPONSE SURFACE REGRESSION ANALYSIS FOR THE SMALL ROUTES IN THE SAMPLE

iv. Appendix four – DOE Analysis of large routes in the sample

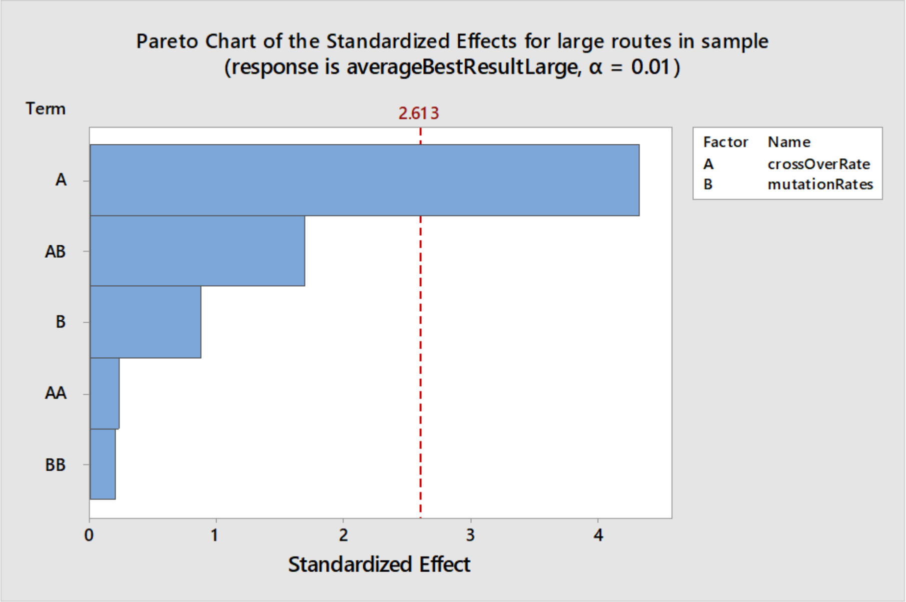
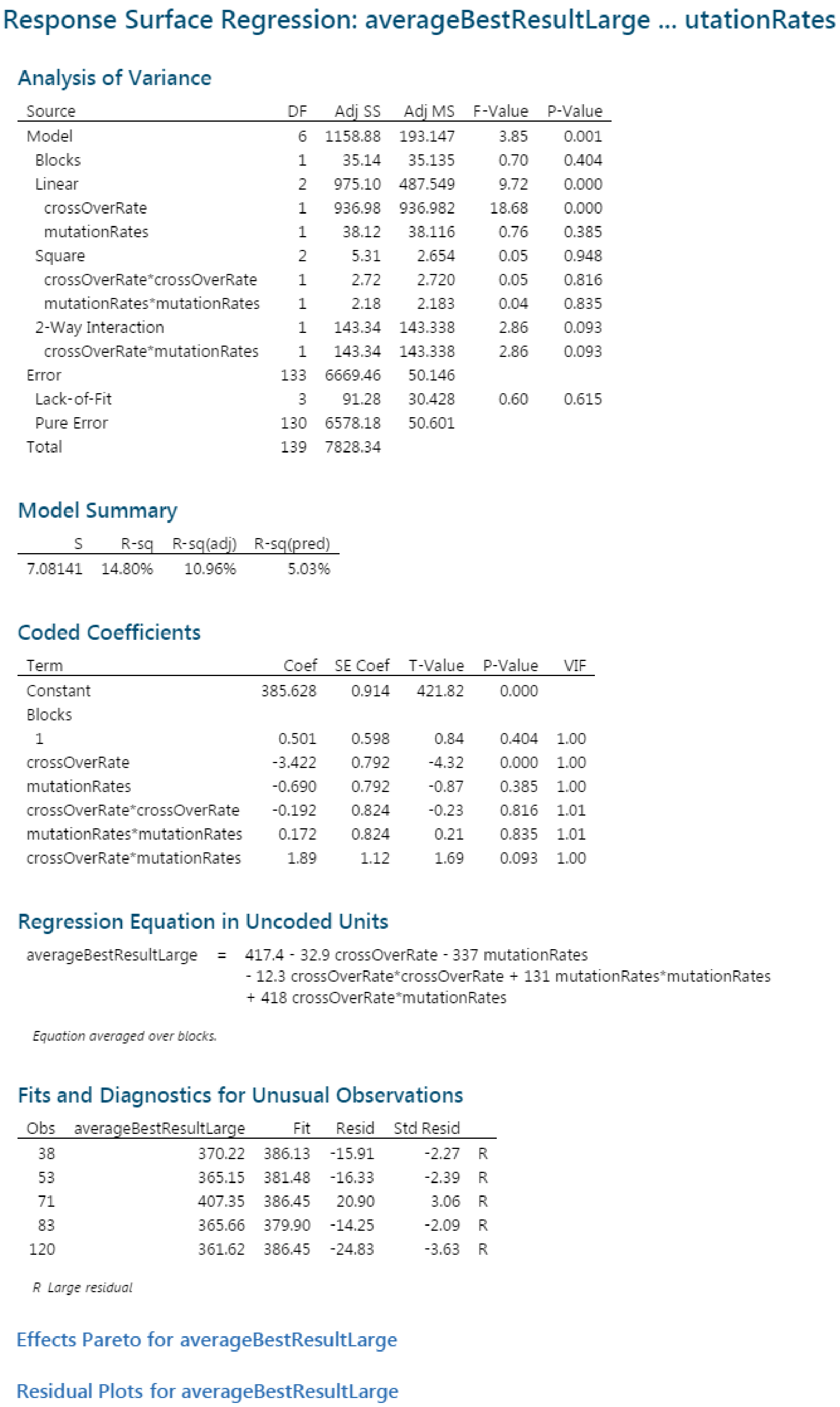


FIGURE 77 PARETO CHART OF THE STANDARDISED EFFECTS OF PARAMETER SETTINGS ON THE LARGE ROUTES ON THE SAMPLE



Response Surface Regression: averageBestResultLarge ... utationRates

Analysis of Variance

```
Source                          DF   Adj SS   Adj MS  F-Value  P-Value
Model                            6  1158.88  193.147     3.85    0.001
  Blocks                         1    35.14   35.135     0.70    0.404
  Linear                         2   975.10  487.549     9.72    0.000
    crossOverRate                1   936.98  936.982    18.68    0.000
    mutationRates                1    38.12   38.116     0.76    0.385
  Square                         2     5.31    2.654     0.05    0.948
    crossOverRate*crossOverRate  1     2.72    2.720     0.05    0.816
    mutationRates*mutationRates  1     2.18    2.183     0.04    0.835
  2-Way Interaction              1   143.34  143.338     2.86    0.093
    crossOverRate*mutationRates  1   143.34  143.338     2.86    0.093
Error                          133  6669.46   50.146
  Lack-of-Fit                    3    91.28   30.428     0.60    0.615
  Pure Error                   130  6578.18   50.601
Total                          139  7828.34
```

Model Summary

```
      S    R-sq  R-sq(adj)  R-sq(pred)
7.08141  14.80%     10.96%       5.03%
```

Coded Coefficients

```
Term                            Coef  SE Coef  T-Value  P-Value   VIF
Constant                     385.628    0.914   421.82    0.000
Blocks
  1                            0.501    0.598     0.84    0.404  1.00
crossOverRate                 -3.422    0.792    -4.32    0.000  1.00
mutationRates                 -0.690    0.792    -0.87    0.385  1.00
crossOverRate*crossOverRate   -0.192    0.824    -0.23    0.816  1.01
mutationRates*mutationRates    0.172    0.824     0.21    0.835  1.01
crossOverRate*mutationRates     1.89     1.12     1.69    0.093  1.00
```

Regression Equation in Uncoded Units

```
averageBestResultLarge  =  417.4 - 32.9 crossOverRate - 337 mutationRates
                           - 12.3 crossOverRate*crossOverRate + 131 mutationRates*mutationRates
                           + 418 crossOverRate*mutationRates
```

Equation averaged over blocks.

Fits and Diagnostics for Unusual Observations

```
Obs  averageBestResultLarge     Fit   Resid  Std Resid
 38                  370.22  386.13  -15.91      -2.27  R
 53                  365.15  381.48  -16.33      -2.39  R
 71                  407.35  386.45   20.90       3.06  R
 83                  365.66  379.90  -14.25      -2.09  R
120                  361.62  386.45  -24.83      -3.63  R
```

R Large residual

Effects Pareto for averageBestResultLarge

Residual Plots for averageBestResultLarge

FIGURE 78 RESULTS OF THE RESPONSE SURFACE REGRESSION ANALYSIS FOR THE LARGE ROUTES IN THE SAMPLE

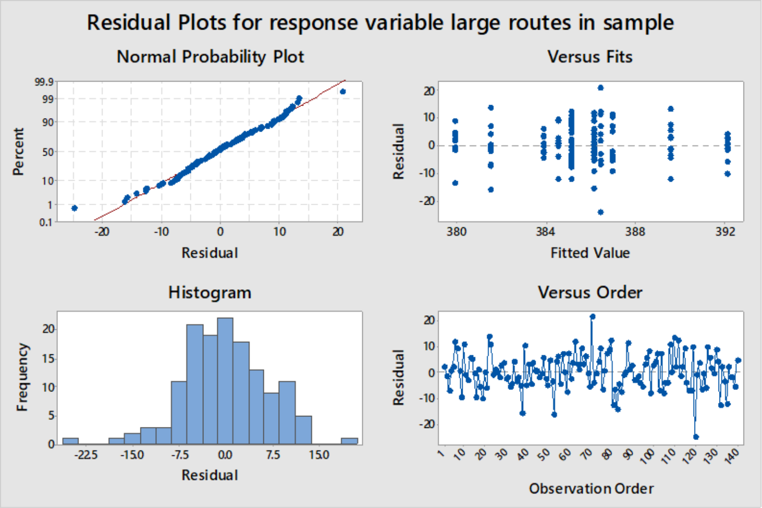


FIGURE 79 RESIDUAL PLOTS FOR THE SMALL ROUTES IN THE SAMPLE

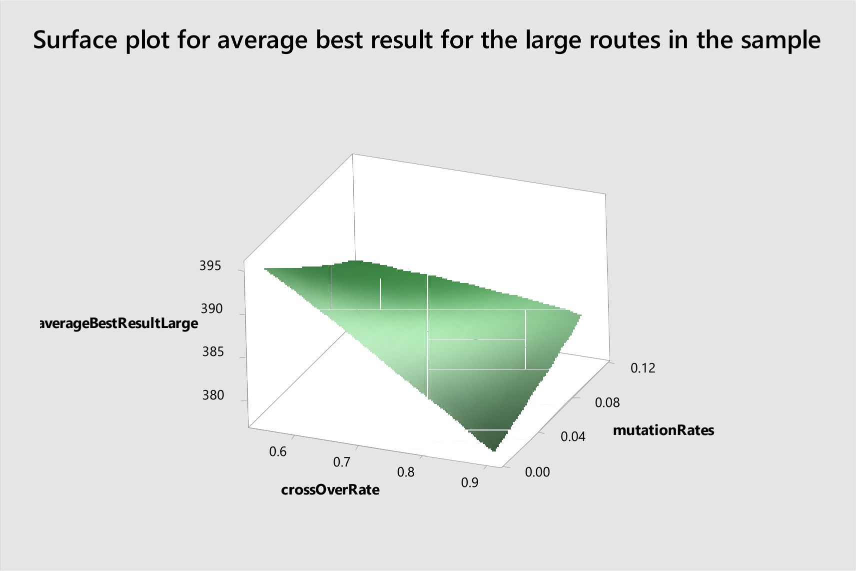
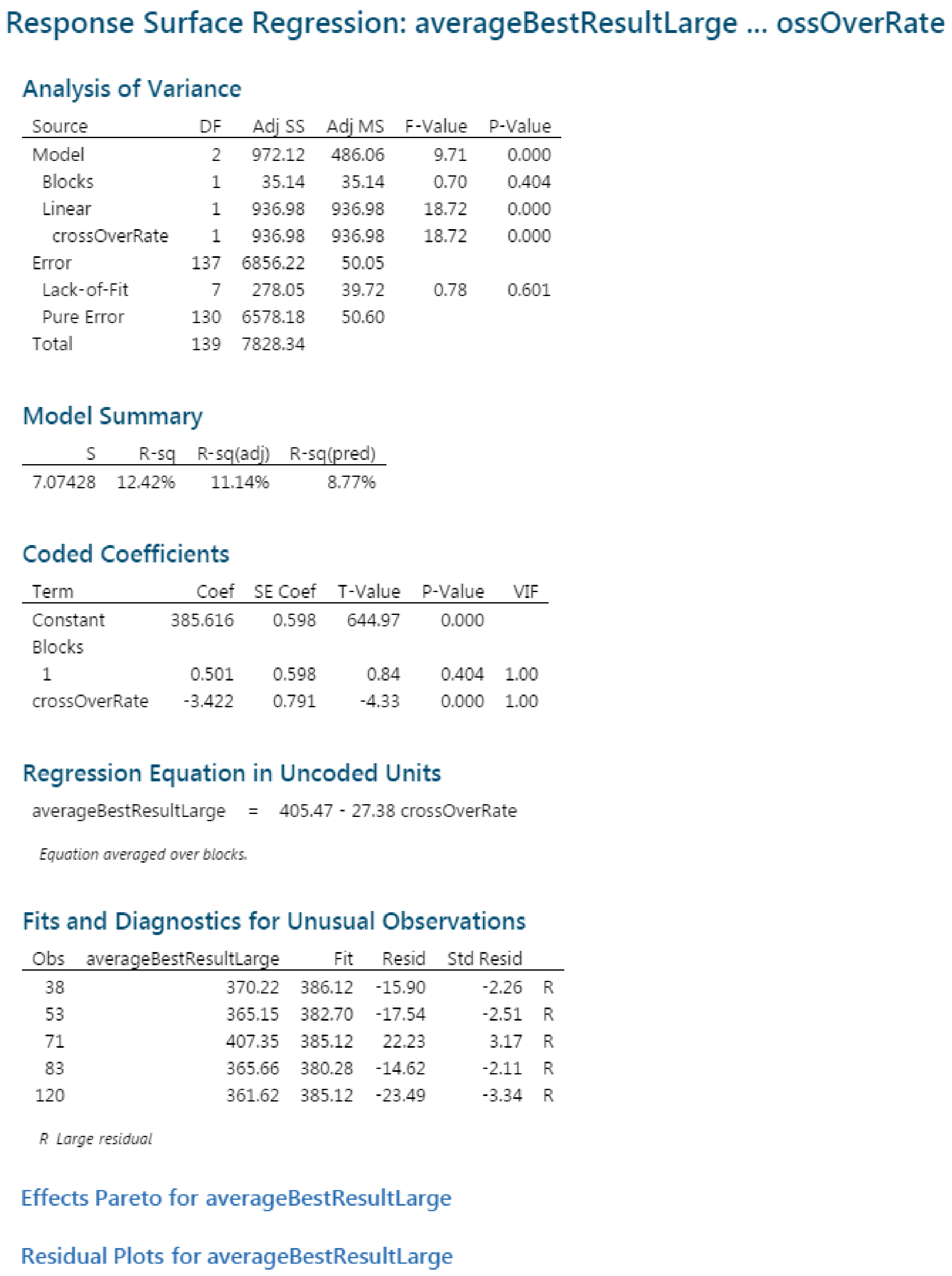


FIGURE 80 SURFACE PLOT FOR THE RESPONSE VARIABLE FOR THE LARGE ROUTES IN THE SAMPLE



Response Surface Regression: averageBestResultLarge ... ossOverRate

Analysis of Variance

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Model	2	972.12	486.06	9.71	0.000
Blocks	1	35.14	35.14	0.70	0.404
Linear	1	936.98	936.98	18.72	0.000
crossOverRate	1	936.98	936.98	18.72	0.000
Error	137	6856.22	50.05		
Lack-of-Fit	7	278.05	39.72	0.78	0.601
Pure Error	130	6578.18	50.60		
Total	139	7828.34			

Model Summary

S	R-sq	R-sq(adj)	R-sq(pred)
7.07428	12.42%	11.14%	8.77%

Coded Coefficients

Term	Coef	SE Coef	T-Value	P-Value	VIF
Constant	385.616	0.598	644.97	0.000	
Blocks					
1	0.501	0.598	0.84	0.404	1.00
crossOverRate	-3.422	0.791	-4.33	0.000	1.00

Regression Equation in Uncoded Units

averageBestResultLarge = 405.47 - 27.38 crossOverRate

Equation averaged over blocks.

Fits and Diagnostics for Unusual Observations

Obs	averageBestResultLarge	Fit	Resid	Std Resid	
38	370.22	386.12	-15.90	-2.26	R
53	365.15	382.70	-17.54	-2.51	R
71	407.35	385.12	22.23	3.17	R
83	365.66	380.28	-14.62	-2.11	R
120	361.62	385.12	-23.49	-3.34	R

R Large residual

Effects Pareto for averageBestResultLarge

Residual Plots for averageBestResultLarge

FIGURE 81 RESULTS OF THE CROSSOVER ONLY RESPONSE SURFACE REGRESSION ANALYSIS FOR THE SMALL ROUTES IN THE SAMPLE

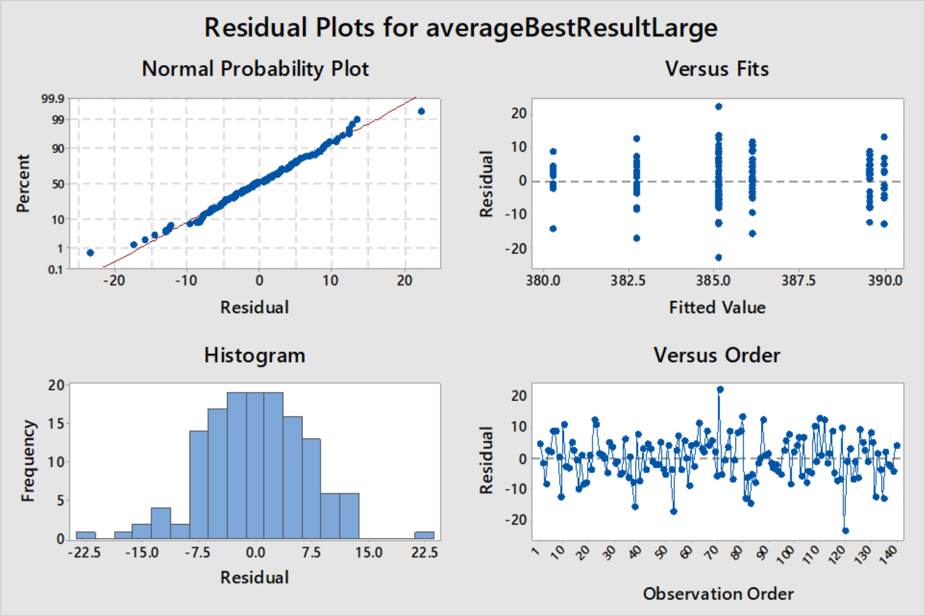
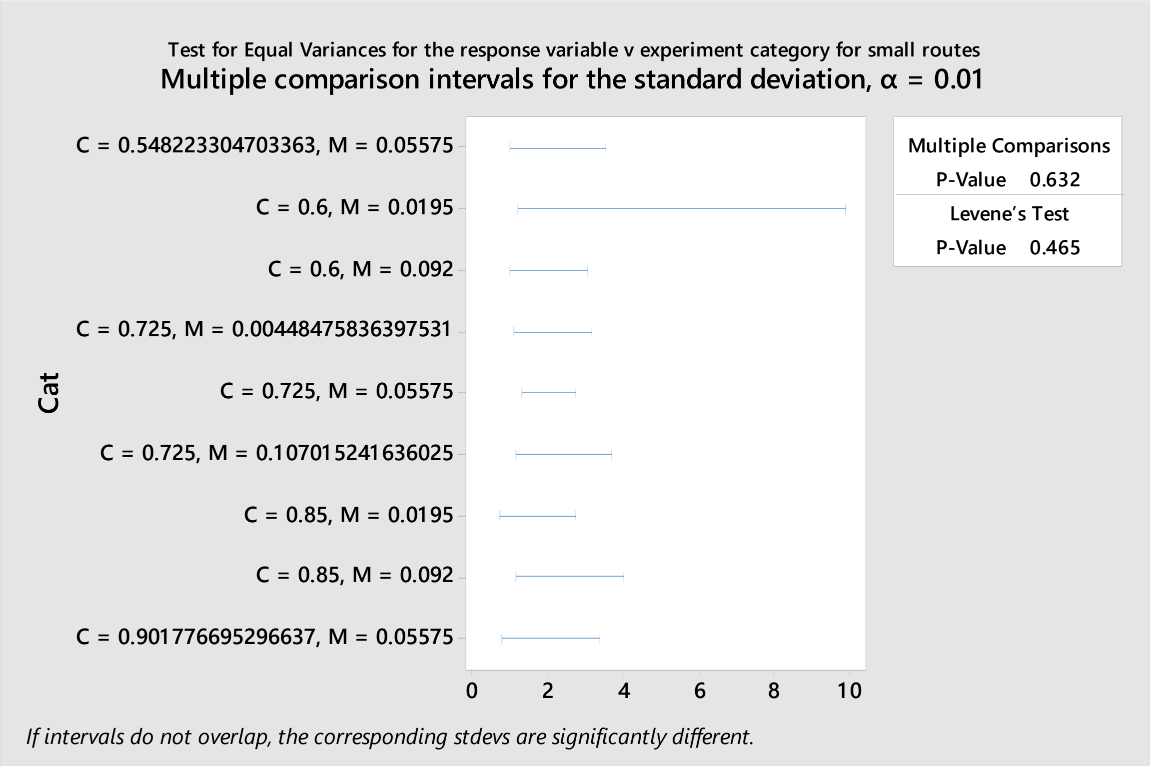


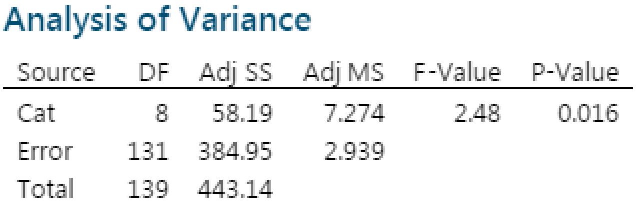
FIGURE 82 RESIDUAL PLOT FOR CROSSOVER ONLY REGRESSION ANALYSIS FOR THE LARGE ROUTES IN THE SAMPLE

v. Appendix five – Do parameter settings affect the response variable for small routes


Test for Equal Variances for the response variable v experiment category for small routes

Multiple comparison intervals for the standard deviation, α = 0.01

If intervals do not overlap, the corresponding stdevs are significantly different.


Analysis of Variance

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Cat	8	58.19	7.274	2.48	0.016
Error	131	384.95	2.939		
Total	139	443.14			

Grouping Information Using the Tukey Method and 95% Confidence

ID	Cat	N	Mean	StDev	99% CI	Grouping
1	C = 0.54822, M = 0.05575	10	288.64	1.458	(287.223, 290.057)	A
2	C = 0.6, M = 0.0195	10	287.851	2.704	(286.434, 289.268)	A
3	C = 0.6, M = 0.092	10	288.908	1.345	(287.491, 290.325)	A B
4	C = 0.725, M = 0.00448	10	287.523	1.477	(286.106, 288.940)	A B
5	C = 0.725, M = 0.05575	60	287.382	1.795	(286.804, 287.961)	A B
6	C = 0.725, M = 0.10701	10	287.612	1.607	(286.195, 289.029)	A B
7	C = 0.85, M = 0.0195	10	287.116	1.073	(285.699, 288.533)	A B
8	C = 0.85, M = 0.092	10	286.851	1.683	(285.434, 288.268)	A B
9	C = 0.90177, M = 0.05575	10	286.178	1.289	(284.761, 287.595)	B

Pooled StDev = 1.71423

Means that do not share a letter are significantly different.

vi. Appendix Six – Do parameter settings affect the response variable for large routes

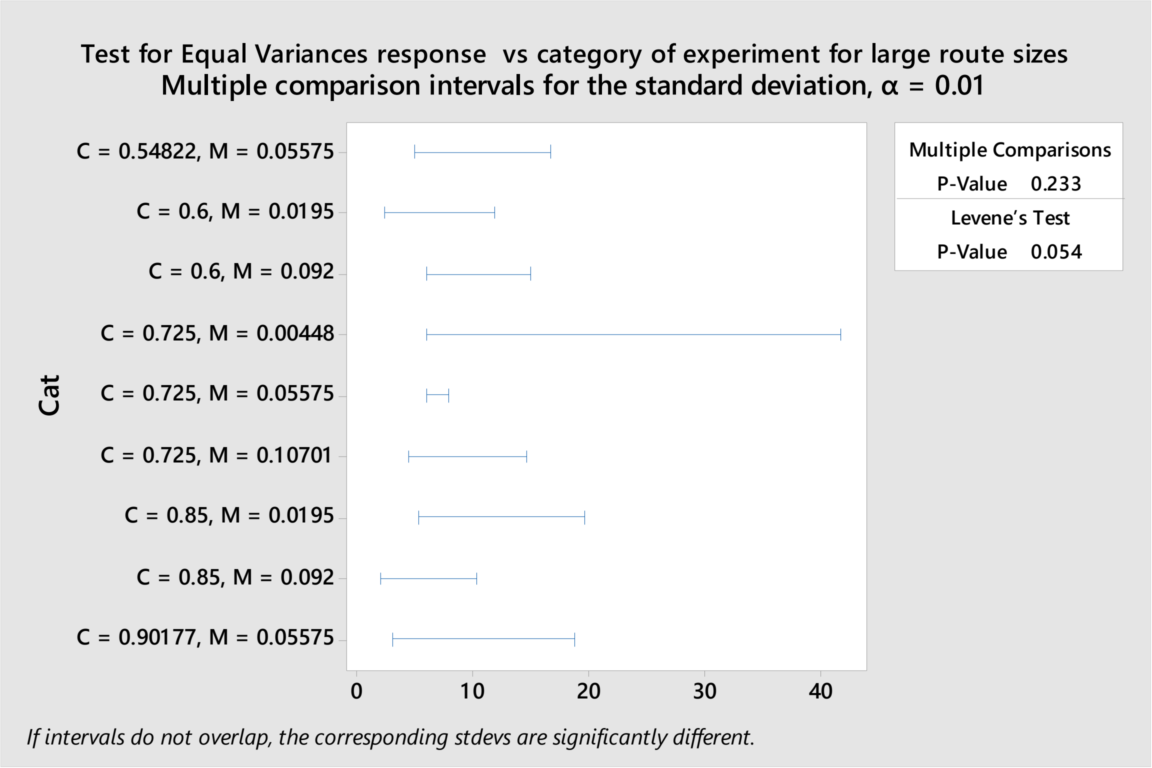
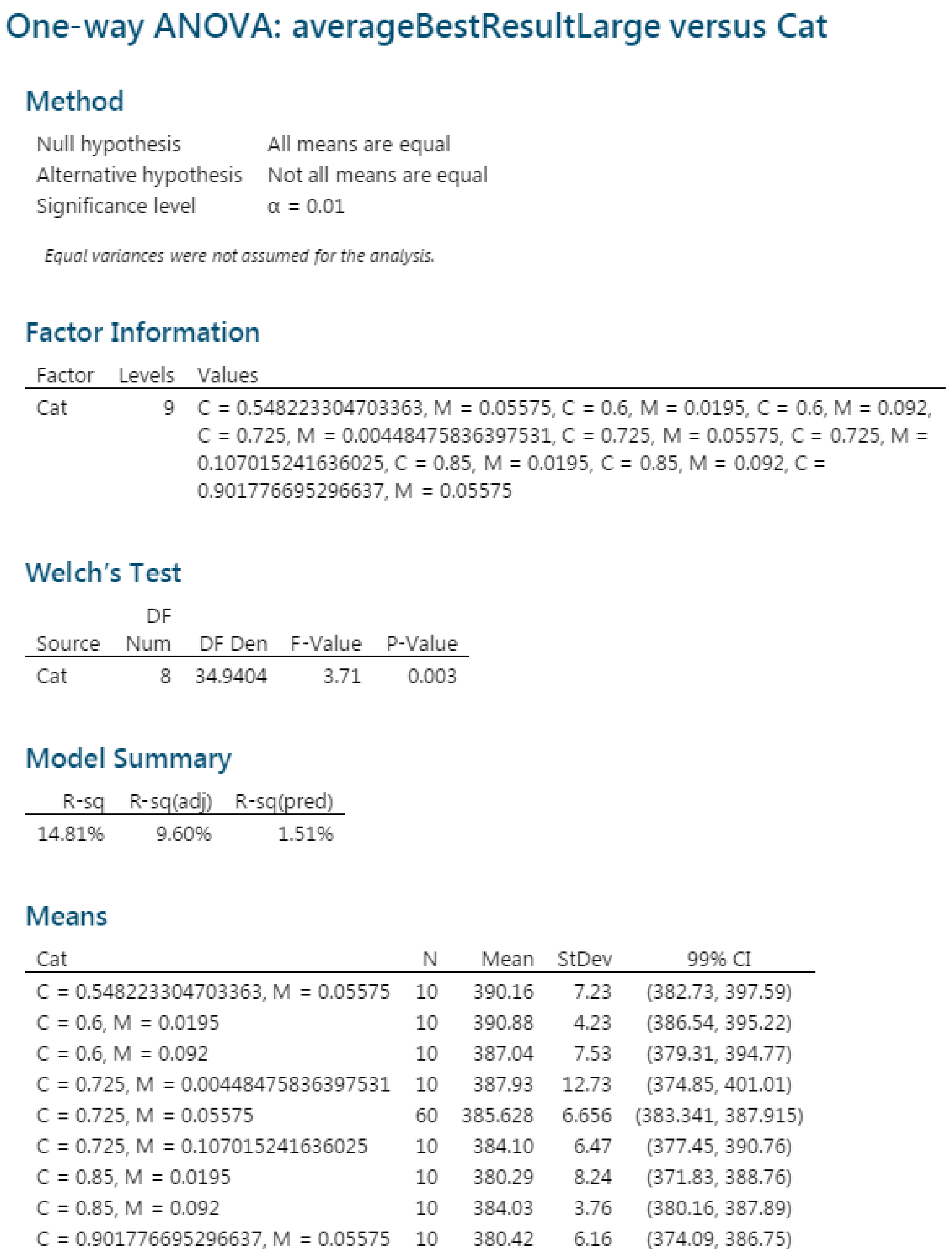


FIGURE 83 LEVENE'S TEST FOR EQUAL VARIANCES RESPONSE VARIABLE AGAINST CATEGORY OF EXPERIMENTS FOR LARGE ROUTES IN THE SAMPLE



One-way ANOVA: averageBestResultLarge versus Cat

Method

Null hypothesis	All means are equal
Alternative hypothesis	Not all means are equal
Significance level	α = 0.01

Equal variances were not assumed for the analysis.

Factor Information

Factor	Levels	Values
Cat	9	C = 0.548223304703363, M = 0.05575, C = 0.6, M = 0.0195, C = 0.6, M = 0.092, C = 0.725, M = 0.00448475836397531, C = 0.725, M = 0.05575, C = 0.725, M = 0.107015241636025, C = 0.85, M = 0.0195, C = 0.85, M = 0.092, C = 0.901776695296637, M = 0.05575

Welch's Test

Source	DF Num	DF Den	F-Value	P-Value
Cat	8	34.9404	3.71	0.003

Model Summary

R-sq	R-sq(adj)	R-sq(pred)
14.81%	9.60%	1.51%

Means

Cat	N	Mean	StDev	99% CI
C = 0.548223304703363, M = 0.05575	10	390.16	7.23	(382.73, 397.59)
C = 0.6, M = 0.0195	10	390.88	4.23	(386.54, 395.22)
C = 0.6, M = 0.092	10	387.04	7.53	(379.31, 394.77)
C = 0.725, M = 0.00448475836397531	10	387.93	12.73	(374.85, 401.01)
C = 0.725, M = 0.05575	60	385.628	6.656	(383.341, 387.915)
C = 0.725, M = 0.107015241636025	10	384.10	6.47	(377.45, 390.76)
C = 0.85, M = 0.0195	10	380.29	8.24	(371.83, 388.76)
C = 0.85, M = 0.092	10	384.03	3.76	(380.16, 387.89)
C = 0.901776695296637, M = 0.05575	10	380.42	6.16	(374.09, 386.75)

FIGURE 84 ANOVA TEST FOR RESPONSE VARIABLE AGAINST CATEGORY OF EXPERIMENTS FOR LARGE ROUTES IN THE SAMPLE

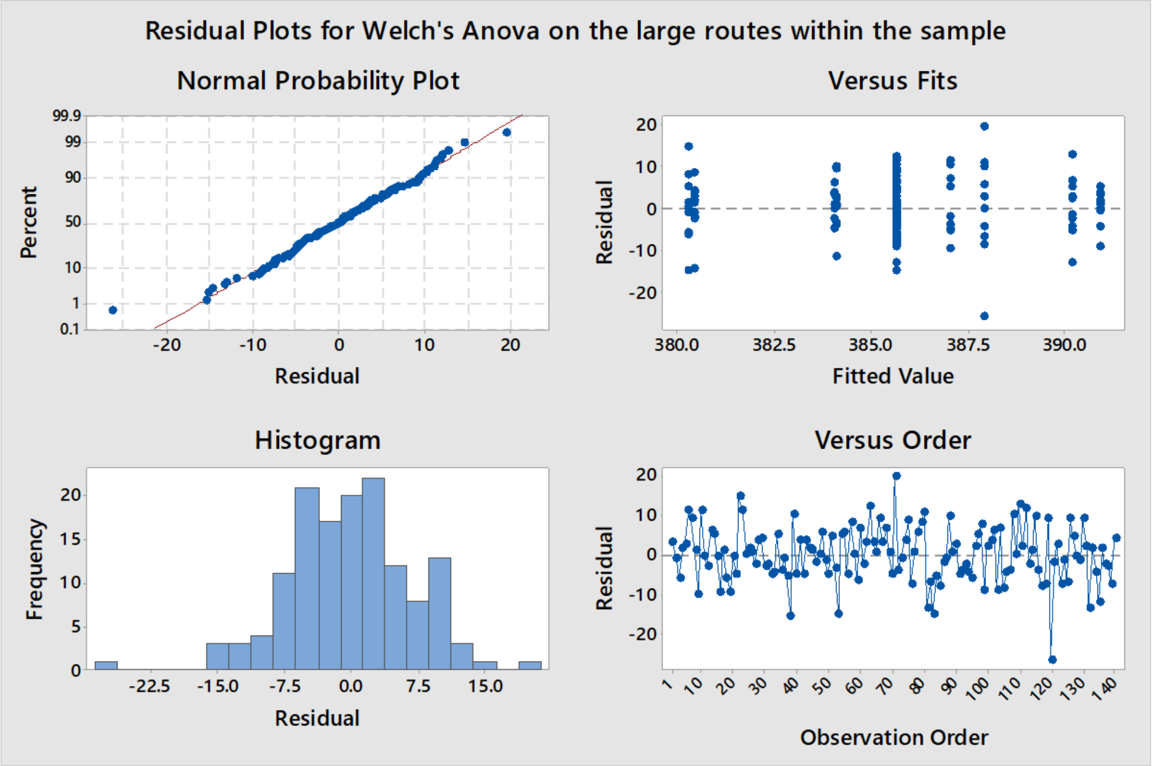


FIGURE 85 RESIDUAL PLOTS FOR WELCH'S ANOVA FOR THE LARGE ROUTES IN THE SAMPLE

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