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Comparison of Different Symbol Detection Techniques with SA-BFO Algorithm in MIMO Systems

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ABSTRACT:

Multi-Input Multi-output (MIMO) technique has attracted numerous research interests in the area of wireless communication due to its capability of providing high data rates through spatial multiplexing. In this paper comparative study of different detection techniques such as Maximum Likelihood (ML), Zero Force Equalisation (ZFE), Self-adaptive Bacterial Foraging Optimization (SA-BFO), Vertical Bell Labs Layered Space-Time (V-BLAST), Genetic Algorithm (GA) is presented. While an optimal Maximum Likelihood (ML) detection using an exhaustive search method is prohibitively complex, simulation results show that the SA-BFO optimized MIMO detection algorithm results in near optimal Bit Error Rate (BER) performance, with significantly reduced complexity.

KEYWORDS: Multi-Input Multi-Output system (MIMO), Bit Error Rate (BER), Self-adaptive Bacterial Foraging Optimization (SA-BFO), Maximum Likelihood (ML), Genetic Algorithm (GA)

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1. INTRODUCTION

The growing demands of multimedia services and the growth of internet related contents lead to increasing interest to high speed communications. Initially higher bandwidth was used to support such high data rate applications. However, the increase in bandwidth is an impractical method and an alternate solution is to adopt some spectral efficient techniques like Multi-Input Muti-Output (MIMO) systems¹. Wireless communication using MIMO antenna architecture also referred to as spatial multiplexed system which promises to play a key role in realizing the tremendous growth in the field of communication. Fading is the one of the major aspect which is considered in the receiver. To cancel the effect of fading, channel estimation and equalization procedure must be done at the receiver before data demodulation²

The inter-symbol interference caused by multipath MIMO channels distorts the MIMO transmitted signal which causes bit errors at receiver.

Optimization problems defined by functions for which derivatives are unavailable or available at a prohibitive cost are appearing more and more frequently in computational science and engineering. Increasing complexity in mathematical modelling, higher sophistication of scientific computing, and abundance of legacy codes are some of the reasons why derivative-free optimization is currently an area of great demand³. In this paper comparative study of different detection techniques such as Maximum Likelihood (ML), Zero Force Equalisation (ZFE), Self-adaptive Bacterial Foraging Optimization (SA-BFO), Vertical Bell Labs Layered Space-Time (V-BLAST), Genetic Algorithm (GA) is presented.

2. MIMO SYSTEM MODEL

MIMO channel model is assumed to be quasi-static. Consider the MIMO system shown in fig.1 where N different signals are transmitted and arrive at an array of M ($N \leq M$) receivers via a rich-scattering flat-fading environment¹. The block transmission is assumed to contain one symbol i.e. $L=1$. Baseband equivalent model of received signal vector at each sampling instant can be represented as:

$$\mathbf{r} = \sqrt{P}/N \mathbf{H}\mathbf{x} + \mathbf{n} \quad (1)$$

Where \mathbf{r} is an $M \times 1$ vector of received symbols at each antenna, \mathbf{x} is an $N \times 1$ vector of symbols transmitted by each antenna, and \mathbf{n} is an $M \times 1$ vector of complex Additive White Gaussian Noise (AWGN) random variables seen at each receive antenna. The channel matrix \mathbf{H} is an $M \times N$ matrix, whose elements \mathbf{h}_{ij} represent the complex fading coefficients experienced by a signal transmitted

from transmit antenna 'j' to receive antenna 'i'. P is total transmit energy for one transmit antenna system and is normalized for N transmit antenna system.

The receiver is also assumed to have perfect knowledge of the channel coefficients. This is a reasonable assumption when the fading is slow enough to allow estimation of the CSI with negligible error, as in the case of fixed wireless systems⁴.

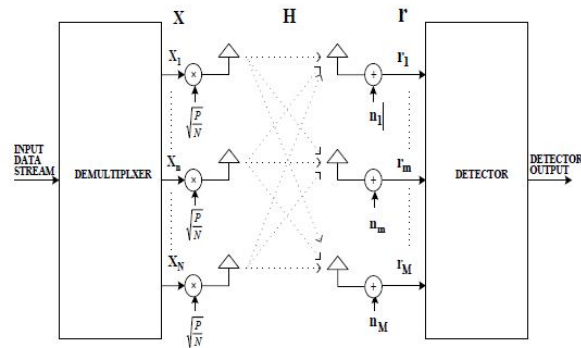


Fig 1. MIMO system model with N transmit and M receive antennas

3. SA-BFO BASED DETECTION FOR MIMO SYSTEMS

A. Steps for SA-BFOA

1) **Chemotaxis:** This process simulates the movement of an E.coli cell through swimming and tumbling via flagella. Suppose $\theta_i(j, k, l)$ represents the i th bacterium at j th chemotactic, k th reproductive, and l th elimination–dispersal step. $C(i)$ is a scalar and indicates the size of the step taken in the random direction specified by the tumble (run length unit). Then, in computational chemotaxis, the movement of the bacterium may be represented by

$$\square^i(j + 1, k, l) = \square^i(j, k, l) + C(i) \frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}} \quad (2)$$

where Δ indicates a unit length vector in the random direction.

2) **Swarming:** Interesting group behaviour has been observed for several motile species of bacteria including E.coli and S. typhimurium, where stable spatiotemporal patterns (swarms) are formed in semisolid nutrient medium. A group of E.coli cells arrange themselves in a traveling ring by moving up the nutrient gradient when placed amid a semisolid matrix with a single nutrient chemo-effector. The cells when stimulated by a high level of succinate release an attractant aspartate, which helps them to aggregate into groups and, thus, move as concentric patterns of swarms with high bacterial density.

3) Reproduction: The least healthy bacteria eventually die while each of the healthier bacteria (those yielding lower value of the objective function) asexually split into two bacteria, which are then placed in the same location. This keeps the swarm size constant.

4) Elimination and Dispersal: To simulate this phenomenon in BFOA, some bacteria are liquidated at random with a very small probability while the new replacements are randomly initialized over the search space³.

B. Step-by step algorithm:

[Step 1] Initialize parameters $n, S, Nc, Ns, Nre, Ned, Ped, C(i)$ ($i=1,2,\dots,S$), \square^i . Where,

n : Dimension of the search space,

S : The number of bacterium,

Nc : chemotactic steps,

Ns : swim steps,

Nre : reproductive steps,

Ned : elimination and dispersal steps,

Ped : probability of elimination,

$C(i)$: the run-length unit during each run or tumble.

[Step 2] Elimination-dispersal loop: $l = l+1$.

[Step 3] Reproduction loop: $k = k+1$.

[Step 4] Chemotaxis loop: $j = j+1$.

[substep a] For $i = 1=1, 2, \dots, S$, take a chemotactic step for bacteria i as follows.

[substep b] Compute fitness function, $J(i,j,k,l)$.

[substep c] Let $J_{last} = J(i,j,k,l)$ to save this value since we may find better value via a run.

[substep d] Tumble: Generate a random vector

$\Delta(i) \square R^n$ with each element $\Delta_m(i), m = 1, 2, \dots, S$, a random number on $[-1, 1]$.

[substep e] Move: Let

$$\square^i(j+1,k,l) = \square^i(j,k,l) + C(i) \frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}} \quad (3)$$

This results in a step of size $C(i)$ in the direction of the tumble for bacteria i .

[substep f] Compute $J(i,j+1,k,l)$ with $\square^i(j+1,k,l)$.

[substep g] Swim:

(i) Let $m = 0$ (counter for swim length).

(ii) While $m < N_s$ (if have not climbed down too long)

- Let $m = m+1$.

- If $J(i,j+1,k,l) < J_{last}$, let $J_{last} = J(i,j+1,k,l)$. then another step of size $C(i)$ in this same direction will be taken as equation (1) and use the new generated $\square^i(j+1,k,l)$ to compute the new $J(i,j+1,k,l)$.

- Else let $m = N_s$.

[substep h] Go to next bacterium ($i+1$): if $i \neq S$ go to (b)

to process the next bacteria.

[Step 5] If $j < N_c$, go to step 3. In this case, continue chemotaxis since the life of the bacteria is not over.

[Step 6] Reproduction:

[substep a] For the given k and l , and for each $i = 1, 2, \dots, S$, let J_{health} be the health of the bacteria. Sort bacterium in order of ascending values.

$$J_{health}^i = \sum_{j=1}^{N_c+1} J(i,j,k,l) \quad (4)$$

[substep b] The S_r bacteria with the highest J_{health} values die and the other S_r bacteria with the best values split and the copies that are made are placed at the same location as their parent.

[Step 7] If $k < N_{re}$ go to step 2. In this case the number of specified reproduction steps is not reached and start the next generation in the chemotactic loop.

[Step 8] Elimination–dispersal: For $i = 1, 2, \dots, S$, with probability ped , eliminate and disperse each bacteria, which results in keeping the number of bacteria in the population constant. To do this, if a bacterium is eliminated, simply disperse one to a random location on the optimization domain. If $l < N_{ed}$, then go to step 2; otherwise end.

In SA-BFO evolution process, each bacterium displays alternatively two distinct search states:

(1) Exploration state, during which the bacterium employs a large run-length unit to explore the previously unscanned regions in the search space as fast as possible.

(2) Exploitation state, during which the bacterium uses a small run-length unit to exploit the promising regions slowly in its immediate vicinity. Each bacterium in the colony permanently maintains an appropriate balance between Exploration and Exploitation states by varying its own run-length unit adaptively. This is achieved by taking into account two decision indicators: a fitness

improvement and no improvement registered lately. The criteria that determine the adjustment of individual run-length unit and the entrance into one of the states are the following:

Criterion-1: if the bacterium discovers a new promising domain, the run-length unit of this bacterium is adapted to another smaller one. Here “discovers a new promising domain” means this bacterium register a fitness improvement beyond a certain precision from the last generation to the current. Following Criterion-1, the bacterium’s behavior will self-adapt into Exploitation state.

Criterion-2: if the bacterium’s current fitness is unchanged for a number K_u (user-defined) of consecutive generations, then augment this bacterium’s run-length unit and this bacterium enters Exploration state. This situation means that the bacterium searches on an un-promising domain or the domain where this bacterium focuses its search has nothing new to offer⁵.

4. LINEAR MIMO DETECTORS

4.1 Zero-Forcing (ZF)

The ZF algorithm attempts to null out the interference introduced from the matrix channel by directly inverting the channel with the weight matrix .

5. NON-LINEAR MIMO DETECTORS

5.1 VBLAST:

VBLAST is the improvement of BLAST receiver. The detection algorithm associated with the BLAST architecture is the successive cancellation (SUC) algorithm. Rather than jointly decoding all of the transmitted symbols, this nonlinear detector decodes the first transmitted symbol by satisfying the ZF or MMSE performance criterion while treating the rest of the data symbols as interference; then it cancels out its contribution to obtain a reduced order integer least-squares problem with $t-1$ unknowns. The process is repeated until all the symbols are detected. In general, this algorithm performs better than the ZF or MMSE receivers, but it suffers from error propagation; its performance quickly degrades if that first symbol was incorrectly decoded. A suggested improvement is the use of ordered successive cancellation (OSUC), an algorithm associated with the VBLAST architecture (6) The main idea behind OSUC is that rather than selecting the symbols to be decoded in their natural order as in SUC, the symbols at the beginning of each decoding stage are ordered in terms of decreasing signal-to-interference noise ratio (SNR), and the symbol with the highest SNR is selected for decoding.

5.2 ML detector: Maximum Likelihood detector is optimal but computationally very expensive. ML detection is not practical in large MIMO systems.

5.3 GA based detection for MIMO systems

GA is an inspiration based on principles of natural genetics and selection. Algorithm starts by defining optimization variables, optimization cost and the cost function. Convergence/Fitness test follows different components of algorithm, as explained.

5.3.1 Initialization of GA

All potential solutions of a problem are encoded in bit level to simplify the following GA recombination operations. In MIMO detection χ that form the ML search space are coded as binary strings called chromosomes. It is common to select the initial population randomly from solution space or derive from a linear/non-linear detector output. Each chromosome is a combination of the probable solution for all transmit antennas. Normally, the population size N_{pop} is taken as the product between N , the number of transmit antennas, and C , the number of all possible solutions of each transmit antenna.

$$N_{pop} = 2^b \times N$$

5.3.2 Fitness evaluation using cost function

Each member of the population at each generation is evaluated, and according to its fitness value (output of the cost function), it is assigned a probability to be selected for reproduction. Following equation acts as the cost function to evaluate the fitness of each chromosome:

$$f = \|r - Hx\|^2 \quad (8)$$

The optimal solution of eq.8 should yield a minimum value. ML detector evaluates $\forall x \in X$ results in computation time that varies exponentially with the number of transmit antennas. As will be explained, the use of GA in a MIMO system can reduce the computation times of eq.8 significantly. The best chromosome in a generation should have the least value of the objective function. If the value of the best chromosome in the present generation is larger than its counterpart in the previous generation, the chromosome with the largest value of the objective function in the present generation will be replaced by the best chromosome of the previous generation. This operation ensures that at least the useful information contained in the present generation is passed on to the next.

5.3.3 Optimality

If the optimal criterion is satisfied, that is, when any one of all f in the population is less than a predetermined threshold, or if the generation number has exceeded a predefined value, which is also commonly taken as the product between N and C , then go to 5.3.8. Otherwise, go to Step 5.3.4.

5.3.4 Selection

This process uses fitness value and serves to provide chromosomes for the subsequent recombination operations. Of N_{pop} chromosomes in a generation, only $N_{keep} = N_{pop} * p_{sel}$ survive for

mating, and bottom $N_{pop} - N_{keep}$ are discarded to make room for new offspring. Deciding how many chromosomes to keep is arbitrary and normally 50% ($P_{sel} = 0.5$) of population survives 'Selection' process after chromosomes have been sorted by cost. This new population of N_{keep} chromosomes forms mating pool of good parents.

5.3.5 Reproduction

This step is intended to replace the chromosome with largest objective function value by the best chromosome of the same generation. The Offspring to replace the bad parents is created by the processes of 'Crossover' and 'Mutation'.

5.3.6 Crossover

Crossover operation is applied to pairs of selected parents and creates offspring. Process of mating by applying crossover operator creates two offspring by combining subparts of bit strings of two selected parents⁶. The crossover point is randomly selected along the chromosome lengths and portions up to that point are exchanged between two parents. Probability of crossover p_c is user controlled and usually set to a high value.

5.3.7 Mutation

These offspring are mutated through mutation operator and new members of next generation are produced. Mutation operator simply alters each bit of the binary chromosome randomly with a user-controlled probability p_m ⁷. Generally, the crossover probability p_c is close to 1 and the mutation probability p_m is close to 0. New individuals replace members of previous populations with worst fitness values. Algorithm iterates until optimization of objective function is achieved. For given predefined number of generations and population size, the computation times of eq.8 vary linearly with $(N_{pop} \times N_{gen})$ for GA based detector, which is much smaller than the factor of $2NXb$ in the ML detection. The improvement is clearly significant.

5.3.8 Decision making

If the defined optimality criterion is met the algorithm terminates its execution and output is generated⁸.

6. SIMULATION RESULTS AND DISCUSSION

We consider a MIMO systems designed for an underlying 4-QAM and 4-PSK constellation with up to 4 transmit and 4 receive antennas. We assume a quasi-static Rayleigh fading channel model which is constant over a frame and varies independently between frames. We assume that the channel exhibits a quasi-static frequency flat Rayleigh fading over the frame duration. Thus, it is constant over one frame and varies independently between frames. We consider a frame size of 100 symbols. We assume perfect channel state information (CSI) is available at the receiver. For

performance comparison, we consider MIMO system which has specifications same as the system described above, the only difference being in the detection/decoding of the received symbols which is done via maximum likelihood (ML) Viterbi decoder. We show that SABFO based detector gives near optimal results with much lower complexity level as compared to the ML detector. SA-BFO gives better results than ZFE and V-BLAST systems if PSK modulation scheme is used.

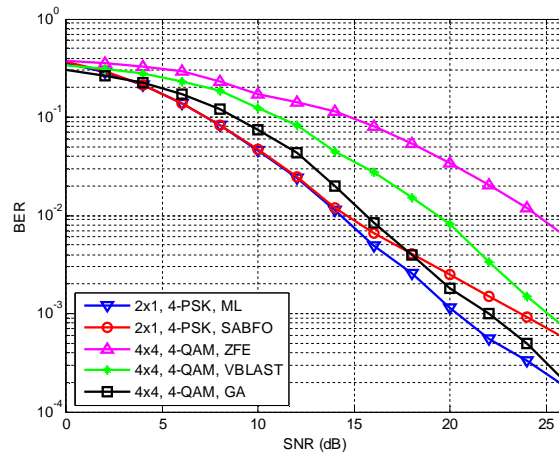


Fig 2. BER performance comparison for 2x1 and 4x4 System using 4-PSK and 4-QAM technique

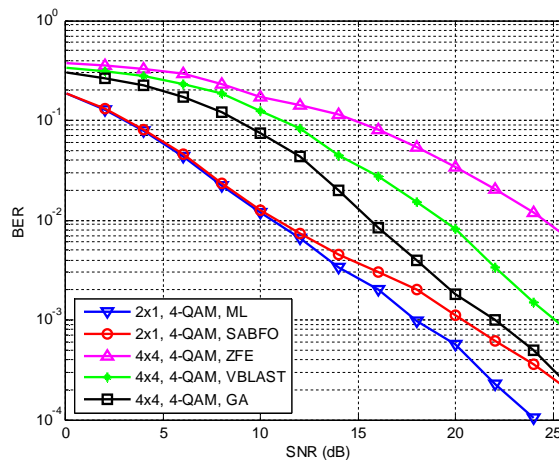


Fig 3. BER performance comparison for 2x1 and 4x4 System using 4-QAM technique.

From fig 3. It is clear that for QAM modulation technique SA-BFO gives better results than Genetic algorithm.

7. CONCLUSION

In this paper, Self-Adaptive Bacterial Foraging Optimization algorithm for symbol detection is presented. SA-BFO based MIMO detector uses a simple model and has lesser implementation complexity. For larger number of antennas and higher modulation schemes, the proposed SA-BFO

algorithm is expected to give near optimal results with much lower complexity level as compared to the ML detector. For QAM modulation technique SA-BFO gives better results than Genetic algorithm as well as ZFE and V-BLAST system.

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