

Genetic Algorithms: Tuning of Parameter K for the Labeling Diversity Problem in Wireless Communications

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Abstract – Recently, the Genetic Algorithm (GA) has been developed to produce Labeling Diversity (LD) mapper designs irrespective of constellation size or shape. However, the parameter space of the GA has not been investigated thoroughly. This paper investigates the parameter space of a GA by parameter varying the parameter K. Tuning results show that the parameter K should be set such that $K \leq 4$ to achieve close-to-optimal mapper designs in significantly less time. Monte Carlo simulations illustrate that when $K = 1, 2, 3$ the 16-APSK constellation exhibits a ≈ 1 dB gain over all other values of K. The 64-APSK constellation is a peculiar case such that close-to-optimal mapper designs are achieved in terms of fitness values but perform equally to other values of K. Thus, in order to design a close-to-optimal mapper design in the least possible time, the value of K should be $K \leq 4$. Furthermore, this study provides a deeper insight into developing more accurate mapper design GAs for future works. **Copyright** © 2022 The Authors.

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Keywords: Wireless Communications, Tuning, Identification, Labeling Diversity, USTLD

Nomenclature

y	Received signal vector [dB]
N_T	Number of transmitting antennas
N_R	Number of receiver antennas
h	Multipath fading matrix
A	Information codeword
$\hat{A}$	Estimated received codeword
n	AWGN noise vector [dB]
s	Arbitrary error correction integer
M	Modulation order
γ	Labelling diversity mapper
σ	Signal-to-noise ratio [dB]
τ	Euclidean distance [units]
ϕ	Fitness of a mapper design
φ	A chromosome
ι	A gene
P	A population of chromosomes
K	Number of swaps parameter
$\mathcal{R}$	Radius of the hypersphere [units]
χ	Total size of the population after crossover
δ	Parameter set chromosome
α	A single parameter of the parameter set
P_m	Mutation rate
Subscripts	
m	Mutation
T	Transmit antennas
R	Receive antennas
F	Frobenius norm
i	The i-th value

t	t -th value
N	N -th parameter value
max	Maximum
Acronyms	
USTLD	Uncoded Space-Time Labelling Diversity
STBC	Space-Time Block Code
GA	Genetic Algorithm
LD	Labelling Diversity
ABEP	Average Bit Error Probability
AI	Artificial Intelligence
MIMO	Multiple-Input Multiple-Output
HSX	Hypersphere Swap Crossover
QAM	Quadrature Amplitude Modulation
APSK	Amplitude Phase Shift Keying

I. Introduction

Uncoded Space-Time Labeling Diversity (USTLD) is an innovative Multiple-Input Multiple-Output (MIMO) scheme that achieves an improved error performance over the Alamouti Space-Time Block Code (STBC) [1], [2]. USTLD systems improve on the performance of STBC systems by applying a MIMO structure while employing the concept of Labeling Diversity (LD). LD is attained by employing symbol-pairs from distinct binary mappings to encode message bitstreams that is to be transmitted. In order to transmit a single message bitstream, there exist M possible symbol-pairs. The modulation order is denoted by M . However, at the receiver, a total of M^2 possible symbol-pairs can be detected. Since only M of the M^2 codewords can be

detected, overall error performance is reduced. The magnitude to which LD is attained depends directly on the mappings used. The main aim of LD is to put adjacent symbols further apart on a new constellation than in its first constellation. [1] has suggested symmetrical heuristic approaches while [3] has suggested an algorithmic approach for producing LD mappers. [4] reports that the branch-and-bound algorithmic solution is far too expensive computationally for $M > 16$. More recently, Patel et al. [4] have proposed a cost effective approach in the form of a Genetic Algorithm (GA) in order to produce LD mappers irrespective of constellation topology. The GA has been later applied to high density constellations in [5]. GAs are meta-heuristic search algorithms that iteratively solve NP-hard optimization problems. GAs form part of a group of stochastic search methods that produce solutions by variation and selection [6]. GAs have the following basic structure: i) chromosome encoding, ii) parent selection, iii) crossover, iv) mutation, v) evaluation and vi) creation of the population for the next generation. The algorithms within this group are based on a generic framework that is controlled by state parameters. These state parameters are customary and selecting good numeric values for these parameters is paramount. In the case of the GA in [4] and [5], its logic is as follows: i) data structures known as chromosomes are created with the respective values from a random LD mapper. Multiple chromosomes are created similarly and added to a population, ii) Two chromosomes are selected at a time – known as parent chromosomes – and are crossed over to produce two child chromosomes. This is performed for all combinations of parent chromosomes from the population, iii) After crossover, the child chromosomes then go through the probabilistic technique, mutation, iv) after crossover and mutation, parent and child chromosomes are added to the population, and evaluated according to a metric function, v) the best chromosomes from the population are then chosen to represent the population for the next generation [7].

It has been stated in [5] that the GA found in [4] has not been effectively a GA, but a Genetic-Inspired Algorithm (GIA). This is because the crossover stage has not created child chromosomes that inherit from both parents, but rather the values contained within the child chromosomes were mostly from the one parent. Hence, [8] has investigated the use of two-parent crossover techniques such as the single-point, multi-point and Davis ordered crossover techniques respectively. These techniques have shown to produce LD mapper designs that match or improve upon the mapper designs found in [9]. However, these improved mapper designs had been produced at the cost of higher computational complexity when compared to the GA in [4], which has been shown in [10]. Further to this improvement, [11] has designed a global neighbourhood algorithm that leveraged the power of the GA in [12] and [13] combined with a local search algorithm. This method had shown a minimal increase in computational costs, but it has been able to produce

mapper designs that have improved upon the existing designs found in [10], [11] and [14]. This had furthered the research of finding an optimal mapper design algorithm without the need for high computational costs.

Selecting parameters for GAs is frequently divided into two classifications, namely i) parameter tuning and ii) parameter control [7]. In parameter control, parameter variables are changed during the run of a GA, while parameter values are not changed during the GA run, hence a single numeric parameter value is changed [7].

Although there are two cases, selecting good parameter values for a given algorithm is hard since there are many options, and very little is known of the effects of EA parameter values on EA performance [7]. GAs rely on many conventions, such as low mutation rates, uniform crossovers and testing combinations. It is important to note that there is a difference between choosing good parameter sets and good biological operators [7]. In recent years, literature has focused on designing optimal parameter settings for GAs using systematic approaches. The resulting outcome has placed more emphasis on parameter tuning. Hence research efforts have been placed on developing systematic and sophisticated approaches to address it [7]. One of the more significant goals in the field of meta-heuristics is transferring the parameter tuning effort to the algorithm.

Hence, the end goal of parameter tuning is to equip meta-heuristics with smart procedures that enable the algorithms to respond to a problem on their own [7]. A study by Solwa et al. [15] has shown that for the genetic algorithm in [4], a meta-genetic algorithm could be produced to fine tune each input parameter. A meta-genetic algorithm is a meta-heuristic search algorithm that uses the GAs hyperparameters as input to be optimized. This approach has many advantages as stated in [16], but the main disadvantage of meta-genetic algorithms is that it adds to the overall time complexity of the GA. However, this approach can be considered a “blind-search”, as it randomly traverses the parameter search space. Additionally, this approach has illustrated the fact that by fine tuning each parameter – even so “blindly” – faster convergence as well as a better output could be observed from the respective GA.

The adoption of Artificial Intelligence (AI) for designing LD mappers has recently been introduced to literature for two transmit and three transmit USTLD systems in the form of a GA [4]. The GA has not been explored for optimal parameter sets. Motivated by the GA innovation, the main objective of this study is to fine tune a single parameter in order to further improve upon mapper designs. Therefore, the contribution of the paper is as outlined as follows:

1. Parameter varying technique to fine-tune a single parameter;
2. Designing secondary mapper designs for $2 \times N_R$ M-QAM and M-APSK USTLD schemes, where $M = 16, 64$;
3. Error performance comparisons of 16-ary MQAM and MAPSK USTLD schemes with the fine tuning of

the parameter.

The rest of the paper is structured according to the following. Section II briefly discusses the USTLD system, the analytical error performance analysis and provides a design metric for evaluating LD mappers.

Section III outlines the GA model that is used to produce LD mappers. Section IV discusses various parameter tuning methodologies and its applications. In section V, the results of the tuning methodology are presented. Furthermore, Section VI presents numerical results, which are confirmed by simulations. Concluding remarks are mentioned in section VII.

II. The System Model

II.1. The USTLD Transmitter Model

The USTLD system in question considers a MIMO structure with $N_T = 2$ and N_R transmit antenna. A single codeword that is of length $r = \log_2 M$ is put through LD mappers γ_1 and γ_2 , which produce symbols $\gamma_1(A)$ and $\gamma_2(A)$ respectively.

The USTLD system transmits two of these codewords $A_{(1)}$ and $A_{(2)}$ over multiple consecutive time slots. For this case, there are two time slots. While transmitting the codewords, the mapper γ_i in the i^{th} , $i \in [1:2]$, time slot is used.

Thus, the $N_R \times 1$ signal vector that is received by the receiver end can be represented as:

$$y_i = \sqrt{\frac{\sigma}{2}} [h_{i,1} \gamma_i(A_{(1)}) + h_{i,2} \gamma_i(A_{(2)})] + n_t \quad (1)$$

In (1), $\sqrt{\frac{\sigma}{2}}$ is the average SNR at each receiver antenna and n is the $N_R \times 1$ AWGN vector. The fading vector $h_{i,a}$, $i, a \in [1:2]$ is the multipath fading experienced by the transmitted symbol from antenna a in time slot i [4].

At the receiver side, the maximum likelihood detection algorithm is employed to estimate transmitted symbols. By assuming perfect Channel State Information (CSI), the estimated detection of the transmitted codewords can be formulated as:

$$\begin{aligned} \hat{A}_{(1)}, \hat{A}_{(2)} &= \\ &= \arg \min_{L_{(1)} \text{ and } L_{(2)}} \left\| y_i - \sum_{u=1}^2 \sqrt{\frac{\sigma}{2}} h_{i,u} \gamma_u(A_{(u)}) \right\|^2, \quad (2) \\ &\quad i \in [1:2] \end{aligned}$$

In (1) and (2), $\hat{A}_{(1)}, \hat{A}_{(2)}$ are the symbols that are estimated to be received and $A_{(1)}, A_{(2)}$ represent the symbols that have been transmitted.

II.2. The Analytical Error Performance of the USTLD System

[1] has shown that by employing the union bound

approach, the average bit error probability (ABEP) has been derived as:

$$ABEP(\rho) = \frac{1}{Mr} \sum_{A=0}^{M-1} \sum_{\substack{\hat{A}=0 \\ \hat{A} \neq A}}^{M-1} \nabla(A, \hat{A}) P(A \rightarrow \hat{A}) \quad (3)$$

where M represents the number of symbols on the constellation, $\nabla(A, \hat{A})$ is the sum of bit errors between transmitted and estimated received symbols. $P(A \rightarrow \hat{A})$ is the Pairwise Error Probability (PEP) that one set of symbols is detected perfectly and the other being detected with error. It is shown from [1] that the PEP is given as:

$$\begin{aligned} P(A \rightarrow \hat{A}) &= \frac{1}{4s} \prod_{t=1}^2 \left(1 + \frac{\sigma \tau_t^2}{8} \right)^{-N_R} + \\ &+ \frac{1}{2s} \sum_{j=1}^n \prod_{t=1}^2 \left(1 + \frac{\sigma \tau_t^2}{8 \sin^2(\frac{j\pi}{2s})} \right)^{-N_R} \end{aligned} \quad (4)$$

where s is the total error correction-based number of iterations such that $s > 10^2$, and $\tau_t = |\gamma_i(A) - \gamma_i(\hat{A})|$, $i \in [1:2]$ is the distance between the points A and $\hat{A}$ on the constellation of γ_i .

For a detailed derivation, readers are pointed to the original paper by Xu et al. ([1], eqn. (4)-(10)). The authors of [1] have shown that at high SNR, $\frac{\sigma \tau_t^2}{8} \gg 1$, $i \in [1:2]$. The PEP can be reduced to the following when the values of SNR are high:

$$\begin{aligned} P(A \rightarrow \hat{A}) &= \frac{1}{4s} \left(\frac{\sigma \tau_1^2}{8} \frac{\sigma \tau_2^2}{8} \right)^{-N_R} + \\ &+ \frac{1}{2s} \sum_{j=1}^n \left(\frac{\sigma \tau_1^2}{8 \sin^2(\frac{j\pi}{2s})} \frac{\sigma \tau_2^2}{8 \sin^2(\frac{j\pi}{2s})} \right)^{-N_R} \end{aligned} \quad (5)$$

The result in (5) hints that the ABEP of USTLD systems is influenced by the product distance $\tau_1 \tau_2$ at high SNR values. Thus, this gives rise to a design metric used to evaluate the degree to which mapper γ_2 achieves labeling diversity, which can be found in [1]. This is given as:

$$\Phi(\gamma_1, \gamma_2) = \min_{\substack{A, \hat{A} \in [0:M-1] \\ A \neq \hat{A}}} \left[\prod_{i=1}^2 |\gamma_i(A) - \gamma_i(\hat{A})| \right] \quad (6)$$

The larger the value of (6), the more LD has been achieved. Therefore, the aim of LD mapper design is to maximize the minimum product distance between constellation points to produce a secondary mapper that achieves the required labeling diversity for USTLD systems.

III. Labeling Diversity Mapper Design Approach

First, a candidate solution to the problem is represented in the form of a chromosome (φ). Each value within a chromosome is called a gene. Each gene, $\iota_i, i \in [0:M-1]$, is a single point on the constellation while the information of each gene is encoded with its associated label [4]. Hence, a chromosome can be defined as:

$$\varphi = [\iota_0, \iota_1, \dots, \iota_{M-1}] \quad (7)$$

Every chromosome denotes a single arrangement of labels of size M . An array of s number of chromosomes is created to build-up the initial population, denoted by P .

$P^{(0)}$ – which represents the starting population – contains an array of randomly chosen chromosomes. If existing mapper designs are found in the literature, these are coded into a chromosome and added to the starting population. It has been reported by [4] that the previous statement will ensure that the GA produces equivalent or better mapper designs. It has been reported in Patel et al. [4] that crossover methods currently in use are not suitable for the labeling diversity application. Hence, [4] has developed a new strategy specific to the LD problem, namely the K -Hypersphere swap crossover (K -HSX).

The relatively new technique has the following number of steps:

1. Choose two parent chromosomes at random;
2. Select a random point in parent chromosome φ_1 , and select the same point in parent chromosome φ_2 . The point selected in both parent chromosomes is located at different constellation points;
3. Enclose all neighboring constellation points in a projected circle or radius $\mathcal{R}$;
4. Choose a swap point such that the chosen swap point falls outside of the projected circle's radius;
5. Swap the points within the chromosome.

The process of the K -HSX is designed such that the offspring that is produced would have new neighboring labels, thus fulfilling the criteria of LD design. It has been reported in [4] that one swap will not produce good offspring.

Thus, K swaps are done to ensure good offspring chromosomes are produced. The authors ask the reader to refer to the original text, section III-B2 [4]. All combinations of parent chromosomes are passed through the crossover stage, with each producing two offspring chromosomes. Hence, the total size of P after crossover during any generation of the GA is numerically presented as:

$$\chi^{(i)} = P + \frac{P!}{(P-2)!} = P^2 \quad (8)$$

Mutation is termed as the genetic exploitation stage of the GA used to explore previously unknown solutions. It is also used to maintain diversity through generations of

populations [5]. Mutation occurs probabilistically within offspring chromosomes. For this GA, the mutation operator will trigger by swapping two randomly selected genes within an offspring chromosome. Mutation probability is represented by P_m . After ‘mating’, parent and offspring chromosomes are placed back into P and evaluated in accordance with the objective found in (6).

These chromosomes are ranked according to their objective value, and the best s number of chromosomes is taken to form the population of the next iteration. It is important to note that φ_1 is known to the user, and each chromosome in P denotes a contender for φ_2 . Finally, the termination of a GA is executed when a convergent solution is found or the maximum number of generations for a population is reached. In the context of this GA, there are two conditions to which the GA will terminate: i) the GA had converge to an optimal solution or ii) the maximum number of generations for the population had been reached, which deems the best solution in the population as sub-optimal. The GA is limited to undergo a maximum of $c_{\max}$ iterations only.

IV. Tuning Methodology

In this section, the authors look at various parameter tuning methodologies for determining “good” parameter sets. Generally, any Evolutionary Algorithm (EA) such as a GA has two types of parameters: i) symbolic parameters: these parameters do not have searchable structures and are treated by using enumerations or grid search methods [7] and ii) numerical parameters. For this paper, the authors focus on finding “good” parameter sets for numeric values only. Finding “good” parameter sets requires complex optimization tasks with non-linear objective functions, interacting variables and interference (noise). EAs are naturally excellent heuristic solvers.

Therefore, one method of determining “good” parameter sets for an EA, an evolutionary approach can be taken. The following subsections discuss four methodology used for finding “good” parameter sets for an EA:

IV.1. Parameter Varying

Parameter Varying (PV) is a simple technique whereby each parameter is changed one at a time to produce “good” parameter sets. The general idea of PV is to choose a sufficient range of values for a given parameters, simulate the parameters and compare the results to other parameter sets of the same nature. Once the limit of the range has been reached, the final parameter set is chosen from the best output. The PV technique can be represented as follows:

$$\delta = [\alpha_0, \alpha_1, \dots, \alpha_{N-1}] \quad (9)$$

where δ is the parameter set, α is the parameter to be tuned and N is the total number of parameters in the parameter set.

IV.2. Meta-Evolutionary Algorithm

Meta-Evolutionary Algorithms (Meta-EAs) has been first proposed by Mercer et al. [11] in order to optimize a set of parameters for an EA.

Due to high computational costs of the Meta-EA, the research has been very limited. Further research has been conducted by Greffenstette et al. [12] in order to show the effectiveness of a Meta-GA.

Each value used in a Meta-EA is vectors of numeric values [12].

Each numeric variable that is passed through the Meta-EA corresponds to a single parameter of the base EA to be tuned. In order to evaluate the vector, the base EA is ran multiple times on the given set of parameter values [11].

This, in a sense, is referred to as a meta-fitness function. In general, any EA can be used as a Meta-EA if it can handle the real-valued numeric vector.

IV.3. Meta-Estimation of Distribution Algorithm

The Meta-Estimation of Distribution Algorithm (Meta-EDA) has been proposed as a technique for Relevance Estimation and Value Calibration of parameters (REVAC) [13]. The basic principle of REVAC is to obtain an optimal parameter vector setting by estimating the distribution of all favourable values over the range of each parameter, and then it creates vectors by choosing values from among the distributions [13]. Essentially, REVAC is very similar to an EA in the sense that it uses a population-based search method to achieve the objective.

The population consists of real-valued parameters that need to be tuned. After each iteration, a single parameter is replaced. The REVAC algorithm can be used to gain insights into the relevance and sensitivity of difference parameters, their costs and benefits of tuning each parameter [13].

IV.4. Sequential Parameter Optimization

Sequential Parameter Optimization (SPO) is a search method more specifically used for parameter tuning and analysis, first proposed by Bartz-Beielstein et al. [14].

This model is similar to a Meta-EA in the sense of utilizing the model landscape to achieve an objective [7].

At the beginning of an SPO, an initial population of vectors is created and tested several times for its output fitness value. Based on the test results, a regression model is used to represent the relationship of the vectors and results [7].

After the regression model has completed fitting, a new set of vectors are created and tested. The points from the most promising results are then added to the population of the EA.

The authors note that regression models are succeeded by stochastic models [7]. In this paper, the authors have chosen the PV approach to selecting “good” parameter values for the baseline GA. The choice is motivated by

low computational costs over other existing methods.

V. Identification of Influential Parameters

GAs are population search based algorithms that iteratively produce better solutions [7]. Generally, many factors play a role in determining the resultant output of a GA, namely i) parameter settings, ii) genetic coding and iii) biological operators and its design. In this paper, the authors focus on identifying the parameters that influence the output of the GA discussed in Section III.

GAs generally depend on population sizes and mutation rates to produce optimal or sub-optimal solutions. A larger population size will thoroughly transverse a search space, hence producing a good candidate solution. The mutation rate should be set to less than 5%. Higher mutation rates increase the chances of destroying a potentially good candidate solution.

The GA has been tested with a range of values over the respective parameters, where the output is compared.

The range of values chosen is summarized as follows:

- Population Size: $8 \leq P \leq 200$;
- Mutation Rate: $1\% \leq P_m \leq 5\%$;
- Number of swaps during crossover: $1 \leq K \leq M$.

The influence of the mutation rate P_m is almost negligible due to a small quantity of offspring chromosomes being mutated. As the population size P increases, improved fitness values for mapper designs are produced, hence being a candidate for an influential parameter.

The number of swaps parameter plays a key role during the crossover stage of the GA. If genes are swapped correctly during crossover, the GA will produce good quality solutions in a short amount of time. Hence, the number of swaps parameter is another candidate for an influential parameter. When comparing the parameters P and K in terms of influence, it is noted that irrespective of the population size, the GA will produce an output that is close to equivalent to other GA outputs. However, the parameter K is the most likely candidate to influence the output of the GA.

As seen in Table I which presents the most significant fitness values, a lower value for K will produce good quality solutions, while increasing the parameter value closer to M produces solutions of a lesser quality. Hence, it can be deduced that the most influential parameter on the GA discussed in Section III is the number of swaps parameter, K .

TABLE I
SIGNIFICANT GA FITNESS VALUES WITH VARYING PARAMETERS

Test Case	P	K	$\phi(\varphi_1, \varphi_2)$
16APSK	10	1	0.5411
16APSK	20	5	0.4278
16APSK	30	10	0.3685
16APSK	40	16	0.2745
64APSK	10	1	0.1163
64APSK	20	10	0.0807
64APSK	30	25	0.0758
64APSK	40	42	0.0112

VI. Results and Discussions

VI.1. Tuning of Influential Parameters

In this section, the authors outline a design metric for fine tuning the parameter K . [4] suggests that the number of swaps K is chosen such that $K = \frac{M-4}{2}$. This ensures that offspring chromosomes are sufficiently different to their parent chromosomes [4]. As seen in Section III, the most dominating function in the GA is the crossover function, i.e. the number of swaps K that determines the convergence of the GA at a local optimal or not.

Therefore, the range of parameters chosen to tune the parameter K is given as:

$$1 \leq K \leq \frac{M-4}{2} \quad (10)$$

where K is the number of swaps during crossover and M is the modulation order. The expression in (10) ensures that each value for K within the range is tested to determine the most optimal parameter setting. Table II summarizes the values that have been tested to tune parameter K on 6 different instances of modulation schemes. For simplicity, the output of each instance of parameter tuned values is denoted as $\phi(\Omega_2, K)$. Each parameter change has been tested at least 5 times and ran for 500 generations. This has ensured that a close-to-optimal mapper design is produced in the fraction of the total number of iterations that the GA runs for.

VI.2. Parameter Tuning Output

First, the parameter tuning has been carried out on 16QAM and 16APSK constellations. In the case of the 16QAM constellation, all the parameter tuned values of K have produced the same fitness output, i.e. $\phi(\varphi_2^{16QAM}, K) = 8.0$. The reason for this observation is that optimal constellation designs have been proposed by Samra et al [4]. In the case of the 16APSK constellation, it can be seen that as the number of swaps K is increased, the solution quality begins to decrease. This is summarized in Table III. It is important to note from Table III that the most optimal parameter value for designing 16APSK – i.e. $\phi(\varphi_2^{16APSK}, K) = 0.5411$ – constellations is by setting the number of swaps $K = 1, 2, 3$ respectively.

TABLE II
SUMMARY OF VALUES TESTED FOR TUNING THE PARAMETER K

Modulation Scheme	Minimum Value	Average Value	Maximum Value
16-ary	1	5	6
64-ary	1	16	30

TABLE III
16APSK LD MAPPERS WITH VARYING VALUES OF K

K	Fitness Output $\phi(\varphi_2, K)$
1,2,3	0.5411
4,5	0.4278
6	0.3685

Next, the 64QAM and 64APSK constellations are tested over all possible values of K . In the case of the 64QAM constellation, the fitness values produced by fine tuning parameter K have produced the same fitness value, i.e. $\phi(\varphi_2^{64QAM}, K) = 8.0$. A possible reason for this observation is that the fitness function applied has not been robust enough in the sense of finding optimality of LD mapper designs. Finally, the 64APSK constellation is tested to determine an optimal parameter value for K .

For $K = 1, 2, 3$ the best mapper designs are produced when compared to other values of K , i.e. $\phi(\varphi_2^{64APSK}, K) = 0.1163$. All other values tested on the 64APSK constellation have produced mapper designs of a less quality. Hence, it can be concluded that for M-ary Quadrature Amplitude Modulation (QAM) and Asymmetric Phase Shift Keying (APSK) constellations, lower values of K produce more optimal mapper designs.

VI.3. General Genetic Algorithm Parameter Settings

For all the applications of the GA, the population size, p , is set to $p = 8$ and mutation rate $P_m = 10\%$. The radius $\mathcal{R}$ is set to $\mathcal{R} = 3$ for M-QAM and for M-APSK constellations, $\mathcal{R} = 1$. The maximum number of generations c_{max} , is set as $c_{max} = 10^4$ for 16-ary constellations and $c_{max} = 10^6$ for 64-ary constellations.

VII. USTLD Simulation Results and Discussions

In this section, the error performance of the mapper designs produced by the GA - $\phi(\varphi_2, K)$ - is presented.

The authors remind the reader that φ_1 is known and φ_2 represents the mapper with the parameter K changed.

The BER curves are generated using the settings in Tables III and Table IV respectively. It is clear from the tables that the value of the fitness output $\phi(\varphi_2, K)$ decreases when the value of K increases. For the 16APSK, in Table III, compared to the value when K is less than 4, the value drops by 21% when K moves to the values 4 and 5 and by 32% when it reaches the value 6.

For the 64APSK values in Table IV, the fitness output value drops by 40% when K changes between 1 and 30.

Analytical results and Monte Carlo simulations are presented in Figure 1 and Figure 2 in the fast-fading channel respectively.

TABLE IV
64APSK LD MAPPERS WITH VARYING VALUES OF K

K	Fitness Output $\phi(\varphi_2, K)$
1	0.1163
2	0.1095
3	0.1031
4	0.0975
5,6	0.0896
7,8,9,10,11,12,13,14	0.0807
15,16,17,18,19,20	0.0739
21,22,23,24,25,26	0.0758
27,28,29	0.0708
30	0.0696

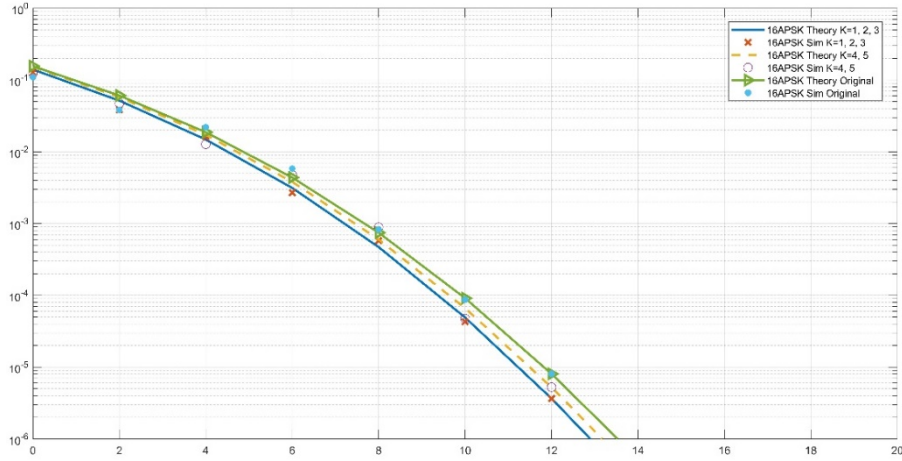


Fig. 1. BER performance of the 16APSK modulation scheme with USTLD

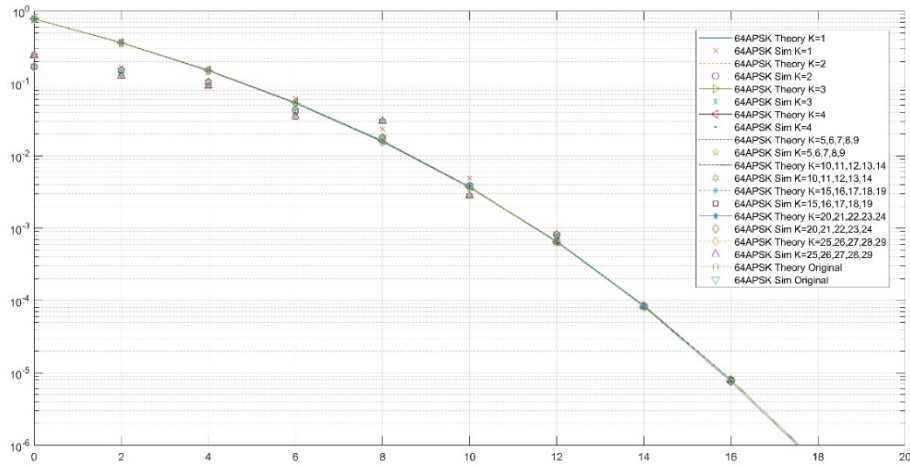


Fig. 2. BER performance of the 64APSK modulation scheme with the USTLD system

The 16-APSK and 64-APSK constellations are modulation schemes of the DVB-s2x standard. The 16-APSK constellation is of the 4+12-APSK structure while the 64-APSK constellation is of the 4+12+20+28-APSK structure. In Figures 1 and 2, analytical results tightly match the Monte Carlo simulation results for the fast-fading channel. The 16-APSK and 64-APSK USTLD scheme is compared by varying the number of swaps parameter, K .

When $K = 1, 2, 3$ the 16-APSK USTLD scheme exhibits a $\approx 1\text{dB}$ gain of the 16-APSK USTLD scheme when $K = 6$, while performing at almost equivalent levels to the 16-APSK USTLD scheme when $K = 4, 5$. For 64-APSK, even though a varying output fitness value is found for every value of K , the error performance of the scheme remained equivalent. This is attributed to the constellation structure and minimal differences in fitness or LD achieved. The findings of this research are critical in developing efficient wireless communication systems that can meet future needs.

Therefore, the primary motivation for increasing research into accurate and high-speed communication networks is to achieve future goals and demands [17]-[30].

VIII. Conclusion

This paper presents a simple, yet effective technique to achieve optimal parameter sets by parameter varying. The technique is used to find optimal values for the number of swaps – K – for the labeling diversity GA. By tuning the parameter K , close-to-optimal mapper designs are found during earlier generations of the GA, hence faster convergence at a local or global optima. The technique has been tested on 16-ary and 64-ary QAM and APSK respectively. In the case of 16- and 64-QAM, mapper designs have matched but have not improved upon existing designs due to optimal mappings already produced in literature. Tuning results show that for $K = 1, 2, 3$ the 16APSK constellation exhibits a gain of $\approx 1\text{dB}$ over other values of K . The 64-APSK constellation has shown increased values of LD but it has exhibited equivalent error performance for all the values of K .

Thus, a deduction can be made that for M-ary constellations the value of K should be chosen such that $K \leq 4$ to achieve close-to-optimal mapper designs with quick convergence. Future scope of this work includes extending this study to modulation orders of $M > 64$ and performing the same study on similar GAs present in the

literature.

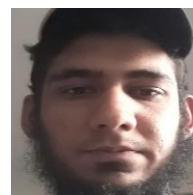
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