Exact Maximum Likelihood Direction Of Arrival Estimation Using Bacteria Foraging Optimization

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Abstract— Source direction of arrival (DOA) estimation is one of the challenging problems in a variety of applications, such as communications, radar, sonar, and seismic exploration. Several methods based on maximum likelihood (ML) criteria has been established in literature. Generally, to obtain the exact ML (EML) solutions, the DOAs must be estimated by optimizing a complicated nonlinear multimodal function over a high-dimensional problem space. Bacteria foraging optimization (BFO) based solution is proposed here to compute the ML functions and explore the potential of superior performances over traditional PSO algorithm. Simulation results confirms that the BFO-EML estimator is significantly giving better performance at lower SNR compared to conventional method like MUSIC in various scenarios at less computational costs.

Keywords- MUSIC, Direction-of-arrival, Maximum Likelihood Estimation, PSO, BFO.

I. INTRODUCTION

DOA estimation is an important problem in the fields of radar, sonar, radio, astronomy, under water surveillance and seismology etc to estimate the source location. One of the simplest versions of this problem is the estimation of the directions-of-arrival (DOAs) of narrow-band sources where the sources are located in the far field of the sensor array [1, 2, 3]. Many high resolution suboptimal techniques have been proposed and analyzed, such as multiple signal classification (MUSIC) [4], the minimum variance method of Capon [5], estimation of signal parameters via rotational invariance technique (ESPRIT) [6] and more [7]. These techniques give better performance at high SNR only. The ML technique is used here because of its superior statistical performance compared to spectral based methods. The ML method is a standard technique in statistical estimation theory. A likelihood function can be formulated easily if we know the observed parametric data [8], [9]. The ML estimate is computed by maximizing the likelihood function or minimizing the negative likelihood function with respect to all unknown parameters, which may include the source DOA angles, the signal covariance, and the noise parameters. Since the ML function is multimodal, so direct optimization is seems to be unrealistic due to large computational burden. So main contribution is to reduce the dimensionality by taking some assumptions on signal, noise and array structure. There are different optimization techniques available in literature for optimization of ML function like AP-AML [10], simulated annealing (SA) [11], genetic algorithms (GA) [12] fast EM and SAGE algorithms [13] and a local search technique e.g. Quasi-Newton methods. GA is one of the most powerful and popular global search tools; however, its implementation is somewhat difficult due to slow convergence. All these techniques have several limitations because of multidimensional cost function which need extensive computation, good initialization is also crucial for global optimization and we cannot guarantee that these local search techniques always have global converge. The evolutionary algorithms like genetic algorithm [14], particle swarm optimization and simulated annealing [11], [15], [16] can be designed to optimize the ML function. Genetic algorithm [12] and particle swarm optimization [17] had already used as a global optimization technique to estimate the DOA for uniform array. In this paper, the bacteria foraging optimization algorithm is applied to ML criterion functions for accurate DOA estimation in uncorrelated Gaussian noise. Recently BFO algorithm has been successfully applied in different applications and shown that it is giving better performance compared to different constrained PSO. Due to multimodal, nonlinear, and high-dimensional nature of the parameter space, the problem seems to be a good application area for BFO, by which the excellent performance of ML criteria can be fully explored. Strategically pairing PSO with EML has the desired advantages over Newton-AML based schemes because of BFO-EML is expected to offer higher quality estimates, BFO has a better chance to attain the global optimum and BFO is less sensitive to initialization, however, a good initial guess speeds up the computation. All these features make BFO more attractive for direction finding applications. Via extensive simulation studies, we demonstrate that with properly chosen parameters, BFO achieves fast and robust global convergence over PSO and MUSIC.

II. DATA MODEL AND MAXIMUM LIKELIHOOD ESTIMATION PROBLEM

A major application of sensor array signal processing is the estimations of parameters of the impinging signal to the array. Parameters to be identified include number of signals, magnitudes, frequency, angle of arrival (AOA), distances

from the sources, and speeds of signals. Of all these parameters, the DOA estimation is has been paid most attention, especially in farfield signal applications, in which case the wave front of the signal may be treated planar, indicating that the distance is irrelevant thus, the topic of current research is also focus on DOA estimation using far-field source consideration. There are two categories of ML are deterministic ML and Stochastic ML depending on the model of assumption on the signal waveform. Deterministic ML algorithms assumes that the signal waveform is deterministic but unknown, while the stochastic ML algorithms assumes that the signal waveform is Gaussian random processes. Both classes of ML algorithms assume zero mean Gaussian random noise. Let us consider an array of M WSN nodes are distributed in an arbitrary geometry and received signals form N narrow band far-field signal sources at unknown locations. The output of sensor nodes modelled by standard equation as

$$x(i) = A(\theta)s(i) + n(i), \text{ i=1,2}\ldots \text{L}. \tag{1}$$

Where s(i) is the unknown vector of signal waveforms, n(i) is unpredicted noise process, L denotes the number of data samples (snapshots). The matrix $A(\theta)$ has the following special structure defined as

$$A(\theta) = [a(\theta 1), \ldots a(\theta_N)] \tag{2}$$

Where a(θ) is called steering vector and $\theta = [\theta_1, \theta_2, \ldots, \theta_N]^T$ are the parameters of interest or true DOA's. The exact form of a(θ) depends on the position of the nodes in sensor network. Further, the vectors of signals and noise are assumed to be stationary, temporarily white, zero-mean complex Gaussian random variables with the following second-order moments given by

$$E[s(i)s(j)^H] = S\delta ij \quad \text{and} \quad E[s(i)s(j)^T] = 0$$

$$E[n(i)n(j)^H] = \sigma^2 I \delta_{ij} \quad \text{and} \quad E[n(i)n(j)^T] = 0 \tag{3}$$

Where δ_{ij} is the Kronecker delta, $(\cdot)_H$ denotes complex conjugate transpose, $(\cdot)_T$ denotes transpose, E$(\cdot)$ stands for expectation.

A. Maximum Likelihood Estimation

In many applications it is appropriate to model the signals as stationary stochastic processes, possessing a certain probability distribution. Then by far most commonly advocated distribution is the Gaussian one. Not only is this for the mathematical convenience of the resulting approach, but the Gaussian assumption is also often motivated by the Central Limit Theorem.

Under the assumptions taken above, the observation process, x(i), constitutes a stationary, zero-mean Gaussian random process having second-order moments

$$E[x(i)x(i)^H] = R = A(\theta)SA^H(\theta)+\sigma^2 I \tag{4}$$

In most applications, no *a-priori* information on the signal covariance matrix and the number of sources are available. But here in this work we assume that the number of signals are known to us. The problem addressed herein is the estimation of θ along with the parameter in S and σ^2(noise power) from a batch of L measured data x(1), . . . , x(L).

Under the assumption of additive Gaussian noise and complex Gaussian distributed signals we can have negative log likelihood function [3], [17] is given as

$$l(\theta, S, \sigma^2) = \log|R| + \text{tr}\{R^{-1}\hat{R}\} \tag{5}$$

where $\hat{R}$ is the sample covariance matrix and it defined as

$$\hat{R} = \frac{1}{N}\sum_{i=1}^{N} x(i)x(i)^H \tag{6}$$

The ML criterion function can be concentrated with respect to S and σ^2 by following [23]–[25]. The stochastic maximum likelihood (SML) estimates of the signal covariance matrix and the noise power are obtained by inserting the SML estimates of θ in the following expressions

$$\hat{S}(\theta) = \left(A^\dagger(\theta)\left(\hat{R} - \hat{\sigma}^2 I\right)A^{\dagger H}(\theta)\right) \tag{7a}$$

$$\hat{\sigma}^2(\theta) = \frac{1}{M-N}\text{Tr}\{P_A^\perp(\theta)\hat{R}\} \tag{7b}$$

Where $A^\dagger$ is the psedo-inverse of A and $P_A^\perp$ is the orthogonal projection onto the null space of A^H and are defined as

$$A^\dagger = (A^H A)^{-1} A^H \tag{8a}$$

$$P_A = AA^\dagger \tag{8b}$$

$$P_A^\perp = I - P_A \tag{8c}$$

Therefore the concentrated form of the UML function now can be obtained by using (7) in (5) as

$$f_{EML}(\theta) = \log\left|\left(A(\theta)\hat{S}(\theta)A^H(\theta) + \hat{\sigma}^2(\theta)I\right)\right| \tag{9}$$

III. BACTERIA FORAGING OPTIMIZATION

Bacterial foraging is a new evolutionary computational method proposed by Passino[26]. The idea of bacteria foraging algorithm is based on the fact that natural selection tends to eliminate animals with poor foraging strategies and favour those having successful foraging strategies. After many generations poor foraging strategies are either eliminated or reshaped into new ones. The E.coli bacteria that are present in our intensities have a foraging strategy governed by four processes namely Chemotaxis, Swarming, Reproduction, Elimination and Dispersal

Step-by-step of the algorithm
[Step 1] Initialize parameters n, S, N_c, N_s, N_{re}, N_{ed}, P_{ed}, $C(i)$ $(i=1,2\ldots S)$, θ^i Where,
n: Dimension of the search space,

S: The number of bacterium,
N_c: chemotactic steps,
N_s: swim steps,
N_{re}: reproductive steps,
N_{ed}: elimination and dispersal steps,
P_{ed}: 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*.
[a] For *i=1,2...,S*, take a chemotactic step for bacteria *i* as follows.
[b] Compute fitness function, *J (i,j,k,l)*.
[c] Let J_{last}= *J(i,j,k,l)* to save this value since we may find better value via a run.
[d] Tumble: Generate a random vector $\Delta(i) \in R^n$ with each element $\Delta_m(i)$, *m* = 1, 2, …, *S*, a random number on [-1, 1].
[e] Move: Let

$$\Theta^i(j+1,k,l) = \Theta^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}} \qquad (10)$$

This results in a step of size *C(i)* in the direction of the tumble for bacteria *i*.
[f] Compute *J(i,j+1,k,l)* with Θ^i*(j+1,k,l)*.
[g] Swim:
(i) Let *m* = 0 (counter for swim length).
(ii) While *m <Ns* (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 Θ^i*(j+1,k,l)* to compute the new *J(i,j+1,k,l)*.
• Else let m = N_s.
[h] Go to next bacterium (*i*+1): if *i • 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:
[a] For the given *k* and *l*, and for each *i* = 1, 2, …,*S*, let J_{health} be the health of the bacteria. Sort bacterium in order of ascending values.

$$J_{health}^i = \sum_{j=1}^{Nc+1} J(i,j,k,l) \qquad (11)$$

[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, …, *S*, with probability P_{ed}, 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.

IV. BFO-EML DOA ESTIMATION

Here we describe the formulation of the BFO algorithm[27] for EML optimization to estimate source DOA's. At first initialize a population of Particles in the search space with random positions and random velocities constrained between 0 and π in each dimension [17]. The *N* dimensional position vector of the *j*th particle takes the form $x_j = [\theta_1, . . . , \theta_N]$, where *θ* represents the DOAs. A particle position vector is converted to a candidate solution vector in the problem space through a suitable mapping. The score of the mapped vector evaluated by a likelihood function f_{EML} which is given in (9), is regarded as the fitness of the corresponding particle. To evaluate the likelihood function f_{EML} required the data from all the elements of the array for K number of snapshots . K=20, n=2, S=10, N_c =20 N_s=4, N_{re} =4 N_{ed}=2, P_{ed}=0.25, C(i)=0.005 are initialized for the optimization algorithm. By using algorithm particles with highest health will be obtained. The optimization iteration will be terminated if the specified maximum iteration number is reached.
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V. SIMULATION RESULTS AND DISCUSSIONS

Here we present a numerical example to demonstrate the performance of BFO based DOA estimation using (9) against PSO and MUSIC [4] which is the best known and well investigated algorithm. The performances of those methods are compared in two ways: (a) the DOA estimation root-meansquared error (RMSE), which is calculated as [12]

$$RMSE = \sqrt{\frac{1}{N N_{run}}\sum_{l=1}^{N_{run}}, \sum_{i=1}^{N}[\hat{\theta}_n(l) - \Theta_n]^2} \qquad (12)$$

where N is the number of sources, $\hat{}_n$(l)) is the estimate of the *n*th DOA achieved in the *l*th run, θn is the true DOA of the *n*th source; and (b) the ability to resolve closely spaced sources known as probability of resolution (PR). By definition, two sources are said to be resolved in a given run if both $|\hat{\theta}_1 - \theta_1|$ and $|\hat{\theta}_2 - \theta_2|$ are smaller than $|\theta_1 - \theta_2|/2$.

A. Example 1

Here our aim is to demonstrate the performance of ML estimator computed by PSO, BFO algorithm, and to compare with MUSIC algorithm. We assume that two equal-power, uncorrelated signals impinge on 8 sensor UCA from 130° and 140°. The number of snapshots is taken as 20, and the SNR varies from -20 dB to 30 dB with the step size of 1 dB taken for simulation. The function f_{EML} is optimized using PSO and APSO algorithms for 20 snapshots in case of

PSO and BFO, but 1000 snapshots taken for MUSIC. The Fig.1 gives the Surface of Exact Maximum Likelihood function f_{EML} corresponding to 0° to 180° is given in. The Fig. 2 gives the DOA estimation RMSE values obtained using PSO-EML, BFO-EML, and MUSIC as a function of SNR. Fig. 3 shows the resolution probabilities (RP) for the same methods. Two sources are considered to be resolved in an experiment if both DOA estimation errors are less than the half of their angular separation.

As can be seen from Fig. 2 and Fig. 3, BFO-EML yields significantly superior performance over PSO-EML as a whole, by demonstrating lower DOA estimation RMSE and higher resolution probabilities. The accurate DOA estimates are observed because 1) EML criterion functions are statistically optimal although computation-extensive, and 2) the designed BFO is a robust and reliable global optimization algorithm. MUSIC, on the other hand, produces less accurate estimates.
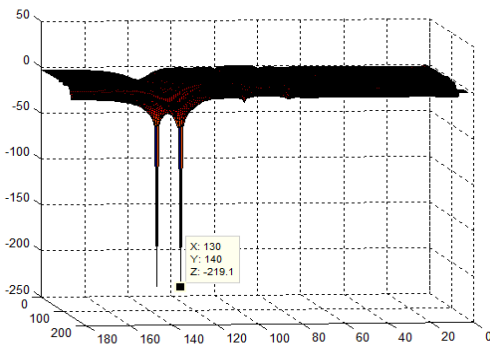

Fig 1: Surface of Exact Maximum Likelihood function corresponding to 0° to 180°.

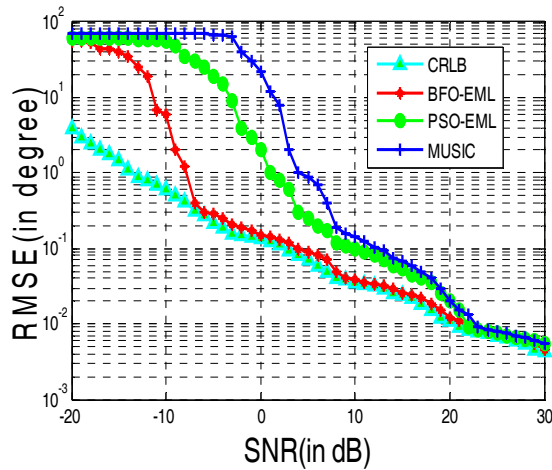

Fig. 2. DOA estimation RMSE values of PSO-EML, APSO-EML, and MUSIC versus SNR. Two uncorrelated sources impinge on 8-sensor UCA at 130° and 140°. Number of snapshots is 20.
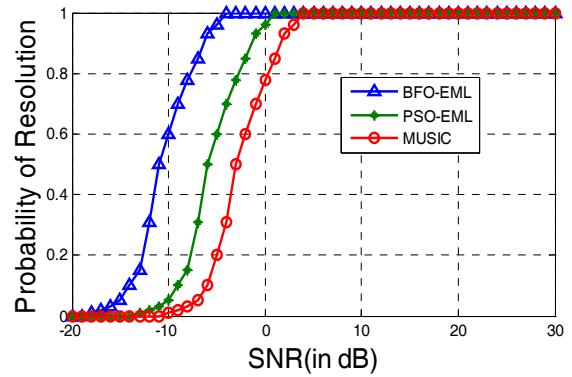

Fig. 3. Resolution probabilities of PSO-EML, BFO-EML and MUSIC versus SNR. Two uncorrelated sources impinge on 8-sensor UCA at 130° and 140° Number of snapshots is 20.

VI CONCLUSION

In this paper, bacteria foraging optimization (BFO) is proposed to estimate the DOA using maximum likelihood function. With newly introduced features matching scheme and intelligent initialization, carefully selected evolution operators and fine-tuned parameters, the BFO-EML estimator achieves fast convergence. Simulation results also demonstrate that BFO-EML outperforms other estimators, MUSIC of the DOA estimation RMSE and source resolution probability, with less computational cost, which is similar to that of MUSIC, and the result estimates asymptotically achieve the stochastic CRLB.

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