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# TUTORIAL ON UNIVARIATE AUTOREGRESSIVE SPECTRAL ANALYSIS

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**ABSTRACT.** In the present paper, the theoretical basis of autoregressive (AR) modelling in spectral analysis is explained in simple terms. Spectral analysis gives information about the frequency content and sources of variation in a time series. The AR method is an alternative to discrete Fourier transform, and the method of choice for high-resolution spectral estimation of a short time series. In biomedical engineering, AR modelling is used especially in the spectral analysis of heart rate variability and electroencephalogram tracings. In AR modelling, each value of a time series is regressed on its past values. The number of past values used is called the model order. An AR model or process may be used in either process synthesis or process analysis, each of which can be regarded as a filter. The AR analysis filter divides the time series into two additive components, the predictable time series and the prediction error sequence. When the prediction error sequence has been separated from the modelled time series, the AR model can be inverted, and the prediction error sequence can be regarded as an input and the measured time series as an output to the AR synthesis filter. When a time series passes through a filter, its amplitudes of frequencies are rescaled. The properties of the AR synthesis filter are used to determine the amplitude and frequency of the different components of a time series. Heart rate variability data are here used to illustrate the method of AR spectral analysis. Some basic definitions of discrete-time signals, necessary for understanding of the content of the paper, are also presented.

**KEY WORDS.** autoregressive modelling, spectral analysis, heart rate variability.

## INTRODUCTION

Autoregressive (AR) modelling utilizes the time history of a signal to extract important information hidden in the signal. It is superior to many other methods in biomedical signal processing because it can take advantage of the noise inherent in a biological system and extract information from propagation of that noise in a signal.

AR modelling is an alternative to the discrete Fourier transform (DFT) in the calculation of a power spectrum density function of a time series. The power spectrum gives information about the frequency content of a time series. In biomedical applications, AR modelling is used notably in the spectral analysis of heart rate variability and electroencephalogram recordings. It provides a smoother and more easily interpretable power spectrum than DFT, but involves the disadvantage of complex model identification. Although there are excellent publications covering the principles of DFT at an elementary level [1, 2], there are no such publications on AR modelling and

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spectral analysis. The aim of the present paper is to explain the theoretical background of the AR methods in simple terms. Some basic concepts of digital signal processing, necessary for understanding of the subject matter, are also presented. The methods are illustrated with a beat-to-beat RR-interval variability signal exhibiting physiological rhythms [3].

## AR MODEL IDENTIFICATION

The basic assumption is that the process to be studied is stationary and stochastic. The AR model predicts the current values of a time series from the past values of the same series. The future dependency on past values can be demonstrated by a function called the autocorrelation function [4]. Autocorrelation is the average of the product of a data sample $x[n]$ with a version of itself advanced by a lag. The autocorrelation function is described by the equation

$$r_{xx}[k] = \frac{1}{N}\sum_{n=1}^{N-k} x[n]x[n+k] \tag{1}$$

where $r_{xx}[k]$ is the autocorrelation value of $\underline{x}$ at sample delay $k$, and $N$ is the number of data points.

For a very small advance, the values of the two signals at any given instant will be very similar. As the lag increases, the difference between the two values becomes larger. If a signal has both a periodic and a random component, the latter gradually disappears as the lag increases (Figure 1). The property is useful for extracting periodic signals from random noise.

Basically, the AR model may be regarded as a set of autocorrelation functions. AR modelling of a time series is based on an assumption that the most recent data points contain more information than the other data points, and that each value of the series can be predicted as a weighted sum of the previous values of the same series plus an error term. The AR model is defined by:

$$x[n] = \sum_{i=1}^{M} a_i x[n-i] + \varepsilon[n] \tag{2}$$

where $x[n]$ is the current value of the time series, $a_1, \ldots, a_M$ are predictor (weighting) coefficients, $M$ is the model order, indicating the number of the past values used to predict the current value, and $\varepsilon[n]$ represents a one-step prediction error, i.e. the difference between the predicted value and the current value at this point.

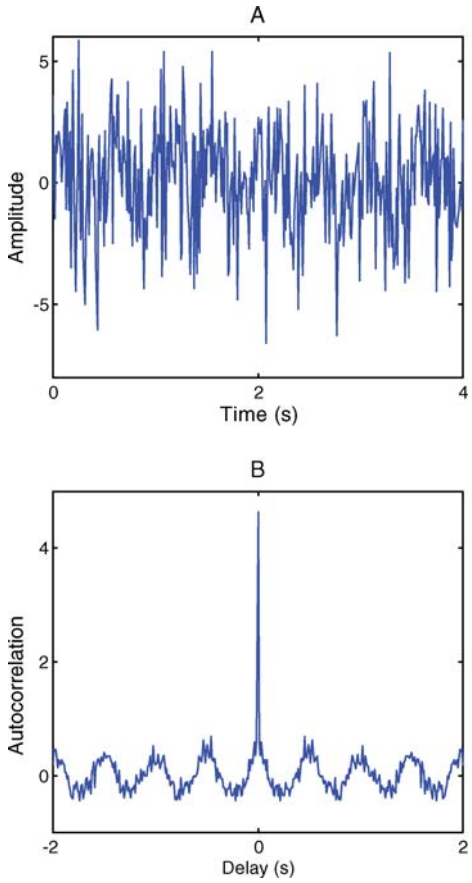


*Fig. 1. A periodic signal plus noise (A) and autocorrelation of the same signal (B). Autocorrelation function can reveal oscillations hidden in the signal, which are not visible to the naked eye.*

The AR model determines an analysis filter, through which the time series is filtered. This produces the prediction error sequence. In the model identification, the AR analysis filter uses the current and past input values to obtain the current output value (Figure 2). By writing (2)

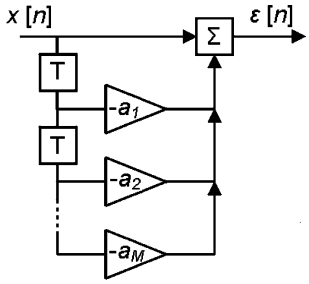


*Fig. 2. AR analysis filter. $x[n]$ and $\varepsilon[n]$ represent input and output sequences, respectively. $T$ is a time delay of one sample period, $a_1, \ldots, a_M$ are predictor coefficients, and the "$\sum$" box represents summation of $a_i x[n-i\,T]$, $i = 1, \ldots, M$ values.*

in a form

$$\varepsilon[n] = x[n] - \sum_{i=1}^{M} a_i x[n-i] \tag{3}$$

we get the filter with an impulse response $[1, -a_1, \ldots, -a_M]$, which produces the prediction error sequence $\varepsilon[n]$.

The predictor coefficients are usually estimated using the least-squares minimization technique so that they produce the minimum error $\varepsilon[n]$. From (2) we get

$$x[n] = a_1 x[n-1] + a_2 x[n-2] + \cdots + a_M x[n-M] + \varepsilon[n] \tag{4}$$

If we use Equation (4) to write the expressions for several estimates of $x[n]$, we get a set of linear equations:

$$\underline{x} = \begin{bmatrix} x[M] & x[M-1] & \ldots & x[1] \\ x[M+1] & x[M] & \ldots & x[2] \\ \vdots & \vdots & \ldots & \vdots \\ x[N-1] & x[N-2] & \ldots & x[N-M] \end{bmatrix} \underline{a} + \underline{\varepsilon} = \underline{X}\,\underline{a} + \underline{\varepsilon} \tag{5}$$

We need $M$ equations to solve the $M$ unknown coefficients $a_i, i = 1, \ldots, M$. The least squares solution is easiest to achieve by matrix calculation. The equations (5) may be rewritten in matrix form:

$$\underline{x} = \begin{bmatrix} x[M] & x[M-1] & \ldots & x[1] \\ x[M+1] & x[M] & \ldots & x[2] \\ \vdots & \vdots & \ldots & \vdots \\ x[N-1] & x[N-2] & \ldots & x[N-M] \end{bmatrix} \times \underline{a} + \underline{\varepsilon} = \underline{X}\,\underline{a} + \underline{\varepsilon} \tag{6}$$

where

$$\underline{a} = \begin{bmatrix} a_1 \\ \vdots \\ a_M \end{bmatrix} \quad \text{and} \quad \underline{\varepsilon} = \begin{bmatrix} \varepsilon[M+1] \\ \vdots \\ \varepsilon[N] \end{bmatrix} \tag{7}$$

In other words, $\underline{X}$ is a square matrix with M rows and M columns, and $\underline{a}$ and $\underline{\varepsilon}$ are column matrices consisting of M rows and 1 column.

When two vectors form a 90 degree angle, and one vector is projected onto the other, the result is a zero vector. The vectors are then said to be orthogonal, and their inner product equals 0. The inner product of any two column vectors $\underline{a}$ and $\underline{b}$ of the same length is defined as $\underline{a}^T\underline{b}$, where $\underline{a}^T$ is the transpose of $\underline{a}$. Transposal means that the rows and columns of a matrix or a vector are interchanged; hence a column vector becomes a row vector when transposed.

The optimum predictor coefficients ($\underline{a}_{\text{opt}}$) can be obtained by applying the orthogonality principle in the least-squares minimization technique. This means that the predictor coefficients are selected so that column vector $\underline{\varepsilon}$ is orthogonal to each explanatory vector $\underline{x}_i$, $i = 1, \ldots, M$, i.e. to each column vector in matrix $\underline{X}$. As in normal regression analysis, this minimizes the mean-square error. Then, $\underline{\varepsilon}$ vector is independent of the data $\underline{X}$, i.e. it contains the part of the time series that can not be explained by $M$ previous data points.

Instead of solving these $M$ equations $\underline{x}_i^T\underline{\varepsilon}$ separately, we can take advantage of the matrix calculation rules and solve them simultaneously. This is done by transposing the matrix $\underline{X}$ containing the explanatory vectors. The transpose is denoted by $\underline{X}^T$. Then

$$\underline{X}^T\underline{\varepsilon} = \underline{X}^T(\underline{x} - \underline{X}\underline{a}_{\text{opt}}) = \underline{0} \Leftrightarrow \underline{X}^T\underline{X}\underline{a}_{\text{opt}} = \underline{X}^T\underline{x} \tag{8}$$

We can solve $\underline{a}_{\text{opt}}$ by multiplying both sides of the matrix equation by the inverse of $\underline{X}^T\underline{X}$, denoted by $(\underline{X}^T\underline{X})^{-1}$, because the product of a matrix and its inverse is the identity matrix $I$. Thus,

$$(\underline{X}^T\underline{X})^{-1}(\underline{X}^T\underline{X})\underline{a}_{\text{opt}} = I\underline{a}_{\text{opt}} = \underline{a}_{\text{opt}} = (\underline{X}^T\underline{X})^{-1}\underline{X}^T\underline{x} \tag{9}$$

This direct least squares solution is called the covariance method [5].

When we study the new matrices $\underline{X}^T\underline{X}$ and $\underline{X}^T\underline{x}$ formed, we find that they consist of sums like in the autocorrelation function with different lags. $\underline{X}^T\underline{X}$ is in the matrix form

$$\frac{\underline{X}^T\underline{X}}{N} \approx \underline{R} = \begin{bmatrix} r(0) & r(-1) & \ldots & r(1-M) \\ r(1) & r(0) & \ldots & \vdots \\ \vdots & \ldots & \ldots & r(-1) \\ r(M-1) & \ldots & r(1) & r(0) \end{bmatrix} \tag{10}$$

That is, $\underline{X}^T\underline{X}$ is quite close to the autocorrelation matrix ($\underline{R}$) of $\underline{x}$. In the case of a univariate real signal, the values of the matrix are symmetrical about the leading diagonal. In practice, a sequence of length $N$ of measured data is available, and the ensemble autocorrelations are replaced by the corresponding sample autocorrelations computed from the given sequence of data.

The other new matrix $\underline{X}^T\underline{x}$ is quite close to the autocorrelation vector ($\underline{r}$) and may be calculated from the sequence of data as well

$$\frac{\underline{X}^T\underline{x}}{N} \approx \underline{r} = \begin{bmatrix} r(1) \\ r(2) \\ \vdots \\ r(M) \end{bmatrix} \tag{11}$$

By combining (10) and (11), we get from (9)

$$\underline{a}_{\text{opt}} = \underline{R}^{-1}\underline{r} \tag{12}$$

The solution is called Yule–Walker equation [6, 7], and it is also known as the autocorrelation method. The recursive method generally used to solve the Yule–Walker equation is called the Levinson–Durbin algorithm [8, 9]. The advantage of the recursive method is that it produces solutions for all model orders lower than the chosen $M$, thus making the selection of $M$ easier.

Either (9) or (12) may be used to estimate the model parameters. There are also other methods to extract reasonable estimates of the model parameters using a sequence of data, but all the other methods are derived from these two basic methods.

The AR model is identified by determining $M$, fitting the model to the data, and checking the prediction error variance. There are several methods for each of these steps. In practice, several models are fitted to the time series while varying the M and the best model is chosen. The most common criterion for the selection of $M$ is Akaike's Information Criterion (AIC) [10], which can be presented as

$$AIC(M) = N\ln\left(\sigma_p^2\right) + 2M \tag{13}$$

where $\sigma_p^2$ is the prediction error variance associated with $M$. The selected $M$ minimizes the value of the criterion. There are also other well-known criteria for this selection, such as Final Prediction Error [11], Criterion Autoregressive Transfer Function [12], and Rissanen Minimum Description Length [13].

After the model has been identified, its validity must be checked. The tests are usually based on the statistical properties of the prediction errors. The most commonly tested properties are whiteness and normality. If $M$ is correct, the error terms should be white (Gaussian) noise with a zero mean.

## AR SPECTRAL ANALYSIS

A signal spectrum shows how the power (variance) is distributed as a function of frequency. Theoretically speaking, total power, which is a frequency domain measure, is mathematically identical to variance, which is a time domain measure. AR spectral analysis can provide the number, centre frequency, and associated power of oscillatory components in a time series. When the AR model is fitted into the time series, the model is inverted, and the prediction error sequence is regarded as an input and the measured time series as an output, to an AR synthesis filter. Properties of the AR synthesis filter are then used to determine the power spectrum of the time series.

When a signal passes through a filter, amplitudes of certain frequencies are rescaled. Different frequencies making up the signal are also delayed by different times, i.e. signals of different frequencies are unravelled and then put back together in a different way [14]. The output sequence of any filter can be found by a technique called convolution, defined mathematically as [15]:

$$y[n] = \sum_{k=-\infty}^{k=\infty} h[k]x[n-k] = h[n] * x[n] \tag{14}$$

where $x[n]$ is the input sequence, $h[n]$ is the impulse response of the filter, $y[n]$ is the resulting output sequence, and * denotes convolution. In other words, the output sequence is found by time-reversing $x[n]$ and multiplying each term in the sequence by each term in $h[n]$ (or vice versa) and adding up the result. With $h[k]$ of length $P$ and $x[k]$ of length $Q$ the equation is:

$$y[n] = \sum_{k=0}^{P+Q-2} h[k]x[n-k] \tag{15}$$

with $P = 3$ and $Q = 3$ we can write the terms for $y[n]$ as:

$$\begin{aligned} y[0] &= h[0]x[0] + h[1]x[-1] + h[2]x[-2] \\ y[1] &= h[0]x[1] + h[1]x[0] + h[2]x[-1] \\ y[2] &= h[0]x[2] + h[1]x[1] + h[2]x[0] \\ y[3] &= h[0]x[3] + h[1]x[2] + h[2]x[1] \\ y[4] &= h[0]x[4] + h[1]x[3] + h[2]x[2] \end{aligned} \tag{16}$$

It is of note that the time reversal is the only difference between autocorrelation and convolution if $h[k]$ is equal to $x[k]$.

Because convolution takes place in the time domain, and calculations are simpler to perform in the frequency domain, the time domain presentation is usually transformed

into the frequency domain presentation, by using DFT. Multiplication in the frequency domain is equivalent to convolution in the time domain. Hence,

$$y[n] = h[k] * x[n] \overset{\text{DFT}}{\underset{\text{IDFT}}{\longleftrightarrow}} H(\omega)\,X(\omega) \tag{17}$$

where $H(\omega)$ and $X(\omega)$ are the DFTs of the impulse response and input sequences, respectively, and IDFT denotes inverse DFT.

In the frequency domain, a transform known as the z-transform is used to facilitate the analysis of the sequences [16]. The $z$-transform can be thought as a time-shift operator, where the $z^{-n}$ term indicates the position of the sample value in the sequence:

| | | | | | |
|---|---|---|---|---|---|
| Sampling period, $T$: | 0 | 1 | 2 | 3 | ... |
| Time series, $x$[time]: | 4[0] | 3[1] | 0[2] | 1[3] | ... |
| z-transform, $X(z)$: | $4\,z^0$ | $3\,z^{-1}$ | $0\,z^{-2}$ | $1\,z^{-3}$ | ... |

Mathematically, this can be expressed as

$$X(z) = \sum_{n=-\infty}^{\infty} x(n) z^{-n} \tag{18}$$

In the $z$-domain, the magnitude and phase response of a filter can be determined by an algebraic input/output relationship called transfer function, $T(z)$, defined as

$$T(z) = \frac{Y(z)}{U(z)} \tag{19}$$

where $U(z)$ is the $z$-transform of the input sequence and $Y(z)$ is the corresponding output sequence.

$T(z)$ is obtained by polynomial division, e.g.

$$T(z) = \frac{1 - 5z^{-1} + 6z^{-2}}{1 - 2z^{-1}} = 1 - 3z^{-1}$$

Equation (2) defines the AR synthesis filter, which is in the z-domain equivalent to

$$X[z] = \sum_{i=1}^{M} a_i\,X[z]z^{-i} + W[z] \tag{20}$$

$$\Leftrightarrow$$

$$X(z) = (a_1 z^{-1} + \cdots + a_M z^{-M})\,X(z) + W(z) \tag{21}$$

$$\Leftrightarrow$$

$$X(z)(1 - a_1 z^{-1} - \cdots - a_M z^{-M}) = W(z) \tag{22}$$

$$\Leftrightarrow$$

$$\frac{X(z)}{W(z)} = \frac{1}{1 - a_1 z^{-1} - \cdots - a_M z^{-M}} = \frac{1}{1 - \sum_{i=1}^{M} a_i z^{-i}} = H(z) \tag{23}$$

where $H(z)$ is the transfer function of the AR synthesis filter. $X(z)$ may be regarded as the output of the AR-filter fed by the prediction error sequence $W(z)$. The AR synthesis filter is a recursive filter, which uses previous output samples to produce the current output value (Figure 3).

A very useful representation of the amplitude and frequency response of a filter is obtained by plotting it on a complex plane, i.e. in a coordinate plane that has real numbers on its horizontal axis and imaginary numbers on its vertical axis (Figure 4). In this representation, frequencies are wrapped around a circle, called the unit circle. At an angle 0 we have 0 Hz, and at $\pm\pi$ Hz we have the highest frequency $[1/(2T)]$. Positive frequencies are wrapped counterclockwise and negative frequencies clockwise around the circle.

If we substitute for a $z$-value a value from the circle, the equation

$$z = e^{j\omega T} \tag{24}$$

defines the unit circle, centred on the origin, and with a radius of 1, where $j$ is the rotation operator, $\omega$ determines angular frequency, and $T$ is the sampling period. Multiplying by $j$ once is the same as rotating counterclockwise 90° around the centre. According to Euler's formula

$$e^{j\theta} = \cos\theta + j\sin\theta \tag{25}$$

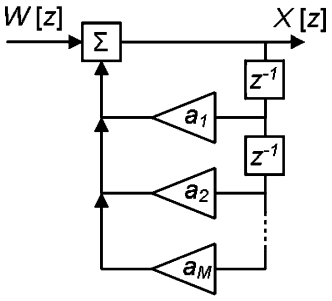


*Fig. 3. AR synthesis filter. W[z] and X[z] represent input and output sequences, respectively. $z^{-1}$ is a time delay of one sample period in the z-domain, $a_1, \ldots, a_M$ are predictor coefficients, and the "$\sum$" box represents summation of $a_i\,X[z^{-i}]$, $i = 1, \ldots, M$ values.*

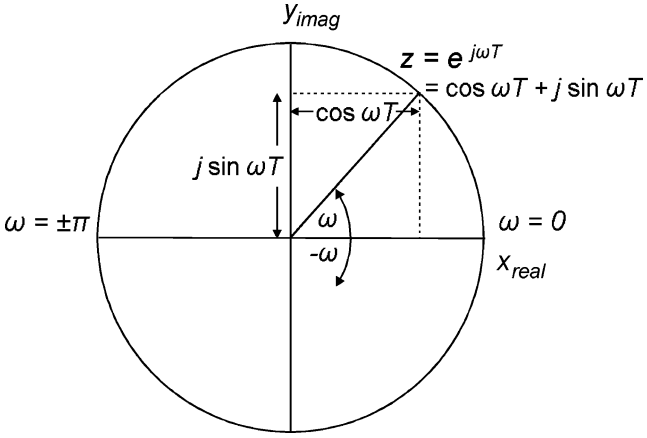


*Fig. 4. Unit circle on the complex plane. $y_{\text{imag}}$ and $x_{\text{real}}$ indicate an imaginary axis and the real axis, respectively; $\omega$ represents angular frequency, $j$ is the rotation operator, and $T$ is the sampling period; sin and cos denote sine and cosine functions, respectively.*

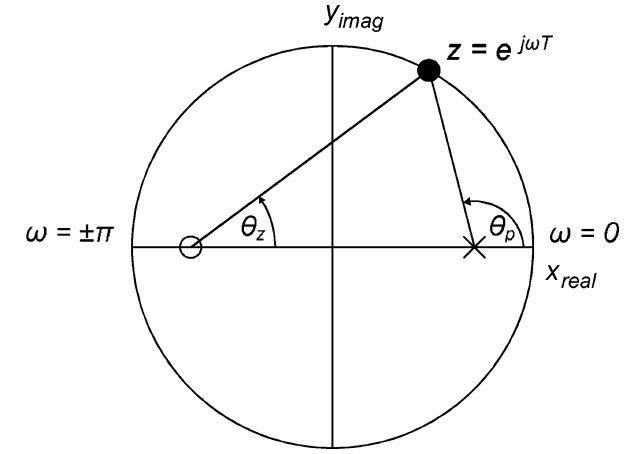


*Fig. 5. Geometric evaluation of the magnitude and phase response of a filter from the pole-zero diagram: ○ zero; × pole; • moving frequency point; $\theta_z$ are $\theta_p$ are the zero and pole angles, respectively. At a particular frequency, the zero vector is drawn from the zero to the frequency point and the pole vector from the pole to the same point. The gain of the filter equals the length of the zero vector divided by the length of the pole vector, and the phase response equals $\theta_z$ minus $\theta_p$.*

where $\theta$ makes an angle with the positive real axis. Because $\theta = \omega T$, we can rewrite

$$z = \cos \omega T + j \sin \omega T \tag{26}$$

Since

$$z^{-k} = (e^{j\omega T})^{-k} = e^{-jk\omega T} \tag{27}$$

from (23) we get

$$H(\omega) = \frac{1}{1 - a_1 e^{-j\omega} - \cdots - a_M e^{-jM\omega}} = \frac{1}{1 - \sum_{i=1}^{M} a_i e^{-ji\omega T}} \tag{28}$$

The $T(z)$ (19) can be presented on the unit circle by displaying its zeros and poles. The zeros are the values that cause $Y(z)$ to become zero, while the poles are the values that result in $U(z)$ becoming zero. The zeros can be anywhere, while the poles of a stable filter always lie inside the unit circle. For real signals, both zeros and poles are either real or in complex conjugate pairs. The poles and zeros located below the origin represent the poles and zeros of the negative frequencies, and result from the mathematical symmetry of polynomials with real coefficients.

At a particular frequency, $Y(z)$ may be represented by a zero vector, drawn from the zero to the relevant frequency point on the unit circle (Figure 5) [17]. $U(z)$ may be represented by a pole vector drawn from the pole to the same frequency point. The magnitude of $T(z)$ is given by the length of the zero vector divided by the length of the pole vector. In a system with many zeros and poles, the magnitude equals

$$\text{Magnitude} = k \frac{\prod \text{zero distances}}{\prod \text{pole distances}} \tag{29}$$

where the numerator is the product ($\Pi$) of all zero vector lengths, the denominator is the product of all pole vector lengths, and $k$ is the pure gain of the system [e.g., if the $T(z) = 2(z-1)/(z+2)$], then $k$ is 2). The phase equals the sum of all zero vector phases minus the sum of all pole vector phases.

The AR filter has an all-pole structure, i.e. it tries to describe the behaviour of a process in the frequency domain by using poles only. The estimates for the different frequency components of a time series can be calculated from the poles of $H(z)$, i.e., the roots of the $X(z)$ polynomial. As the frequency point moves around the unit circle, the magnitude of $H(z)$ peaks whenever the frequency point on the circle passes close to a pole. The nearer to the unit circle a pole is located, the higher and sharper is the peak it creates. Using the poles ($p_i, i = 1, \ldots, M$), $H(z)$ may be presented as

$$H(z) = \frac{1}{(1 - p_1 z^{-1})(1 - p_2 z^{-1}) \cdots (1 - p_M z^{-1})} \tag{30}$$

The spectrum of the modelled time series, $R(e^{j\omega})$, is obtained by multiplying the prediction error variance with the square of the transfer function. In other words, from

(28) we get

$$R(e^{j\omega}) = |H(e^{j\omega})|^2\sigma_p^2 = \frac{\sigma_p^2}{|1 - a_1e^{-j\omega} - \cdots - a_Me^{-jM\omega}|^2} \quad (31)$$

Frequency resolution is one of the main differences between the DFT and model-based AR spectral analysis. In DFT, the frequency resolution is determined by the number of data points used for calculation, whereas in the model-based methods the spectrum can be evaluated at an arbitrary number of frequency points and the frequency resolution is not affected by the length of the given sequence of data. Estimation of the signal spectrum with the AR model also enables the frequency components to be determined more exactly than by DFT, provided that the model is good enough.

When analysing cardiovascular variability signals, for example, a clearly higher $M$ than that given by AIC is often used. The higher the $M$ chosen, the better will the identified model fit the measurements. A high $M$ offers better frequency resolution, but allows less robust power estimates. Very high $M$ may also lead to line splitting and spurious peaks [18]. Line splitting means that a single peak in a spectrum splits into two peaks. Spurious peaks are false spectral peaks at a frequency where no peak should exist. Thus, only a small number of parameters can be reliably determined from a limited amount of measurement data. We must appraise the pros and cons according to our demands. Some applications require high-frequency resolution at the cost of robustness of the power estimates and vice versa.

## APPLICATION EXAMPLE

Spectral analysis of RR-interval fluctuations is of clinical importance in the assessment of cardiovascular regulatory mechanisms. Figure 6 shows how the time between successive heart beats varies around its mean in a healthy man in a standing position. The original RR-interval time series has first been resampled at 1 Hz sampling frequency. The mean value and very slow variations of the signal have been removed by subtracting a mean value of 50 consequent data points at each point. The resulting 300-point time series is then subjected to the AR modelling process. In this case, the minimum value for $M$ given by the AIC is 5 (Figure 7).

The first 10 data points (D) of the time series are

$$D = [-12.52 \quad 23.61 \quad -10.98 \quad -47.98 \quad 3.01 \quad 32.56 \quad -54.20 \quad -116.06 \quad -71.07 \quad -24.87 \cdots]$$

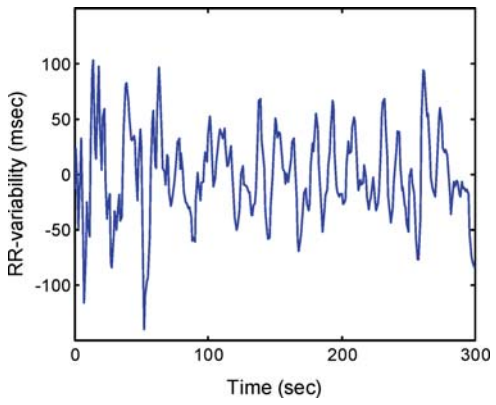


*Fig. 6. Pre-processed RR-interval signal.*

The autocorrelation value at zero delay (R_estimate_0) is calculated by multiplying each data point by a non-delayed version of itself, summing the products and dividing the result by the number of data points. With these 10 points the result would be

$$\text{R\_estimate\_0} = (-12.52 * -12.52 + 23.61 * 23.61 + (-10.98 * -10.98) + \cdots)/10 = 2628$$

The more data points are used, the better the correlation estimate. Using the whole data (300 points) results in a correlation estimate of

$$\text{R\_estimate\_0} = 1603$$

The next autocorrelation value at one sample delay (R_estimate_1) is calculated by multiplying each data point by a delayed version of itself:

$$\text{R\_estimate\_1} = (-12.52 * 23.61 + 23.61 * -10.98 + (-10.98 * -47.98) + \cdots)/10 = 1557$$

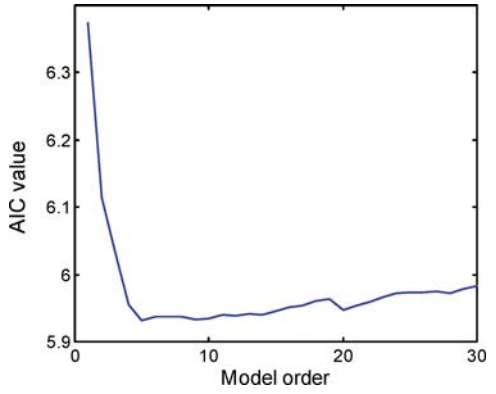


*Fig. 7. Akaike's Information Criteria (AIC) values for model orders of 1 to 30 for an instantaneous heart rate signal.*

Again, using the whole data the result is

R_estimate_1 = 1279

The autocorrelation values for every delay up to $M = 5$ are calculated by the same principle and put together into a matrix that has zero delay values on its diagonal (see Equation (10)). The matrix is symmetric because the autocorrelation values for the delays $d$ and $-d$ are the same. The resulting autocorrelation matrix $R$ up to delay of $M-1$ samples is

$$R = \begin{bmatrix} 1603 & 1279 & 739 & 384 & 149 \\ 1279 & 1603 & 1279 & 739 & 384 \\ 739 & 1279 & 1603 & 1279 & 739 \\ 384 & 739 & 1279 & 1603 & 1279 \\ 149 & 384 & 739 & 1279 & 1603 \end{bmatrix}$$

For comparison, the $(X^T X)/N$ matrix for this data is

$$(X^T X)/N = \begin{bmatrix} 1596 & 1279 & 734 & 374 & 146 \\ 1279 & 1583 & 1261 & 716 & 371 \\ 734 & 1261 & 1565 & 1247 & 712 \\ 374 & 716 & 1247 & 1557 & 1242 \\ 146 & 371 & 712 & 1242 & 1556 \end{bmatrix}$$

The autocorrelation vector $\underline{r}$ from delay 1 to delay $M$ is

$$r = [1279 \quad 739 \quad 384 \quad 149 \quad -139]^T$$

Using $(X^T x)/N$ matrix we get

$$(X^T x)/N = [1301 \quad 755 \quad 389 \quad 151 \quad -141]^T$$

Using Yule–Walker solution [12] we get for the $M$ of 5 coefficients $a_1, \ldots, a_5$

$$\underline{a} = [-1.35 \quad 0.94 \quad -0.48 \quad 0.04 \quad 0.17]^T$$

and the resulting coefficients using the covariance method [9] are

$$\underline{a} = [-1.45 \quad 1.08 \quad -0.59 \quad 0.10 \quad 0.16]^T$$

We get the transfer function estimate using the estimated $\underline{a}$ values. Yule–Walker solution results in

$$\widehat{H}(e^{j\omega}) = \frac{1}{1 - 1.35e^{-j\omega} + 0.94e^{-j2\omega} - 0.48e^{-j3\omega} + 0.04e^{-j4\omega} + 0.17e^{-j5\omega}}$$

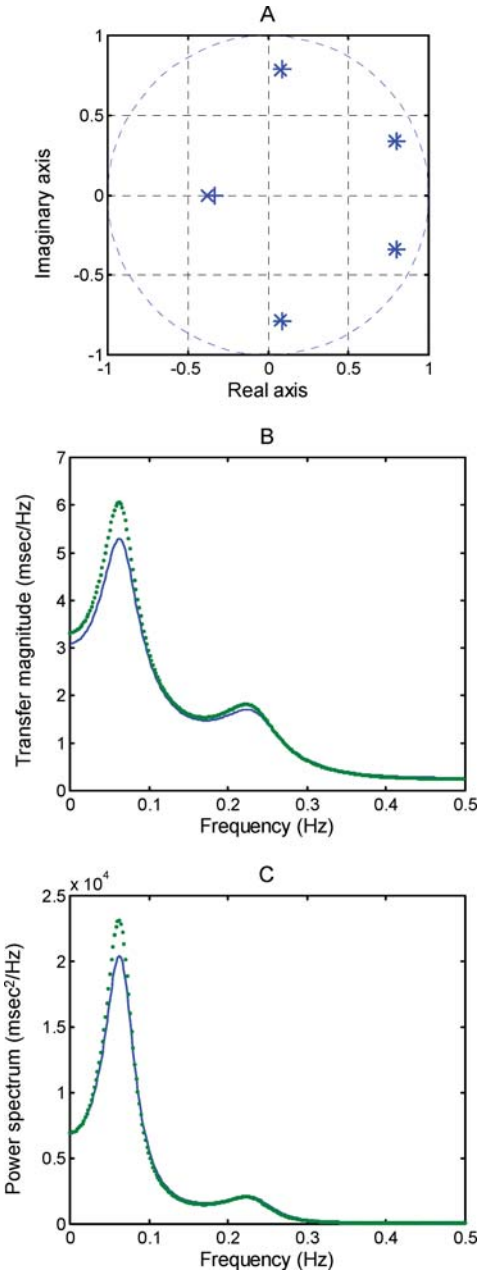


*Fig. 8. Pole-zero plot (A). × and + denote the poles of autocorrelation and covariance methods, respectively. The closer to the unit circle a pole lies, the higher the magnitude of the response it creates (B). The transfer function and spectrum of the autocorrelation method is shown as a solid line and the corresponding results of the covariance method as a dotted line. The frequencies shown in the RR-interval power spectrum correspond to respiration rate (0.24 Hz) and vasomotor activity (0.06 Hz) (C).*

When we solve the roots of the $X(\omega)$ polynomial, we get the poles of the AR model. The poles are located at points $0.79 \pm 0.34i$, $0.08 \pm 0.78i$ and $-0.38$. The complex pole pairs represent two separate peaks in the transfer function, at

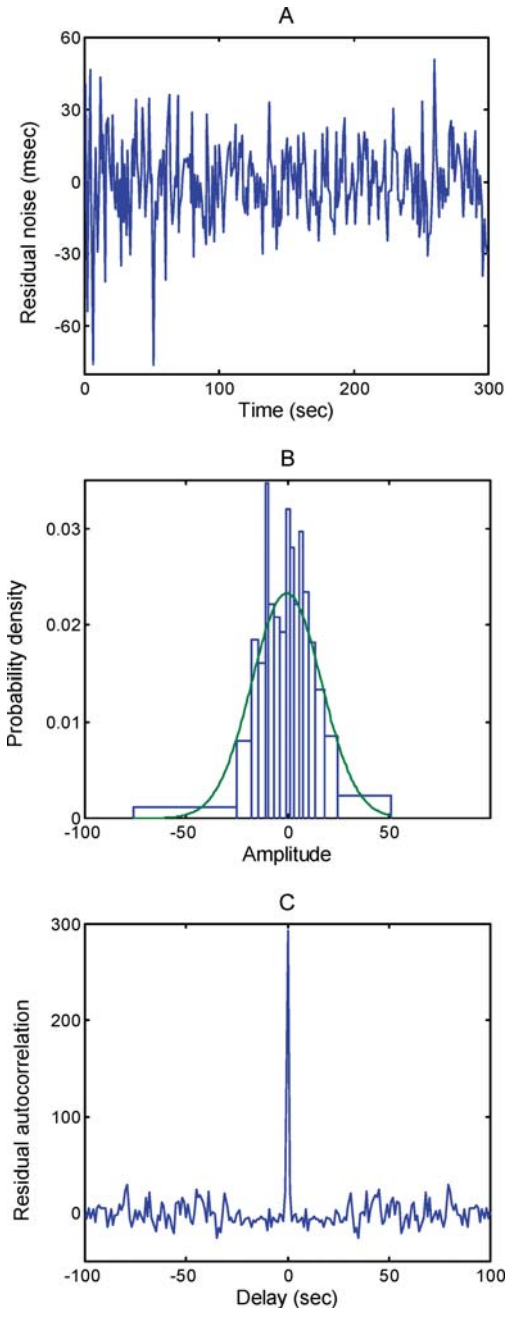


*Fig. 9. Residual noise (A), its distribution compared to normal distribution (bell-shaped curve) (B) and its autocorrelation (C).*

locations 0.4 and 1.47 rad. The corresponding frequencies at 1 Hz sampling frequency are

$$0.4\,\text{rad} * \frac{1\,\text{Hz}}{2\pi\,\text{rad}} = 0.06\,\text{Hz}$$
$$1.47\,\text{rad} * \frac{1\,\text{Hz}}{2\pi\,\text{rad}} = 0.23\,\text{Hz}$$

The real pole at $-0.38$ is relatively far from the unit circle. Therefore, it does not create a separate peak in the transfer function. The transfer function (magnitude response) and spectrum are shown in Figure 8. The selected model produces prediction error distribution that is nearly normal (Figure 9).

If we use the covariance method, the poles are located at points $0.80 \pm 0.34i$, $0.09 \pm 0.79i$ and $-0.33$, and the two separate peaks in the transfer function and spectrum are located at 0.06 Hz and 0.23 Hz (Figure 8). In the literature, differences between the autocorrelation and covariance method are a matter of debate, but in practise they result in very similar spectra.

MATLAB m-files for univariate AR analysis are available at the web site: http://www.mit.tut.fi/staff/hytti/AR_modelling.html.

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