NEUVIEME COLLOQUE SUR LE TRAITEMENT DU
SIGNAL ET SES APPLICATIONS

NICE du 16 au 20 MAI 1983

UNE NOUVELLE TECHNIQUE POUR DETERMINER L'ORDRE D'UN PROCESSUS ARMA

A NEW ORDER DETERMINATION TECHNIQUE FOR ARMA PROCESSES

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RESUME

Lors d'une estimation spectrale à l'aide d'un modèle, il est généralement reconnu que les modèles de type ARMA (autoregressive-moving average) donnent des estimations ayant une plus grande résolution que les modèles autoregressifs seuls [1,2]. Cependant, il manque pour l'instant une méthode acceptable pour déterminer l'ordre d'un processus de type ARMA à partir de sa sortie.

Le critère d'information de Akaike [1] peut être utilisé pour déterminer l'ordre de la partie AR du processus , cependant le problème demeure pour trouver l'ordre de la partie MA. Les quelques rares techniques qui existent pour évaluer cet ordre sont basées sur des méthodes empiriques d'essais et corrections.

Ce paper présente une nouvelle méthode qui détermine l'ordre d'un processus ARMA en une seule opération. Il s'agit d'une modification de la méthode de Chow [6] qui fait usage de la procedure d'orthonormalisation de Gram-Schmidt pour déterminer la dépendance linéaire des colonnes dans une matrice d'autocorrélation. Le développement théorique est vérifié par des simulations qui donnent également des résultats sur la détermination d'ordres de processus seulement à partir de séquences de sortie.

SUMMARY

It is generally recognized that when performing spectral estimation via the modelling approach, autoregressive-moving average (ARMA) models can provide estimates of higher resolution than autogressive models alone [1,2]. However, there is lacking an acceptable method for determining the orders of an ARMA process from its output.

The Akaike information criterion [1] can be used to find the order for the AR part, but the problem of determining the MA order remains. Of the very few order determination techniques in existence, most are trial and error based.

This paper presents a new method that determines the ARMA orders in one pass. It is a modification of the method of Chow [6] and uses the Gram-Schmidt orthonormalization procedure to determine linear dependency of the columns in an autocorrelation array. The theoretical development is verified by simulation, which also includes results on order determination from output sequences alone.

I. INTRODUCTION

In applying the modelling approach to spectral estimation and in system identification, where a sequence is to be represented as the output of an autoregressive-moving average (ARMA) process, the determination of the proper ARMA orders and the estimation of the ARMA coefficients are presently two important research areas. Very little results are available on the determination of the orders of an ARMA process [1,2]. The Akaike information criterion [1] can be used to find the AR order, but the problem of determining the MA orders remains. Some ARMA spectral estimation techniques avoid the MA part of the modelling approach completely by taking the Fourier transform of the residuals [3], the result of which is the MA spectrum. Nevertheless, information on the complete model is needed in other ARMA spectral estimators [1,2], as well as in system identification.

Two methods in the literature on order determination are trial and error based [4,5], but neither of them provides a constructive algorithm. Chow in [6,7] did give procedures to establish the ARMA orders. The AR order is first determined by testing for singularity of a correlation matrix, then the AR coefficients are estimated, and finally the MA order is obtained from the relationship expected of the correlation of an ARMA process.

This paper presents a new ARMA order determination method that is non-iterative, giving the answer in one pass without having to calculate the AR coefficients. The principle used in finding the AR order is similar to Chow's [7], but the implementation is different and simpler. Instead of calculating the determinant of a correlation matrix to test for singularity, the linear dependency of an array of correlation functions are checked via the Gram-Schmidt ortho-normalization procedure. The position at which the first linear dependency occurs gives the AR order. Then the check continues until an independent column appears and the MA order is computed from a simple equation. The whole process is systematic and eliminates the estimation of the AR coefficients (required in Chow [7]), which adds uncertainties to the determination of the MA order. The procedures are developed in Section II, followed by the simulation results in Section III. Using the whiteness of the residuals and the mean squared errors as the performance criteria, comparisons are made of the estimation results obtained from models with estimated and actual ARMA orders. In many instances, especially when the number of samples is small (say 100), the estimated ARMA orders are superior. The conclusions are in Section IV.

II. ARMA ORDER DETERMINATION

Given a finite sequence $\{x_n\}$, n=0,1,...,N-1, as the output of an ARMA process

$$x_n = \sum_{k=1}^{p} a_k x_{n-k} + \sum_{i=0}^{q} b_i w_{n-i} \qquad (1)$$

where $\{w_n\}$ is a band-limited white noise (BLWN) sequence [5]. The problem is to determine, from the sequence $\{x_n\}$ only, the orders (p,q) of the ARMA process.

Let

$$R_{wx}(\ell) \triangleq E\{w_{n+\ell} x_n\} \qquad (2)$$

$$R_{xx}(\ell) \triangleq E\{x_{n+\ell} x_n\} = E\{x_n x_{n-\ell}\} \qquad (3)$$

be the cross and auto-correlations of $\{w_n\}$ and $\{x_n\}$ and $\{x_n\}$, respectively. Then it follows immediately from (1) that

$$R_{xx}(\ell) = \sum_{k=1}^{p} a_k R_{xx}(\ell-k) + \sum_{i=0}^{q} b_i R_{wx}(\ell-i) \qquad (4)$$

Further, since

$$R_{wx}(j) = 0 \quad \text{for} \quad j > 0 \qquad (5)$$

which is a consequence of $\{w_n\}$ being BLWN and x_n is a function only of w_n and the past values $w_{n-1}, w_{n-2}, \ldots$, etc., (4) reduces to, for $\ell > q$,

$$R_{xx}(\ell) = \sum_{k=1}^{p} a_k R_{xx}(\ell-k) \qquad (\ell > q) \qquad (6)$$

In addition, for $\ell \le q$

$$R_{xx}(\ell) \neq \sum_{k=1}^{p} a_k R_{xx}(\ell-k) \qquad (\ell \le q) \qquad (7)$$

A set of procedures to determine p and q can now be constructed based on (6) and (7) as follows.

(i) Form, assuming the **true** $R_{xx}(\cdot)$ are available at the moment, the (a+1+b)×(a+1+b) array

$$\begin{array}{ccccccccc} R_{xx}(a) & R_{xx}(a-1) & \cdots & R_{xx}(0) & R_{xx}(1) & R_{xx}(2) & \cdots & R_{xx}(b) \\ R_{xx}(a+1) & & & R_{xx}(1) & R_{xx}(0) & R_{xx}(1) & & \vdots \\ \vdots & & & & R_{xx}(1) & R_{xx}(0) & & \vdots \\ \vdots & & & & & \vdots & & \vdots \\ R_{xx}(2a+b) & & \cdots & & & & & R_{xx}(a) \end{array} \qquad (8)$$

where a is larger than the maximum possible MA order and b is larger than the maximum AR order. These maxima can always be roughly deduced from a priori knowledge.

(ii) Label the columns in the array as $\bar{c}_i$, i=0,1,..., a+b, and normalize each column by their norm to give $c_i = \frac{\bar{c}_i}{\|\bar{c}_i\|}$. Apply the Gram-Schmidt ortho-normalization procedure [8] to the columns, giving

$$u_1 = c_1, \quad v_1 = \frac{u_1}{\|u_1\|}$$

$$u_i = c_i - \sum_{k=1}^{i-1} \langle v_k, c_i \rangle, \quad v_i = \frac{u_i}{\|u_i\|}$$

(iii) Check the remaining norms $\|u_i\|$ against a threshold TH (=0.1 for example) and let u_k be the first vector such that $\|u_k\| \le TH_1$. Then from (6), p=k.

(iv) Check the remaining norms $\|u_i\|$, i=l+1,...,a+b, against another threshold TH_2 (=0.1 for example). Let u_m be the first vector such that $\|u_m\| \ge TH_2$. Then from (7), q=p-(m-a). This simple relation comes from the observation from (8) that $R_{xx}(q)$ is the first element of the column which lies p columns to the left of the vector u_m, and m-a is the number of columns between the vector u_m and the column whose first element is $R_{xx}(0)$.

Several remarks are in order concerning the implementation of the method. In practice, the $R_{xx}(\cdot)$ are not known and must be replaced by the estimate.

$$\hat{R}_{xx}(\ell) = \frac{1}{N-\ell} \sum_{n=\ell}^{N-1} x_n x_{n-\ell} \qquad (9)$$

For a fixed number of samples N, the accuracy of (9) deteriorates with increasing ℓ, hence it is important that the values a and b in (i) not be unnecessarily high. With $\hat{R}_{xx}(\ell)$ replacing the true autocorrelations in (8), it is possible that there is no $\|u_k\|$ that is smaller than TH_1. In that case, TH_1 can be increased. Or, the value of 'a' should first be decreased (this will eliminate some of the less accurate $\hat{R}_{xx}(\ell)$ at large lags that cause linear independence), then increased (to see if p is larger than expected), repeating step (iii) each time. If linear independency persists, (p,q) are simply set to their expected maxima. This condition appeared infrequently in the simulation and essentially means that some of the $\hat{R}_{xx}(\ell)$ are inaccurate to the extent that they creat linear independence in (8), even if a is larger than q. Also, since q=p-(m-a) and q≥0, the check on $\|u_m\|$ should stop at m=a+p. If no $\|u_m\| \ge TH_2$, q is set to zero.

Thus far, the choosing of TH_1 and TH_2 nas not been addressed. Clearly, they play a critical role in determining (p,q). Raising TH_1 will probably give a smaller p while lowering TH_2 will probably result in a smaller q (assuming p>q). It turns out that TH_1, which really decides how small the norm of an orthonormalized vector is before the vector is considered linearly dependent on the other columns, can be chosen according to the degree of spectral resolution required. The relationship between TH_1 and spectral resolution, defined as the ability to distinguish two closely spaced sinusoids, is developed next.

It is shown in [9] that for a sequence $\{s_n\}$ containing M pure sinusoids of amplitudes A_i and frequencies ω_i, the sample s_n is exactly a linear combination of its past 2M samples. Thus the autocorrelations of s_n satisfy, for M=2

$$R_{ss}(m) = \sum_{k=1}^{4} d_k R_{ss}(m-k) \qquad (10)$$

where the coefficients d_k are functions of ω_1 and ω_2 and

$$R_{ss}(m) = \sum_{i=1}^{2} \frac{A_i^2}{2} \cos\omega_i m \qquad (11)$$

In [10], the correlations are expressed as, for $A_i = 1$,

$$R_{ss}(m) = \cos\bar{\omega}m \cos\Delta m \qquad (12)$$

where

$$\Delta = \frac{\omega_2-\omega_1}{2} \qquad \bar{\omega} = \frac{\omega_1+\omega_2}{2} \qquad (13)$$

Substituting (12) into (10) gives

$$\cos\bar{\omega}m \cos\Delta m = \sum_{k=1}^{4} d_k \cos\bar{\omega}(m-k)\cos\Delta(m-k) \qquad (14)$$

If Δ and m are sufficiently small so that $\cos\Delta(m-k)\approx 1$ for k=1,...,4, then (14) becomes

$$\cos\bar{\omega}m \approx \sum_{k=1}^{4} d_k \cos\bar{\omega}(m-k) \qquad (15)$$

With this approximation, only a single frequency $\bar{\omega}$ appears in (15). Hence following the same argument that leads to (10), (15) can also be expressed as

$$\cos\bar{\omega}m \approx \sum_{k=1}^{4} \bar{d}_k \cos\bar{\omega}(m-k) \qquad (16)$$

where it is shown in [9] that $\bar{d}_1 = 2\cos\bar{\omega}$ and $\bar{d}_2 = -1$.

Returning to (8), if $\{x_n\}$ is a sequence containing two closely spaced sinusoids ω_1 and ω_2, it can be seen from the preceding (equations (12) to (16)) that depending on 'a', the starting value and ω_1 ω_2, the third column u_2 may take on a very small norm $\|u_2\|$. If indeed $\|u_2\| \le TH_1$, then choose p=2 and the spectrum obtained from the ARMA model will only indicate a sinusoid at $\bar{\omega}$. Thus it is important that TH_1 be sufficiently small whenever very fine spectral resolution is required. As a guide to choosing TH_1, Figure 1 gives a plot of $\|u_2\|$ versus 'a', with $\omega_1=\frac{0.2204}{\pi}$ and $\omega_2 = \frac{0.2794}{\pi}$ and an array size of 15. This plot is constructed from setting up (8) with the correlations calculated from (11) for the given ω_1 and ω_2 and then applying the Gram-Schmidt orthonormalization to obtain $\|u_2\|$. From the figure, it is seen that if the estimated spectrum must contain distinct ω_1 and ω_2, then TH_1 must be smaller than 0.1 if the starting value a in (8) is 4.

III. SIMULATION RESULTS

Several experiments were conducted to confirm the theoretical developments and to evaluate the practicality of the method. The computations were performed on a PDP 11/34 computer with an attached AP120B array processor.

First the processes (see (1) for definition).

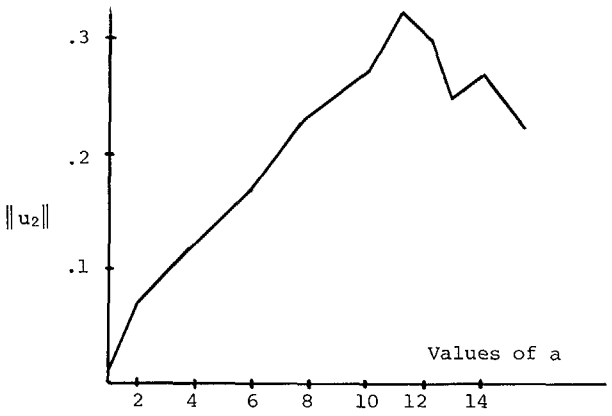

Figure 1. $\|u_2\|$ for two sinusoids.

(a) $\begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \end{bmatrix} = \begin{bmatrix} 2.7607 \\ -3.8106 \\ 2.6535 \\ -0.9238 \end{bmatrix} \qquad \begin{bmatrix} b_0 \\ b_1 \end{bmatrix} = \begin{bmatrix} 1 \\ 1\times 10^{-3} \end{bmatrix}$

whose a_k are identical to those in an example in [10], and

(b) $\begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix} = \begin{bmatrix} 0.1 \\ -0.3 \\ 0.3 \end{bmatrix} \qquad \begin{bmatrix} b_0 \\ b_1 \\ b_2 \\ b_3 \end{bmatrix} = \begin{bmatrix} 1 \\ 0.15 \\ -0.35 \\ 0.42 \end{bmatrix}$

were used to verify the algorithm as outlined in Section II. The true autocorrelations were used. They are computed from the difference equation (1) and knowledge of the a_k, b_i coefficients and an input noise variance $\sigma_w^2 = 1$. The array (8) was set up and indeed the true orders were detected for both processes. However, it should be noted that for process (a), whose spectrum contains two peaks at the two frequencies of 0.2204 and 0.2794 [10], if the start value is at a=4 and b=10 (hence 15 columns), $\|u_2\| = 0.0736$ so that a $TH_1 = 0.1$ will erroneously give p=2. On the other hand, if a=10 and b=4 (still 15 columns), $\|u_2\| = 0.17$, $\|u_3\| = 0.106$ and $\|u_4\| = 7.7\times 10^{7}$ so that $TH_1 = 0.1$ will give the correct result of p=4. The $\|u_2\|$ values are close to those predicted in Figure 1, which of course is for the special case of two pure sinusoids. The purpose of studying process (a) is to stress the fact that TH_1 should be selected for each application, in particular with reference to the degree of spectral resolution required.

Next, only estimates (see (9)) of the autocorrelations were used in (8). Since only a finite sequence length is available for estimating the ARMA orders, there is no reason to believe that the estimated orders should equal the true orders. Indeed, they were not in many instances. As an evaluation of the fitting properties of the ARMA models with estimated orders, comparisons were made between the models with estimated orders and true orders.

Consider again the ARMA process

$$x_n = \sum_{k=0}^{p} a_k x_{n-k} + \sum_{i=0}^{q} b_i w_{n-i} .$$

Let (p,q) and $(\hat{p},\hat{q})$ be the true and estimated orders, respectively and (a_k,b_i), k=1,...,p; i=1,...,q and $(\hat{a}_k,\hat{b}_i)$ k=1,...,$\hat{p}$; i=1,...,$\hat{q}$ be the coefficients estimated, by least squares, from the sequences $\{x_n\}$ and $\{w_n\}$, n=0,...,N-1. The least squares solution for $(\bar{a}_k,\bar{b}_i)$ are

$$\begin{bmatrix} \bar{a}_1 \\ \bar{a}_2 \\ \vdots \\ \bar{a}_p \\ \hline \bar{b}_0 \\ \bar{b}_1 \\ \vdots \\ \bar{b}_q \end{bmatrix} = \begin{bmatrix} \hat{R}_{xx}(0) & \cdots & \hat{R}_{xx}(p-1) & \hat{R}_{xw}(-1) & \cdots & \hat{R}_{xw}(q-1) \\ \hat{R}_{xx}(1) & & & & & \\ \vdots & & & & & \\ \hat{R}_{xx}(p-1) & & \hat{R}_{xx}(0) & \hat{R}_{xw}(-p) & & \hat{R}_{xw}(q-p) \\ \hline \hat{R}_{xw}(-1) & & \hat{R}_{xw}(-p) & \hat{R}_{ww}(0) & & \hat{R}_{ww}(0) \\ \vdots & & & & & \\ \hat{R}_{xw}(q-1) & \cdots & \hat{R}_{xw}(q-p) & \hat{R}_{ww}(q) & \cdots & \hat{R}_{ww}(0) \end{bmatrix}^{-1} \begin{bmatrix} \hat{R}_{xx}(1) \\ \vdots \\ \hat{R}_{xx}(p) \\ \hline \hat{R}_{xw}(0) \\ \vdots \\ \hat{R}_{xw}(q) \end{bmatrix} \tag{17}$$

The solution for $(\hat{a}_k, \hat{b}_i)$ are similar, except with $(\hat{p},\hat{q})$ instead of (p,q). The $\hat{R}_{xx}(\cdot)$ and $\hat{R}_{xw}(\cdot)$ are computed from $\{x_n\}$ and $\{w_n\}$ according to (9). If $\{w_n\}$ is not available, techniques other than (17) are required to compute the coefficients but this is of no concern here.

Two criteria for comparisons were considered. The mean squared error (MSE), given by

$$\sum_{n=0}^{N-1} \bar{\epsilon}_n^2 = \left(x_n - \sum_{k=1}^{p} \bar{a}_k x_{n-k} - \sum_{i=0}^{q} \bar{b}_i w_{n-i}\right)^2 \tag{18}$$

and

$$\sum_{n=0}^{N-1} \hat{\epsilon}_n^2 = \left(x_n - \sum_{k=1}^{\hat{p}} \hat{a}_k x_{n-k} - \sum_{i=0}^{\hat{q}} \hat{b}_i w_{n-i}\right)^2 \tag{19}$$

is one, the other is the residual whiteness test [5] which computes the residuals

$$\bar{r}_n = x_n - \sum_{k=1}^{p} \bar{a}_k x_{n-k} - \sum_{i=1}^{q} \bar{b}_i w_{n-i} \tag{20}$$

TABLE 1

Process (a) Comparison of MSE, N=100

p=4 , q=1 MSE	$\hat{p}$	$\hat{q}$	MSE
48	3	0	27
27	4	0	27
38	4	0	38
50	4	0	50
18	3	0	9
55	4	0	55
107	4	0	107
53	4	0	53
49	4	0	49
27	4	0	27
31	2	0	9
19	4	0	19
52	4	0	52
47	4	0	47
68	4	0	68
32	4	0	32
97	4	0	97
53	4	0	53
48	4	0	48
28	4	0	28
30	4	0	30
24	4	0	24
39	4	0	39
46	4	0	46
32	4	0	32
60	4	0	60
18	4	2	19
65	4	0	65
15	4	0	15
26	4	0	26
48	4	0	48
22	4	0	22
60	4	0	60
32	4	0	32
57	4	0	57
13	3	1	7
39	4	0	39
29	4	0	29
66	4	0	66
34	4	0	34

and

$$\hat{r}_n = x_n - \sum_{k=1}^{p} \hat{a}_k x_{n-k} - \sum_{i=1}^{q} \hat{b}_i w_{n-i} \tag{21}$$

and tests the whiteness of $\bar{r}_n$ and $\hat{r}_n$. The idea behind (18) to (21) is that if the fitting is proper, the MSE should be small and $\bar{r}_n$ and $\hat{r}_n$ should be very close to $b_0 w_n$, which is a BLWN sequence. Let

$$R_{\bar{r}\bar{r}}(\ell) = \frac{1}{N-\ell} \sum_{n=\ell}^{N-1} \bar{r}_n \bar{r}_{n-\ell} \tag{22}$$

be the sample correlations of $\bar{r}_n$. The whiteness test [5] states that $\bar{r}_n$ is a white noise sequence if for $\ell=0,\ldots,L$, less than 5% of the $c_\ell = \left|\frac{R_{\bar{r}\bar{r}}(\ell)}{R_{\bar{r}\bar{r}}(\ell)}\right|$ exceeds $\frac{1.96}{\sqrt{N}}$. The same applies to $\{\hat{r}_n\}$.

The processes (a) and (b) were tested and 40 independent runs were performed to give the statistical results in Tables 1 to 3. In each table, the heading COW stands for coefficient of whiteness, and is the percentage of the number of times, out of a total of L=40, that c_ℓ exceeds $1.96/\sqrt{N}$. Due to the large variances associated with estimating correlations with small samples, the COW is not given for the N=100 runs.

For process (a), where $b_1 = 1\times10^{-3}$, it is essentially an AR process and is so estimated in the majority of cases in Table 1. For the few runs where $(\hat{p},\hat{q})$ are smaller than (4,1), the MSE are also smaller, indicating that for those particular sequences, a smaller order fit is better. For N=4000, all $(\hat{p},\hat{q})=(4,0)$ and the MSE are equal (to within third decimal place) to the MSE

TABLE 2

Process (b) Comparison of MSE, N=100

p=3 q=3 MSE×10^{-4}	$\hat{p}$	$\hat{q}$	MSE×10^{-4}
70	13	13	86
78	12	9	12
300	10	9	4
192	11	9	35
67	11	8	63
137	11	8	4
727	10	7	21
14	12	9	4
132	11	9	18
181	13	13	5
422	12	9	13
213	13	13	25
7	13	13	4
57	11	9	5
111	13	13	43
3	13	13	42
159	12	9	103
40	12	9	18
92	13	13	36
266	9	9	153
195	13	13	36
194	13	13	18
287	13	13	132
7	13	13	30
4	13	13	7
275	12	9	9
182	11	8	19
5	12	9	10
35	12	9	6
15	13	13	23
213	12	9	9
9	12	9	12
426	10	7	13
574	11	8	142
4	11	8	6
35	11	8	15
115	12	9	13
122	12	9	22
285	13	13	12
62	12	9	11

TABLE 3
Process (b) Comparison of MSE and COW, N=4000

p=3 MSE×10^{-4}	q=3 COW	$\hat{p}$	$\hat{q}$	MSE×10^{-4}	COW
3	5	12	9	3	6
3	1	12	9	3	1
3	2	13	13	.05	2
3	6	12	9	2	6
3	2	8	8	5	3
3	5	10	9	0.2	4
3	6	12	9	3	6
3	8	10	8	6	10
3	1	8	8	5	1
3	13	10	7	10	14
3	5	9	9	0.2	5
3	7	10	9	0.4	8
3	6	13	13	.05	6
3	4	12	9	2	4
3	6	11	9	2	6
3	5	13	13	.004	5
3	7	8	9	5	8
3	2	12	9	2	3
3	4	12	9	5	4
3	6	10	7	9	8
3	3	8	8	6	4
3	8	9	9	0.3	7
3	3	9	9	0.08	4
3	2	8	8	5	4
3	4	11	8	3	3
3	7	13	13	.05	7
3	7	10	9	0.2	6
3	4	11	9	3	3
3	4	8	8	5	4
3	6	13	13	0.2	5
3	4	13	13	0.02	4
3	6	11	8	3	5
3	8	12	9	2	10
3	2	12	9	2	5
3	6	10	7	10	9
3	3	11	9	3	3
3	5	10	8	8	4
3	3	13	13	.003	3
3	3	11	8	3	3
3	5	12	9	2	6

from (4,1). Hence the results are not shown. The TH_1 used was 0.01 and TH_2 = 0.1. Such a small TH_1 was necessary to ensure that the frequency components 0.2204 and 0.2794 are resolvable.

Table 2 gives the process (b) results for N=100. In 31 out of 40 runs, the MSE from $(\hat{p},\hat{q})$ are smaller. At N=4000 in Table 3, the MSE from $(\hat{p},\hat{q})$ are smaller in 29 runs. For whiteness test, $(\hat{p},\hat{q})$ and (p,q) have equal COW in 17 runs and for 6 runs, $(\hat{p},\hat{q})$ has smaller COW.

Finally, it is noted that for process (a), the $(\hat{p},\hat{q})$ are consistently very close to (p,q) while for process (b) they are much higher than the true orders (3,3). This can be explained by the fact that process (a) essentially contains two periodic components so that the correlation estimates, even at large lags, still have comparable magnitudes with respect to those at small lags. For a fixed variance, the reliability of the correlation estimates do not decrease with large lags. Process (b) is just the opposite. Its correlation values drop off in magnitude rapidly after 4 lags and it is much more difficult to obtain (percentage wise) correlation estimates that are small (compared with the magnitude at zero shift). These inaccuracies manifest themselves in (8) by giving linear independency to the columns when theoretically they should not be. The result is that high $(\hat{p},\hat{q})$ orders are estimated.

IV. CONCLUSIONS

Determination of the orders of an ARMA process from its output sequence is a necessary step in some spectral estimation and system identification techniques. A one pass method is proposed to estimate the ARMA orders without the need for trials nor the intermediate steps of calculating the AR coefficients. Simulation results have demonstrated the effectiveness of the new method. Using MSE and COW as performance criteria, models with $(\hat{p},\hat{q})$ orders in general give better results than models with (p,q) orders. This is particularly evident at low sample points, when the correlation estimates are less reliable.

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