

MOEA Design of Robust Digital Symbol Sets

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1. INTRODUCTION

Bandwidth efficient modulation techniques using bounded bandwidth is sought in digital communications. Symbol set design is the minimizing of the probability of bit error (P_b) at a specific normalized signal-to-noise ratio ($\frac{E_b}{N_o}$) [4]. Optimal constellations with lower P_b at specified $\frac{E_b}{N_o}$ have numerous applications in digital communications. Lowering the inter-symbol interference reduces P_b , but normally this comes at cost of increased signal power or decreased noise interjection. Typical links have distortion elements in channel filters and amplifier nonlinearities that cannot be eliminated or, in some cases, reduced. Military communications face all types of noise interjection when an enemy attempts to reduce allied information exchange. Therefore, optimizing symbol set constellations is absolutely necessary for lowering this inter-symbol interference.

Investigated¹ is the ability of a Multiobjective Evolutionary Algorithm (MOEA), the multiobjective fast messy GA (MOMGA-IIa), to optimize two dimensional (4, 8, ..., and 256)-ary symbol set design for a decreased P_b at certain ($\frac{E_b}{N_o}$). The combinatorics of this problem call for a stochastic search algorithm that can be used in optimizing both single- and multi-objective problems because the models generated to capture this symbol set design problem are constructed as both single and multi-criteria problems [5].

2. ALGORITHM

The MOMGA-IIa is a multiobjective version of the fmGA that has the ability to achieve a semi-partitioned search in

¹The views expressed in this article are those of the authors and do not reflect the official policy of the United States Air Force, Department of Defense, or the U.S. Government.

both the genotype and, in multiobjective mode, phenotype domains during execution. It is an algorithm that exploits *good* building blocks (BBs) in solving optimization problems. These explicit BBs represent *good* information in the form of partial strings that can be combined to obtain better solutions. The MOMGA-IIa algorithm executes in three phases: Initialization, Building Block Filtering, and Juxtapositional.

Beginning with the Probabilistically Complete Initialization (PCI) Phase, the algorithm randomly generates a user specified number of population members. These population members are constructed to a specified chromosome length and each is evaluated to determine its respective fitness values. A binary alphabet is used.

The Building Block Filtering (BBF) Phase follows by randomly deleting loci and their corresponding allele values in each of the population member's chromosomes. This process completes once the length of the population member's chromosomes have been reduced to a predetermined BB size. These reduced chromosomes are referred to as underspecified² population members. In order to evaluate population members that have become underspecified, competitive templates (CTs) are utilized to fill in the missing allele values. Evaluation consists of the partial string being overlaid onto a CT just prior to evaluation. CTs are fully specified chromosomes that evolve as the algorithm executes. CT replacement is done after each BB generation. In the MOMGA-IIa, *competent* CTs that partition both the phenotype and genotype are selected for advancement. This innovative balance is achieved through two mechanisms: Orthogonal CT generation and Target Vector (TV) guidance. Orthogonal CT generation is used to partition the genotype space, while TV guidance is used, when MOMGA-IIa is running in multiobjective mode, to partition the phenotype space. TVs are normalized fitness markers that capture one solution per vector for future CT replacement. In the MOMGA-IIa, target vectors are used in a manner to divide the normalized fitness space of pareto-front members and select a distribution of CTs that fall nearest to each TV. Also, an orthogonal bank of chromosomes is used to filter a randomly selected CT through for creation of a set of orthogonal CTs.

The BBF process is alternated with a selection mechanism to keep only the *best* BBs found, or those with the *best* number of fitness values. In the case of a tie, where two strings each have an equal number of better fitness values (i.e. each have $\frac{m}{2}$ *best* fitness values), the string is randomly

²An underspecified chromosome is chromosome where some, but not all locus positions have an associated allele value.

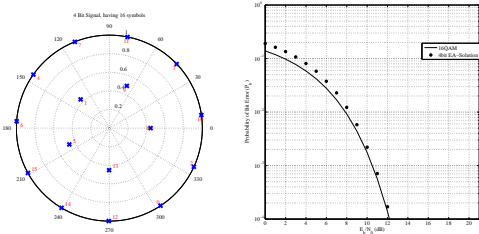


Figure 1: Presented is the best constellations and associated SNRs found for 4 bit symbol set.

selected between the two. In MOMGA-IIa each string has $f = (c * m + i + o) * m$ fitness values associated with it – corresponding to the m objective functions to optimize, c competitive templates, i inverse templates (equal to $c * m$), and o orthogonal templates.

Finally, the juxtapositional phase uses BBs found in the BBF phase and recombination operators to create chromosomes that are fully specified. The MOMGA-IIa has an outer and inner loop that must be completely iterated through using each BB size and epoch before terminating. Next, the problem domain is described in detail.

3. FITNESS FUNCTION

Previous researchers either use different coding methods or symbol positioning to get better P_b at particular $\frac{E_b}{N_o}$ [1, 3, 4]. In our models the MOMGA-IIa optimizes both by assigning each symbol its bit-wise representation while assigning it a location in space. However, the challenge was found not to be what to optimize or how to represent the problem, but what model (fitness function) best represented the Monte Carlo simulation used to check constellations for goodness. Normally, new constellations would be tested using a Monte Carlo simulator where a random stream of symbols are encoded into a signal, s , using the amplitude and phase of symbols identified in a designed constellation. Next, noise is added to the generated signal, $(s + n)$, to simulate the transmission process. The amount of noise added to the signal is related to the $\frac{E_b}{N_o}$ under test. Then, the signal is decoded and a reconstructed symbol stream is generated from the noisy signal. Finally, the number of bit errors are calculated by comparing the reconstructed symbol stream to the originally transmitted symbol stream. This test is re-run until enough data is collected to assign a P_b rate to that particular constellation at the $\frac{E_b}{N_o}$ under test. Four different analytical models are designed in search of the optimal balance between computational time and model correctness. Five models are tested. The first four designs are analytical approximates for this digital system and the fifth design is the Monte Carlo simulation.

Each model uses symbols placed inside a unit circle for amplitude and phase characteristics for each symbol [2]. Each symbol bit pattern is defined to be in one and only one place within the genome. Placement is in binary order, {00, 01, 10, 11}, and each symbol has $d = 2$ degrees of freedom to define its location in the space.

3.1 Brute force model:

The brute force model takes into account our intuition about how to represent this problem using a high level of

understanding of the problem domain. A maximization constellation fitness function is sought; therefore, a negative exponential decay of the distance is used to emphasize a larger space between symbols is better. The exponential decay is modified using a constant K value to increase or decrease the rate of decay depending on the number of symbols in the constellation. Finally, to account for the bit error increasing when encountering a high hamming code distance between symbols, the exponential decaying distance is multiplied by the hamming code distance, found in the \mathcal{H} matrix, of the two symbols.

4. RESULTS AND ANALYSIS

MOMGA-IIa constellations having 2, 3, 4, and 5 bits all compete well with the x -rectangular constellation theoretical best. The 4 bit comparisons are graphically presented in Figure 1.

The MOMGA-IIa has found good constellations using the brute force model. Although MOMGA-IIa solutions did not beat the x -rectangular constellation theoretical best, they did compete rather well. This is validated using standard Amplitude Modulation techniques in use today. Theoretically, there exists a constellation that have lower P_b than the x -rectangular constellations at certain $\frac{E_b}{N_o}$ s; however, those constellations evade researchers in the field today and the MOMGA-IIa so far.

Since, this is a new angle on an old problem. Many different techniques can be used to increase the effectiveness of the MOMGA-IIa in solving this problem. Right now, the model needs to be modified to yield maximum fitness value at the same constellation that the Monte Carlo simulation validates to be the lowest P_b . So far, a better model escapes us. Our current models show little correlation to the current simulation model. Once a model is found for finding good constellations for use on signals subject to additive White Gaussian Noise, a new model can be derived to find constellations for noisy signals having other types of noise. In fact, the ultimate goal would be to have a channel noise probe identify the noise over a channel and back propagates this information to an EA that searches for an optimal symbol set for that channel. Once the symbol set was defined for the unknown noise in the channel, communicators would have the best symbol set for that digital system.

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