ESTIMATION OF MIXED SPECTRUM USING GENETIC ALGORITHM

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ABSTRACT

This paper proposes a method for estimating the mixed spectrum which is composed of line and continuous spectra, the latter of which is characterized by an AR or ARMA noise model. Line spectrum is represented by multiple sinusoids. In order to avoid simultaneous minimization of a prediction error criterion with respect to all unknown parameters, we give an efficient iterative algorithm for estimating the frequencies of the sinusoids and other parameters separately. By adopting the genetic algorithm in choice of initial values of the AR or ARMA parameters in the iterative estimation, we can attain a globally optimal estimates of unknown parameters. The frequency estimate is given by a modified Toeplitz approximation method using a shifted correlation matrix of observed signals. The effectiveness of the proposed algorithm is validated in numerical simulations.

1. INTRODUCTION

Estimation of mixed spectrum which is composed of line and continuous spectra plays an important role in wide area of digital signal processing. Continuous spectrum can be expressed by a sum of multiple sinusoids, while line spectrum is characterized by an AR, MA or ARMA noise model. This problem was first investigated by using the periodgram [1] via a non-parametric approach. From a parametric point of view, an AR, MA or ARMA spectral estimation method is applicable, however, we cannot discriminate the continuous spectral signal from the sinusoids.

On the other hand, for estimation of line spectrum only, we can apply the maximum likelihood (ML) method [2] and the subspace approaches such as the Pisarenko's method, the Toeplitz approximation (TA) method [3], the MUSIC etc. The separable estimation of the mixed spectrum have also been studied in [4]-[8]. The ML methods normally search all unknown parameters simultaneously so that the prediction error criterion may be minimized [4][5]. However, the simultaneous minimization needs the search of too many parameters and suffers from traps into local minima.

The purpose of this paper is to clarify a high-resolution estimation method for the mixed spectrum incorporating with the genetic algorithm (GA). If the ARMA model is known, we can implement a filter with the ARMA parameters, then apply a modified TA method to a correlation matrix of its shifted matrix of the filtered signals to estimate the frequencies of sinusoids. That implies that the total estimation problem can be reduced to the iterative search of the ARMA parameters minimizing a prediction error criterion. Another feature of the proposed method is that GA is efficiently utilized in the choice of initial values of the ARMA parameters in the iteration, that can save computational burden and time. Finally, the effectiveness of the proposed algorithm is investigated in numerical simulations including a benchmark example.

2. SIGNAL MODEL WITH MIXED SPECTRUM

2.1 Problem Statement

It is assumed that the observed signal $y(k)$ is composed of multiple sinusoids and autoregressive moving-averaged (ARMA) noise process as

$$y(t) = \sum_{m=1}^{M} \alpha_m \sin(2\pi f_m t + \phi_m) + v(t) \tag{1}$$

$$v(t) + \sum_{i=1}^{p} a_i v(t-i) = w(t) + \sum_{j=1}^{q} b_j w(t-j) \tag{2}$$

where f_m, α_m, and ϕ_m are the frequency, amplitude and phase of each sinusoid respectively, $\{a_i\}$ and $\{b_j\}$ are the coefficient parameters of the ARMA noise process which is actuated by a white Gaussian noise $w(t)$ with zero mean and variance σ_w^2. M is the number of sinusoids and p and q is the order of the AR and MA part respectively. These model parameters $\{f_m\}$, $\{\alpha_m\}$, $\{\varphi_m\}$, $\{a_i\}$, $\{b_j\}$, σ_w^2, M, p and q are all unknown.

2.2 Parametrization of Signal Model

Let the polynomials $A(z^{-1})$ and $B(z^{-1})$ be stable and be defined by

$$A(z^{-1}) = 1 - \sum_{k=1}^{p} a_k z^{-1}, \quad B(z^{-1}) = 1 + \sum_{k=1}^{q} b_k z^{-1} \tag{3}$$

Multiplying $A(z^{-1})$ with the both sides of (1) gives

$$\begin{aligned} z(t) &= A(z^{-1}) y(t) \\ &= A(z^{-1}) \cdot \sum_{m=1}^{M} \alpha_m \sin(2\pi f_m + \phi_m) + B(z^{-1}) w(t) \\ &= \sum_{m=1}^{M} c_m \sin(2\pi f_m t) + \sum_{m=1}^{M} d_m \cos(2\pi f_m t) \\ &\qquad + B(z^{-1}) w(t) \end{aligned} \tag{4}$$

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where the coefficients c_m and d_m depend on the unknown parameters $\{\alpha_m\}, \{a_i\}, \{f_m\}$ and $\{b_j\}$, but the expressions are omitted for the sake of space.

Moreover, dividing the both sides of (4) by $B(z^{-1})$, we can obtain another model description as

$$\begin{aligned}\eta(t) &= \frac{1}{B(z^{-1})} z(t) \\ &= \sum_{m=1}^{M} c_m \frac{1}{B(z^{-1})} \sin 2\pi f_m t \\ &\qquad + \sum_{m=1}^{M} d_m \frac{1}{B(z^{-1})} \cos 2\pi f_m t + w(t) \end{aligned} \qquad (5)$$

3. OUTLINE OF SEPARATION ALGORITHM

Conventional parameter estimation schemes such as the ML estimation are based on the signal model (4) which shows all the parameters $\{a_i\}, \{c_m\}, \{d_m\}, \{f_m\}$ and $\{b_j\}$ explicitly. Thus the schemes require search of too many parameters and then sometimes suffer from traps into local minima.

An outline of a scheme proposed in this paper is summarized as follows: First if the ARMA parameters are given correctly, we can estimate the frequencies by applying a modified Toeplitz approximation method to the signal model (4), as is described in the next section. Then, secondly if the ARMA parameters and the frequencies are given correctly, we can estimate the parameters $\{c_m\}$ and $\{d_m\}$ of the model (5) by utilizing the ordinary least squares (LS) estimation method, and then calculate the amplitudes and phases of sinusoids from all of the given or estimated parameters as

$$\phi_m = \arg\{(\beta c_m + \gamma d_m) + j(\beta d_m - \gamma c_m)\} \qquad (6)$$

$$\alpha_m = \frac{c_m}{\beta \cos \phi_m - \gamma \sin \phi_m} \qquad (7)$$

respectively, where

$$\beta = 1 + \sum_{k=1}^{p} a_k \cos(2\pi f_m k), \qquad \gamma = \sum_{k=1}^{p} a_k \sin(2\pi f_m k)$$

Thirdly the final problem is how to estimate the ARMA parameters $\{a_i\}$ and $\{b_j\}$ if the other parameters are given. In order to execute the estimation, we rewrite the signal representation (4) into

$$A(z^{-1}) y(t) = x(t) + B(z^{-1}) w(t) \qquad (8)$$

$$x(t) = \sum_{m=1}^{M} c_m \sin(2\pi f_m t) + \sum_{m=1}^{M} d_m \cos(2\pi f_m t) \qquad (9)$$

Let the ARMA parameter vector be denoted by

$$\theta = (a_1, \cdots, a_p, b_1, \cdots, b_q)^T$$

and the prediction error $\varepsilon(t,\theta)$ by

$$\varepsilon(t,\theta) = y(t) - \hat{y}(t \mid \theta) \qquad (10)$$

where the predicted output $\hat{y}(t \mid \theta)$ of a model is given by

$$\begin{aligned}\hat{y}(t \mid \theta) &= \left[1 - \frac{A(z^{-1})}{B(z^{-1})}\right] y(t) + \frac{1}{B(z^{-1})} x(t) \\ &= (1 - A(z^{-1})) y(t) + x(t) - (1 - B(z^{-1}))\varepsilon(t,\theta) \\ &= \varphi^T(t,\theta)\theta + x(t) \end{aligned} \qquad (11)$$

where $\varphi(t,\theta)$ is the regressor signal defined by $\varphi^T(t,\theta) = (-y(t-1), \cdots, -y(t-p), \varepsilon(t-1,\theta), \cdots, \varepsilon(t-q,\theta))$. We take a prediction error criterion for the parameter estimation as

$$J(\theta) = \frac{1}{N} \sum_{t=1}^{N} \{y(t) - \hat{y}(t \mid \theta)\}^2 \qquad (12)$$

Applying a Newton type of nonlinear optimization algorithm to minimization of (12), we obtain the estimate of $\hat{\theta}$ in an iterative manner. The derivatives of $\hat{y}(t \mid \theta)$ with respect to the ARMA parameters which are needed in the minimization are given by

$$\frac{\partial}{\partial a_i} \hat{y}(t \mid \theta) = -\frac{1}{B(z)} y(k-i) \qquad (13a)$$

$$\frac{\partial}{\partial b_j} \hat{y}(t \mid \theta) = -\frac{1}{B(z)} \varepsilon(k-j,\theta) \qquad (13b)$$

Thus, instead of simultaneous minimization with respect to all the parameters, the estimation algorithm is reduced to the iterative search of only ARMA parameters. A genetic algorithm is efficiently introduced into decision of initial ARMA parameters in the iterative search for escaping from traps into local minima, as will be described in Section 4.

3. MODIFIED TOEPLITZ APPROXIMATION

Ordinary TA method can be employed when the signal consists of sinusoids and white noise [3]. We consider some extension to a case subjected to MA noise as

$$z(t) = \sum_{m=1}^{M} \alpha'_m \sin 2\pi f_m t + B(z^{-1}) w(t) \qquad (14)$$

When the noise is an MA process, we should enlarge the correlation matrix R_z so much as we can use the fact that the autocorrelation functions of the MA process are zero for lags n larger than q. Let the lower left block of $\tilde{R}_z$ be denoted by

$$\tilde{R}_z = \begin{bmatrix} r_z(n) & r_z(n-1) & \cdots & r_z(n-2M+1) \\ r_z(n+1) & r_z(n) & \cdots & r_z(n-2M+2) \\ \vdots & \vdots & \ddots & \vdots \\ r_z(N'-1) & \cdots & \cdots & r_z(N'-2M) \end{bmatrix} \qquad (15)$$

where the shifted lag should satisfies $n > q + 2M - 1$. Let C be a matrix defined by

$$C = \begin{bmatrix} 0 & \cdots & 0 & 1 \\ \vdots & .\cdot^{\cdot} & 1 & 0 \\ 0 & .\cdot^{\cdot} & .\cdot^{\cdot} & \vdots \\ 1 & 0 & \cdots & 0 \end{bmatrix}$$

The first step is to take the singular value decomposition of the Hankel matrix $R_z C$ as $R_z C = U \Sigma V^T$ where the rank of the diagonal matrix Σ will become $2M$ if M is the number of sinusoids. Secondly calculate the matrix as $\Phi = U \Sigma^{1/2}$ and then the system matrix F as $F = (\Phi^{\downarrow T} \Phi^{\downarrow})^{-1} \Phi^{\downarrow T} \Phi^{\uparrow}$, where $\Phi^{\downarrow}$ is Φ deprived from its last row, and $\Phi^{\uparrow}$ is Φ deprived from its first row. Finally calculate the frequency estimates $f_m = \omega_m / 2\pi$ from the eigenvalues of F given by $\exp(\pm j \omega_m)$.

4. GENETIC ALGORITHM FOR ARMA MODEL

4.1 Genetic Algorithm

The basic element processed by a genetic algorithm (GA) is the string (genes) formed by concatenating substrings, each of which is a binary coding of a parameter of the search space. Each string represents a possible solution to the optimization problem. The genetic algorithm works with a set of strings, not a single string, which is called the population, This population then evolves from generation to generation through the application of three basic genetic operators: *reproduction*, *crossover* and *mutation* [9]. The outline of the genetic algorithm utilized in the proposed scheme is given as follows:

(a) *Coding*: Coding is required to map a finite length of string to the initial conditions $\hat{\theta}^{(0)} = (\hat{a}_1^{(0)}, \cdots, \hat{a}_p^{(0)}, \hat{b}_1^{(0)}, \cdots \hat{b}_q^{(0)})^T$ of the iterative search of the ARMA parameters. It is one of the advantages of the proposed scheme that the ARMA parameters themselves are not directly coded, therefore this coding may be rather rough. Fig.1 shows an example of the coding of $\hat{\theta}^{(0)}$. A set of strings are referred to as the population.

$$\underbrace{0101}_{1.25} \cdots \underbrace{1101}_{-1.25} \underbrace{1101}_{-1.25} \cdots \underbrace{0111}_{1.75}$$

$$\begin{array}{cccc} \downarrow & \downarrow & \downarrow & \downarrow \\ \hat{a}_1^{(0)} & \hat{a}_p^{(0)} & \hat{b}_1^{(0)} & \hat{b}_q^{(0)} \end{array}$$

Fig.1 An example of binary coding of the initial values to present a string.

(b) *Evaluation of fitness function*: The fitness of the nth string is denoted by $g(n)$ which is defined by $1/J_n(\theta)$, where $J_n(\theta)$ is given in (12). In this paper, the scaling of $1/J_n(\theta)$ by the ranking is performed so that average strings and best strings get nearly the same number of copies in the next generation.

(c) *Reproduction*: Reproduction is an operation in which individual strings are copied in probabilistic ways according to the fitness values. Moreover we employ two schemes: One is the stochastic remainder selection without replacement by which the strings with the fitness higher than average can have more than one offspring. The other is the scheme in which the best string is always copied.

(d) *Crossover*: Reproduction directs the search toward the best copy of strings but does not produce new strings. This operation is divided into two steps. First two strings from reproduced population are mated at random. Then each pair of strings are cut randomly between any two bits on the strings. The new pair of strings are then created by interchanging the tails. Thus the new offsprings are created from their parent strings.

(e) *Mutation*: Mutation is introduced to produce a new string by flipping the state of a bit from 0 to 1 or vice versa. However, this operation should be used with small probability.

4.2 Separation Algorithm

We will apply the genetic algorithm to the choice of initial value of the ARMA parameters for starting the iterative search to avoid traps into local minima of the prediction error criterion. The algorithm is given below:

(Step 1) Set M, p and q.

(Step 2) Set the population size S and the initial population of the strings $\{\hat{\theta}^{(0)}(1), \cdots, \hat{\theta}^{(0)}(S)\}$.

(Step 3) Maximize the fitness $g(n) = 1/J_n(\theta)$ (see (12)) for the each *new* string with respect to θ in an iterative way.

(3-1) Calculate the filtered output $z^{(i)}(t)$ in (4) by using $\{\hat{\theta}^{(i)}\}$ and apply the proposed modified TA method to the output $z^{(i)}(t)$ to obtain the estimate $\{\hat{f}_m^{(i)}\}$.

(3-2) Calculate the LS estimate $\{\hat{c}_m^{(i)}\}$ and $\{\hat{d}_m^{(i)}\}$ on a basis of the model (5) to obtain the estimates of the amplitudes and phases in (6) and (7).

(3-3) Update the estimate of ARMA parameters $\{\hat{\theta}^{(i)}\}$ by the Newton method as

$$\hat{\theta}^{(i+1)} = \hat{\theta}^{(i)} - \mu [J_n''(\hat{\theta}^{(i)})]^{-1} J_n'(\hat{\theta}^{(i)})$$

and return (3-1) until $\hat{\theta}^{(i+1)}$ and $J_n(\hat{\theta}^{(i+1)})$ converge to a constant $\bar{\theta}$ and $J_n(\bar{\theta})$ respectively. Store the value of the fitness function for the each string.

(Step 4) Scale the fitness $g(n)$ by ranking $J_n(\bar{\theta})$.

(Step 5) Operate the reproduction including the two schemes stated above (see (c)).

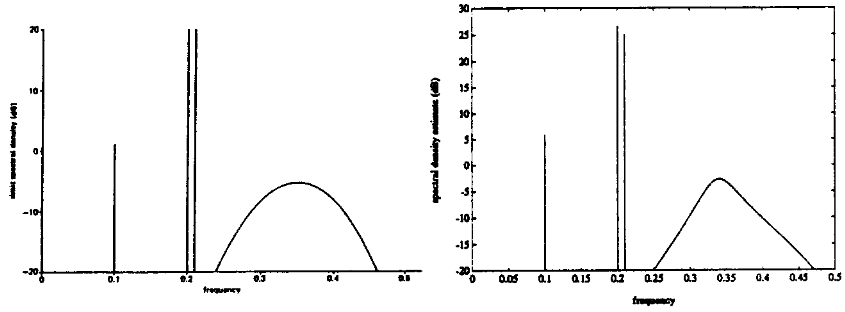
(Step 6) Perform the crossover on the each string.

(Step 7) Take mutations on the each string.

(Step 8) Return Step 3 and produce the next generation until the minimum of J_{n° is not more updated.

4.3 Optimal Decision of Number of Sinusoids and Order of ARMA Noise

In the last section we presented the iterative algorithm assuming that the number (M) of sinusoids and the order (p, q) of the ARMA model. We will discuss how to decide M, p and q. In this paper, we apply the χ^2 statistical test to validate the triplet (M, p, q) by testing the whiteness of the predicted error $y(t) - \hat{y}(t \mid \bar{\theta}_{n^\circ})$ for the obtained best string. The null hypothesis H_0 is that the prediction error is white. Let α be the level of significance indicating the risk probability of rejecting H_0 when H_0 holds. Normally α is chosen between 0.01 and 0.1. The decision rule is summarized as follows:



(a) (b)

Fig.2 True and estimated mixed power spectra

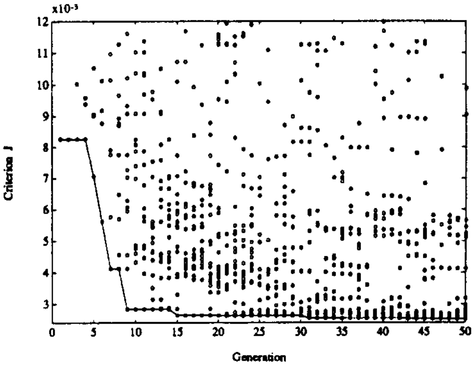


Fig.3 Criterion J of each string at each generation.

1) For all triplets (M,p,q), first apply the χ^2-test for validating the whiteness of the prediction error of the best string minimizing J in order to simplify the order decision procedure.

2) For the each validated triplet (M,p,q), calculate the estimate $\hat{M}$ that minimizes the criterion given in [10][11] by using the filtered data $\hat{\eta}(t)$.

3) If there is only one $\hat{M}'$ that coincides with the assumed M, the number of sinusoids is decided as $\hat{M}'$. The order (p,q) of the ARMA model is chosen by using the AIC.

4) If there are more than two $\hat{M}$, the number of sinusoids is decided as the maximum $\hat{M}'$ among $\hat{M}$'s.

5 ILLUSTRATIVE EXAMPLE: BENCHMARK TEST

We applied the proposed algorithm to the signal data given in [12], which was often used for benchmark tests. The true power spectrum is given in Fig.2a. The number of data is $N = 64$, and the risk rate is chosen $\alpha = 0.03$. In the genetic algorithm given in Section 4, we take that the population size is $S = 30$, the maximum generation is 50, the coding of the initial value $\hat{\theta}^{(0)}$ is performed by assuming that $\hat{\theta}^{(0)}$ take between -2 and 2, and the precision is $1/2^{10}$. The crossover is processed at a single position with probability one. The number of sinusoids and the order of ARMA model were decided as $M = 3, p = 3$ and $q = 5$ by the scheme given in Section 4.3. The estimated power spectrum is satisfactorily close to the true one as shown in Fig.2b. Finally Fig.3 illustrates the process of the search by the genetic algorithm and shows that the number of genes giving smaller value of $J(\bar{\theta})$ increases and the minimum of $J_{n^o}(\bar{\theta})$ can be attained by the best gene, as the generation proceeds.

6. CONCLUSIONS

The GA-based estimation of the mixed spectra has been presented to discriminate the line and ARMA spectra. The genetic algorithm enables that the estimation of all the unknown model parameters is reduced to the optimal choice of only the initial guess of the ARMA parameters, since the frequency estimate can be obtained by the Toeplitz approximation approaches if the ARMA parameters are given.

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