Artificial Intelligence Based Design Optimizations for Improving Diversity in Wireless Links

Shaheen Solwa

A dissertation submitted in fulfilment of the requirement for the degree of

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Submission 1:

S. Solwa, "A Performance Study of a Genetic Algorithm Based Mapper Design for Uncoded Space-Time Labeling Diversity", 2021

Preparing for Submission

Submission 2:

S. Solwa, "An Ordered Crossover Approach to Designing Labelling Diversity Mappers", 2021

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Dedication

Unremitting gratitude to the All Mighty for his abundant blessing in affording me the ability to execute the current dissertation.

The author extends multitudes of love to parents and family members, who displayed continual support throughout the duration of the research programme.

The author's sincerest gratitude is sent towards the ever helpful supervisors, Dr. Tahmid Quazi and Mr. Bashan Naidoo, whose optimistic attitude was displayed through their excellent guidance and advice to always believe in myself. Both supervisors have added great value to the current research thesis.

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Inexhaustible love goes out the authors closest friends, for the immense support and belief throughout the 2 years of the authors postgraduate career.

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Abstract

Uncoded space-time labelling diversity (USTLD) is a recent, innovative multi-diversity scheme that improves the error performance of space-time block codes (STBC) by employing labelling diversity (LD) to transmit information codewords. LD is achieved by employing mapper designs with different binary encodings to encode information codewords. Current approaches for designing LD mapper designs are constrained to high computational costs or dependability on symmetry-based heuristics. Recently, a Genetic algorithm (GA) solution was proposed to overcome these limitations. GAs are powerful meta-heuristic tools that are loosely based on the theory of evolution and natural selection. Primarily, GAs are used when little is known about the solution space or the search space is unreasonably large. Research interests in GAs are found to be in both its theory and application. On one side, modifications to the GA parameters and genetic operators allow them to solve problems faster, more accurately and more reliably. On the other hand, GAs are used to solve complex and novel optimization problems in new applications.

Due to high computational costs for design LD mappers of size $M > 16$, where M is the order of modulation, the first contribution in this dissertation is to apply the GA to high-density M-ary constellations. Such an application has not been studied in open literature to date. Results show that for M-QAM systems, the GA produces mapper designs that match, but do not improve upon existing heuristic designs. The GA had produced mapper designs for M-PSK and M-APSK (symmetric and asymmetric) constellations that have exhibited diversity gains of $\approx 3dB$ to $\approx 9dB$ over existing heuristic mapper designs and the Alamouti STBC respectively. Additionally, a complexity analysis was performed on the GA and compared to complexities of exhaustive mapper design techniques. Analysis shows that the GA, in the worst-case scenario, has a computational complexity of $\mathcal{O}(M^2)$. When compared to existing exhaustive mapper design techniques, which have computational complexities of $\mathcal{O}(M!)$ and $\mathcal{O}(M^5)$, the GA is observed to require significantly less computational resources. Finally, the GA produces mapper designs that illustrate a close to or equivalent performance in comparison to exhaustive search approaches.

Motivated by the recent GA innovation the application of new genetic operators to increase genetic diversity are considered. The previous GA applied a single-parent crossover technique, where genetic diversity comes from mutation making the process rather random. Therefore, it can be classified as a Genetic-Inspired Algorithm(GIA). The second extension of the application of the GA is applying two-parent crossover techniques to introduce genetic diversity during both crossover and mutation, thereby decreasing randomness and increasing genetic diversity. The enhanced GA is studied in the context of producing close-to-optimal mapper designs and achieving higher values of LD. Analysis of two-parent crossover techniques show that single-point crossover, multi-point crossover as well as the Davis ordered crossover 1 and Enhanced ordered crossover 2 conforms to LD mapper design constraints. The Davis ordered crossover 1 was chosen over the other crossover techniques because the technique introduced more genetic diversity in offspring chromosomes. The algorithm is tested on 16-ary (symmetric and asymmetric) constellations only. Results show that for 16QAM and 16PSK, the enhanced-GA produced mapper designs that match but do not improve upon existing GA and Exhaustive Search mapper designs. However, the enhanced-GA converged to a solution for both 16QAM and 16PSK systems in less than 15 iterations, while the GIA converged to a solution after more than 100 iterations. The mapper designs produced by the enhanced-GA demonstrated a diversity gain between $\approx 0.5dB$ to $\approx 4dB$ over the GIA mapper designs. A critical comparison study between the LD GAs had been performed. The enhanced-GA is found to be significantly more computationally complex ($\mathcal{O}(M!)$) than the GIA ($\mathcal{O}(M^2)$) but comes with its added advantages such as requiring lower mutation rates (less than 10%) and produces LD mapper designs that match or improve upon existing GA designs. Finally, an observation can be made that the enhanced-GA also requires a significantly lower amount of time to converge to a local or global optimum solution.

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List of Acronyms

ABEP	Average Bit Error Probability
APSK	Amplitude Phase Shift Keying
AWGN	Additive White Gaussian Noise
BER	Bit Error Rate
DVB-s2x	Digital satellite television broadcast standard 2x
ED	Euclidean Distance
GA	Genetic Algorithm
i.i.d	Independent and Identically Distributed
K-HSX	K-point Hypersphere Swap Crossover
LD	Labeling Diversity
MIMO	Multiple-Input Multiple-Output
OX	Ordered Crossover
PEP	Pairwise Error Probability
PSK	Phase Shift Keying
QAM	Quadrature Amplitude Modulation
QAP	Quadratic Assignment Problem
SNR	Signal-to-Noise Ratio
USTLD	Uncoded Space-Time Labeling Diversity

Preface

The research discussed in this dissertation is carried out in the College of Agriculture, Engineering and Science of the University of Kwa-Zulu Natal, Durban, from July 2019 until May 2021 by Shaheen Solwa under the supervision of Dr. Tahmid Quazi and co-supervised by Mr. Bashan Naidoo.

As the candidate's supervisor, I, Tahmid Quazi, agree agree to the submission of this dissertation.

Signed: TAHMID QUAZI Date: 24/05/2021

As the candidate's co-supervisor, I, Bashan Naidoo, agree to the submission of this dissertation.

Signed: BASHAN NAIDOO Date: 24/05/2021

I, Shaheen Solwa, hereby declare that all the material incorporated in this dissertation are my own original work, except where acknowledgement is made by name or in the form of a reference. The work contained in herein has not been submitted in any form for any degree or diploma to any other institution.

Signed: SHAHEEN SOLWA Date: 01/07/2021

University of KwaZulu-Natal, October 16, 2021

Part I

Introduction

1 Overview of Wireless Communications and Application of Artificial Intelligence

Wireless Communications technology has revolutionised the way in which the world connects. More recently, wireless communications have been more prominent in mobile devices such as smartphones. In the last decade alone, the need for high speed, reliable and efficient wireless communications have risen exponentially. The most recent technological advancement in wireless communications include the fifth generation systems (5G) and the current experimental sixth generation wireless systems (6G) [1]. The advancements in wireless communications technology usage leads to bottle necking of data throughput, increased interference, and other destructive shortfalls.

Space-time block coding (STBC) is a recent technique used to achieve reliable, high data rate wireless communications using multiple-input multiple-output (MIMO) systems [2]. STBCs leverage its characteristic of sending and receiving multiple copies of a radio signal through multiple transmit and receive antenna. This mitigates the effects of wireless channel impairments, such as fading. Alamouti [3] was the first to propose an orthogonal, full diversity STBC scheme, which has been extended to other reliable schemes that use two or more transmit antenna. The orthogonality of Alamoutis STBC ensures the decoupling of signals at the receiver of a STBC system with coherent detection [3].

More recently, the uncoded space-time labelling diversity(USTLD) scheme was proposed as a direct extension to Alamoutis STBC [3]. The most significant difference between the Alamouti STBC and the USTLD system is that Alamouti employs only one mapper, while USTLD employs two mappers, hence leveraging on labelling diversity (LD). LD is achieved by using symbol pairs from constellations with different binary mappings. The degree to which LD is achieved depends on the binary mappers used to encode information [4]. The aim of LD mapper design is to position adjacent symbols on a constellation further apart than in its base constellation. A design metric has been suggested in [5] that evaluates the extent to which the mapper has achieved LD. The design metric was of a combinatorial nature, hence too computationally expensive to implement.

LD has been studied in various research, such as in [4]. [4] proposed an algorithmic approach to solving for the optimal LD mapper design by employing an instance of the quadratic assignment problem(QAP). [4] reports that optimality had been achieved, but the approach was too computationally expensive for modulation order $M > 16$. Other LD work in [6], [7] suggests most algorithmic approaches are, naturally, computationally expensive. Other limitations of current mapper design approaches include i) symmetry based heuristics cannot be applied to asymmetric constellations and ii) heuristics may not produce good quality mapper designs. This prompted research into applying artificial intelligence(AI) to LD mapper design.

Patel et al [8] proposed the use of a Genetic Algorithm(GA) to solve for near optimal mapper design. GAs are powerful meta-heuristic tools that leverage a population-iteration based approach to solving optimization problems. By employing the GA, it is ensured that significantly less computational and time resources are used when compared to other algorithmic approaches. From [8], the GA is to designed to produce mapper designs irrespective of constellation size or shape. Hence, both symmetric, asymmetric and high-density mapper designs can now be produced without any limitations.

In this dissertation, the authors apply the GA from [8] to high-density M-ary constellations (symmetrical and asymmetrical) to design LD mappers for two transmit USTLD systems. Furthermore, a proposed enhancement on the GA is made by the application of two-parent crossover techniques.

2 Notation

In terms of notation, this dissertation contains the following mathematical notations:

N_T and N_R are the number of transmit and receive antenna. All vectors and scalars are represented by Bold Face and italics respectively. $\|\cdot\|_F$ represents the Frobenius norm while $|\cdot|$ represents the absolute value of the euclidean distance between transmitted and estimated received symbol. $\arg\min_w$ represents the minimum argument with respect to w. $\binom{n}{k}$ is the number of combinations that can be produced from n total number of objects by choosing k number of objects.

3 Diversity Techniques

Due to the fluctuation of signal power in a wireless channel, signal power decreases substantially, at the point which the channel is said to be fading. Diversity is a technique used in MIMO systems that makes up for channel impairments by employing wireless link enhancements at a low cost [9]. Diversity is used to reduce depth and duration of the fading experienced by the receiver in a flat-fading channel [10]. This technique uses multiple inputs at the receiver such that the fading of the received signals are i.i.d, i.e. the fading channel is uncorrelated. If one signal path undergoes a significant fade, another signal path may contain a strong signal at the receiver. Hence, information codewords are transmitted as multiple copies of each other that do not undergo significant fading [11]. The mean power in each diversity technique branch are approximately equal [11]. The following types of diversity are discussed with respect to the dissertation.

3.1 Space Diversity

Space diversity is a technique whereby multiple transmit and receive antenna are used to decrease channel impairments due to physical separation of the antennas by a wavelength size of one half or more [12]. The actual antenna distance separation decides the channel correlation among branch signals and the size of mutual coupling between adajcent branch antenna [12]. Spatial diversity is employed due to its low cost, simplicity and its ease of implementation. Coupled with these advantages, spatial diversity also provides a gain in error performance without the need of sacrificing bandwidth of the transmitted power sources.

3.2 Time Diversity

Time diversity utilizes channel coding and interleaving to tackle fading at a cost of added delay and bandwidth efficiency loss [10]. In this scheme, multiple copies of information codewords are transmitted over multiple time-slots, providing full diversity privileges [12]. If the time between transmitted signals are sufficiently spaced out, the sequential amplitude signals will be uncorrelated, and the time spacing should be at least the reciprocal of the fading bandwidth [13]. Another technique to achieving time diversity is to introduce redundancy into the transmitted signals in the temporal domain by using repetition of channel coding.

3.3 Labelling Diversity

The idea of labelling diversity(LD) was first introduced for bit-interleaved(BI) coded systems with iterative decoding [5]. In these systems, convolutional coding was used, hence higher power consumptions and higher latencies were experienced. More recently, due to these setbacks, LD was applied to uncoded systems [4, 6, 7]. In 2014, Xu et el [5] proposed a scheme that was a direct extension to the Alamouti STBC, called uncoded space-time labelling diversity(USTLD). In USTLD systems, LD is achieved by employing binary mappers with different binary encodings. The end-goal of LD mapper design is to place adjacent points on a constellation further apart than in its base constellation.

4 Space-Time Coding

Space-time coding (STC) is a channel code that is widely adopted for MIMO schemes for its power and spectral efficiency and does not sacrifice diversity gains over wireless channels [13]. The coding scheme uses a combination of conventional channel coding techniques, modulation schemes and a MIMO structure within the design criteria [13]. STC schemes introduce spatial and temporal correlation into signals that are transmitted from different antennas which provide diversity gains at the receiver [10]. This scheme also provides a coding gain over the uncoded scheme without the need to sacrifice additional bandwidth resources [12]. The STC scheme also contributes to an improved error performance rate when compared to uncoded STC schemes [10]. Various forms of STC schemes are adopted for MIMO techniques. For this dissertation, only the Space-Time Block Code is considered.

5 Space-Time Block Coding

Space-time block coding (STBC) is a simple technique used in wireless communications that mitigate the effects of fading channel impairments due to multipath fading, hence, improving link reliability in MIMO systems. STBC systems make use of redundancy of several transmissions between transmitter and receiver by sending multiple versions of information signals with a good probability that some signals are less attenuated than others [14]. At the receiver these signals are combined optimally [3]. Therefore, overall link reliability is improved [3]. A novel transmit diversity scheme using STBC was proposed by [3], called the Alamouti STBC (ASTBC). The ASTBC employed a $N_T N_R$ MIMO system ($N_T = 2$) that transmits information codewords (symbol-pairs) in two time slots. The ASTBC achieves full-diversity error performance with symbol rate of one [3]. The modulated codewords are transmitted over multipath fading channels with additive white gaussian noise (AWGN), where fading is assumed to be constant over the two time slots and assumed different values from one pair of time slots to another [3]. An assumption is made that perfect channel state information (CSI) is known at the receiver. From [3], the transmission matrix of the ASTBC is mathematically given as:

$$A_x = \begin{bmatrix} x_1 & x_2 \\ -x_2^* & x_1^* \end{bmatrix}$$

Where x_1 and x_2 are symbols from a M-QAM or M-PSK constellation transmitted in time slot 1 and x_1^* and x_2^* are the complex conjugate symbol pairs that are transmitted in time slot 2 from each antenna. The ASTBC is an orthogonally full-rate STBC system, such that $A^H A = (|x_1|^2 + |x_2|^2)I_2$ [3], [10]. This is exploited for low complexity (LC) linear decoding.

6 Uncoded Space-Time Labelling Diversity

Uncoded space-time labelling diversity (USTLD) is a recent innovated STBC scheme and is a direct extension to the Alamouti STBC [8]. USTLD employs a $N_T N_R$ MIMO structure and implements labelling diversity (LD) to improve error performance in the presence of multi-path fading. The USTLD scheme achieves space diversity by employing N_T transmit antenna, time diversity by transmitting symbols over t time slots and LD by employing N_T number of binary constellations which reduce redundancy [5]. USTLD has a lower decoding complexity and offers better energy efficiency when compared to coded systems such as bit-interleaved space-time coded modulation (BI-STCM) [8]. The transmission matrix of USTLD systems are not orthogonal, hence a higher detection complexity is found at the receiver since the maximum likelihood (ML) detector performs an exhaustive joint symbol pair detection over all possible symbol pairs [13].

7 Labelling or Mapping Diversity

The labelling diversity (LD) problem is stated as "Adjacent symbols on another constellation has to be spaced further apart than in its consequent base constellation". Samra et al [4] proposed an exhaustive search approach to designing LD mappers, but was reported to be too computationally expensive for constellations of size $M > 16$, where M is the modulation order, due to the search space. Xu et al [5] proposed a LD technique for symmetric M-QAM and M-PSK constellations that swapped diagonal symbol pairs. [7] proposed an innovative matrix technique that ensured adjacent rows and columns in the constellation are spaced further apart by bit-flipping. In essence, current mapper design techniques have the following constraints:

- Existing techniques can only be applied to constellations with symmetry
- Are highly computationally expensive for $M > 16$

8 Application of Artificial Intelligence to the Labelling Diversity Problem

Recently, Patel et al [8] proposed applying AI in the form of a genetic algorithm(GA) to solve the constraints surrounding the LD problem. By applying AI, not only do we solve for solutions faster, we also use fewer computational resources when compared to algorithmic and exhaustive search approaches. Hence, the next section discusses GAs and applying it to the LD problem.

9 Genetic Algorithms

9.1 Design Optimization and Meta-Heuristics

9.1.1 Design Optimization

An excellent design technique to find optimal solutions to the given LD problem is by employing design optimization and meta-heuristic algorithms. Design optimization is the problem of selecting a set of design parameters that will optimize a given objective function [15]. Its interests can be found in many design problems, especially NP-hard problems. For example, when designing the most optimal route for a salesman to travel from one city to another, one needs to consider the distances from the start point to every other point such that each point is only visited once [16]. Design optimization can be classified into two categories, namely functional and combinatorial optimization [17]. Functional optimization aims to optimize a given cost function, whereas combinatorial optimization considers possible, discrete combinations of parameters that form finite states of the problem that affects the optimization objective is a certain way. Major problems in combinatorial problems are:

- Solution space is exponentially large
- Relationship between design parameters and optimization objectives are not clearly understood, hence they cannot be solved through analytical methods.

9.1.2 Meta-Heuristics

Meta-heuristic algorithms are efficient tools that solve combinatorial optimization problems. They can be formally defined as an iterative process that guides a sample heuristic by combining different concepts for exploration and exploitation of a given search space. Learning methods are used to structure information such that near optimal solutions can be found efficiently. Meta-heuristic algorithms are approximate rather than deterministic [17]. Deterministic algorithms always find the most optimal solution in a given time-frame for a finite size instance of a problem [17], but lead to high computational costs and computation times. Approximate algorithms(meta-heuristics), however, sacrifice the need to find the most optimal solution for finding good solutions in a small amount of time [16]. Most meta-heuristic algorithms rely on probabilistic decisions to produce good solutions in a search space. The only difference between a pure random search and a meta-heuristic is that instead of only relying on randomness, meta-heuristic randomness is not used blindly, but in an intelligent, biased form. The most common and widely-adopted methodologies of meta-heuristics include GAs, neural networks (NN) and simulated annealing (SA) [17]. Due to this dissertation being one of combinatorial optimization, GAs are used for its robustness to produce high-quality solutions and parse through a search space quickly by relying on biologically inspired operators such as crossover and mutation.

9.1.3 The Logic of Genetic Algorithms

9.1.3.1 Chromosome Representation

The very first step in a GA is to represent candidate solutions in the form of a chromosome. Each value within a chromosome is known as genes. Different problems require different representations of chromosomes. For example, the travelling salesman problem (TSP) requires the use of floating-point values to represent the distance from the starting point to other points on the map. However, there is also not one distinct way to represent a chromosome. The TSP problem can also be represented using key-value pairs that place each city with a corresponding $X - Y$ co-ordinate pair. A typical chromosome can be represented as:

$$\delta = [m_1, m_2, \cdots, m_i] \tag{1}$$

Where δ is the chromosome and m_i is each gene within the chromosome and $i \epsilon [0 : S - 1]$ where S is the maximum length of the chromosome.

9.1.3.2 Generation of a Population

The population contains all chromosomes in a generation. There is no accepted norm of the population size per problem instance [17]. Population sizes are chosen based on intuition, either by using small population sizes or extremely large population sizes that exceed the solution space. Each of these has its own trade-offs, with the most notable being:

- The larger the population size, the quicker the solution space can be explored.

- The smaller the population size, convergence is found quicker.

The above two points however, are not confined to either of them. For example, the larger population size could achieve convergence faster than a smaller population size while the smaller population size may produce more fit chromosomes.

9.1.3.3 Fitness Function

For a particular problem, the fitness of a chromosome can be arrived at in an infinite number of ways as there are an infinite number of equivalent representations [15]. For example, the transformation of a $1-$bit representation into a $1+1-$bit representation can be performed without changing the fitness function by ignoring the new bit. The most important requirement for a fitness function is as the population gets closer to a solution, the relative fitness values should be higher. This is very loosely defined and does not appeal to practicality. The fitness function has to reward chromosomes in an way that pushes the population to a desired solution.

9.1.3.4 Parent Selection

After chromosomes are placed into the population, chromosomes are selected based on their fitness to be parents for future generations. In a few cases, the most fit chromosomes from the i-th generation can be taken over into the $i+1$-th generation often referred to as elitism. However, in other cases, chromosomes are selected based on their contribution to genetic material. There exists many selection strategies, hence this indicates that there is no agreement into which selection strategy is the most optimal [16].

9.1.3.5 Crossover Operator

Crossover is a technique by which parent chromosomes that are selected pass on their genetic material to the chromosomes of the next generation (offspring). The most common type of crossover is called the K-point crossover. The K-point crossover takes two selected parent chromosomes from the population, splits each chromosome K number of times, and fragments from each are swapped to produce two offspring chromosomes. The example in Fig. B.5 further illustrates the use of the K-point Crossover.

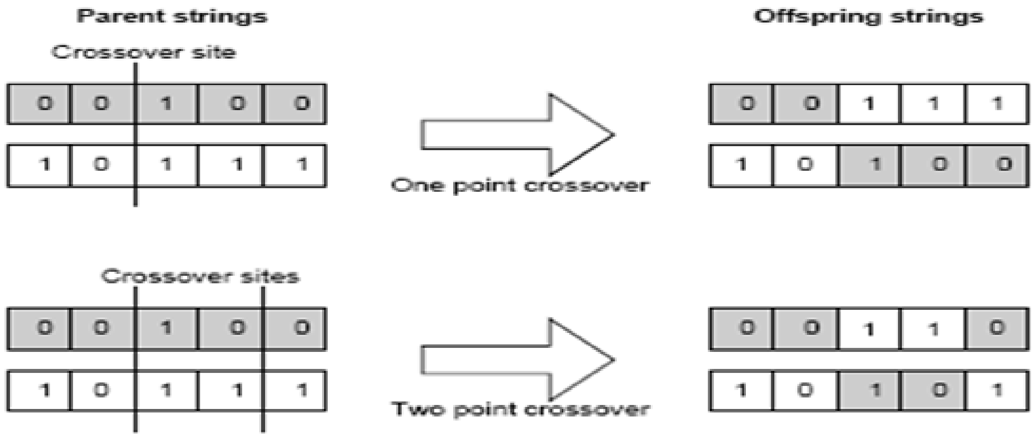

Fig. 1: K-Point Crossover of two Parent Chromosomes

In addition to the K-point crossover, other crossover techniques such as the Davis ordered crossover (OX1), partially mapped crossover (PMX) and cycle crossover(CC) can also be applied to increase genetic diversity. Currently, there is no agreement as to which crossover technique is the most optimal [17]

9.1.3.6 Mutation Operator

Mutation is a probabilistic event that an offspring chromosome undergoes further change after crossover. Generally, during each generation, each chromosome in the population will have a very small probability (typically $< 10\%$) of undergoing further change. Mutation rates do not have an optimal parameter but can be set with the value that works best with the particular problem at hand [17]. Actually, it can be easily shown that different mutation rates will allow the GA to converge more quickly by varying the problem size.

Initially, mutation was inspired by biological evolution rather than practical requirement [17]. Nevertheless, mutation helps a population avoid being stuck in a local optima. In some cases, pre-mature convergence is found when an entire population converges uniformly to a sub-optimal solution. Without mutation, populations have no means to further change to a more optimal solution since all chromosomes in the population would be identical [16].

9.1.3.7 Application and Research

Since the creation of the GA, applications have been found in many areas of research. In the area of design engineering, [18] used a GA to produce design parameters for manufacturing cells while [19] used a GA for the kinematic design of turbine blade fixtures. More recently, [20] used a GA to design detection strategies for face recognition. In the area of cloud computing, GAs are being used for Load Balancing strategies for infrastructure.

Due to the GA being non-problem-specific, the application is not confined within problems of the physical realm, and therefore can be applied to many combinatorial optimization problems in distinct areas.

9.1.3.8 Computational Complexity

The study of computational complexity aims to classify classes of problems based on the rate of growth of space, time and other essential units of measure with respect to the size of the input. The study aims to answer one important question, what problems are computationally controllable in the sense that the resource requirements do not increase significantly with larger instances [17]. A complexity analysis, on the other hand, is the method of providing reason behind the advantages and disadvantages of using a particular approach over other existing or new approaches. To illustrate the difference between computational complexity and complexity analysis, consider the sort problem (sorting n number of elements in a pre-defined manner) [21]. If there is only a few elements that are out of order, the algorithm will converge much quicker than if all elements are out of order [21]. Therefore, an analysis is based on problem instances that is concerned with the features of the particular instance that causes it to converge slower than others. The computational complexity analysis, however, is concerned with the complexity of the problem over all possible instances, sizes and representations [16].

9.2 Research and Objectives

9.2.1 The Original Genetic Algorithm

The Genetic-inspired algorithm(GIA) was proposed by [8] to produce LLD mapper designs irrespective of constellation shape or size. Initially, the GIA was only applied to 16-, 32- and 64-ary constellations. Hence the first extension was the application of high-density M-ary constellations to the GIA. Furthermore, [8] did not perform a thorough computational complexity analysis on the GIA. Therefore, the second extension to the GIA was to perform an overall computational complexity analysis and compare it to other existing exhaustive and algorithmic approaches.

9.2.2 The Enhanced-Genetic Algorithm

The GIA in [8] was proposed as a simple Crossover-Mutation-Evaluation approach, and did not employ any biological techniques such as a two parent crossover or the carrying over of the most fit chromosomes(elitism) from each generation. Furthermore, genetic diversity was introduced only during the mutation stage, thereby being almost purely random. Hence, the following enhancements were made to improve the Genetic Algorithm's ability to produce close-to-optimal LD mappers for M-ary constellations:

The first proposed enhancement to the GIA in this dissertation is to introduce elitism into the GIA. Elitism is the process that carries over the best chromosomes from the population of the i-th generation into the $i+1$-th generation. By including elitism, not only do we ensure that the best chromosomes are kept in future generations, we also allow the search to be expanded through other channels as well, hence producing better offspring. The second enhancement of the GIA is introducing biological or two-parent crossover techniques, hence increasing diversity among offspring chromosomes. The crossover technique used in [8] followed a single-parent, virtual second-parent structure imitating the reproduction of plant organisms. The main advantage of using two-parent crossover techniques is that randomness is reduced. Again, a computational complexity analysis will be performed and compared to the GIA.

9.3 Contributions

9.3.1 Chapter A

S. Solwa, A Performance Study of a Genetic Algorithm Based Mapper Design for Uncoded Space-Time Labelling Diversity. The summary of the chapter is as follows: The extent to which uncoded space-time labelling diversity (USTLD) mappers achieve labelling diversity (LD) depends on the binary mappers used to encode information. Current mapper designs, however, are limited and constrained due to high computational costs and do not extend to larger constellations. The current works based on designing LD Mappers using the genetic algorithm (GA) has not been exhaustively tested for higher order and irregular constellations. Due to improved complexity, this chapter tests the GAs ability to produce LD mappers for higher order constellations as well as irregular constellations that do not exhibit any symmetry. Additionally, this chapter uses the QAP optimization algorithms found in previous studies as a benchmark to verify that the GA does indeed have a reduced space complexity. The algorithm was tested on 128-, 256- and 512-ary QAM, 64-, 128- and 256-ary PSK and 32-, 64-, 128- and 256-ary APSK and irregular APSK constellations, respectively. The LD mappers produced by the GA match the current best heuristic designs for 128QAM, 256QAM and 512QAM. In the case of PSK constellations, the 64PSK, 128PSK and 256PSK constellations exhibited a gain of $\approx 5dB$, $\approx 4dB$ and $\approx 8dB$ when compared to the best available heuristic designs. Next, 128APSK and 256APSK constellations produced showed gains of $\approx 3dB$ and $\approx 6dB$ respectively. Finally, the GA was tested on irregular, non-symmetrical 32APSK, 64APSK, 128APSK and 256APSK. These constellations exhibited gains of $\approx 5dB$, $\approx 17dB$, $\approx 5dB$ and $\approx 5dB$ over the Alamouti STBC system respectively. The GA was found to have a computational complexity of $\mathcal{O}(M^2)$ which is exponentially less expensive than the exhaustive search and other algorithmic techniques. Additionally, the GA is able to produce LD mapper designs that match or improve upon the LD achieved by exhaustive search and algorithmic approaches.

9.3.2 Chapter B

S. Solwa, An Ordered Crossover Approach to Designing Labelling Diversity Mappers. The summary of the chapter is as follows: Genetic algorithms(GA) is a population-based search optimization technique that mimic the process of evolution and natural selection. GAs are an effective way to finding feasible solutions to complex problems. Recently, GAs have been applied to designing LD mappers, and have shown great promise. However, the approach implemented did not apply biological processes during 'mating', and therefore, could not be classified as a GA, but rather a genetic-inspired algorithm(GIA). Since the GA for designing LD mappers was developed, no further studies have been produced to suggest any improvement to the system. In reproduction with two distinct parents, the offspring acquires genetic diversity from the crossover are from the distinct parent genes. When there is only one parent, genetic diversification is gained only from mutation. In such a case, evolution becomes a random process rather than one that is guided by parent propensities; and the promised value of the GA is not realised. This chapter investigated four biological crossover techniques and two hybrid techniques, namely, single point, multi-point, OX1 and OX2 and cycle and partially mapped crossovers, respectively. The proposed GA with the Davis ordered (OX1) crossover technique was tested on the 16QAM, 16PSK, 16APSK and three 16APSK constellations that do not exhibit any diagonal symmetry. In the case of symmetric 16QAM and 16PSK, mapper designs produced by the proposed GA had matched but not improved upon existing heuristic and the previous GA mapper designs. However, results show that for the Asymmetric 16APSK and Single Symmetry 16APSK constellations, LD values have increased from $\omega(\mu_1, \mu^{Patel}_{GA,AS-16APSK}) = 0.0981$ to $\omega(\mu_1, \mu^{Davis}_{GA,AS-16APSK}) = 0.3008$ and $\omega(\mu_1, \mu^{Patel}_{GA,SS-16APSK}) = 0.4020$ to $\omega(\mu_1, \mu^{Davis}_{GA,SS-16APSK}) = 0.4053$ respectively, and led to

$\approx 4dB$ and $\approx 2dB$ gains respectively when compared to the results of mappers produced by the GIA. In the cases of the 11+5APSK and 16APSK, even though improvement in the LD of the mapper design is observed ($\omega(\mu_1, \mu_{GA,115APSK}^{Davis}) = 0.7171$ from $\omega(\mu_1, \mu_{GA,11+5APSK}^{Patel}) = 0.6766$) for the 11+5APSK constellation and $\omega(\mu_1, \mu_{GA,16APSK}^{Patel}) = 0.3685$ to $\omega(\mu_1, \mu_{GA,16APSK}^{Davis}) = 0.5427$ for the 16APSK constellation), only a small gain of $\approx 0.5dB$ was achieved. More significantly, the proposed GA achieved significant performance improvement in terms of time complexity but used more computational resources $(\mathcal{O}(M!))$ when compared to the GIA $(\mathcal{O}(M^2))$. A test on mutation rates on the proposed GA was performed, with the objective of utilizing lower mutation rates instead of relatively high mutation rates used in the GIA. Results have shown that higher mutation rates are needed for single parent reproduction, and thus the process is purely random. However, the converse is also true, where two parents produce a set of offspring chromosomes and thus, randomness is reduced and genetic diversity is increased. The results also showed that a more guided search (mating of two parents) is more effective at genetic diversity than pure random searches as in the case of single parent reproduction.

9.4 Structure of the Dissertation

The dissertation work presented has been detailed in chapter A and chapter B and is presented in Chapter II and Chapter III respectively. Chapter IV concludes the dissertation and provides possible future research objectives and direction.

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Part II

Included Chapters

Paper A

A PERFORMANCE STUDY OF A GENETIC ALGORITHM BASED MAPPER DESIGN FOR UNCODED SPACE-TIME LABELING DIVERSITY

1 Abstract

The extent to which uncoded space-time labelling diversity (USTLD) mappers achieve labelling diversity (LD) depends on the binary mappers used to encode information. Current mapper designs, however, are limited and constrained due to high computational costs and do not extend to larger constellations. Recently, a genetic algorithm(GA) has been proposed to produce LD mappers irrespective of size of shape of the constellation. The current works based on designing LD mappers using the GA has not been exhaustively tested for higher order and irregular constellations. Due to improved complexity, this chapter tests the GAs ability to produce LD mappers for higher order constellations as well as irregular constellations that do not exhibit any symmetry. Additionally, this chapter uses the QAP optimization algorithms found in previous studies as a benchmark to verify that the GA does indeed have a reduced computational complexity. The algorithm was tested on 128-, 256- and 512-ary QAM, 64-, 128- and 256-ary PSK and 32-, 64-, 128- and 256-ary APSK and irregular APSK constellations, respectively. The LD mappers produced by the GA match the current best heuristic designs for 128QAM, 256QAM and 512QAM. In the case of PSK constellations, the 64PSK, 128PSK and 256PSK constellations exhibited a gain of $\approx 5dB$, $\approx 4dB$ and $\approx 8dB$ when compared to the best available heuristic designs. Next, 128APSK and 256APSK constellations produced showed gains of $\approx 3dB$ and $\approx 6dB$ respectively. Finally, the GA was tested on irregular, non-symmetrical 32APSK, 64APSK, 128APSK and 256APSK. These constellations exhibited gains of $\approx 5dB$, $\approx 17dB$, $\approx 5dB$ and $\approx 5dB$ over the Alamouti STBC system respectively. The GA was found to have a computational complexity of $\mathcal{O}(M^2)$ which is exponentially less expensive than the exhaustive search techniques. Additionally, the GA is able to produce LD mapper designs that match or improve upon the LD achieved by exhaustive search techniques.

Index Terms - Genetic algorithms, labelling diversity, mapper design, quadratic assignment problem, complexity, STBC

2 Introduction

Uncoded space-time labelling diversity (USTLD) is a recent innovative multi-diversity scheme proposed by Xu et al [1], and is a direct extension and improvement upon the Alamouti space-time block codes (ASTBC). The original work proposed by [2] used a multiple-input multiple-output (MIMO) structure with two transmit antenna and N_R receive antenna. By employing the MIMO structure and implementing labelling diversity (LD), the bit error rate (BER) is reduced. Initially, LD was proposed for bit-interleaved(BI) coded systems, which employed convolutional coding. When compared to BI systems, USTLD has a lower decoding complexity and offers better efficiency [1]. Other areas of the application of LD included decode-and-forward relay systems [3] and hybrid automatic requests (ARQs) [4]. In order to transmit a single codeword, there exists M possible symbol pairs that can be transmitted over the two time slots. However, at the receiver, a total of M^2 possible symbol pairs could be detected. Therefore, since on M out of the possible M^2 symbol pairs can be detected, the error performance is improved [5].

The extent to which USTLD achieves LD depends on the design of binary mappers Ω_1 and Ω_2. The aim of the mapper design for USTLD systems is to place adjacent points on the constellation further apart in the second constellation than in its base constellation. From literature, for a modulation order M, there exists $M!$ possible designs [5]. In the context of USTLD systems with two binary mappings, there exits $(M!)^2$ possible mapper designs [5]. Due to the large search space, research on determining mapper optimality remains open [5]. Although the research remains open, both Patel et al [5] and Quazi et al [6] have recently proposed design metrics to prove optimality for these mappers.

Xu et al [1] proposed a design metric for these mapping structures, as well as a symmetrical-based heuristic mapper design for M-ary quadrature amplitude modulation (M-QAM) and M-ary phase shift keying (M-PSK) constellations. Further work done by Quazi et al [6] exploited the symmetrical-based design to extend LD for M-ary amplitude phase shift keying (M-APSK) constellations. Other heuristic-based designs have been proposed in [3] for 16QAM and 64QAM. Other research that has been done on LD, such as [7], proposed an algorithmic design to achieve a 16QAM and 16PSK constellations for convolutionally coded systems. A more generalised approach can be found in [4], which can be seen as an instance of the quadratic assignment problem (QAP). [4] shows that to design x LD mappers, there exists $(M!)^x$ possible solutions to the QAP. Due to the large search space, [4] uses the lower-bound approach that iteratively find x number of optimal LD mapper solutions one at a time. Although the search space complexity is reduced when compared to the QAP, [4] reports that the algorithm is too computationally expensive for $M > 16$. The reliance on

heuristics for mapper designs constrains the constellations that can be applied to USTLD systems [5]. Current limitations for designing LD mappers are as follows; i) symmetry based heuristic mapper designs cannot be applied to asymmetric constellations. Also, these heuristic mapper designs may not produce good mappers for symmetrical ones [1, 5], ii) current heuristic and exhaustive algorithms for designing LD mappers are too computationally expensive and infeasible [4] for $M > 16$, iii) current heuristic designs for symmetrical and asymmetrical constellations do not exceed $M = 64$ and iv) the current proposed Genetic Algorithm(GA) has not been tested on producing LD mappers for $M > 64$. Thus, to overcome these limitations, the aim of this chapter is to design LD mappers using the GA proposed in [5] for higher order M-ary constellations and perform a complexity study to assess the work done in [5]. The authors in [2] report that by employing the GA, LD mappers can be produced unconstrained by the modulation order or symmetry. The use of Higher order modulation schemes has become very attractive for applications to wireless communications due to its high spectral efficiency, higher throughput and data rate within a limited bandwidth. Higher order modulation schemes have recently been investigated and implemented in 5G and in LTE-A based systems [8].
According to Chen et al [9], APSK constellations have the following advantages: i) reduced sensitivity to carrier synchronization errors due to the small angular separation between constellation points, ii) channel estimation and complex equalization can be alleviated which simplifies the receiver, and iii) non-linear (phase and amplitude) distortion caused by the high power amplifier which has to be operated close to saturation to improve power efficiency is alleviated. An algorithmic optimization technique carried out by [5] resulted in irregular, asymmetric constellations that improved on the original APSK constellation by $\approx 1dB$ for both the 16APSK and 64APSK modulation schemes. This prompted studies of applying these asymmetric constellations to USTLD systems as seen in [5].

Patel et al [5] produced a GA based mapper design for USTLD systems but did not assess the computational complexity of the algorithm. Other heuristic and QAP mapper designs proposed in [1, 3, 4, 10] are deemed infeasible due to the high computational costs involved $O(M^5)$. Hence, the second contribution of this chapter is to investigate the complexity of different mapper design techniques. Additionally, the complexity analysis investigates different optimization techniques such as the QAP solvers found in [4] and [3]. The authors only consider Space Complexity, as Time Complexity of the GA outperforms the other optimization techniques [11].

The remainder of the chapter is structured as follows: Section 2 describes the system model and discusses the USTLD system. This section also looks at the possible design metric benchmark (fitness function) that was extracted from [1]. Section 3 discusses the QAP [12] and the proposed GA by [5]. In Section 4, analytical results are verified with Monte Carlo simulations. The results were based on the mapper designs produced by the GA and compared to other heuristic designs and the Alamouti STBC. Section 5 expands and discusses more in detail about performance studies based on space complexity and compares current heuristic and exhaustive mapper deigns to that of the GA, thereby assessing the work done in [5]. The final conclusion is discussed in Section 6.

In terms of notation for this chapter, vectors and scalars are in boldface and italics respectively. $\|\cdot\|$ represents the Frobenius norm of a vector, $|\cdot|$ represents the absolute value of a scalar and $(\cdot)!$ represents the factorial of a scalar.

3 System Model

Consider a MIMO system with $N_T = 2$ and N_R receive antenna. A codeword of length $r = log_2(M)$ is passed through $\Omega_1$and Ω_2 to produce symbols $\Omega_1(L)$ and $\Omega_2(L)$ respectively. The USTLD system employs a MIMO structure with two transmit antenna and N_R receive antenna. The USTLD system transmits two codewords $L_{(1)}$ and $L_{(2)}$ across two consecutive time slots. When transmitting information codewords, the binary mapper Ω_t in the $t-th, t \ \epsilon \ [1:2]$, time slot is used. Thus, the $N_R \times 1$ received signal vector can be represented as:

$$y_t = \sqrt{\frac{\rho}{2}}\left[h_{t,1}\Omega_1(L_{(1)}) + h_{t,2}\Omega_2(L_{(2)})\right] + \boldsymbol{n}_t \tag{A.1}$$

In (A.1), $\sqrt{\frac{\rho}{2}}$ is the average signal-to-noise ratio at each receiver and $\boldsymbol{n}$ is the $N_R \times 1$ Additive White Gaussian Noise vector. Each entry of the vector matrix $\boldsymbol{n}$ follows a complex normal distribution with zero mean and variance of $\frac{E_s}{2}$ per dimension. The vector $h_{(t,u)}, t, u \ \epsilon \ [1:2]$ is the multipath fading experienced by the symbol that is transmitted from antenna u in time slot t. The fading is assumed to be frequency flat and follows a Rayleigh amplitude distribution with zero mean and a unit variance. Over the two time slots, fading can either be fast of quasi-static. The phase distribution of the noise and fading is assumed to be uniform. At the receiver, the maximum likelihood(ML) detection is used to estimate the transmitted information codewords. Assuming that perfect channel state information is available at the receiver, the detection may be formulated as:

$$\widehat{L_{(1)}}, \widehat{L_{(2)}} = \arg \min_{L_{(1)},L_{(2)}} \left\| y_t - \sum_{u=1}^{2} \sqrt{\frac{\rho}{2}} h_{(t,u)} \Omega(\widehat{L_{(u)}}) \right\|^2, t \ \epsilon \ [1:2] \tag{A.2}$$

In (A.1) and (A.2), the estimated codewords at the receiver is given as $\widehat{L_{(1)}}, \widehat{L_{(2)}}$ and $L_{(1)}, L_{(2)}$ Are the symbols that are being transmitted over the consecutive time slots.

3.1 Theoretical Error Performance of USTLD

Based on the model described in the previous section, an analytical union bound was used to derive the average bit error probability (ABEP) of the USTLD system in [1]. The resulting expression is:

$$ABEP(\rho) = \frac{1}{Mr} \sum_{L=0}^{M-1} \sum_{\widehat{L}=0}^{M-1} N(L, \widehat{L}) P(L \to \widehat{L}) \tag{A.3}$$

Where M is the number of points in the constellation, $N(L, \widehat{L})$ is the number of bit errors between the transmitted and the estimated received symbol. P$(L \to \widehat{L})$ is the pairwise error probability of one symbol being detected perfectly and the other being detected with error. It is shown from [1] that the PEP can be given as:

$$P(L \to \widehat{L}) = \frac{1}{4n} \prod_{t=1}^{2} \left(1 + \frac{\rho d_t^2}{8}\right)^{-N_R} + \frac{1}{2n} \sum_{k=1}^{n} \prod_{t=1}^{2} \left(1 + \frac{\rho d_t^2}{8sin^2(\frac{k\pi}{2n})}\right)^{-N_R} \tag{A.4}$$

Where n is a large integer, $n > 10$, and $d_t = \left|\Omega_t(L) - \Omega_t(\widehat{L})\right|, t \ \epsilon \ [1:2]$ is the Euclidean distance between the points L and $\widehat{L}$ on the constellation of Ω_t. For a detailed derivation, readers are pointed to the original literature by Xu et al [1][eqn. $1-3$]. The authors of [1] show that at high SNR, $\frac{\rho d_t}{8} >> 1, t \ \epsilon \ [1:2]$. At high SNR values, the PEP can be reduced to the following:

$$P(L \to \widehat{L}) = \frac{1}{4n} \left(\frac{\rho d_1^2}{8} \frac{\rho d_2^2}{8}\right)^{-N_R} + \frac{1}{2n} \sum_{k=1}^{n} \left(\frac{\rho d_1^2}{8sin^2(\frac{k\pi}{2n})} \frac{\rho d_2^2}{8sin^2(\frac{k\pi}{2n})}\right)^{-N_R} \tag{A.5}$$

The result in (A.5) indicates that at high SNR, the ABEP of USTLD systems is dominated by the product Euclidean distance $d_1 d_2$. Thus, the minimum product Euclidean distance sets an error floor, which gives rise to a design metric used to evaluate the extent to which mappers Ω_1 and Ω_2 achieve LD. The metric is given as:

$$\phi(\Omega_1, \Omega_2) = \min_{L,\widehat{L} \ \epsilon \ [0:M-1], L \neq \widehat{L}} \left[\prod_{t=1}^{2} \mid \Omega_t(L) - \Omega_t(\widehat{L}) \mid \right] \tag{A.6}$$

Higher values of (A.6) indicate that more LD has been achieved. Therefore, the objective of the mapper design is to maximise the minimum product Euclidean distance to produce a second mapper that achieves LD. This process can be described as an instance of the QAP [1, 4].

4 labelling Diversity Mapper Design

4.1 Quadratic Assignment Problem

The QAP is a labelling optimization problem that assigns each of M variables to M locations, in order to optimise a cost function [12]. In the context of mapper design, M-ary constellation variables are each of the constellation points $P, P \; \epsilon \; [0 : M-1]$ and their respective locations are the constellation points. The cost function for optimisation is given in (A.6). For this particular application, the QAP has $M!$ complexity which exceeds 10^{13} for constellations $M > 16$. In order to decrease computation complexity, a GA can be applied to find a solution. This GA is described in the next section.

4.2 Genetic Algorithm for labelling Diversity Mapper Design

4.2.1 Genetic Coding

With any GA, the first step is to represent a candidate solution to the problem in the form of a chromosome, Φ. Each chromosome, Φ, contains information known as Genes. Each gene, $\iota_i, i \; \epsilon \; [0 : M-1]$, represents a point on the constellation and the information contained in the Gene is the label associated with it. A single chromosome can be defined as:

$$\Phi = [\iota_0, \iota_1, \ldots, \iota_{M-1}] \tag{A.7}$$

Each chromosome represents a unique permutation of distinct labels, and therefore, no label can be duplicated in, or excluded from a chromosome. A set of p chromosomes represents the population and is denoted by P_t. The initial population, $P_t^{(0)}$, contains a set of randomly chosen chromosomes. Where heuristic and exhaustive search mappers are available, these are encoded as chromosomes and are added to the initial population. This ensures that the GA will either match or improve on the best heuristic design available [12]. It is important to note that the terms chromosome and constellation will be used interchangeably. Each chromosome in the population will take the following form:

$$P_t = [\Phi_0, \Phi_1, \ldots, \Phi_{M-1}] \tag{A.8}$$

4.2.2 Crossover Operator

For developing secondary mappers, Patel et al [5] designed a new crossover technique called the κ-hyper-sphere swap crossover (κ-HSX). The κ -HSX swaps κ number of points from parent chromosomes to produce offspring chromosomes. From the original work [5], parent chromosomes are selected at random. A random gene is chosen on the first parent chromosome and the same gene is chosen on the second parent chromosome. A Hyper-sphere of radius $\Re$ is then constructed around the randomly chosen gene such that the Hyper-sphere encloses all adjacent neighbours on both parent chromosomes. Offspring chromosomes are then produced by swapping genes with the chosen random gene that fall outside of the Hyper-sphere κ number of times. This ensures that offspring chromosomes will have different adjacent neighbours when compared to its parent chromosomes, hence increasing the value of LD achieved. For a detailed study, the authors refer the reader to the original work, section III-B2 [5].

All combinations of parent chromosomes are crossed over, each producing a pair of offspring chromosomes. Therefore, the total size of the population after crossover in the $i - th$ iteration after crossover can be denoted as:

$$\chi^{(i)} = P_t + 2 \times \binom{P_t}{2} = P_t + \frac{P_t!}{(P_t - 2)!} = P_t^2 \tag{A.9}$$

Therefore, at any iteration, i, the total number of chromosomes in the population will always be P_t^2.

4.2.3 Mutation Operator

Mutation in the context of a GA is the probabilistic event that further change occurs in an offspring chromosome after crossover. For this GA, mutation occurs by swapping any two genes in the offspring chromosome. This, however, is not dependant on parent chromosomes [2]. The probability of mutation is denoted by P_m.

4.2.4 Evaluation of Chromosomes

After the crossover and mutation stages, natural selection is imitated. All chromosomes are evaluated according to a fitness function given in (A.6). The fitness function found in (A.6) was extracted from Patel et al [5] to use as a comparison benchmark. The best p chromosomes are then selected to form the next generation, $P_t^{(i+1)}$. The authors remind the reader than Ω_1 is known, and each solution in $_t$ represents a candidate mapper for Ω_2.

4.2.5 Termination of the Genetic Algorithm

Termination of a GA occurs under two conditions, 1) convergence of the population, P_t or 2) optimality has been reached. As in [2], the GA will terminate at the most optimal solution when all chromosomes in the population$_t$ converge to the same value, i.e. $\phi(\Omega_1, \Phi_a) = \phi(\Omega_1, \Phi_b), \ \forall \ \Phi_a, \Phi_b \ \epsilon \ P_t$. In the case of this chapter, however, the GA will terminate for the following two conditions; 1) A stable, convergent solution had been found, and 2) the GA would terminate if no optimal, stable or convergent solutions can be found, after which the chromosome with the highest fitness will be deemed the sub-stable chromosome. The algorithm is constrained to perform only n_{max} number of iterations. If the GA does not converge, the chromosome in P_t with the highest fitness is deemed sub-optimal.It is important to note that setting $n_{max} \ll M^5$ ensures that the GA is less time expensive when compared to the QAP solvers discussed in [4].

5 Results and Discussion

In this section, the output of the GA used to design the secondary mapper, Ω^2_{GA}, for USTLD systems, is evaluated. From the work in Xu et al [1], the error performance for $2 \times N_R$ USTLD systems are demonstrated and compared to $2 \times N_R$ Alamouti STBC systems [13]. This is a fair comparison as both systems employ the same structure, i.e. $2 \times N_R$ MIMO configuration and transmission over two time slots. Due to the similar structure between the Alamouti STBC and USTLD systems, the performance of the Alamouti STBC can be obtained from (A.3) by setting $d_1 = d_2$. For all applications of the GA, the parameters used are summarized in Table A.1 and set $n_{max} = 10^6$. All binary mappings are represented by their decimal equivalents for brevity.

Table A.1: Summarized parameter values for the Genetic Algorithm

Constellation Size	Population Size (P_t)	Mutation Rate (P_m)
64PSK	8	10%
128QAM, 128PSK, 128APSK	10	10%
256QAM, 256PSK, 256APSK	12	15%
512QAM	16	20%
$4 + 11 + 17$APSK	8	10%
$7 + 13 + 19 + 25$APSK	10	10%
$11 + 18 + 26 + 33 + 40$APSK	12	15%
$25 + 32 + 39 + 46 + 53 + 61$APSK	16	20%

5.1 Square Constellations: M-QAM

The GA is tested on large M-QAM constellations where $M = 128, 256$ and 512. These mappers were benchmarked against the mapper found using the design in Xu et al [1]. For a design analysis of the mapper proposed by [1], the reader is referred to the work done in [1]. Evaluating the mappers using the fitness function found in (A.6), which produced the results $\phi\left(\Omega_1, \Omega^2_{Xu,128}\right) = 8.0$ for 128QAM. The GA converged to chromosomes with fitness $\phi\left(\Omega_1, \Omega^2_{GA,128}\right) = 8.0$ for 128QAM. As seen, the GA matches but does not improve upon the existing heuristic design. The GA was then tested for 256QAM and 512QAM, where benchmark mappers are found using the design technique in [1]. The mappers found in [1] converge to a fitness of $\phi\left(\Omega_1, \Omega^2_{Xu,256}\right) = 8.0$ and $\phi\left(\Omega_1, \Omega^2_{Xu,512}\right) = 8.0$. The GA converges with chromosomes with a fitness of $\phi\left(\Omega_1, \Omega^2_{GA,256}\right) = 8.0$ and $\phi\left(\Omega_1, \Omega^2_{GA,512}\right) = 8.0$ respectively. Again, the GA design matches but does not improve upon the best existing heuristic design. The authors suggest a few reasons for the results:

- Larger population sizes mean faster convergence of the GA
- Fitness function used was not robust enough
- Starting population may have had Fitter individuals

In order to mitigate the problem, [14] proposed design metrics that could be used in order to further evaluate the LD mappers produced by the GA, which will not be used in this chapter but mentioned for future work for the GA.

5.2 Circular Constellations

5.2.1 M-PSK Constellations

Next, the output of the GA is tested on larger PSK constellations where $M = 64, 128$ and 256. Again, since no algorithmic benchmark mappers have been designed, the design found in [1] is employed as a benchmark mapper. Again, the reader is referred to the original work done in [1]. The 64PSK mapper designed from [1] has a fitness of $\phi\left(\Omega_1, \Omega^2_{Xu,64PSK}\right) = 0.019231$. The output mapper from the GA, however, converged to a value of $\phi\left(\Omega_1, \Omega^2_{GA,64PSK}\right) = 0.057532$. The GA was then tested on the 128PSK and 256PSK. The heuristic based mappers have a fitness of $\phi\left(\Omega_1, \Omega^2_{Xu,128PSK}\right) = 0.004731$ and $\phi\left(\Omega_1, \Omega^2_{Xu,256PSK}\right) = 0.001201$. The output of the GA for 128PSK and 256PSK converged to chromosomes of fitness $\phi\left(\Omega_1, \Omega^2_{GA,128SPK}\right) = 0.009628$ and $\phi\left(\Omega_1, \Omega^2_{GA,256PSK}\right) = 0.003615$. The curves shown in Fig. A.1 - A.3 show the theoretical performance of these systems in the fast fading channel. These results are then verified by Monte Carlo simulations using the system model described in section 2. The results show that there is a significant improvement when compared to the heuristic mapper. When considering the BER results, 64PSK shows an improvement of $\approx 5dB$, 128PSK shows an improvement of $\approx 4dB$ and 256PSK shows an improvement of $\approx 8dB$ gains at BER of 10^{-5}. This is expected as stated in section 2, the higher the fitness, the higher achievement of LD.

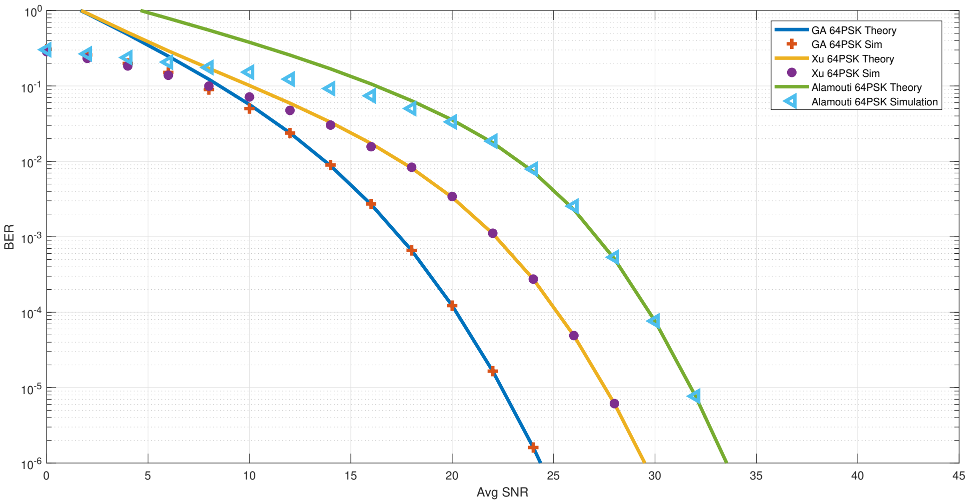


Fig. A.1: Bit Error Rate Performance of 64PSK Alamouti and USTLD systems

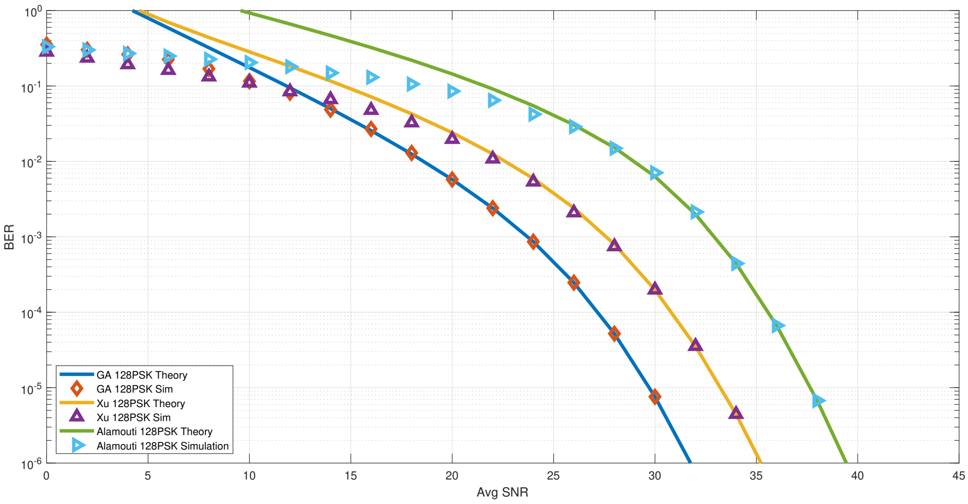


Fig. A.2: Bit Error Rate Performance of 128PSK Alamouti and USTLD systems

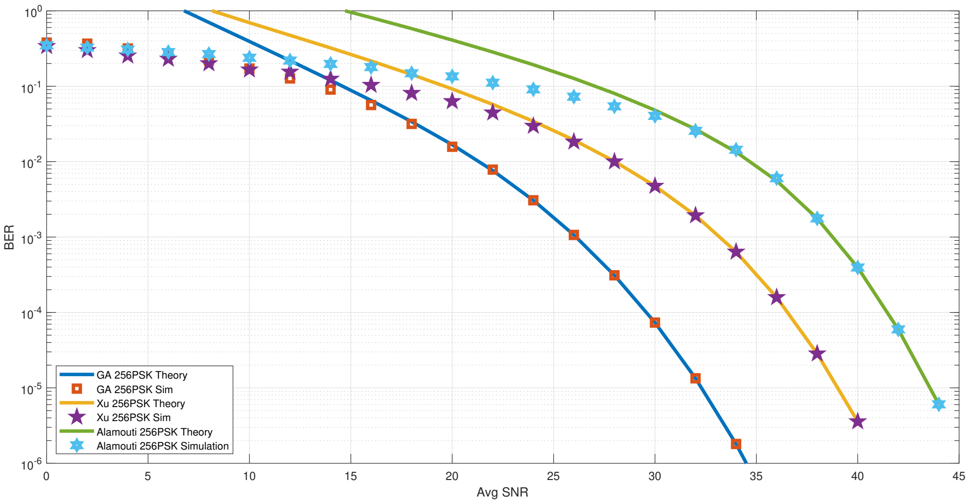


Fig. A.3: Bit Error Rate Performance of 256PSK Alamouti and USTLD systems

5.2.2 M-APSK Constellations

The GA is now tested with APSK constellations. The work done by Patel et al [5] that for $M = 8, 16, 32$ and 64, the GA shows significant improvement when compared to the Alamouti STBC and the mapper design by [1, 14]. In terms of this chapter, the DVB-s2x modulation has been employed to design the candidate mappers. Again, no heuristic mappers have been designed for APSK constellations $M > 64$. Therefore, the design from [1] is employed for $M = 128$ and 256. The heuristic based mapper for 128APSK (DVB-s2x) has a fitness value $\phi\left(\Omega_1, \Omega^2_{Xu,128APSK}\right) = 0.0203076$. The output of the GA showed a convergence of chromosomes of fitness $\phi\left(\Omega_1, \Omega^2_{GA,128APSK}\right) = 0.0545484$. It can then be seen from Fig. A.4 that the mapper designed by the GA has a $\approx 3dB$ gain over the heuristic mapper design at the BER of 10^{-6}. Next, the GA is tested with the 256APSK (DVB-s2x) constellation. The heuristic design has a fitness of $\phi\left(\Omega_1, \Omega^2_{Xu,256APSK}\right) = 0.001789$. The output of the GA shows a convergence fitness value of $\phi\left(\Omega_1, \Omega^2_{GA,256APSK}\right) = 0.0119273$. From the BER curve in Fig. A.5, it can be seen that the GA has a $\approx 6dB$ improvement over the heuristic mapper design at the BER of 10^{-6}.

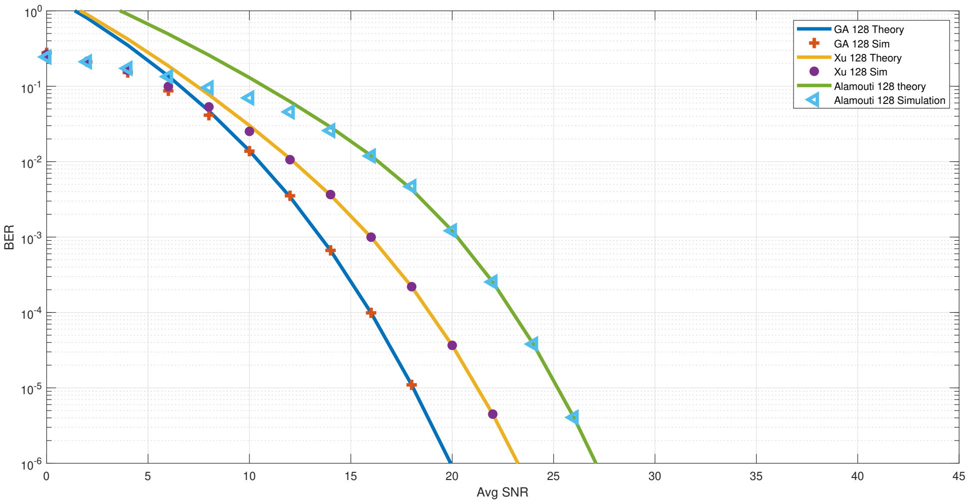


Fig. A.4: Bit Error Rate Performance of 128APSK Alamouti and USTLD systems

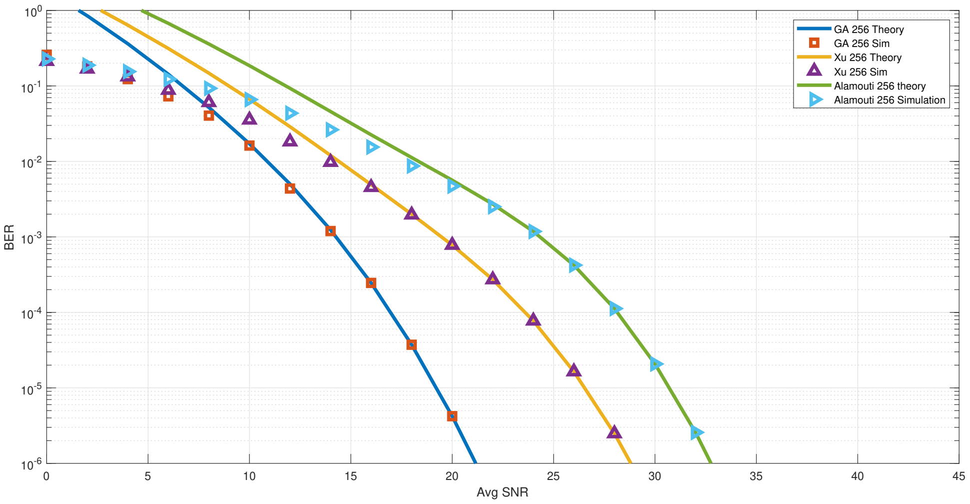


Fig. A.5: Bit Error Rate Performance of 256APSK Alamouti and USTLD systems

5.2.3 Irregular Shaped M-APSK Constellations

Finally, the GA is tested with irregular constellations proposed by [9]. No existing mapper designs for USTLD are available to benchmark. Additionally, due to non-symmetry and irregular design, the design found in [1] cannot be directly applied to these constellations. The constellations considered are:

- The optimized 4+11+17APSK constellation
- The optimized 7+13+19+25APSK constellation

- The optimized 11+18+26+33+40APSK constellation
- The optimized 25+32+39+46+53+61APSK constellation

Table A.2: Details of Irregular APSK Constellations and their respective Fitness values

Constellation	Arrangement	Fitness	Convergence
32APSK	$4+11+17$	0.4178441	No
64APSK	$7+13+19+25$	0.0950093	Yes
128APSK	$11+18+26+33+40$	0.0804309	No
256APSK	$25+32+39+46+53+61$	0.0559774	Yes

Since no other constellations have been designed using these configurations, the GA is fed with the pseudo gray binary mapping that is used to generate the secondary mapper to achieve LD. Fig. A.6 - A.7 shows the optimized 4+11+17APSK and 7+13+19+25APSK constellations respectively. The fitness values for each constellation is given in Table A.2. Again, the USTLD system is compared to the Alamouti system in order to test its quality. At a BER of 10^{-6}, the 4+11+17APSK constellation shows a $\approx 5dB$ gain over the Alamouti system. For the 7+13+19+25APSK constellation, the graph shows a significant gain of $\approx 17dB$ gain over its Alamouti comparison at a BER of 10^{-6}. Finally, for both the 11+18+26+33+40APSK and 25+32+39+46+53+61APSK when compared to the Alamouti STBC system, the graphs in Fig. A.8 - A.9 show a $\approx 5dB$ gain at a BER of 10^{-6}. Although the GA had found the values in Table A.2, the Maximum Euclidean Distance reported in [9] has not been achieved.

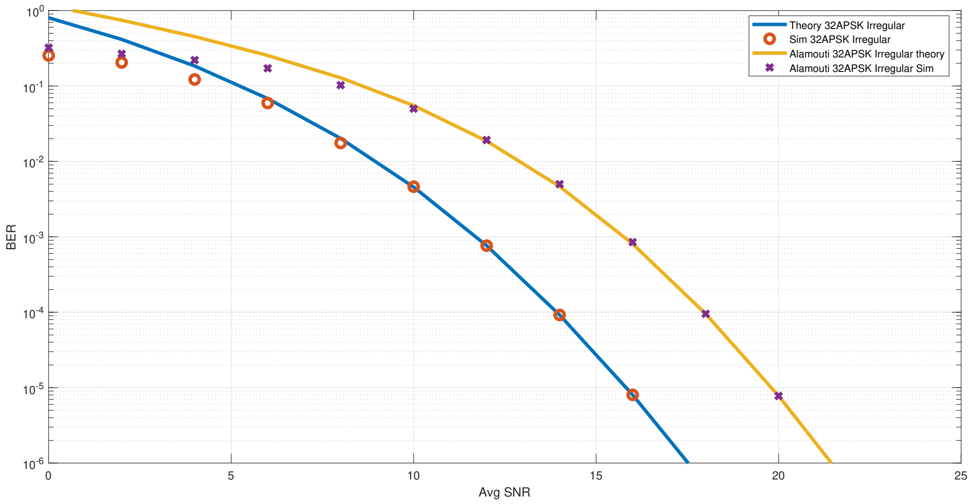


Fig. A.6: Bit Error Rate Performance of Irregular 32APSK Alamouti and USTLD

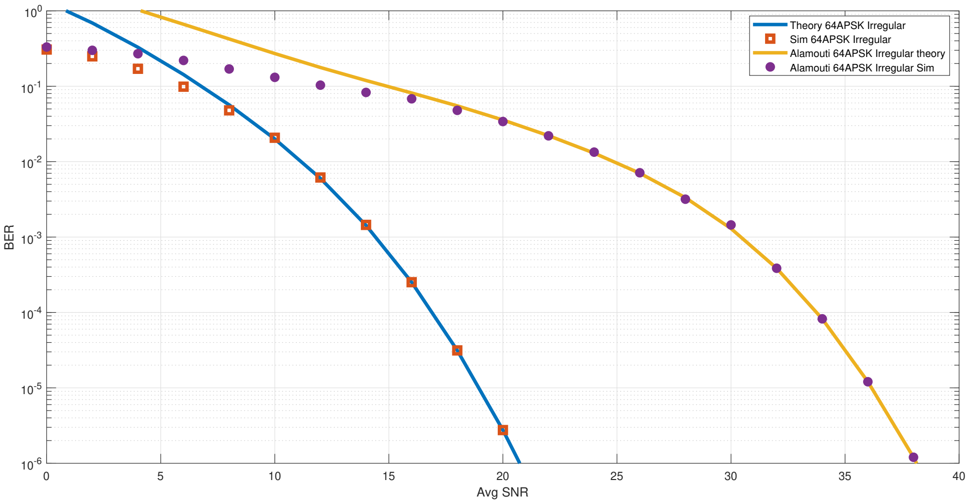


Fig. A.7: Bit Error Rate Performance of Irregular 64APSK Alamouti and USTLD

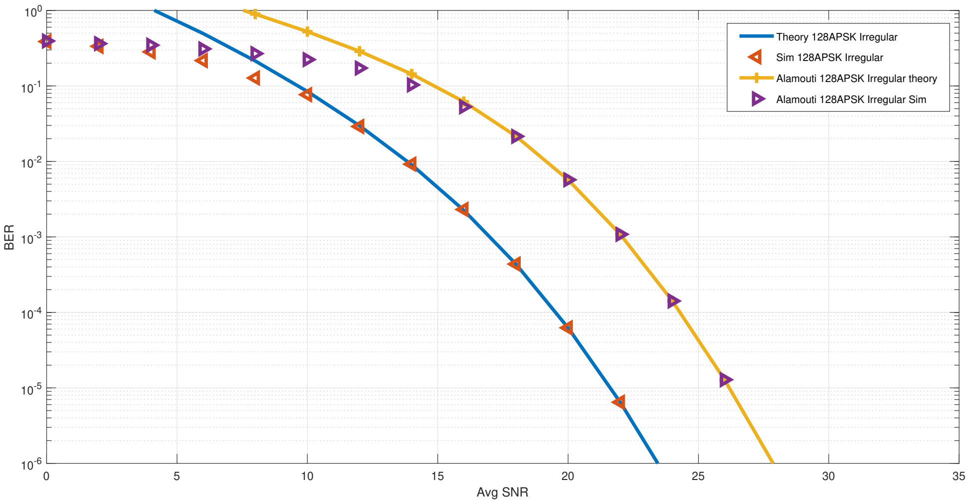


Fig. A.8: Bit Error Rate Performance of Irregular 128APSK Alamouti and USTLD

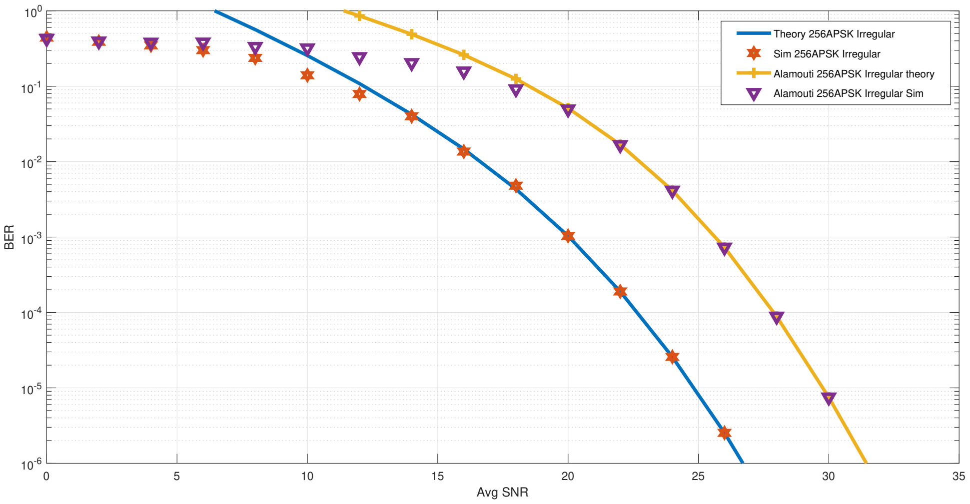


Fig. A.9: Bit Error Rate Performance of Irregular 256APSK Alamouti and USTLD

6 Complexity Performance Study

Computational complexity is the study of a problem class based on the rate of change in growth, time and other fundamental units of measure as a function of a chosen system parameter [15]. Space complexity is the total quantity of computational resources or memory used with respect to the input whereas Time Complexity is defined as the total amount of time required for an algorithm to complete with respect to the chosen system parameter. Complexity studies aim to classify and rank tasks based on their computational costs over all possible instances and algorithms. Complexity analyses of a particular algorithm, however, also aims to answer another question, namely are there advantages or disadvantages in the point of view of a resource over other possible methods?. In the case of the LD problem, the main question arises Is the GA significantly less computationally expensive than existing methods mentioned in [4]?. [2] stated that by setting $n_{max} \ll M^5$ will ensure that the GA will always be significantly less computationally expensive than the QAP solvers proposed in [4]. This assumption is based on Time Complexity of an algorithm, and cannot be compared to the computational complexity of the algorithms in [4]. Therefore, in order to compare each algorithm, a computational complexity analysis based on computational resources is performed. For the analysis of this GA, the author uses the procedures of Computational Complexity analysis from [15, 16].

6.1 Computational Complexity Analysis

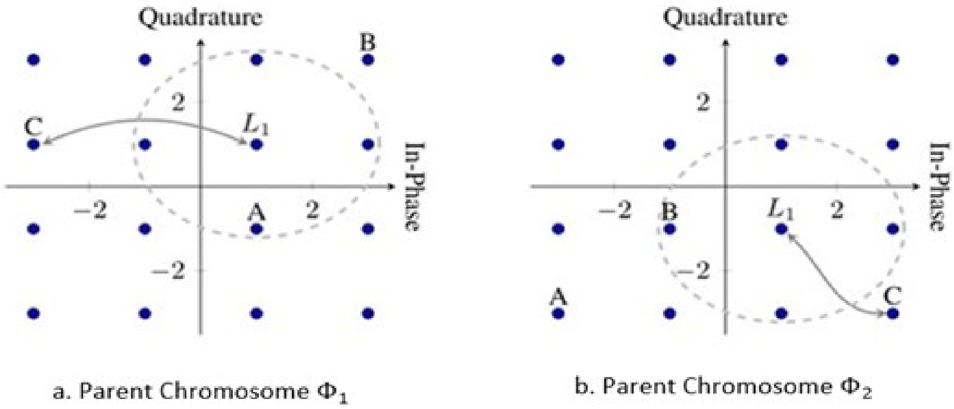
The first step of a computational complexity analysis is to outline all basic operations of the GA loop. From [15], the basic operations of any GA are Fitness Calculation, Selection Operator, Crossover

Operator and Mutation Operator. In GAs, pre-processing functions such as the population initialization are not considered for analysis [15]. Since no Selection Operator is used in this GA application, the basic operators are the Fitness function, Crossover Operator, Mutation Operator and the Evaluation of Chromosomes Function. The second step is to calculate the worst-case computational complexity for each of the basic operators.

From the fitness function in (A.6), the expression requires a double iteration to compute the Euclidean distance from point L in mapper Ω_t to all other points $\widehat{L}$ in mapper Ω_t respectively, where $t \, \epsilon \, [1:2]$. Each point L or $\widehat{L}$ represent one of M number of constellation points in $\Omega_t(L)$ and $\Omega_t(\widehat{L})$, where M is the order of modulation. The single constraint on the fitness function in (A.6) is that all distances from points $\Omega_t(L)$ and $\Omega_t(\widehat{L})$ are to be computed except when $L = \widehat{L}$. The authors remind the reader that Ω_1 is known. Since there are M number of constellations points on Ω_1 and Ω_2, this requires $M(M-1)$ number of computations over Ω_1 and Ω_2 respectively. The fitness function will compute over all chromosomes in the population, P_t^2 given as (A.6). Hence, the total Computational Complexity of the fitness function, denoted by $S_{fitness}$, is given by

$$S_{fitness} = P_t^2 M \left(M-1\right) \tag{A.10}$$

where P_t^2 is the total number of chromosomes after crossover and M is the order of modulation.



a. Parent Chromosome Φ_1

b. Parent Chromosome Φ_2

Fig. A.10: Illustration of the κ-Hyper-sphere Swap Crossover technique

The κ-HSX technique proposed by [2] is best described using the diagram in Fig. A.10. Consider a 16QAM constellation as an example. Let Fig. A.10a be the first parent chromosome Φ_1 and Fig. A.10b as the second parent chromosome Φ_2. A random point on Φ_1, L_1 is chosen. The corresponding point to L_1 from Φ_1 in Φ_2 is also chosen. A hyper-sphere of radius $\Re$ is constructed around the chosen points L_1 such that all of its adjacent neighbours N are contained within the hyper-sphere. Next, another random point L_2 is chosen as a candidate to swap with L_1. For simplicity, Fig. A.10a and

A.10b show three points A, B and C as candidates for L_2. Candidates A and B cannot be chosen as L_2 as the point A falls within the hyper-sphere of Φ_1 and point B falls within the hyper-sphere of Φ_2. The point C however, falls outside of the hyper-sphere. Hence, point C is chosen as the desired candidate for L_2 and swapped with L_1 that produces two offspring chromosomes. [2] stated that performing one swap does not produce offspring that are sufficiently different to its parent chromosomes. Hence, κ number of swaps are implemented per crossover. From [2], an arbitrary value for κ was chosen such that the number of swaps should be less than half that of the number of constellation points, is given as

$$\kappa = \frac{M-4}{2} \tag{A.11}$$

This crossover operator requires two sets of computations, namely the Euclidean distance calculations to find all adjacent neighbours, N to L_1 and the number of swaps κ candidate constellation points for L_2 such that $L_1 \neq L_2$ and L_2 is not found within the hyper-sphere. This requires $\kappa + N = \frac{M-4}{2} + N$ number of computations for a single parent to produce an offspring chromosome. Hence, for any two parent chromosomes, the crossover operator requires $2\left(\frac{M-4}{2} + N\right) = M - 4 + 2N$ number of computations for both parent chromosomes. From [2], it is stated that the GA produces two offspring chromosomes per combination of two parent chromosomes, hence making the total number of chromosomes in the population P_t^2 after crossover. Hence, to get the total number of computations, we subtract the number of chromosomes after crossover from the initial population, $P_t^2 - P_t$. There, the total computational complexity of the crossover technique, denoted by $S_{crossover}$ is given by

$$S_{crossover} = \left(P_t^2 - P_t\right)(M - 4 + 2N) \tag{A.12}$$

where P_t is the initial number of chromosomes, P_t^2 is the total number of chromosomes in the population after crossover, M is the order of modulation and N is the number of distance calculations of the adjacent neighbours of L_1

Mutation is a probabilistic occurrence in nature such that an offspring chromosome undergoes more change after crossover. In the context of this GA, mutation will occur when any two genes within an offspring chromosome are swapped. It is reiterated that the number of offspring chromosomes after crossover is given as $P_t^2 - P_t$. The number of offspring chromosomes that will undergo mutation, which depends the mutation rate P_m. Hence, the total computational complexity of the mutation operator, denoted by $S_{Mutation}$ is given as

$$S_{Mutation} = P_m \left(P_t^2 - P_t\right) \tag{A.13}$$

where P_t is the initial number of chromosomes, P_t^2 is the number of chromosomes after crossover and P_m is the probability of mutation.

In order to generate the population for the next generation, all parent and offspring chromosomes are added back into the population and evaluated according to the fitness function given in (A.6). The authors remind the reader that Ω_1 is known and each chromosome in the population is a candidate for Ω_2. Hence, the total computational complexity of the Evaluation function, S_{Eval} is given as

$$S_{Eval} = P_t^2 \left(M^2 - M\right) \tag{A.14}$$

where P_t^2 is the total number of chromosomes after crossover and M is the modulation order.

Hence, adding up all the number of computations gives the total complexity of the GA as

$$S_{GA} = S_{Fit} + S_{Crossover} + S_{Mutation} + S_{Eval} \tag{A.15}$$

$$= P_t^2 \left(M^2 - M\right) + \left(P_t^2 - P_t\right)\left(M - 4 + 2N\right) + P_m \left(P_t^2 - P_t\right) + P_t^2 \left(M^2 - M\right) \tag{A.16}$$

$$= 2M^2 P_t^2 - MP_t^2 + \left(P_m - 4\right) P_t^2 + 2NP_t^2 + \left(4 - M - 2N - P_m\right) P_t \tag{A.17}$$

Converting expression (A.17) to big-$\mathcal{O}$ notation, we set $P_t = 8$ and $P_m = 0.1$ which further reduces the computational complexity to

$$S_{GA} = 128M^2 - 64M - 249.6 + 128N + 8\left(3.9 - M - 2N\right) \tag{A.18}$$

$$= 128M^2 - 72M + 112N - 218.4 \tag{A.19}$$

The number of adjacent neighbours, N is a variable that scales with the modulation order M. By considering one of the four most inner points on an M-ary constellation as seen in Fig. A.10, it can be noted that for $16-, 32-$ and $64-$ary constellations have the following arithmetic progression for the maximum number of neighbours

$$5 \qquad 21 \qquad 37 \qquad ..... \tag{A.20}$$

From (A.20), it can be seen that a common difference $d = 16$ is found. Hence the arithmetic progression of the number of neighbours is stated as

$$N_n = a + \left(n - 1\right) d \tag{A.21}$$

$$= 5 + \left(n - 1\right)\left(16\right) \tag{A.22}$$

$$= 16n - 11 \tag{A.23}$$

Where a is the first term in the sequence, n represents the number of bits from an $M-$ary constellation such that $M = 2^n$ and $n = log_2(M)$

Therefore, the total computational complexity can be further stated as:

$$S_{GA} = 128M^2 - 72M + 112\,(16n - 11) - 218.4 \tag{A.24}$$

$$= 128M^2 - 72M + 112\,(16\log_2(M) - 11) - 218.4 \tag{A.25}$$

Finally, in big-$\mathcal{O}$ notation, we consider the most dominating term of the complexity equation in (A.25), which then leads to the final computational complexity stated as

$$\mathcal{O}\,(GA) = \mathcal{O}\left(M^2\right) \tag{A.26}$$

6.2 Evaluation of the Complexity of LD Mapper Design Techniques

Table A.3: Summary of different Search Optimization Techniques for Comparison

Technique	Definition	Space Complexity
Genetic Algorithm	Genetic Algorithms mimic the process of evolution and natural selection to optimize a given cost function in an iterative manner.	$\mathcal{O}\left(M^2\right)$
Quadratic Assignment Problem	a labelling optimization problem that assigns each of M variables to M locations, in order to optimise a cost function [17].	$\mathcal{O}\,(M!)$ [4]
Quadratic Assignment Problem (Lower Bound)	a labelling optimization problem that assigns each of M variables to M locations, in order to optimise a cost function [17], Used to develop mapper designs for [4]	$\mathcal{O}\left(M^5\right)$ [4]

n_{max} = maximum number of iterations, M = modulation order

In order to evaluate the complexity of each technique, authors make use of the big-Omicron (big-$\mathcal{O}$) notation, which is the widely used standard for measuring complexities and compares the LD mapper designs produced by each algorithm in terms of fitness values. Table A.3 summarises each optimization technique and their respective Space Complexities. From the big-$\mathcal{O}$ notation in Table A.3, complexity equations show that the Lower Bound QAP approach uses significantly less computational resources than the QAP algorithm. The GA, however, is shown to require M^3 less computational resources than the lower bound QAP solver in [4]. Therefore, the GA answers the main question above, which shows that the GA provides a significant advantage in terms of

Computational and Time complexity [2] over existing exhaustive search and algorithmic approach algorithms.

7 Conclusion

Due to high computational complexities and symmetry-based heuristics, USTLD mapper designs are limited. This chapter employs the GA from the work done by Patel el al [5] to design LD mappers of a higher modulation order and irregular symmetry. The algorithm was tested on 128,256 and 512-ary constellations for the QAM modulation, 64,128 and 256-ary constellations for the PSK modulation and 128 and 256-ary constellations for the APSK modulation. Furthermore, the algorithm was tested on four irregular APSK constellations, namely 4+11+17APSK, 7+13+19+25APSK, 11+18+26+33+40APSK and 25+32+39+46+53+61APSK respectively. These irregular constellations were used to prove that the GA can indeed produce a LD mapper irrespective of symmetry. Results presented in this chapter show that for the M-QAM constellations considered, the GA produced corresponding LD mappers that match, but do not improve on the best available heuristic design. The reason for this could be that the fitness function used was not robust enough or the population size was too large and converged faster. The 64PSK, 128PSK and 256PSK have demonstrated gains of $\approx 5dB$, $\approx 4dB$ and $\approx 8dB$ respectively. When considering APSK constellations, 128APSK and 256APSK outperformed the best available heuristic mappers by $\approx 3dB$ and $\approx 6dB$ respectively. Finally, the GA was tested on irregular constellations such as 4+11+17APSK, 7+13+19+25APSK, 11+18+26+33+40APSK and 25+32+39+46+53+61APSK, which exhibited gains of $\approx 5dB$, $\approx 17dB$, $\approx 5dB$ and $\approx 5dB$ over the Alamouti STBC respectively. Furthermore, a complexity comparison between the GA and Exhaustive Search algorithms was done. The GA was shown to have a much lower complexity when compared to the algorithms proposed in [3, 4], hence, proving the GA having the lowest space complexity.

Future works in this area include improved crossover and mutator operations, better termination conditions and employing other metrics for determining the fitness of mappers such as the metrics found in [14].

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Paper B

AN ORDERED CROSSOVER APPROACH TO DESIGNING LABELLING DIVERSITY MAPPERS

1 Abstract

Genetic Algorithms(GA) is a population-based search optimization technique that mimic the process of evolution and natural selection. GAs are an effective way to finding feasible solutions to complex problems. Recently, GAs have been applied to designing Labelling Diversity mappers and have shown great promise. However, the approach implemented did not apply biological processes during mating, and therefore, could not be classified as a GA, but rather a Genetic-Inspired Algorithm (GIA) . Since the GA for designing Labelling Diversity mappers was developed, no further studies have been produced to suggest any improvement to the system. In reproduction with two distinct parents, the offspring acquires genetic diversity from the crossover are from the distinct parent genes. When there is only one parent, genetic diversification is gained only from mutation. In such a case, evolution becomes a random process rather than one that is guided by parent propensities; and the promised value of the GA is not realised. This chapter investigated four biological crossover techniques and two hybrid techniques, namely, single point, multi-point, OX1 and OX2 and cycle and partially mapped Crossovers, respectively. The proposed GA with the OX1 crossover technique was tested on the 16QAM, 16PSK, 16APSK and three 16APSK constellations that do not exhibit any diagonal symmetry. In the case of symmetric 16QAM and 16PSK, mapper designs produced by the proposed GA had matched but not improved upon existing heuristic and the previous GA mapper designs. However, results show that for the Asymmetric 16APSK and Single Symmetry 16APSK constellations, Labelling Diversity values have increased from $\omega\left(\mu_1, \mu_{GA,AS-16APSK}^{Patel}\right) = 0.0981$ to $\omega\left(\mu_1, \mu_{GA,AS-16APSK}^{Davis}\right) = 0.3008$ and $\omega\left(\mu_1, \mu_{GA,SS-16APSK}^{Patel}\right) = 0.4020$ to $\omega\left(\mu_1, \mu_{GA,SS-16APSK}^{Davis}\right) = 0.4053$ respectively, and led to $\approx 4dB$ and $\approx 2dB$ gains respectively when compared to the results of mappers produced by the previous GA. In the cases of the 11+5APSK and 16APSK, even though improvement in the Labelling Diversity of the mapper design is observed ($\omega\left(\mu_1, \mu_{GA,115APSK}^{Davis}\right) = 0.7171$ from $\omega\left(\mu_1, \mu_{GA,11+5APSK}^{Patel}\right) = 0.6766$ for the 11+5APSK constellation and $\omega\left(\mu_1, \mu_{GA,16APSK}^{Patel}\right) = 0.3685$ to $\omega\left(\mu_1, \mu_{GA,16APSK}^{Davis}\right) = 0.5427$ for the 16APSK constellation), only a small gain of $\approx 0.5dB$ was achieved. More significantly, the proposed GA achieved significant performance improvement in terms of time complexity but used more computational resources ($\mathcal{O}(M!)$) when compared to the previous GA $\mathcal{O}(M^2)$. A test on mutation rates on the proposed GA was performed, with the objective of utilizing lower mutation rates instead of relatively high mutation rates used in the previous GA. Results have shown that higher mutation rates are needed for single parent reproduction, and thus the process is purely random. However, the converse is also true, where two parents produce a set of offspring chromosomes and thus, randomness is reduced and genetic diversity is increased. The results also

showed that a more guided search (mating of two parents) is more effective at genetic diversity than pure random searches as in the case of single parent reproduction.

Index Terms - Genetic algorithms, labelling diversity, mapper design, complexity, STBC, mutation rate

2 Introduction

Evolutionary algorithms (EAs) are adaptive meta-heuristic search algorithms which use techniques inspired by natural selection and evolution to iteratively and efficiently solve combinatorial optimization problems. EAs and Evolutionary programming combined provide an excellent approach to effectively sample large search spaces and produce feasible results [1]. Both exploration and exploitation are largely responsible for the performance and success of any GA [1]. Exploitation can be defined as the use of existing knowledge to find possibly better solutions to a problem, while Exploration refers to finding a solution from an unknown in a search space [1]. Both exploration and exploitation exist in the mating process of the EA namely the crossover and mutation stages respectively. Uncoded space-time labelling diversity (USTLD) is a recent innovative, multi-diversity scheme that was proposed to improve on the performance of space time block coded (STBC) Systems in the presence of multipath fading. USTLD systems employ a multiple-input multiple-output (MIMO) configuration consisting of two transmit antenna and N_R receive antenna. USTLD uses the concept of labelling diversity which employs two mapper designs, Ω_1 and Ω_2, together with its MIMO configuration to reduce the bit error rate (BER). The extent to which labelling diversity (LD) is achieved in USTLD systems is based on the design of binary mappers Ω_1 and Ω_2. The end goal of LD mapper designs is to place adjacent points as far as possible in the second constellation than in its base constellation. Previous works based on search algorithms and exhaustive approaches have proven to be too computationally expensive to design LD mappers. Recently, Patel et al [2] proposed a GA to tackle the LD problem and design LD mappers irrespective of size or shape. A summary of the GA proposed in [2] is summarized in Section III-B2, and authors encourage readers to refer to the original paper. Candidate solutions chromosomes that is represented by θ contain encoded information, known as genes represented by ζ_i where $i \ \epsilon \ [0 : M-1]$ and M is the order of modulation. Each gene represents a symbol on the M-ary constellation. A single chromosome can be defined as:

$$\theta = [\zeta_0, \zeta_1, \cdots, \zeta_{M-1)}] \tag{B.1}$$

It is important to note that each chromosome is a unique permutation of distinct symbols (genes), and therefore, no label can be duplicated in, or excluded from a chromosome.

In [2], we see that new crossover technique being proposed, the κ-Hyper-sphere Swap Crossover κ-HSX). This crossover technique in summary works on the following principles: i) choose two parent chromosomes, Y_1 and Y_2, ii) select a gene from the first parent chromosome, L_1, Y_1, iii) select the same gene L_1 that is found in the second parent chromosome, L_1, Y_2, iv) project a hyper-sphere of radius R around the two genes, L_1 and L_2 on both parent chromosomes enclosing all adjacent genes in the hyper-sphere, v) Choose another random point from Y_1 and Y_2 such that they fall outside of the hyper-sphere radius, $\hat{L}_2, Y_1$ and $\hat{L}_2, Y_2$, vi) swap L_1, Y_1 with $\hat{L}_2, Y_1$ and L_1, Y_2 with $\hat{L}_2, Y_2$ and vii) repeat κ number of times.

The illustration in Fig. B.1 further simplifies the mechanisms of the κ-HSX principle:

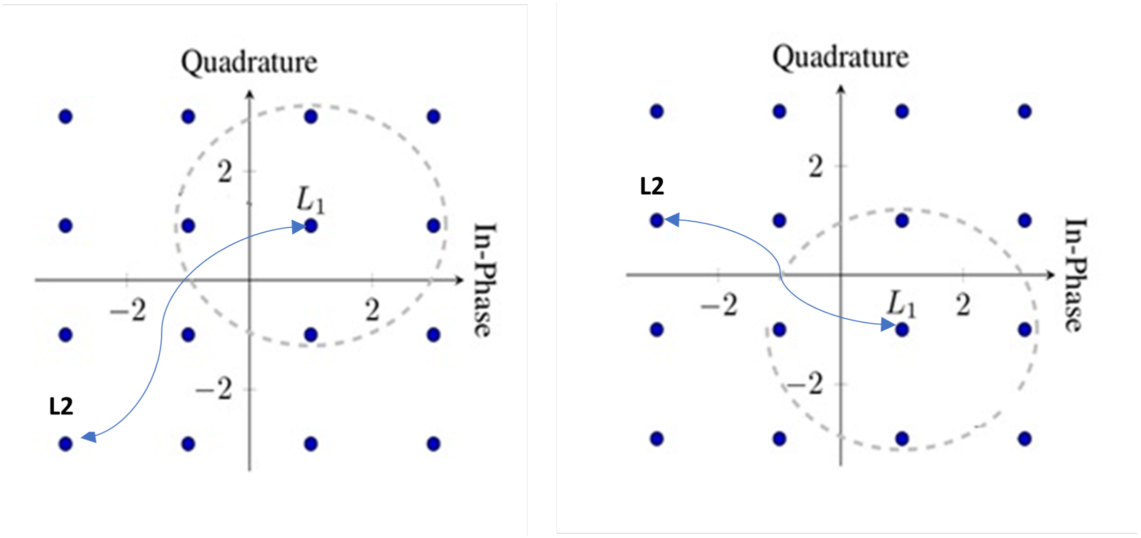

Fig. B.1: Simplified Diagram of the κ-Hyper-sphere Swap Crossover [2]. Parent Chromosome Y_1 is illustrated on the left and Y_2 on the right

From Fig. B.1, it can be seen that the approach in [2] is not of a genetic (two parent reproduction) nature, but that of a genetic-inspired (single parent reproduction) nature, thus creating pure randomness when generating offspring and reducing genetic diversity. This technique has not been applied to other optimization problems, and therefore no validity to produce optimal results can be shown. Therefore, in attempting to reduce randomness and increase genetic diversity, the first aim of this chapter is to introduce two-parent crossover techniques to the LD GA is to apply a two-parent crossover technique that produces LD mapper designs with higher values of LD with respect to the problem constraints. Coupled with the aim of applying two-parent crossover techniques, the aim of the chapter is to gain further insight into achieving a close-to global optimal solution irrespective of size, shape or modulation. The following crossover operators were considered for the GA [1]:

- Single-Point Crossover One random crossover point is selected, the tails of both parents are swapped and offspring are produced
- Multi-Point Crossover An extension to the Single-Point Crossover. Multiple crossover points are selected and swapped between the parents to produce offspring
- Davis Ordered Crossover (OX1) a permutation-based crossover technique used with the intention of transmitting information about relative order of the offspring
- Ordered Crossover (OX2) extension to the OX1 crossover.
- Cyclic Crossover offspring is created from parents where every position is occupied by a corresponding element from one of the parents
- Partially Mapped Crossover Two random crossover points are selected on parent chromosomes creating a segment. One parents segment is mapped onto the other parents segment, and remaining information is exchanged.

From [3], a complexity analysis of the GA from [2] was performed. The computational complexity of the GA was shown to be significantly less complex than available algorithmic and exhaustive search approaches, while producing mapper designs that are equal in fitness. Hence, the second contribution of this chapter is to investigate the complexity of the proposed GA and compare it to the complexity of the GA found in [2, 3].

The remainder of the chapter is structured as follows: Section 2 describes the general architecture of GAs. Section 3 describes the system model and discusses the USTLD system. This section also looks at the possible design metric benchmark fitness function). Section 4 summarises all current works of LD mapper design, which includes the GA proposed in [2]. Section 5 contains detailed study of the proposed GA with crossover study. Sections 6 and 7 contains the experimental setup of the system and discusses the results of the proposed GA as well as Monte Carlo simulations that illustrate the improvements that the proposed GA has to offer. Concluding thoughts are mentioned in Section 8.

In terms of notation for this chapter, vectors and scalars are in boldface and italics respectively. $\cdot$ represents the Frobenius norm of a vector, $|\cdot|$ represents the absolute value of a scalar and $\cdot)!$ represents the factorial of a scalar.

3 Genetic Algorithms

GAs are powerful meta-heuristic algorithms that are employed to solve various combinatorial optimization problems. GAs imitate evolution and natural selection, and apply these concepts to complex problems. Each solution produced by the GA is treated as a single individual whose fitness is determined by an objective function. GAs use the concept of survival of the fittest to maintain a population. A structured, yet randomized information exchange between two individuals (parent chromosomes) crossover operator give rise to new offspring that could be better performing individuals, while genetic diversity is also added to the population by changing random genes mutation operator or bringing in new individuals (immigration operator) [1]. The GA iteratively applies this process until a feasible local or global minimum/ optimum - is found.

In literature, there have been many proposed methods for implementing GAs, while others have proposed enhanced GAs by employing local searches to further better the chances of reaching a global maximum [1]. In this context, there are two types of reproduction systems to consider:

- Generational Reproduction A large number of parent chromosomes are selected and reproduction occurs typically half the population or more. Population from the previous generation is replaced by the population of the new generation
- Steady-State Reproduction Two parents a selected, reproduction occurs and two offspring are produced

For this research study, we have employed a GA that uses a steady-state reproduction system as opposed to a generational reproduction system, which was not investigated as elitism is introduced.

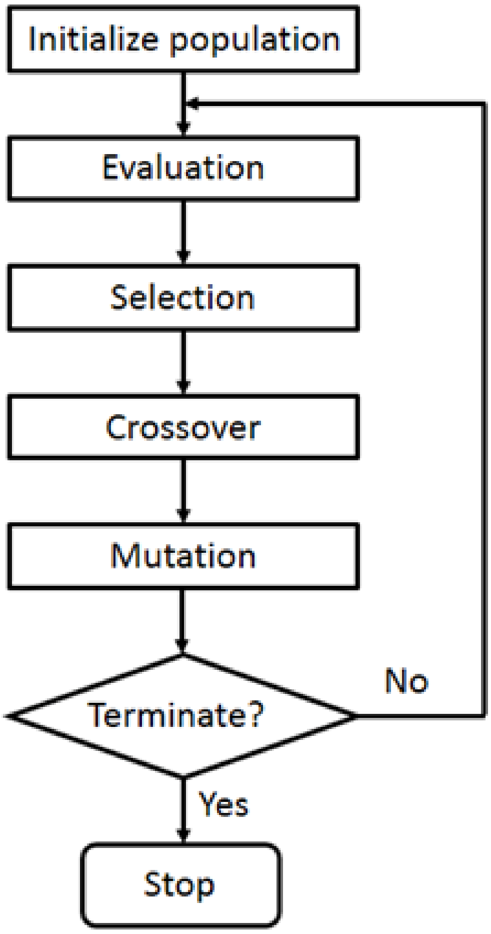

Fig. B.2: Flow Diagram of a General Genetic Algorithm

The most important process in any GA is mating of chromosomes, which consist of the crossover stage and the mutation stage. The crossover stage by definition uses existing information from parent chromosomes to produce offspring. This stage is also known as Exploitation. The mutation stage, however, is the Exploration operator, where a novel and unknown solution is found by randomly exchanging information within an offspring chromosome. During each iteration, natural selection is imitated and the best chromosomes are chosen to form the population of the next generation. Natural Selection is the process whereby each chromosome in the population undergoes evaluation using a fitness function, after which the best p number of chromosomes are selected to represent the population in the next generation. The GA will terminate when all chromosomes in the population have converged to a single fitness value or the algorithm had reached the maximum number of iterations; which is then said to contain an unstable solution. If a GA converges, the solution is deemed to be locally optimal (not necessarily globally optimal).

4 USTLD System Model

The traditional USTLD model considers a MIMO technique with $N_T = 2$ number of transmit antenna and N_R number of receive antenna. Two message information bit streams, $m_1 = [m_{1,1}, m_{1,2}, ., m_{(1,r)}]$ and $m_2 = [m_{2,1}, m_{2,2}, ., m_{(2,r)}]$ of length $r = log_2 (M)$ are passed through two binary mappers, μ_1 and μ_2 which produces symbols $\mu_1(\nu) = \nu_1$ and $\mu_2(\nu) = \nu_2$. After symbol mapping, $\mu_1(\nu)$ and $\mu_2(\nu)$ are transmitted over two consecutive time slots. Therefore, the resultant $N_R \times 1$ received signal vector can be represented as:

$$y_t = \sqrt{\frac{\alpha}{2}} \left[h_{t,1}\mu_1(\nu_1) + h_{t,2}\mu_2(\nu_2) \right] + \mathbf{n}_t \tag{B.2}$$

From (B.2), $\sqrt{\frac{\alpha}{2}}$ is the average signal-to-noise (SNR) ratio at each receiver antenna and $\mathbf{n}_t$ is the $N_R \times 1$ additive white gaussian noise (AWGN) vector in time slot t. In the vector matrix $\mathbf{n}_t$, each value follows a complex normal distribution with zero mean and $\frac{E_s}{2}$ variance per dimension, where E_s is the transmit energy per symbol. The $h_{t,u}, t, u \; \epsilon \; [1 : 2]$ vector is the multipath fading experienced by the transmitted symbol from antenna u in time slot t. Fading is assumed to be frequency flat fading and follows a Rayleigh amplitude distribution with zero mean and unit variance. Fading channels can either be fast or quasi-static fading. The phase distribution of noise and fading is assumed to be uniform.

At the receiver, to detect transmitted symbols, the maximum likelihood detector is employed to estimate these transmitted symbols. We assume perfect channel state information (CSI) is available at the receiver, the detection algorithm can be stated as:

$$\widehat{\nu_{(1)}}, \widehat{\nu_{(2)}} = \arg \min_{K_{(1)}, K_{(2)}} \left\| y_t - \sum_{t,u=1}^{2} \sqrt{\frac{\rho}{2}} h_{t,u}\mu_1(\nu_{(u)}) \right\|^2 , t, u \; \epsilon \; [1 : 2] \tag{B.3}$$

In (B.3), $\widehat{\nu_{(1)}}, \widehat{\nu_{(2)}}$ is the estimated codewords at the receive which is detected across two consecutive time slots.

4.1 Theoretical Error Performance of USTLD

From [4], the base USTLD model used an analytical union bound to derive the average bit error probability (ABEP) which resulted in the following expression:

$$ABEP(\rho) = \frac{1}{Mr} \sum_{\nu=0}^{M-1} \sum_{\widehat{\nu}=0, \nu \neq \widehat{\nu}}^{M-1} \beta\left(\nu, \widehat{\nu}\right) P\left(\nu \to \widehat{\nu}\right) \tag{B.4}$$

In (B.4), M is the modulation order, $\beta(\nu, \widehat{\nu})$ is the number of bit errors between transmitted and received symbols and $P(\nu \to \widehat{\nu})$ is the pairwise error probability (PEP) that one symbol is detected perfectly and the other symbol is detected with error. From [4], the PEP is derived as:

$$P(\nu \to \widehat{\nu}) = \frac{1}{4n}\prod_{t=1}^{2}\left(1+\frac{\alpha D_t^2}{8}\right)^{-N_R} + \frac{1}{2n}\sum_{s=1}^{n}\prod_{t=1}^{2}\left(1+\frac{\alpha D_t^2}{8sin^2(\frac{s\pi}{2n})}\right)^{-N_R} \tag{B.5}$$

Where n is a large integer, $n > 10$ and $D_t = \|\mu_t(\nu) - \mu_t(\widehat{\nu})\|, t \ \epsilon \ [1:2]$ is the euclidean distance between the estimated symbol and all other points on the M-ary constellation μ_t. Authors encourage the readers to [4] for a detailed derivation. At high SNR, $\frac{\alpha D_t^2}{8} >> 1, t \ \epsilon \ [1:2]$, the PEP can be approximated as:

$$P(\nu \to \widehat{\nu}) = \frac{1}{4n}\left(\frac{\alpha D_1^2}{8}\frac{\alpha D_2^2}{8}\right)^{-N_R} + \frac{1}{2n}\sum_{s=1}^{n}\left(\frac{\alpha D_1^2}{8sin^2(\frac{s\pi}{2n})}\frac{\alpha D_2^2}{8sin^2(\frac{s\pi}{2n})}\right)^{-N_R} \tag{B.6}$$

From (B.6), at high SNR, the PEP is dominated by the product euclidean distance D_1D_2. Thus, this sets an error floor and indicates a design metric that can be used to evaluate USTLD mapper designs. The resultant metric is given as:

$$\omega(\mu_1, \mu_2) = \min_{\nu,\ \widehat{\nu}\ \epsilon\ [0:M-1], \nu \neq \widehat{\nu}} \left[\prod_{t=1}^{2}\|\mu_t(\nu) - \mu_t(\widehat{\nu})\|\right] \tag{B.7}$$

From (B.7), higher values of ω indicates higher values of Labelling Diversity achieved. Hence, the overall aim of USTLD mapper design is to maximise the minimum product Euclidean distance to produce a secondary mapper that achieves Labelling Diversity.

5 Current Mapper Design Models

5.1 Algorithmic/ Exhaustive Search Approaches

Samra et al [5] proposed a mapper design solutions for Labelling Diversity by brute-forcing the quadratic assignment problem QAP). [5] showed that for a system that requires S number of LD mappers, there are $(M!)^S$ possible solutions for the QAP. Due to the high computational complexity involved, [5] uses a lower-bound approximate approach to solving the QAP. This approach uses an iterative solver that finds S optimal mapper designs one at a time, therefore reducing the search space to $M! \times S$. But, due to the complexity of the algorithm, [5] reported that the algorithm is unfeasible for larger constellations of order M, where $M > 16$. Xu et al [4] proposed a simple, yet effective mapper design solution that swapped diagonal pairs on a constellation. This proved to be equal in performance to the algorithmic approaches in [5–7]. Although this approach was effective, mapper designs for constellations found in [4] cannot be applied to this design and larger constellations are too tedious. Other algorithmic mapper design approaches include Seddik et al [8] which produced mapper designs for LD constellations by bit-flipping and a more traditional brute-force approach in [7].

5.2 Labelling Diversity Genetic Algorithm

Recently, a GA for producing LD mapper designs was proposed by [2]. Candidate mapper design solutions are encoded as chromosomes, and each value inside the chromosome called genes represent a single point on the constellation. These chromosomes are encoded and added to a population P_t. The initial population, $P_t^{(0)}$ contains a set of randomly generated chromosomes as well as heuristic and exhaustive search mapper designs that have been produced in previous literature this ensures that the GA will either match or beat the heuristic and exhaustive mapper designs. By keeping in mind the Labelling Diversity problem Maximise the minimum distance between two points from its base constellation to its new constellation, [2] proposed a new crossover technique, called the κ-Hyper-sphere Swap Crossover. This technique utilized two parent chromosomes and selects a single gene which is found within each parent chromosome. A circle of radius R is projected around the selected gene in both constellations, thereby encapsulating each of its adjacent points. Another gene is selected at random such that the new selected point is not found within either circle that encapsulates each of its adjacent points. These two genes are then swapped in both parent chromosomes and hence producing offspring chromosomes. This process is performed κ number of times. Mutation in the context of this GA is a probabilistic event that explores new, unknown solutions by swapping two randomly selected genes in an offspring chromosome. The objective function in (B.7) was used to evaluate candidate solutions to carry over to the next generation. Termination of the GA will occur in either two instances: i) the population converges to a single fitness value and the population is said to contain a stable solution or ii) the maximum number of iterations had been reached, the population is said to contain unstable solutions.

6 Proposed Genetic Algorithm

6.1 Genetic Encoding

The very first step of any GA is to represent a candidate solution to the problem in the form of a chromosome, ϕ. Information encoded into each chromosome is known as genes. Each gene, $\iota_i, i \,\epsilon\, [0 : M-1]$, represents a point on the constellation and the information contained in the gene is the label associated with it. A single chromosome can be defined as:

$$\phi = [\iota_1, \iota_2, \cdots, \iota_{M-1}] \tag{B.8}$$

Each chromosome represents a unique permutation of distinct labels, and therefore, no label can be duplicated in, or excluded from a chromosome.

6.2 Population and Elitism

A set of p chromosomes represents the population and is denoted by P_t. The initial population, $P_t^{(0)}$, contains a set of randomly chosen chromosomes. All existing heuristic and algorithmic LD mapper designs are also encoded as chromosomes and are added to the initial population. This ensures that the GA will either match or improve on the best LD mapper design available [2]. It is important to note that the terms chromosome and constellation will be used interchangeably. The population P_t can be represented as

$$P_t = [\phi_0, \phi_1, \cdots, \phi_{M-1}] \tag{B.9}$$

A simple, yet effective technique Elitism was implemented to find better solutions and convergence times. Elitism aims to keep the fittest chromosomes from the current generation and carries them over to the next generation, unaltered. This guarantees that the solution quality obtained by the GA will not depreciate from one generation to the next.

6.3 The Crossover Operator

Crossover is a genetic operator that introduces genetic diversity into chromosomes from one generation to the next. During crossover, two parent chromosomes are mated and produce offspring chromosomes that retain the most desirable properties from parent chromosomes. [2] reports that [9] investigated various crossover techniques for constellation assignments but were not suitable for LD mapper design. [2] proposed a new crossover technique called the κ-Hyper-sphere Swap Crossover (κ-HSX) that used two parents independently to produce offspring chromosomes. When a single parent is used to produce offspring chromosomes, genetic diversity is only gained by mutation, hence becoming a purely random process rather than a process that is guided by parent chromosome properties. The true value of the GAs potential is then not realised. Genetic diversity during crossover is realised by introducing two-parent crossover techniques which reduces randomness in offspring chromosomes. The following two-parent crossover operators were investigated [1, 10]: i) single-point crossover, ii) multi-point crossover, iii) Davis ordered (OX1) crossover, iv) Davis 2 ordered (OX2) crossover, v) cyclic crossover and vi) partially mapped crossover

The crossover operator that was to be chosen for this GA had to conform with the following constraint: "No duplicate genes in chromosomes"

Firstly, both the cycle and partially mapped crossover techniques are not suitable for the implementation of this GA as most offspring chromosomes produced contain duplicate genes, hence violating the constraints. From literature [10], when these operators were applied to the travelling salesman problem (TSP), near optimal results for many datasets - such as the Berlin52 dataset have been achieved. Therefore, the single-point crossover, multi-point crossover and both OX1 and OX2 crossover techniques were considered for application to the system. Initial trial runs in Fig. B.3 - have shown that the single- point, multi-point and OX2 crossover techniques match but do not improve upon existing GA mapper designs. However, OX1 had shown the best results in terms of performance and improvement of mapper designs, as shown in Fig. B.3. Therefore, the Davis ordered crossover (OX1) had been chosen as the crossover operator for this implementation.

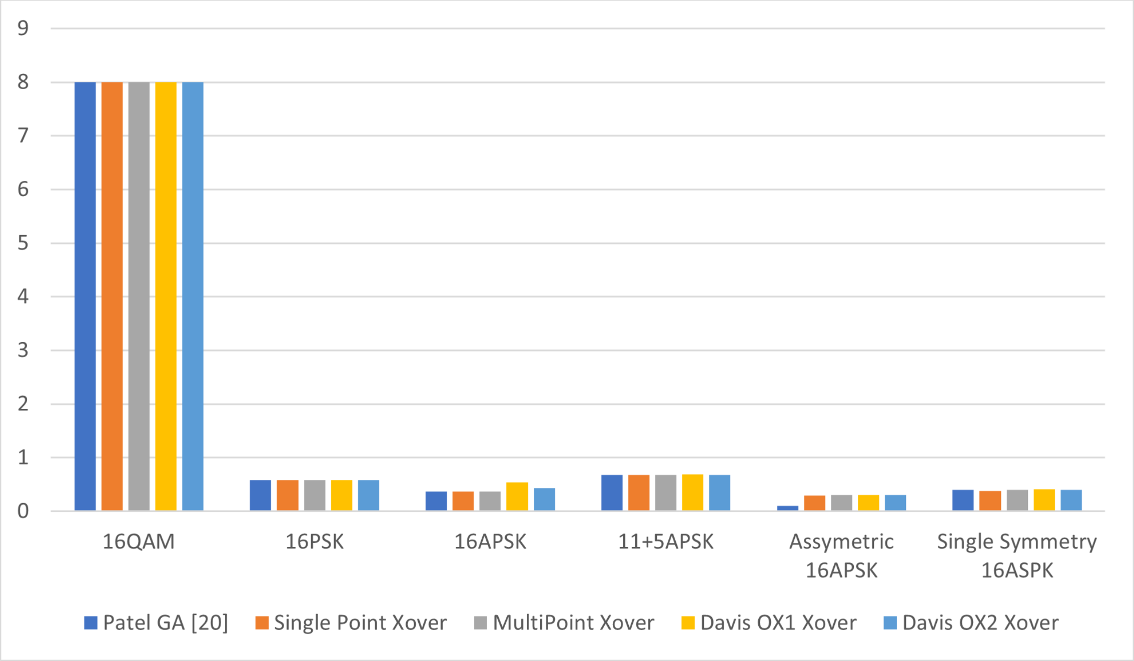

Fig. B.3: Histogram Comparing the final fitness values of the chosen Crossover techniques to be used

The Davis Ordered Crossover (OX1) was proposed by [11] which was used for chromosomes for permutation encoding [1]. Given two parent chromosomes, two random crossover points are selected partitioning them into a left, middle and right portion. The ordered two-point crossover behaves in the following way: The first offspring inherits its left and right section from both parent chromosomes, and its middle section is determined by first parent. The converse is also true for the second offspring chromosome.

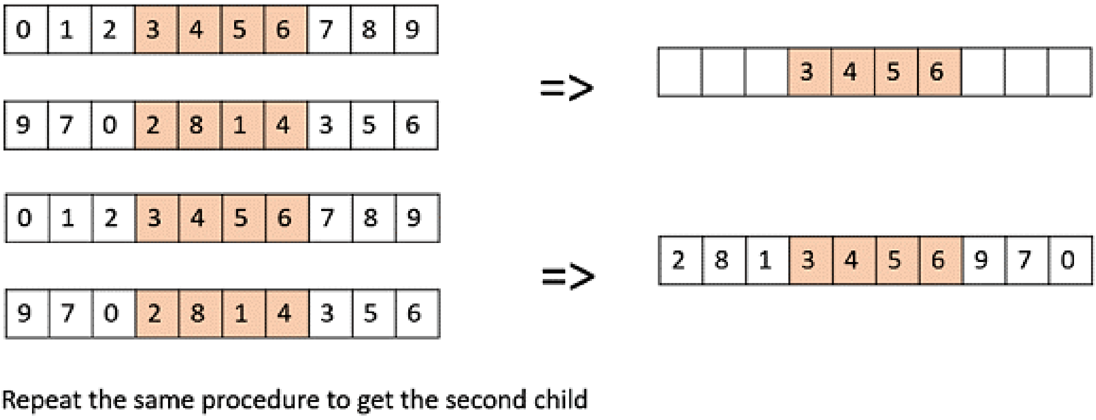

Fig. B.4: Simplified Diagram of the Davis Ordered (OX1) Crossover Operator

All possible combinations of parent chromosomes are crossed over, with each pair producing two offspring. Authors note that the implementation contained a duplicate chromosome remover, and therefore had less chromosomes in the population. Therefore, the total size of the population after crossover in the i-th iteration can be denoted as:

$$P_t^{(i)} = (P_t + 1)^2 \tag{B.10}$$

where P_t is the total population size

6.4 Mutation

Mutation is a genetic operator used to maintain diversity from one generation of the population to the next. It is a probabilistic event that further changes offspring chromosomes. In the context of this GA, mutation will occur of two randomly selected points are swapped. The probability of mutation is denoted by P_m.

Fig. B.5: Illustration of Mutation that occurs within offspring chromosomes

6.5 Evaluation of Chromosomes

After the process of mating (crossover and mutation), natural selection is imitated. All chromosomes parent and offspring are put back into the population and are evaluated according to the fitness function found in (B.7). The best p chromosomes are then selected to form the new generation, $P_t^{(i+1)}$. The authors remind the reader than μ_1 is known, and each solution in the population, P_t, represents a candidate mapper for μ_2.

6.6 Filtering of Illegal Chromosomes

There exists a constraint on labelling diversity mappers, which can be simply stated as "no duplicate values on a constellation/ chromosome". For this reason, a filter was employed to mitigate this issue. The filter is illustrated in Fig. B.6:

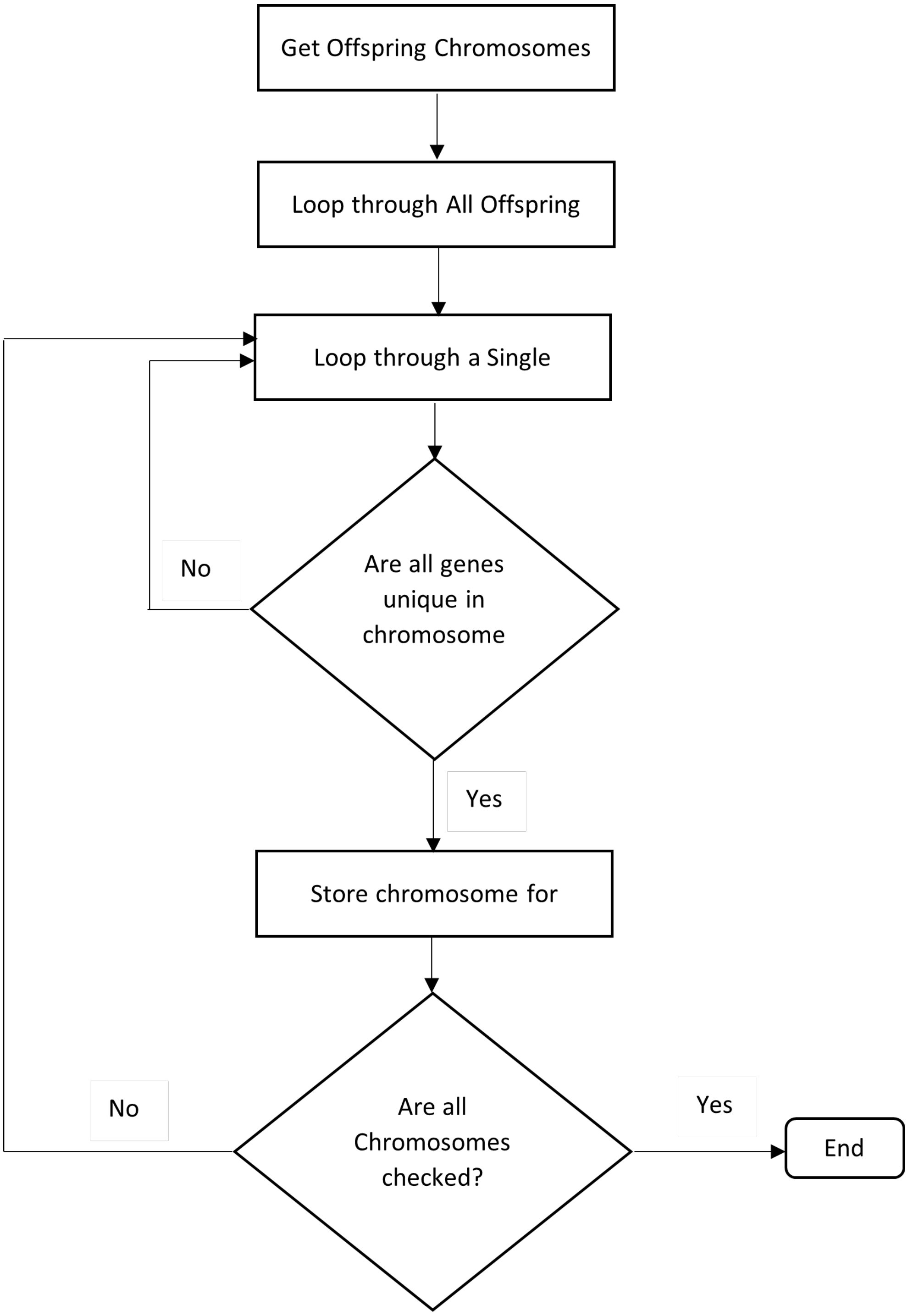

Fig. B.6: Flow Diagram of the Filter Algorithm

6.7 Termination Conditions

Termination of a GA occurs under two conditions, 1) convergence of the population, or 2) optimality has been reached. As in [9, 12], the GA will terminate at the most optimal solution when all chromosomes in the population converge to the same value, i.e. $\omega(\mu_1, \phi_a) = \omega(\mu_1, \phi_b), \forall\ \phi_a, \phi_b\ \epsilon\ P_t$. In the case of this chapter, however, the GA will terminate for the following two conditions; 1) a stable, convergent solution had been found, and 2) the GA would reach the maximum number of iterations and terminate if no optimal, stable or convergent solutions can be found, after which the chromosome with the highest fitness will be deemed the sub-stable chromosome. The algorithm is constrained to perform only n_{max} number of iterations. If the GA does not converge, the chromosome in P_t with the highest fitness is deemed sub-optimal.

7 Experimental Setup

Designing close-to-optimal LD mappers has been a challenge in recent times, since the only method of designing these mappers were the brute-force approach. More recently, a GA proposed by [2] has shown significant improvement for designing such mappers using less computational resources and reducing time complexity. It is also reported by [2] that only a locally optimal solution has been achieved, which prompted studies into new methods of improving the GA. As such, the 16-ary constellations which include 16QAM, 16PSK, 16APSK, 11+5APSK, asymmetric 16ASPK and single symmetry 16APSK are tested on the proposed system. Since 16QAM and 16PSK systems already have optimal configurations, Fig. B.7 shows optimal mapper designs for 16QAM and 16PSK constellations respectively.

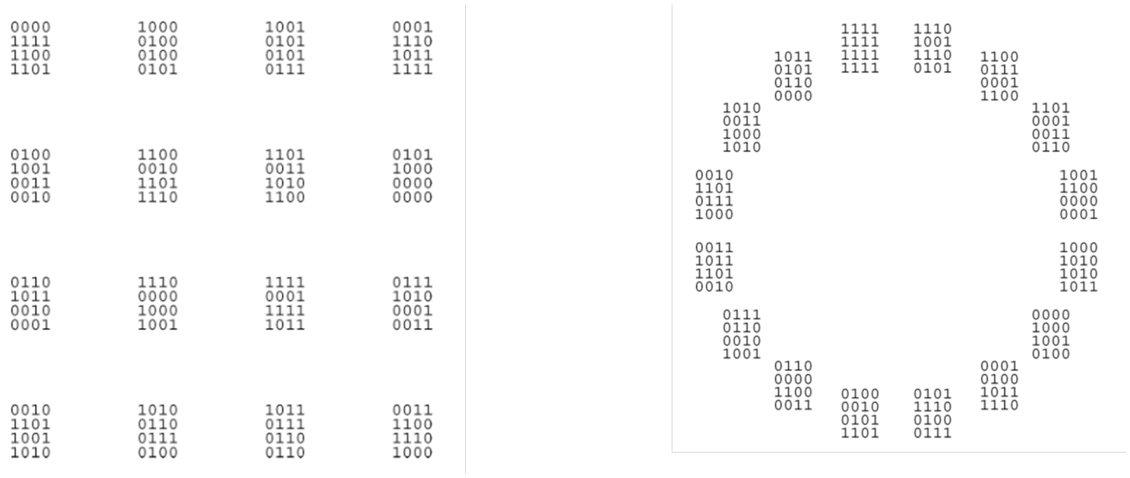

Fig. B.7: Optimal Mapper designs for 16QAM and 16PSK Constellations [5]

The values of each parameter used in the proposed GA in this chapter is summarized in Table B.1. Each parameter had been tested over an arbitrary range of values.

Table B.1: Summary of Variable Values used in the Genetic Algorithm

Modulation	Population Size (P_t)	Mutation Rate (P_m)	Number of Generations
16QAM	10 – 100	$1\% - 9\%, 10\% - 90\%$	10^5
16PSK	10 – 100	$1\% - 9\%, 10\% - 90\%$	10^5
16APSK	10 – 100	$1\% - 9\%, 10\% - 90\%$	10^5
11+5APSK	10 – 100	$1\% - 9\%, 10\% - 90\%$	10^5
Asymmetric 16APSK	10 – 100	$1\% - 9\%, 10\% - 90\%$	10^5
Single Symmetry 16APSK	10 – 100	$1\% - 9\%, 10\% - 90\%$	10^5

From literature, there exists three methods - to the author's knowledge - for determining good parameter settings for a GA, namely; i) a meta-genetic algorithm - the use of a GA to determine good parameter sets [13, 14], ii) sensitivity analysis - the process of comparing results from multiple analyses of a dataset using variations of an analysis workflow [15, 16] and iii) parameter varying. For this application, the author has chosen the parameter varying approach to select good parameter settings for the GA. Parameter varying is a simple approach that changes one parameter value at a time with respect to the output [17]. The parameter technique can be described as follows:

$$\Lambda_i = [\lambda_0, \lambda_1, \cdots, \lambda_{N-1}] \tag{B.11}$$

where Λ is the i-th, $i \ \epsilon \ [0 : N-1]$, set of parameters applied to the proposed GA and N is the number of parameters that tune the GA.

For the application of the proposed GA, the parameter varying technique is represented as:

$$\Lambda_i = [P_t^{(i)}, P_m^{(i)}] \tag{B.12}$$

where i represents the i-th value, $i \ \epsilon \ [0 : N-1]$ and N is the number of parameters that tune the GA.

The mutation rate P_m must be chosen such that $P_m \leq 10\%$. When mutation rates are much higher, offspring chromosomes could be destroyed and may not have a good fitness value [1]. Since the search space for designing LD mappers depends on the modulation order M, a larger population size is needed to transverse the search space. For any modulation order M, there exists $M!$ number of mapper designs [2, 5]. Due to the large number of producible mapper designs, the range of population sizes were chosen as $P_t \geq 10$.

The programming was done in Python and Matlab on a PC machine with Intel Core TM) $i7$ $2.50GHz$ processor and $8GB$ of RAM with the Windows 10 Operating System.

8 Results and Discussion

In this section, the output of the GA used to design the secondary mapper, μ_{GA}^{Davis}, for USTLD systems, is evaluated and benchmarked against the GIA solutions found in [2] -denoted as μ_{GA}^{Patel}. From the work in Xu et al [4], the error performance for 2 × N_R USTLD systems with 16-ary QAM, PSK, APSK and asymmetric APSK constellations in a rayleigh fast fading channel are demonstrated. All parameters and corresponding values are summarized in Table B.1. The authors note that besides the 16QAM and 16PSK mapper designs, no other constellation studied in this chapter has been produced using an exhaustive search, hence the term "close-to global optimal" will be used.

All binary mappings are represented by their decimal equivalent. The results of the proposed GA on the 6 different instances of 16-ary constellations are summarized in Table B.2 and is compared to the mapper designs produced from [2].

Table B.2: Summary of Results of the Genetic-Inspired Algorithm [2] vs the Proposed Genetic Algorithm

Type	Genetic-Inspired Algorithm				Proposed Genetic Algorithm		
Instance	P_t	κ	P_m	μ_{GA}^{Patel}	P_t	P_m	μ_{GA}^{Davis}
16QAM	8	6	10%	8.0	100	7%	8.0
16PSK	8	6	10%	0.5857	100	5%	0.5857
16APSK	8	6	10%	0.3685	100	9%	0.5427
11+5APSK	8	6	10%	0.6766	100	5%	0.7171
Asymmetric 16APSK	8	6	10%	0.0981	100	5%	0.3008
Single Symmetry 16APSK	8	6	10%	0.4020	100	7%	0.4053

From Table B.2, the common parameters and fitness value output from (B.7) of the proposed GA are being compared to the genetic-inspired algorithm (GIA). The parameters used for the GIA were kept to the original values that can be found in Patel et al [2], section IV. The parameter κ has been constrained to $\kappa = \frac{M-4}{2}$ while P_t and P_m remained constant.

In the case of the proposed GA, the parameters were chosen after the Parameter Varying process was conducted, and the most suitable parameters were chosen. A large population size ($P_t = 100$) was chosen while the mutation rates chosen were lower than 10%. The author brings to the readers attention that for a population size $P_t > 100$, no significant improvements in fitness values are found.

As seen in Table B.2, the proposed GA produced matching and higher LD fitness values for the 16-ary systems presented when compared to the GA in [2]. In the cases of 16QAM and 16PSK, it can be seen that no improvements can be found. The authors note that since the proposal by Samra et al [5] had used an exhaustive search algorithm, 16QAM and 16PSK mapper designs has achieved the best Labelling Diversity mapper design. Significant improvements in fitness values can be seen for the 16APSK and asymmetric 16APSK constellations. This is attributed to the larger search space being transversed by the use of a larger population size.

8.1 16QAM and 16PSK

The first two constellations tested on the GA was the 16QAM and 16PSK constellations. Both constellations were benchmarked against mapper designs found in [4, 5, 8] and the GA mapper design in [2]. Since [8] had implemented an exhaustive search algorithm, it has been taken as the most optimal solution as stated in the paper. The mapper designs found in [4, 5, 8] are denoted by μ_2^{Samra}, μ_2^{Seddik} and μ_2^{Xu} respectively. First we consider the 16QAM system. By evaluating these mapper designs with the equation in (B.7), we arrive at the following fitness values; $\omega\left(\mu_1, \mu_{2,16QAM}^{Samra}\right) = 8.0$, $\omega\left(\mu_1, \mu_{2,16QAM}^{Seddik}\right) = 8.0$ and $\omega\left(\mu_1, \mu_{2,16QAM}^{Xu}\right) = 8.0$. Furthermore, $\mu_{2,16QAM}^{Patel}$ is also found to have a fitness value of $\omega\left(\mu_1, \mu_{2,16QAM}^{Patel}\right) = 8.0$. The proposed GA converges to $\omega\left(\mu_1, \mu_{GA,16QAM}^{Davis}\right) = 8.0$. Thus, the mapper design has matched, but not improved upon existing GA mapper designs. Next, the 16PSK constellation is tested. $\mu_{2,16PSK}^{Samra}$, $\mu_{2,16PSK}^{Xu}$ and $\mu_{2,16PSK}^{Patel}$ are both evaluated according to (B.7) and have a fitness value $\omega\left(\mu_1, \mu_{2,16PSK}^{Samra}\right) = \omega\left(\mu_1, \mu_{2,16PSK}^{Xu}\right) = \omega\left(\mu_1, \mu_{2,16PSK}^{Patel}\right) = 0.5857$. The proposed GA converges to a value of $\omega\left(\mu_1, \mu_{GA,16PSK}^{Davis}\right) = 0.5857$. Therefore, the mapper design has matched but not improved upon existing heuristic and GA mapper designs. Since the 16QAM and 16PSK mappers have been produced by utilizing an exhaustive search [5], these mapper designs are deemed optimal. Although no improvements can be observed, authors note that from the Fig. B.8, a significant improvement in the number of generations to reach convergence has been observed for both cases. Authors note that the reason for this improvement is that since all possible combinations and permutations are produced with respect to already existing heuristic mappers faster convergence not pre-mature convergence is achieved.

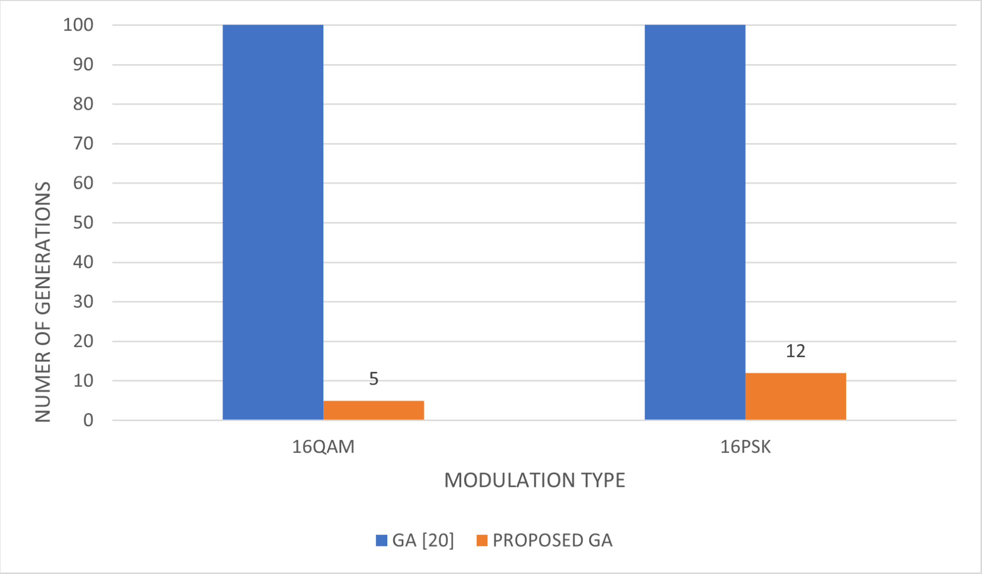

Fig. B.8: Convergence time comparison off the Proposed Genetic Algorithm and Patel et al [2] Genetic Algorithm

8.2 16APSK

The first circular constellation the proposed GA was tested on is the 16APSK constellation. Quazi et al [18] had proposed an approach for designing Labelling Diversity mappers for the APSK system. However, this approach relies on symmetry and tedious when applied to higher order APSK constellations. Therefore, the 16APSK system (along with the 8APSK, 32APSK and 64APSK) systems have been passed through the GA in [2]. Since it was reported in [2] that the values obtained from the GIA were local optimal values, the same system was applied to the proposed GA. The GA in [2] had converged to a value of $\omega\left(\mu_1, \mu_{GA,16APSK}^{Patel}\right) = 0.4278$, while the mapper design produced by the proposed GA converged to a value of $\omega\left(\mu_1, \mu_{GA,16APSK}^{Davis}\right) = 0.5427$. The proposed GA has produced a mapper design with a higher value of LD being achieved. Hence, a close-to global optimal solution has been reached. Thus, the objective of producing a mapper design for the 16APSK with a higher value of LD has been achieved.

The analytical results were validated by a tight fit with the Monte Carlo simulations at high SNR values. As seen in Fig. B.9, even though an improvement in fitness has been observed, only a small gain of $\approx 0.5dB$ at 10^{-6} has been achieved. Above an SNR value of $6dB$, the performance of the proposed GA system extends away from the existing GA system, hence becoming more efficient.

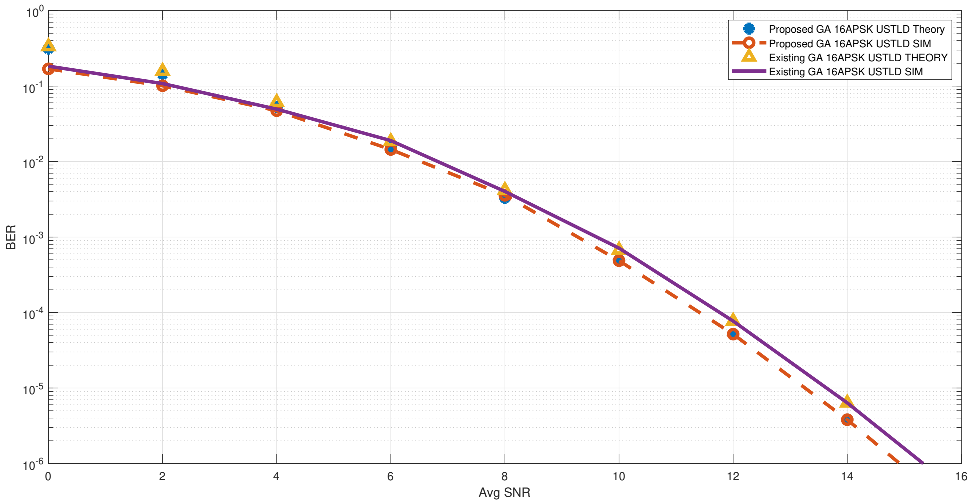

Fig. B.9: BER Curve of the 16APSK system - Genetic Algorithm in [2] and Proposed Genetic Algorithm

8.3 11+5APSK

The next system that was tested on the GA is the 11+5APSK constellation that was proposed by [19] which does not exhibit any diagonal symmetry. The authors note that prior to the GA in [2], there had been no attempts at designing LD mappers for systems like these. Furthermore, techniques from [4] and [18] cannot be modified and applied to these constellations due to the asymmetric nature of the M-APSK constellations. Since no LD mapper designs exist outside the GA produced by [2], pseudo gray mappers were selected for μ_1 and the proposed GA was used to create the secondary mapper, $\mu_{GA,11+5APSK}^{Davis}$. The GA in [2] had converged to a value of $\omega(\mu_1, \mu_{GA,11+5APSK}^{Patel}) = 0.6766$, while the mapper design produced by the proposed GA converged to a value of $\omega\Big(\mu_1, \mu_{GA,16APSK}^{Davis}\Big) = 0.7171$. Chen et al [19] had only obtained a local minima optimized mapper design for the 11+5APSK constellation (Maximum Euclidean Distance $= 0.5975$), while Patel et al [2] had produced a local optimal mapper design. Hence, a close-to global optimal mapper design has been reached for the 11+5APSK constellation. Thus, the objective of producing a mapper design for the 11+5APSK with a higher value of LD has been achieved.

Table B.3 summarizes the mapper designs produced (presented in polar co-ordinates). The analytical results were validated by a tight fit with the Monte Carlo simulations at high SNR values From Fig. B.10, at a BER of 10^{-6}, again only a small gain of $\approx 0.5dB$ has been observed. Above the SNR value of $8dB$, the performance of the proposed 11+5APSK system extends away from the existing 11+5APSK system, thus making the proposed system more efficient.

Table B.3: Mapper design comparisons for 11+5APSK system

11+5APSK Mapper Comparison				
RADIUS	PHASE	Mapper 1	Mapper 2 [2]	Proposed Mapper Design
0.5501	0.000	10	7	5
	1.2566	13	4	8
	2.5133	15	11	13
	3.7699	6	0	11
	5.0265	8	1	4
1.1476	0.0000	7	13	3
	0.5712	3	12	14
	1.1424	5	8	12
	1.7136	4	2	0
	2.28487	11	9	10
	2.85607	0	14	1
	3.4272	9	3	15
	3.9984	14	6	6
	4.5696	1	10	2
	5.1408	12	5	7
	5.7120	2	15	9

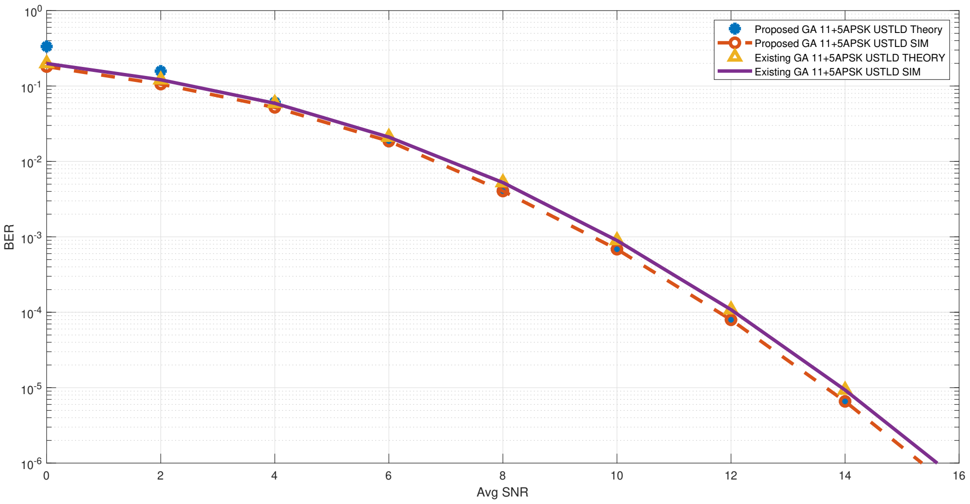

Fig. B.10: BER Curve of the 11+5APSK system - Genetic Algorithm in [2] and Proposed Genetic Algorithm

8.4 Asymmetric 16APSK

The next system tested on the proposed GA is the asymmetric 16APSK constellation proposed by [19]. Again, a pseudo gray mapper was used as μ_1 and the proposed GA was used to design $\mu^{Davis}_{GA,AS16APSK}$. Table B.4 summarises the new mapper designs produced presented in polar co-ordinates). From the fitness equation in (B.7), we see that the GA in [2] had converged to a fitness of $\omega\Big(\mu_1, \mu^{Patel}_{GA,AS16APSK}\Big) = 0.0981$. However, the proposed GA had converged to a fitness value of $\omega\Big(\mu_1, \mu^{Davis}_{GA,AS16APSK}\Big) = 0.3008$, hence achieving higher values of LD, and producing a mapper design that is close-to a global optimum solution. The analytical results were validated by a tight fit with the Monte Carlo simulations at high SNR values. At a BER of 10^{-3}, we see from the BER curve illustrated in Fig. B.11 that the proposed GA showed a diversity gain of $\approx 4dB$ over existing GA mapper designs. As seen from [2], the GA had reached pre-mature convergence, hence there was still a lot of room for even higher fitness values and subsequently higher values of LD being achieved.

Table B.4: Mapper design comparisons for Asymmetric 16APSK system

Asymmetric 16APSK Mapper Comparison				
RADIUS	PHASE	Mapper 1	Mapper 2 [2]	Proposed Mapper Design
0.9593	4.7453	1	10	14
	3.1109	5	5	10
	1.5490	9	14	5
	0.4687	13	3	12
1.000	5.0872	0	4	3
	4.3400	2	13	7
	3.7447	3	1	1
	3.4121	4	11	11
	2.7071	6	8	15
	2.2326	7	6	6
	1.8925	8	2	2
	1.2567	10	0	9
	1.0438	11	7	13
	0.7340	12	9	4
	0.2205	14	15	0
	0.0699	15	12	8

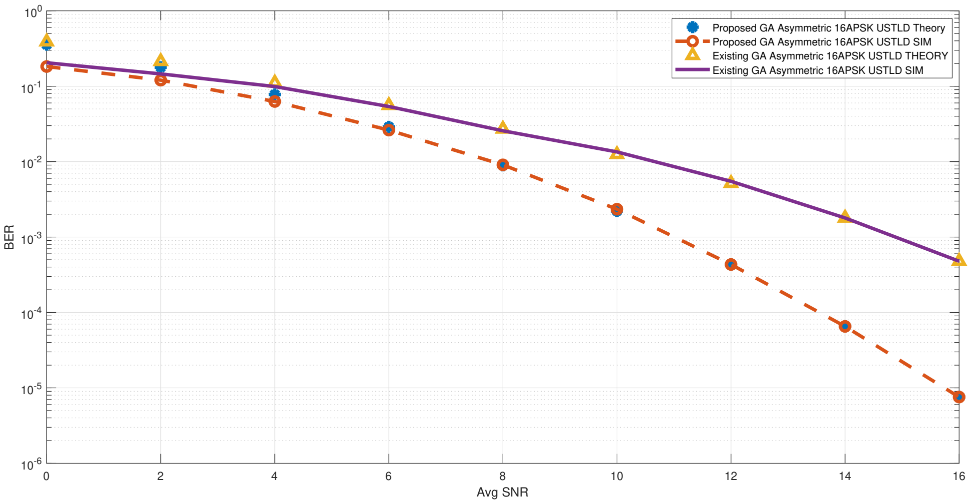

Fig. B.11: BER Curve of the Asymmetric 16APSK system - Genetic Algorithm in [2] and Proposed Genetic Algorithm

8.5 Single Symmetry 16APSK

The single symmetry 16APSK constellation is quite peculiar, having a horizontal axis of symmetry, and was proposed by [19]. Furthermore, from the work done by [19], they show that the single symmetry 16APSK constellation is more optimal than the Asymmetric 16APSK constellation. Again, a pseudo gray mapper was used as μ_1 and the proposed GA was used to design $\mu_{GA,AS16APSK}^{Davis}$. Table B.5 summarises the new mapper designs produced presented in polar co-ordinates). From the fitness equation in (B.7), we see that the GA in [2] had converged to a fitness of $\omega\left(\mu_1, \mu_{GA,AS16APSK}^{Patel}\right) = 0.4020$. Again, the proposed GA had converged to a fitness value of $\omega\left(\mu_1, \mu_{GA,AS16APSK}^{Davis}\right) = 0.4053$, which achieved a higher value of Labelling Diversity. This also indicates that a close-to global optimum solution has been achieved. The analytical results were validated by a tight fit with the Monte Carlo simulations at high SNR values. The BER curve is illustrated in Fig. B.12. At the BER of 10^{-5}, the proposed GA produced a mapper design that improved the systems performance by $\approx 2dB$.

Table B.5: Mapper design comparisons for Single Symmetry 16APSK system

Single Symmetry 16APSK Mapper Comparison				
RADIUS	PHASE	Mapper 1	Mapper 2 [2]	Proposed Mapper Design
0.9627	2.3592	1	4	4
	1.2107	5	6	10
	−2.3592	9	2	1
	−1.2107	13	15	15
1.000	2.5650	0	11	8
	2.0128	2	14	6
	1.7317	3	1	13
	1.4188	4	9	3
	0.8849	6	12	12
	0.5372	7	3	2
	−2.5650	8	13	9
	−2.0128	10	8	7
	−1.7317	11	7	0
	−1.4188	12	0	14
	−0.8849	14	5	5
	−0.5372	15	10	11

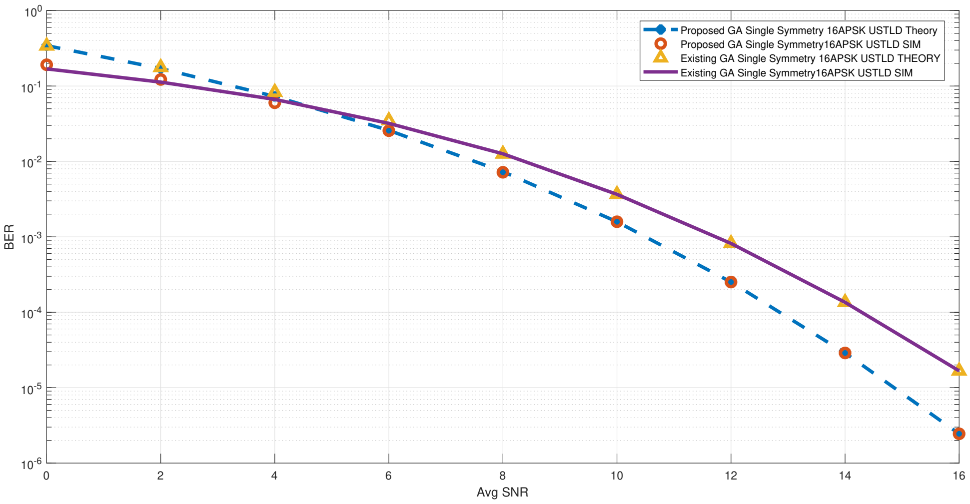

Fig. B.12: BER Curve of the Single Symmetry 16APSK system - Genetic Algorithm in [2] and Proposed Genetic Algorithm

9 Performance of the Genetic Algorithm

9.1 Computational Complexity Analysis

From [2, 3], the base GA consisted of four functions, namely fitness function, crossover operator, mutation operator and evaluation of chromosomes for the next generation. [3] extended the work done in [2] by performing a computational complexity analysis on the GA from [2]. All common functions from the GA in [2] fitness function, mutation and evaluation of chromosomes have been applied to the proposed GA with the exception of the crossover function. Hence, all existing complexities from [3] are used. All complexities are analysed in terms of the modulation order, M. Authors note that the proposed GA will achieve convergence faster than the previous GA because it transverses a much larger search space while producing mapper designs of equal or improved LD.
The common function complexities have been extracted from [3] and are given as:

$$S_{Fitness} = (P_t + 1)^2 \left(M^2 - M\right) \tag{B.13}$$

$$S_{Mutation} = P_m \left((P_t + 1)^2 - P_t\right) \tag{B.14}$$

$$S_{Eval} = (P_t + 1)^2 \left(M^2 - M\right) \tag{B.15}$$

Where P_t is the initial population size, P_m is the mutation rate and M is the order of modulation

Consider two parent chromosomes, P_1 and P_2 that undergo crossover using the Davis Ordered Crossover technique and produce two offspring chromosomes C_1 and C_2 respectively. Two random crossover points are created in both parent chromosomes, creating a segment. The segment from the parent chromosome P_1 is copied onto offspring chromosome C_1 and the segment from parent chromosome P_2 is copied onto offspring chromosome C_2. In order to generate the first offspring chromosome, copy all of the unused genes from P_2 into C_1. Hence, C_1 is produced. C_2 is generated similarly. As stated in section 6.3, the Davis ordered crossover technique in this implementation was a brute force approach needing computations for all possible permutations and combinations of offspring chromosomes. The number of permutations requires computations on all possible arrangements of each offspring chromosome of size M. Hence, this requires $M.M!$ number of computations. Since all possible combinations of parent chromosomes produce two offspring chromosomes and each crossover requires two parent chromosomes, the total computational complexity of the Davis Ordered Crossover for this implementation is given by

$$S_{OrderedCrossover} = 2MM! \left((P_t + 1)^2 - P_t\right) \tag{B.16}$$

Where P_t is the initial population size and M is the order of modulation

Hence, adding up all the complexities gives the total computational complexity of the GA as

$$S_{GA} = S_{fitness} + S_{Mutation} + S_{Eval} + S_{OrderedCrossover} \tag{B.17}$$

$$S_{GA} = (P_t+1)^2 \left(M^2 - M\right) + P_m \left((P_t+1)^2 - P_t\right) + (P_t+1)^2 \left(M^2 - M\right) + 2MM! \left((P_t+1)^2 - P_t\right) \tag{B.18}$$

Converting expression (B.18) to big-$\mathcal{O}$ notation, we set P_t as the largest population size used, hence $P_t = 100$ and the average mutation rate $P_m = 5\%$ which further reduces the computational complexity to

$$S_{GA} = 20402M^2 - 20402M + 505.05 + 20202M.M! \tag{B.19}$$

Hence, the final big-$\mathcal{O}$ notation expression considering the worst-case scenario of all variables is stated as

$$\mathcal{O}\left(enhanced - GA\right) = \mathcal{O}\left(M!\right) \tag{B.20}$$

9.2 Computational Complexity Comparison

The general case is that the GA in [2] will always utilize less computation resources $\left(\mathcal{O}\left(M^2\right)\right)$ and take less time $(n_{max} \ll M^5)$ to produce a solution than other algorithmic/ exhaustive approaches [2, 3]. However, the proposed GA has a much larger computational complexity $(\mathcal{O}\left(M!\right))$ compared to the GA in [2]. This is attributed to the large search space that the GA transverses through to further improve on the LD of mapper designs produced. Even though the enhanced-GA has a larger computational complexity, by traversing through a larger search space, improved mapper designs are produced while taking significantly less time to reach local or global optimum solution.

9.3 Statistical Performance Comparison of the Genetic Algoirthm

Performance studies on algorithms are based on a number of factors that include i) Running Time The time the algorithm takes to complete one cycle or the time the algorithm takes to completion, ii) Convergence Time number of generations taken for the algorithm to converge, iii) Variables used in the algorithm and iv) Space Complexity, denoted by (B.20)

Firstly, we need to analyse the number of parameters needed and the role that they take on when applied to each system. In the case of the GA in [2], three variables namely; population size, number of swaps κ) and mutation rate P_m) is needed, while the proposed system in this chapter only requires two variables namely; population size and mutation rate. The authors note that relatively high mutation rates were used in [2], while lower mutation rates were used in the proposed system in this chapter. From [2], it can be shown that the most important parameter is the Number of Swaps κ) while in the proposed algorithm, the population size had the most influence on the output. The next aspect to be analysed is the changes made to the base system. When comparing the two algorithms, the only change is a new crossover operator OX1) has been applied to the system. In terms of time complexity, the OX1 technique is said to be the fastest crossover algorithm as it can process more generations over a given period of time than others [1]. Fig. B.13 illustrates the time comparison for both algorithms to complete one generation on the 16QAM system. From Fig. B.13, we see that the algorithm in [2] takes less time to complete a single generation as compared to the OX1 technique. The reason for this is that less computations are done in the algorithm from [2] whereas the OX1 operator has a more complex computation and computes much more due to the number of chromosomes after mutation. But the overall number of generations to convergence using the OX1 operator is decreased immensely as seen in Fig. B.13.

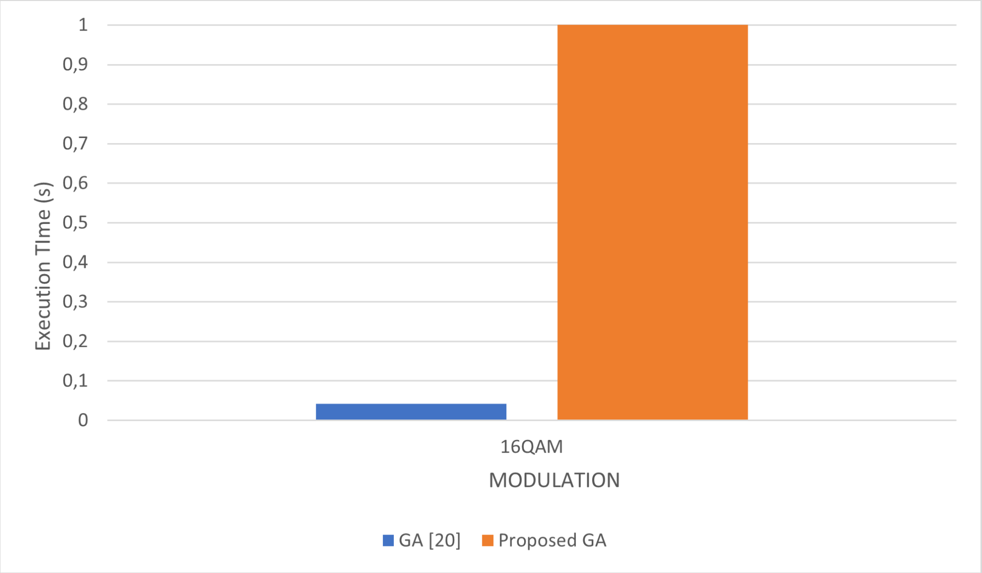

Fig. B.13: Execution time for a single generation for Patel et al [2] Genetic Algorithm and the Proposed Genetic Algorithm

Fig. B.14 shows the fitness comparison between the proposed GA in this chapter and the GA found in [2]. The proposed GA performs fairly consistently, beating the mapper designs produced by [2] across all constellations. This shows a step forward in designing close-to-global optimal solutions for mapper designs and is in line with the expectations for the GA.

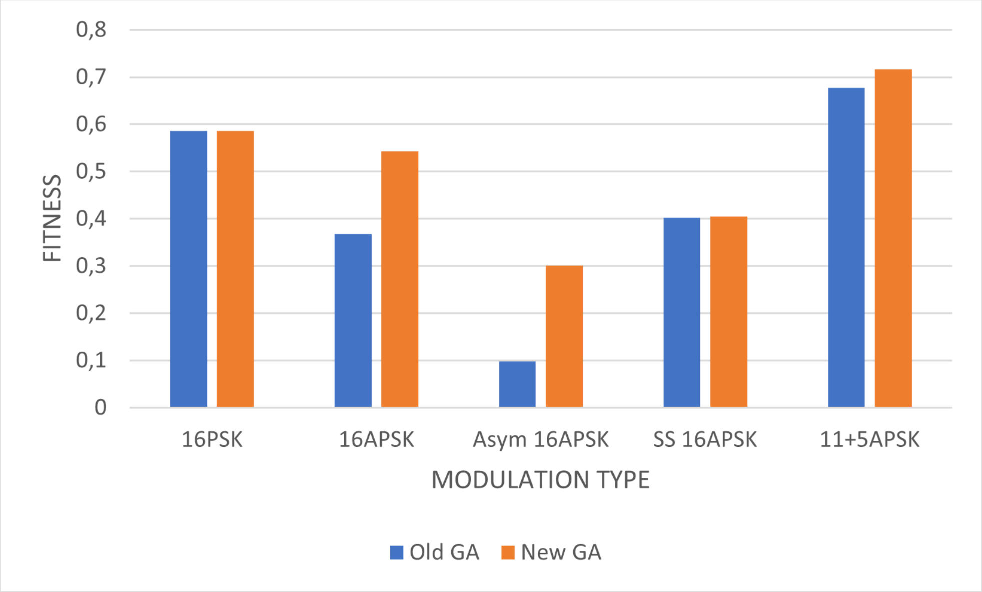

Fig. B.14: Solution Comparison of Patel's GA [2] and the Proposed GA

In terms of convergence time as illustrated in Fig. B.15 the proposed algorithm has shown a decrease in time complexity, as well as a very small convergence time. Highlighted in Fig. B.15, the convergence time of the GA is an inverse logarithm. This suggests that even for larger constellations, the algorithm will have a lower running time than that of the GA in [2].

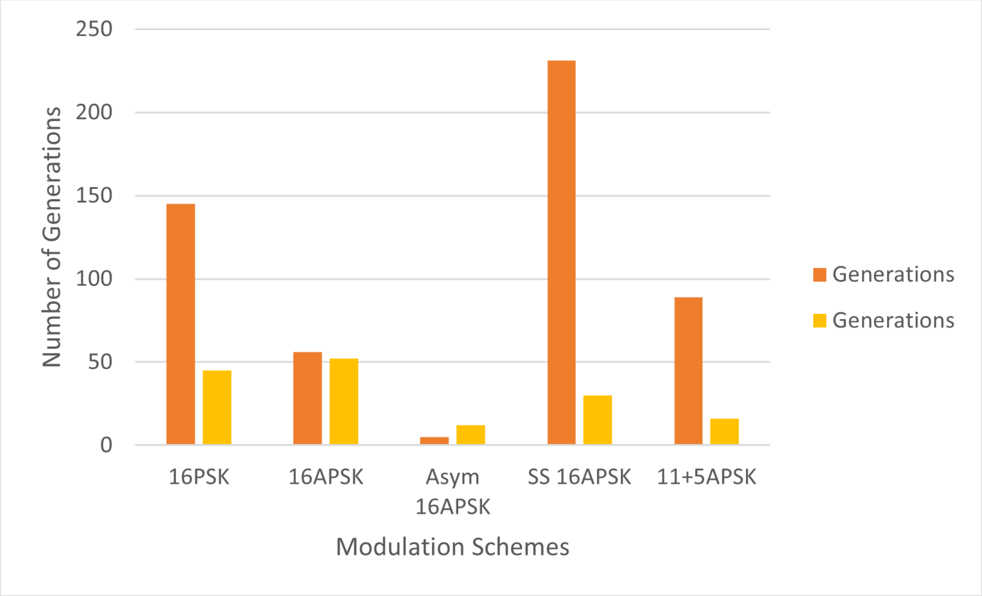

Fig. B.15: Convergence Time Comparison between the Proposed Genetic Algorithm and Patel et al [2] Genetic Algorithm

A study using various mutation rates have been applied to determine the effects on fitness values produced by the GA. From the parameters settings in [2], it was noted that a relatively high mutation rate ($P_m = 10\%$) was used. This in some respect contradicts the principles of evolution [20].

Therefore, when designing the GA in this chapter, the authors aimed for using lower mutation rates, as seen in section 6, Results and Discussion.

Using the equation in (B.18), we see that by using smaller mutation rates, fewer computations are needed, and thus the overall complexity of the GA is decreased. This is best shown by example. First we consider Patel et al [2] algorithm, with population size of $P_t = 8$ and a mutation rate $P_m = 10\%$. [2] states that after crossover, there will be P_t^2 number of computations before mutation. At a mutation rate of $P_m = 10\%$, 6 more computations will be needed to carry out the mutation. This equates to a total of $P_t^2 + 6$ number of computations at any given generation after mutation. Consider the proposed system, with the same population size of $P_t = 8$, a lower mutation rate of $P_m = 1\%$ and the same architecture of the proposed system in [2] that is after crossover, there will be $(P_t + 1)^2$ number of computations before mutation, without any additional computations. By using a mutation rate of $P_m < 10\%$, we ensure that mutation does not occur in some generations, hence decreasing overall number of computations - hence, complexity - of the system. This can be attributed to lower number of offspring chromosomes being mutated. In Fig. B.16, the mutation rates used compared two lower mutation rates ($Pm = 5\%, 7\%$ and 9%) and compared the fitness scores at convergence to a higher mutation rate ($Pm = 10\%, 40\%, 60\%$ and 90%). These values were chosen as they exhibited the best fitness performance of the GA after testing a range of mutation rate values ($Pm = 1\% - 90\%$). The 11+5APSK system produced the best results when the mutation rate was set to $P_m = 7\%$, while the Asymmetric 16APSK system all produced matching fitness values. In the case of the Single Symmetry 16APSK system although the results cannot be seen visually in the figure due to very small changes in values the mutation rate at $P_m = 7\%$ produced the best results.

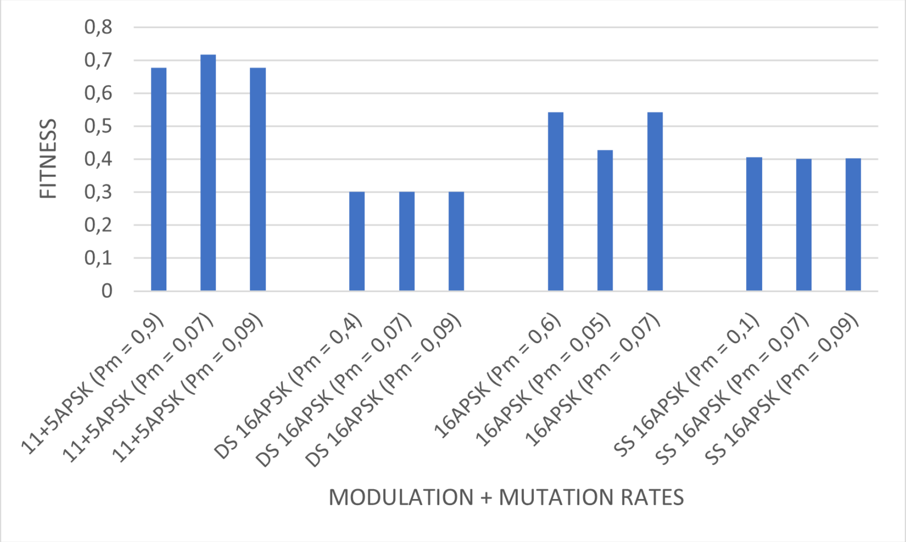

Fig. B.16: Fitness Values vs Different Mutation Rates for the Proposed Genetic Algorithm

10 Conclusion

Recently, AI techniques were applied to the LD problem in the form of a GA. By utilizing a GA, designing LD mappers for constellations $M > 64$ which were practically impossible to produce using exhaustive search or symmetry-based heuristics could be produced. From previous research, a local optima was achieved this is proven by the GAs output of the asymmetric 16APSK constellation where the fitness of the output mapper design was relatively low as compared to the others. This prompted studies into biological GA operators that could further produce mapper designs with higher values of LD. Biologically inspired techniques have been widely applied to GA problems but were yet to be applied to the LD Problem. Analysis of biological crossover techniques on the TSP hinted at the possibility of achieving higher values of LD for mapper designs. Finally, the most promising crossover technique the Davis ordered crossover (OX1) was chosen to further improve on the LD mapper designs produced. The proposed GA was tested on 16-ary constellations, namely; 16QAM, 16PSK, 16APSK and three 16APSK constellations that do no exhibit diagonal symmetry. In the case of 16QAM and 16PSK, an optimal mapper design have already been produced in literature, and no further improvements were made by the GA. In the case of the 16APSK and 11+5APSK constellations, both have achieved higher values of LD. The 16APSK had achieved a LD of $\omega(\mu_1, \mu^{Davis}_{(GA,16APSK)}) = 0.5427$, while the previous GA produced a mapper design with a LD of $\omega(\mu_1, \mu^{Patel}_{(GA,16APSK)}) = 0.3685$, while the 11+5APSK achieved a LD value of $\omega(\mu_1, \mu^{Davis}_{(GA,11+5APSK)}) = 0.7171$, thereby improving the previous LD value of $\omega(\mu_1, \mu^{Patel}_{(GA,11+5APSK)}) = 0.6766$. However, for both these constellations, only a small gain of $\approx 0.5dB$ had been observed on the BER curves. In the case of Asymmetric 16APSK, the mapper design was improved by a magnitude of $\approx 3dB$ ($\omega(\mu_1, \mu^{Davis}_{(GA,AS16APSK)}) = 0.3008$), while showing gains of $\approx 4dB$. This large gain is attributed to the pre-mature convergence ($\omega(\mu_1, \mu^{Patel}_{(GA,AS16APSK)}) = 0.0981$) in the previous GA. In the case of the Single Symmetry 16APSK, a very small improvement was made by the GA $\omega(\mu_1, \mu^{Patel}_{(GA,SS16APSK)}) = 0.4020$ compared to $\omega(\mu_1, \mu^{Davis}_{(GA,SS16APSK)}) = 0.4053$ -, but a $\approx 2dB$ gain was observed. Analysis on the complexity of the proposed GA showed that much more computational resources - $\mathcal{O}(M!)$ - are needed to execute the algorithm, but the time taken to produce mapper designs of equal or improved LD was significantly less then the previous GA. Furthermore, the proposed GA was seen to have a more guided search with lower mutation rates, while the previous GA needed higher rates of mutation making the system purely random.

Future works in this area include utilizing a better crossover method, such as the ring crossover, better mutation operators, better initialization operators for initial populations and a Meta-Parameter tuning model for optimized parameters for the GA for even faster convergence and more improved mapper designs.

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Part III

Conclusion

1 Conclusion

In this dissertation, the Genetic Algorithm(GA) mapper design technique has been applied to high density mappers and enhanced by introducing two-parent crossover to improve genetic diversity. In addition, each GA is analysed and studied in terms of its computational complexity. Table B.1 provides a summary of the key results obtained from the research presented. The main research contributions and outcomes in this dissertation can be summarized as follows

Table B.1: Summary of Key Results

Chapter	Results
Chapter II.A	• Application of the GA high density M-ary QAM, PSK and APSK Constellations. • For all M-QAM constellations, simulation results obtained show that the GA was able to match but not improve upon existing heuristic designs. • Simulation results have shown that the GA produced Labelling Diversity mapper designs that illustrated diversity gains between $\approx 3dB$ to $\approx 9dB$ over existing heuristic designs for M-PSK and M-APSK constellations. • The computational complexity of producing LD mappers from the GA increases as the modulation order M increases and is $\mathcal{O}(M^2)$
Chapter II.B	• Introduce two-parent crossover techniques to the GA to achieve higher values of LD. • For all 16-ary constellations tested, the proposed enhanced-GA produced matching or improved Labelling Diversity values. • The computational complexity of the enhanced-GA was found to be significantly more complex than the corresponding GIA and is $\mathcal{O}(M!)$. • The enhanced-GA converged to a local or global optimum in under 15 iterations for all constellations tested • Larger population sizes and reduced mutation rates allowed for the search space to be explored much faster.

Paper A extends the application of the GA to high-density mappers for $2 \times N_R$ USTLD systems. The GA had produced matching LD or fitness values for high-density M-QAM mappers, while the GA produced higher values of LD or fitness for M-PSK, DVB s2X M-APSK and Asymmetric M-APSK mappers. Monte Carlo simulation results have shown that the GA produced mapper designs that illustrated diversity gains of $\approx 4dB$ to $\approx 9dB$ respectively over heuristic mapper designs. In addition, the GAs computational complexity was studied and compared to exhaustive search and algorithmic approaches. Results demonstrated that the GA is significantly less computationally complex ($O(M^2)$) than exhaustive search approaches ($O(M!)$ and $O(M^5)$). Furthermore, the GA was able to produce mapper designs (close-to)-equivalent in LD to the exhaustive search approaches.

Paper B proposed an enhancement to the genetic-inspired algorithm(GIA) by applying a biological or two-parent crossover technique to achieve higher values of LD. The enhanced-GA was tested on 16-ary constellations only. Simulations show that the enhanced-GA produced mapper designs that either matched or improved upon existing exhaustive, heuristic or GA mapper designs. Monte Carlo simulation results demonstrated an improved error performance when compared to mapper designs from the Genetic-Inspired Algorithm. Additionally, the computational complexity of the enhanced GA ($O(M!)$) was proven to be significantly larger than the Genetic-Inspired Algorithm ($O(M^2)$). Finally, the enhanced GA was found to converge in less than 15 iterations for all instances of $16-$ary constellations, required mutation rates of $P_M \leq 10\%$ and due to large population sizes ($P_t \geq 10$), the search space is explored faster, which in turn produces mappers with higher values of LD.

In conclusion , the dissertation presented provides insight into further applying AI to optimize LD mappers. Furthermore, by using AI, not only does it produce matching or improved mapper designs, the computational resources and time taken to produce mapper designs irrespective of constellation shape or size are reduced significantly. Hence, the aim of producing high density mapper designs as well as enhancing the GA has been successfully fulfilled.

2 Future Research

The GAs presented in this dissertation can be improved and extended to other areas of AI and wireless communications. The following areas have been identified as research areas of interest:

2.1 Davis Ordered Crossover for High Density Mappers

The enhanced-GA is one of the contributions of this research to literature. In this dissertation, the enhanced-GA was applied to $16-$ary constellations only. Motivated by achieving higher values of LD, future research for the enhanced-GA should aim towards applying the enhanced-GA to higher order constellations ($M > 16$) to produce improved mapper designs.

2.2 Application of Neural Networks to Labelling Diversity

Keeping in light with AI, the design of a neural network(NN) to design LD mappers should be investigated. NNs are able to learn and model non-linear and complex relationships, and therefore will be the next big topic to investigate.

2.3 Application of Improved Crossover and Mutation Operators

Everyday, researchers are finding new and improved forms of biological diversity in nature. Taking inspiration from these discoveries, new crossover and mutation techniques can be found and applied to further improve the optimality of the GA. Furthermore, the application of already existing mutation operators such as the shuffle mutation technique can be used jointly with diversified crossover methods to introduce pure randomness and diversity, hence creating offspring that may provide optimality.

2.4 Meta-Parameter Optimization for Genetic Algorithms

Meta-Parameter optimization is a technique whereby an algorithm is trained over different sets of parameters. This technique selects some of the best parameter sets for the algorithm. The advantage of using meta-parameter optimization techniques has faster convergence times without pre-mature convergence, and significantly less computational resources are need.

2.5 Application of the Genetic Algorithm Mapper design to $N_T \times N_R$ USTLD Systems

As stated in [1], using the GA technique to design LD mappers for $3 \times N_R$ USTLD systems should be investigated in future research. Hence, the GA should be applied to $N_T \times N_R$ USTLD systems respectively. Furthermore, the GA should be used to design all N_T mapper designs as it produces close-to-optimal LD mappers.

2.6 Application of Optimized Mappers for $N_T \times N_R$ USTLD and USTPLD Systems

Patel et al [2] proposed a direct extension to the USTLD system by introducing polarization(USTPLD). Further research should include applying the mapper designs produced by the GA for a $3 \times N_R$ USTLD and USPTLD systems respectively.

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