Adaptive Spectral Peak Estimation with aid of Genetic Algorithm

Norikazu Ikoma and Hiroshi Maeda
Department of Computer Science,
Kyushu Institute of Technology
1-1 Tobata-ku, Kita-Kyushu, 804-8550 Fukuoka Japan
Phone: +81-93-884-3216, Fax: +81-93-871-5835
email:ikoma@comp.kyutech.ac.jp

ABSTRACT: An adaptive method to estimate time-varying peaks of power spectrum with aid of genetic algorithm is proposed. The model used here is based on time-varying coefficient autoregressive model nonlinearly parametrized by characteristic roots of complex conjugate pair. Since the characteristic root denotes a peak frequency by its exponential part, the model can directly estimate time-varying spectral peaks by doing state esitmation using non-Gaussian filtering. As the non-Gaussian filtering method, we employ Monte Carlo filtering that uses particles sampled from the non-Gaussian distribution. It is known that the procedure of Monte Carlo filter is similar to the procedure of genetic algorithm, and collaboration between them is possible. The model used here also has time-varying order of autoregressive, we apply genetic operation for the estimation of it. Simulational result shows the efficiency of the model.

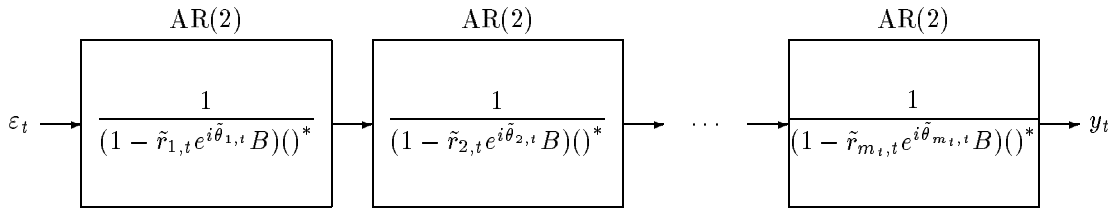
KEYWORDS: Genetic algorithm, spectral analysis, adaptive estimation

INTRODUCTION

Spectral analysis is widely used in many field of researches and designs. The analysis of stationary case is well established, however, nonstationary anaylsis is still a topic to investigate. Several method to estimate nonstationary spectrum by using time domain model have been researched e.g., time-varying coefficient autoregressive(AR) model proposed by Kitagawa and Gersch(1985). Almost all the analysis used time domain model, the order of autoregression is assumed to be constant though the time series data. However, it is not always satisfactory for the anaylsis when the data contain some structural changes or arrivals of signal. For such situation, we propose a new model that can treat the changes of autoregressive order within the time series data.

We firstly extend the time-varying coefficient autoregressive model to have time-varying order of autoregression, and it is also assumed that the autoregressive coefficients are parametrized by the roots of characteristic equation in order to make a direct estimation of peaks of power spectrum. Then we introduce a "gene" to express the choice of peaks from the state vector of the model and apply genetic operations to the gene to obtain optimal selection of peaks and autoregressive order. Another parameters in state vector, such as parameters that specify the spectral peaks, are estimated by a state estimation method for non-Gaussian model since our model is nonlinearly formulated. As a method for non-Gaussian state estimation, we use Monte Carlo filtrer proposed by Kitagawa(1997). The Monte Carlo filter has similar procedure to genetic algorithm except there is no crossover operation. So a collaboration between Monte Carlo filter and genetic algorithm can easily be done.

In the followings, we firstly summarize the basic of time series model for the nonstationary spectral analysis briefly, and next we define our model for the analysis in the situation mentioned above. Secondly, the method for state estimation is explained. The procedure of Monte Carlo filtering is summarized and the use of genetic algorithm in our model is mentioned here. Finally, a simple simulational experiment shows the efficiency of our model to estimate nonstationary spectral peaks with changes of the number of peaks.



$()^*$ denotes conjugate pair of preceding complex

Figure 1: Sequential system of AR(2) consists of selected peaks

MODEL

FOUNDATION

Let us consider time-varying coefficient autoregressive model of the follwing form,

$$y_t = \sum_{j=1}^{2m_t} a_{j,t} y_{t-j} + \varepsilon_t \tag{1}$$

where ε_t is i.i.d. random variable of normal distribution with zero mean and time-varying variance σ^2. We also assume the order of autoregression denoted by m_t is varying with time. By using z operator, which shifts time as $zy_t = y_{t-1}$, the above model can be written as follows,

$$\left(1 - \sum_{j=1}^{2m_t} a_{j,t} z^j\right) y_t = \varepsilon_t \tag{2}$$

Assume that all the roots of characteristic equation

$$1 - \sum_{j=1}^{2m_t} a_{j,t} z^j = 0 \tag{3}$$

are complex(conjugate pair) denoted by $\tilde{r}_{k,t}e^{\pm i\tilde{\theta}_{k,t}}$, $k = 1, 2, \cdots, m_t$. The time-varying autoregressive model (1) can be rewritten by using conjugate pair of characteristic roots as follows,

$$\prod_{k=1}^{m_t} \left(1 - \tilde{r}_{k,t}e^{i\tilde{\theta}_{k,t}}z\right)\left(1 - \tilde{r}_{k,t}e^{-i\tilde{\theta}_{k,t}}z\right) y_t = \varepsilon_t \tag{4}$$

By considering equation (4) as data generation process in which white noise ε_t is fed into the process, it can be written in sequential system of second order AR models as shown in Figure 1.

Note that by comparing equation (2) and (4), time-varying coefficients can be identified by characteristic roots, and we use this fact for the definition of our model. This type of modeling is proposed by Ikoma(1996) except the order of the model is varying with time.

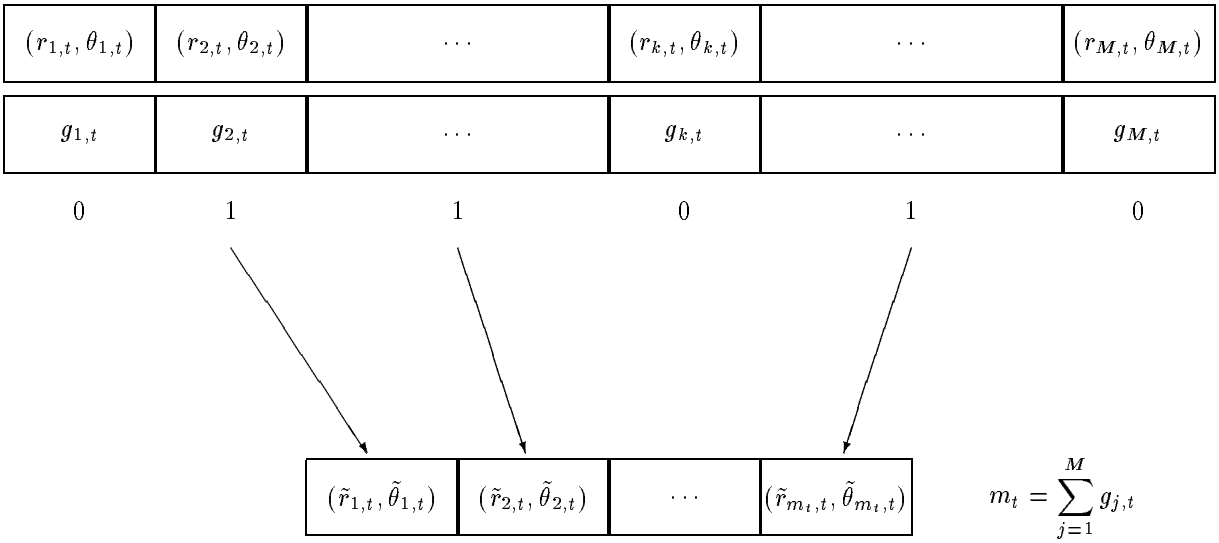


Figure 2: Selection of peaks by gene

COEFFICIENTS

For the explicit notation of autoregressive coefficients, we firstly denote characteristic roots by $c_{j,t}$, $j = 1, \cdots, m_t$, as equation (4) becomes

$$\prod_{j=1}^{2m_t} (1 - c_{j,t} z)\, y_t = \varepsilon_t \tag{5}$$

where $c_{j,t}$'s are defined

$$c_{j,t} = \begin{cases} \tilde{r}_{k,t} e^{i\tilde{\theta}_{k,t}} & j \text{ is odd}, \\ \tilde{r}_{k,t} e^{-i\tilde{\theta}_{k,t}} & j \text{ is even}, \end{cases} \tag{6}$$

for $k = [(j+1)/2]$, here $[\cdot]$ is Gauss's symbol. Then we can explicitly denote autoregressive coefficients

$$a_{j,t} = (-1)^j \sum_{c_{i1} \cdots c_{ij}} c_{i1} \cdots c_{ij} \tag{7}$$

where summation is taken $i1, \cdots, ij$, for all combination of each different value.

MODEL DEFINITION

Consider M conjugate pairs characteristic roots where twice of M is upper limit of autoregressive order. We define a state space model with observation equation is basically defined by the equation (1) with equations (6),(7), and system equation consists of linear part

$$\tilde{\mathbf{x}}_t = \tilde{\mathbf{x}}_{t-1} + \mathbf{w}_t \tag{8}$$

and nonlinear part

$$\mathbf{g}_t = f(\mathbf{g}_{t-1}, \mathbf{w}_{g,t}) \tag{9}$$

By noting the state vector

$$\mathbf{x}_t = \left[\tilde{\mathbf{x}}_t^T, \mathbf{g}_t\right]^T \tag{10}$$

system equation is written as following general form

$$\mathbf{x}_t = \mathbf{g}\left(\mathbf{x}_{t-1}, \mathbf{w}_t\right) \tag{11}$$

State vector of linear part consists of parameters of characteristic roots and variance,

$$\tilde{\mathbf{x}}_t = \left[\mathbf{r}_t^T, \theta_t, \sigma_t^2\right]^T \tag{12}$$

and vector of system noise

$$\mathbf{w}_t = \left[\mathbf{w}_{r,t}^T, \mathbf{w}_{\theta,t}^T, w_{\sigma,t}\right]^T \tag{13}$$

where $[\cdot]^T$ denotes transpose of vector, and the followings are the definition of the vectors used above,

$$\mathbf{r}_t = \left[r_{1,t}, \cdots, r_{M,t}\right]^T \tag{14}$$

$$\theta_t = \left[\theta_{1,t}, \cdots, \theta_{M,t}\right]^T \tag{15}$$

$$\mathbf{w}_{r,t} = \left[w_{r,1,t}, \cdots, w_{r,M,t}\right]^T \tag{16}$$

and

$$\mathbf{w}_{\theta,t} = \left[w_{\theta,1,t}, \cdots, w_{\theta,M,t}\right]^T \tag{17}$$

Althourh we have several choice of the distribution of system noise since we will use non-Gaussian state esimation method, however for the practical reason, we assume Gaussian distribution for each items of system noise vector with common variance in $\mathbf{w}_{r,t}$, $\mathbf{w}_{\theta,t}$ and $\mathbf{w}_{\sigma,t}$. The variance parameters are denoted by τ_r^2, τ_θ^2 and τ_σ^2.
Nonlinear part of system equation has state vector $\mathbf{g}_t$ of bit sequence with length M,

$$\mathbf{g}_t = \left[g_{1,t}, \cdots, g_{M,t}\right]^T \tag{18}$$

and we call $\mathbf{g}_t$ "gene" of genetic algorithm in Goldberg(1989). The function $f(\cdot,\cdot)$ denotes the result of genetic operations such as mutation and crossover. The gene works as that if k-th bit is equal to 1, the corresponding pair of characteristic root denoted by $r_{k,t}e^{\pm i\theta_{k,t}}$ is used in observation equation, otherwise, i.e. another k'-th bit is equal to 0, the corresponding pair is not used. This is illustrated in Figure 2.
The function of gene is written as the autoregressive notation as follows,

$$\prod_{k=1}^{M}\left(1 - g_k r_{k,t}e^{i\theta_{k,t}}z\right)\left(1 - g_k r_{k,t}e^{-i\theta_{k,t}}z\right)y_t = \varepsilon_t \tag{19}$$

Note that in observation equation defined by the equation (1), (6) and (7), in equation (6), only the characteristic roots that have value 1 of corresponding bit of gene are used as $c_{j,t}$.

ESTIMATION

MONTE CARLO FILTER

Since the model defined in the previous section is nonlinear, we have to use non-Gaussian filtering method for the state estimation. As the state estimation method, we use Monte Carlo filter proposed by Kitagawa(1996), and we will briefly summarize the method as follows.

Let us first denote the observation by

$$Y_N = [y_1, \cdots, y_N]^T \tag{20}$$

The aim of filtering is to estimate the conditional distribution of state vector given observation such as one-step-ahead prediction distribution $p(\mathbf{x}_t|Y_{t-1})$ and filtering distribution $p(\mathbf{x}_t|Y_t)$. In the Monte Carlo filter, these non- Gaussian distributions are approximately represented by particles that are sampled from the distributions as follows,

$$\{\mathbf{p}_{1,t}, \cdots, \mathbf{p}_{K,t}\} \text{ is sampled from } p(\mathbf{x}_t|Y_{t-1}) \tag{21}$$

$$\{\mathbf{f}_{1,t}, \cdots, \mathbf{f}_{K,t}\} \text{ is sampled from } p(\mathbf{x}_t|Y_t) \tag{22}$$

where each $\mathbf{p}_{j,t}$ and $\mathbf{f}_{j,t}$ takes a value of state vector $\mathbf{x}_t$. By starting from appropriate initial distribution $p(\mathbf{x}_0|Y_0)$ and alternatively calculating the distributions of one-step-ahead prediction and filtering, we can estimate state for all time $t = 1, \cdots, N$. The calculation of each distribution is as follows. One-step-ahead prediction is done by simply applying each particle to system equation (11),

$$\mathbf{p}_{j,t} = \mathbf{g}\left(\mathbf{f}_{j,t-1}, \mathbf{w}_{j,t}\right) \tag{23}$$

by generating random vector $\mathbf{w}_{j,t}$ according to the distribution of system noise $\mathbf{w}_t$. For filtering, firstly calculate the likelihood of each particle by

$$\alpha_{j,t} = p(y_t|\mathbf{p}_{j,t}) \tag{24}$$

note that this can easily calculated by p.d.f. of Gaussian distribution from prediction error of y_t and observation variance σ_2. Then according to the value of likelihood $\alpha_{j,t}$, we can obtain the filtering particles by resampling as follows,

$$\mathbf{f}_{j,t} = \begin{cases} \mathbf{p}_{1,t} & \text{with probability} \quad \alpha_{1,t}/\sum\alpha \\ \vdots & \qquad\qquad\quad \vdots \\ \mathbf{p}_{K,t} & \text{with probability} \quad \alpha_{K,t}/\sum\alpha \end{cases} \tag{25}$$

where $\sum\alpha = \sum_{j=1}^{K} \alpha_{j,t}$. Log-likelihood of the model can be calculated from the result of filtering as follows,

$$l(\vartheta) = \sum_{t=1}^{N} \log p(y_t|Y_{t-1}) \simeq \sum_{t=1}^{N} \log\left(\frac{1}{K}\sum_{j=1}^{K}\alpha_{j,t}\right) \tag{26}$$

GENETIC OPERATION

There is a research of a similarity of Monte Carlo filter and genetic algorithm by Higuchi(1997). In this research, particles appear in Monte Carlo filter are considered as individual ,and one-step-ahead prediction corresponds to mutation, filtering corresponds to selection. This relationships are summarized in Table 1.

Thus Monte Carlo filter is equivalent to a special case of genetic algorithm with zero crossover rate. The research proposed to approach both from Monte Calro filter to genetic algorithm and vice versa. In our research, we incorporated genetic operation into Monte Carlo filter by defining the state vector of our model as previously defined. By this definition, the gene $\mathbf{g}_t$ of state vector selects spectral peaks from linear part of state vector denoted by $\tilde{\mathbf{x}}_t$. In the above notation of Monte Carlo filter for our model, equation (23) contains equation (9) is the genetic operation including mutation and crossover. Although several parameters such as mutation and crossover rate for genetic operation, they can be determined by maximizing the likelihood function as in Akaike(1980).

Table 1: Relationship between genetic algorithm and Monte Carlo filtering

genetic algorithm	Monte Carlo filtering
population	distribution
individual	particle
mutation	one-step-ahead prediction
crossover	-
fitness	likelihood
selection	resampling

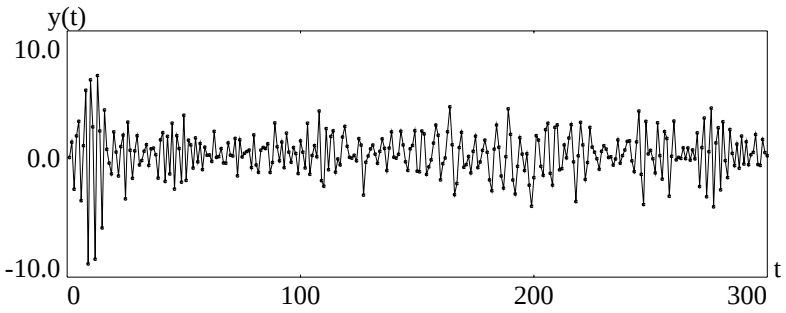


Figure 3: Simulation data

SIMULATION

A simple simulational experiment has been done. We firstly generate an artificial time series by simulation with time varying coefficient with three different order of autoregression. The length of data is 300 and they are divided into three part corresponding to the three different autoregressive order, the first part has order 2, the second order 4, and the last part has the order of 6. Thus the number of peak are 1,2, and 3 respectively. The data are shown in Figure 3. The time changes of the frequency of the peaks are plotted in Figure 5. We assume in this experiment that only the frequency changes, i.e., another part of state vector such that $\mathbf{r}_t$ and σ_t^2 are not changing with time. Thus, in the following experiment, we only estimate the time-varying frequency of spectral peak.

To this artificial data, we have applied our model with the following conditions. The number of particles is 1000, maximum number of peaks is 10, and initial value of peak frequency for each particle is taken uniformly random in range $[0, \pi]$. All another values that are constant in time is assumed to be known. With mutation rate 0.01 and crossover rate is 0, we estimate the state vector by Monte Carlo filter and genetic algorithm.

The estimation result of time-varying order of autoregression is shown in Figure 4. Since the result consists of distribution of particles in autoregressive order $0, 1, \cdots, 10$, we use contour map to figure the distribution on the paper. Estimated result of peak frequencies are shown in Figure 5 with true frequencies with dotted three lines as mentioned above. Estimated peaks are denoted by plots in the figure for each time.

By looking the result of estimated order, the true order can be estimated in most of the series. Also looking the result of peak estimation, estimated plots follow the true peak and new peak appears when the order of autoregression is changed.

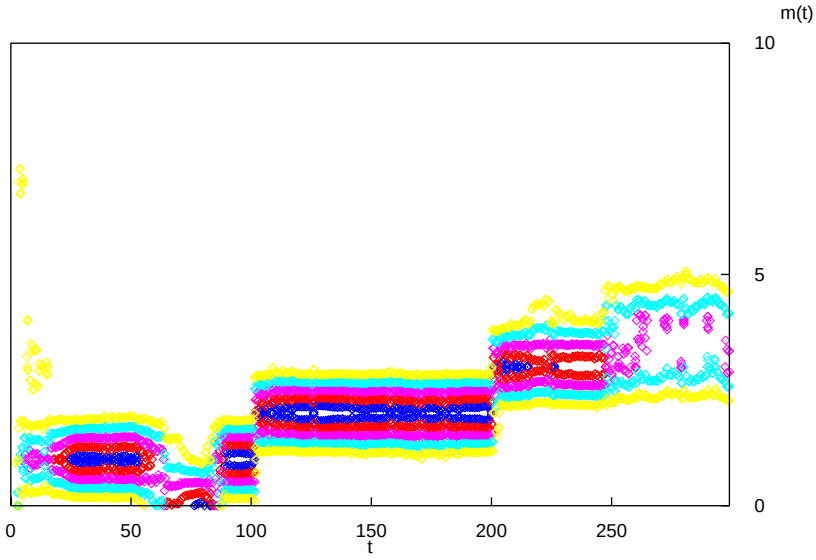


Figure 4: Estimated order of autoregressive

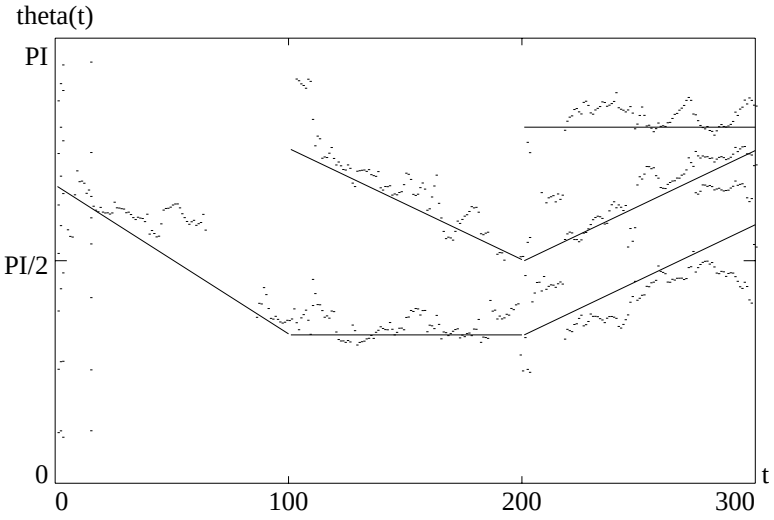


Figure 5: Estimated peaks

CONCLUSION

A new model for nonstationary spectral analysis with time-varying order of autoregression is proposed. The model is an extension of time-varying coefficient autoregressive model to have time-varying order of autoregression. For the state estimation of the mode is done by Monte Carlo filter and genetic operation. For continuous parameters in state, such as spectral peak parameters, can be estimated by Monte Carlo filter, and combination of peaks among state vector can be estimated by genetic operations. Through the genetic operation, the optimal order of autoregression can be obtained in the same time. By a simple simulational experiment, the esimation result of spectral peaks and autoregressive order for artificially generated data has been demonstraited.

ACKNOWLEDGEMENT

This research was supported by the Grant-in-Aid for Encouragement of Young Scientists by the Japanese Ministry of Education, Science, Sports and Culture.

REFERENCES

Akaike, Hirotugu, 1980, "Likelihood and Bayes procedure", in Bayesian Statistics, University Press, Valencia, Spain , pp. 143 - 166.

Goldberg, David Edward, 1989, "Genetic algorithms in search, optimization, and machine learning", MA/USA.

Higuchi, Tomoyuki, 1997, "Monte Carlo filter using the Genetic algorithm operators", Journal of Statistical Computation and Simulation, Vol.59, No.1, pp. 1 - 23.

Ikoma, Norikazu, 1996, "Estimation of time varying peak of power spectrum based on non-Gaussian nonlinear state space modeling", Journal of Signal Processing, Vol.49, No.2, pp. 85 - 95.

Kitagawa, Genshiro, 1996 "Monte Carlo Filter and Smoother for Non-Gaussian Nonlinear State Space Model", Journal of Computational and Graphical Statistics, Vol.5, pp.1-25.

Kitagawa, Genshiro, 1998, "A Self-Organizing State-Space Model", Journal of the American Statistical Association, Vol.93, No.443, pp. 1203 - 1215.

Kitagawa,Genshiro; Gersch, Will, 1985, "A smoothness Priors Time-Varying AR Coefficient Modeling of Nonstationary Covariance Time Series", IEEE Transaction on Automatic Control, Vol.AC-30,No.1, pp.48-56.