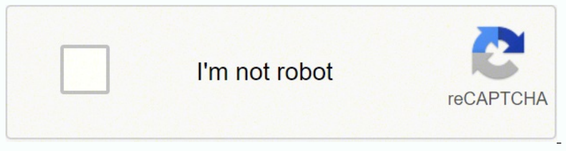

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Dependent Variable: $D4LNGDP$				
Method: Least Squares				
Date: 06/30/07 Time: 15:22				
Sample (adjusted): 1982Q2 2006Q4				
Included observations: 99 after adjustments				
Variable	Coefficient	Std. Error	t-Statistic	Prob.
$D1$	0.023682	0.069117	0.342640	0.7327
$D2$	0.021555	0.069275	0.311146	0.7564
$D3$	0.022655	0.069099	0.327870	0.7438
$D4$	0.024569	0.069475	0.353632	0.7245
$LNGDP(-4)$	-0.001483	0.006427	-0.230790	0.8180
$D4LNGDP(-1)$	0.760041	0.096776	7.853634	0.0000
$D4LNGDP(-2)$	0.171648	0.112739	1.522527	0.1314
$D4LNGDP(-3)$	-0.060442	0.113433	-0.532844	0.5955
$D4LNGDP(-4)$	-0.579852	0.113701	-5.099803	0.0000
$D4LNGDP(-5)$	0.387072	0.093588	4.135898	0.0001

Statistics:			
R-squared	0.634339	Mean dependent var	0.021517
Adjusted R-squared	0.597362	S.D. dependent var	0.016270
S.E. of regression	0.010324	Akaike info criterion	-6.213125
Sum squared resid	0.009486	Schwarz criterion	-5.950991
Log likelihood	317.5497	Durbin-Watson stat	2.011525

Nonlinear time-series analysis revisited[a]

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In 1980 and 1981, two pioneering papers laid the foundation for what became known as nonlinear time-series analysis: the analysis of observed data—typically univariate—via dynamical systems theory. Based on the concept of state-space reconstruction, this set of methods allows us to compute characteristic quantities such as Lyapunov exponents and fractal dimensions, to predict the future course of the time series, and even to reconstruct the equations of motion in some cases. In practice, however, there are a number of issues that restrict the power of this approach: whether the signal accurately and thoroughly samples the dynamics, for instance, and whether it contains noise. Moreover, the numerical algorithms that we use to instantiate these ideas are not perfect; they involve approximations, scale parameters, and finite-precision arithmetic, among other things. Even so, nonlinear time-series analysis has been used to great advantage on thousands of real and synthetic data sets from a wide variety of systems ranging from roulette wheels to lasers to the human heart. Even in cases where the data do not meet the mathematical or algorithmic requirements to assure full topological conjugacy, the results of nonlinear time-series analysis can be helpful in understanding, characterizing, and predicting dynamical systems.

PACS numbers: 05.45.Tp
Keywords: time series analysis, other things

Nonlinear time-series analysis comprises a set of methods that extract dynamical information about the succession of values in a data set. This framework relies critically on the concept of reconstruction of the state space of the system from which the data are sampled. The foundations for this approach were laid around 1980, when deterministic chaos became a popular field of research and scientists were looking for evidence of chaos in natural and laboratory systems. One of the first—and still most spectacular—applications was the prediction of the path of a ball on a roulette wheel, which nicely demonstrated the power of these methods. Since then, nonlinear time-series analysis has left this narrow niche and moved into much broader use across all branches of science and engineering, as well as social science, the humanities, and beyond.

I. WHY NONLINEAR TIME SERIES ANALYSIS?

The goal of time-series analysis is to learn about the dynamics behind some observed time-ordered data. Early approaches to this employed linear stochastic models—more precisely, autoregressive (AR) and moving average (MA) models[1]. These stationary Gaussian stochastic processes are fully characterized by their two-point auto-correlation function

$$c(\tau) = \frac{\langle (x_t - x_{t+\tau})^2 \rangle}{\langle x_t^2 \rangle} \qquad (1)$$

or by their power spectrum, respectively. There are many data sets where this type of analysis leads to a good characterization, such as temperature anomalies: differences between the daily (maximum, mean, minimum) temperature at a given place and the many-year average of that quantity for the corresponding calendar day. Data of this type possess an almost Gaussian distribution with an almost exponentially decaying auto-correlation function; typically the null hypothesis that they are generated by an AR(1) process cannot be rejected easily on the basis of observed data.

Of course, we know that temperatures can be predicted much more accurately by high-dimensional physics-based models of the atmosphere than by AR(1) models. That scalar temperature data look like AR data comes from the projection of dynamics in a high-dimensional state space onto a single quantity. This illustrates that, depending on one's point of view and one's access to a system's variables, the very same system might appear to have very different complexity.

As in any other analysis, the choice of a specific time-series analysis method requires justification by some hypothesis about the appropriate data model. Time-series analysis is essentially data compression: we compute a few characteristic numbers from a large sample of data. This reduced information can only enhance our knowledge about the underlying system if we can interpret it, and it becomes interpretable through the fact that the

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A Time Series Analysis of Microarray Data

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Abstract

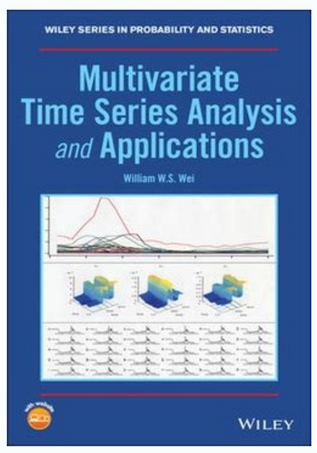
As the capture and analysis of single-time-point microarray expression data becomes routine, investigators are turning to time-series expression data to investigate complex gene regulation schemes and metabolic pathways. These investigations are facilitated by algorithms that can extract and cluster related behaviors from the full population of time-series behaviors observed. Although traditional clustering techniques have shown to be effective for certain types of expression analysis, they do not take the biological nature of the process into account, and therefore are clearly not optimized for this purpose. Moreover, the current approaches provide internal comparisons for the experiments utilized for clustering, but cross-comparisons between clustered results are qualitative and subjective. We present a combination of current and novel methods for the analysis of time series gene expression data. We focus on an actual study we have performed for Haemophilus influenzae which is a major cause of otitis media in children. We first perform a discretization of the gene expression data that takes both positive and negative correlations into consideration and then develop a clustering algorithm optimized for such data that allows elucidation and searching of time-series patterns. The resulting approach allows time-series data to be usefully compared across multiple experiments. We demonstrate the success of our algorithm by showing some of the genes that it finds to be co-regulated are not detected by current methods. As a result we are able to identify several signal pathways that initiate competence development, and to characterize the transcriptomes of wild-type and an adenylate cyclase mutant (cya) strains under both nutrient-limiting and nutrient-complete growth conditions.

1. Introduction

Genes are the code of proteins that are fundamental components of all living cells and carry out vital organism functions. Before being translated into protein, this code must be transcribed from chromosomal DNA into messenger RNA (mRNA). The rate of transcription by the cell for some genes can be varied, and therefore the amount of certain mRNAs in the cell cytoplasm is a measure of the production speed of corresponding protein in the cell. Depending on the environment of the cell (and other factors), different amounts of some proteins are required; hence different concentrations of mRNAs for different genes exist in the cell. The relationship between the amount of an mRNA observed under experimental conditions, versus the amount observed under control conditions is called the expression level. Immobilized DNA microarrays (aka. probe arrays) are a tool for high-throughput gene expression studies. In microarray studies, probes (i.e. oligonucleotide sequences) with known identity are placed on glass or nylon substrates in a grid and used to determine expression levels through hybridization to bulk unknown populations of sequences (11). In the results we see the relative expression levels of genes.

As the capture and analysis of single-time-point microarray expression data becomes routine, investigators have started examining time-series expression data to investigate complex gene regulation schemes and metabolic pathways. The current approach is basically to cluster the time-series sequences based on common methods such as k-means. These algorithms provide internal comparisons for the experiments utilized for clustering, but cross-comparisons between clustered results are qualitative and subjective. In this paper, we present a combination of current and novel methods for the analysis of time series gene expression data. We first perform a discretization of gene expression data that takes both positive and negative correlations into consideration and then develop a clustering algorithm optimized for such data that allows both elucidation and searching of time-series patterns. The resulting approach allows time-series data to be usefully compared across multiple experiments.

The proposed technique can be used as a decision support tool for a researcher who is searching for candidate



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The native characteristics or structural parameters of a system that generates the time series, for example, the natural frequency and damping of a civil structure. Control¢ÃÂÂYou can use the predicted values of a time series to determine appropriate corrective actions that you take to specify optimal settings for the controller and keep a physical system or process operating properly. For example, you can obtain a multivariate time series by recording the values of pressure, flow, and temperature simultaneously in an industrial process. For example, you can explain the dynamic properties of a physical system by analyzing the input time series to and output time series from the system. For example, to measure the trends or periodicity, you can plot the time series. Single-source observations generate univariate time series, and multi-source observations form multivariate time series, or vector time series. Generally speaking, if the statistical characteristic of a time series contains no systematic change, the time series is stationary. The signals are acquired simultaneously from seven acceleration sensors located at different positions on the beam. Prediction¢ÃÂÂYou can use observed values to predict the future values of a time series. Stationary Time Series and Nonstationary Time Series In theory, given a behavioral model for a system, you can predict future values of a time series measured from that system, based on past observations. The LabVIEW Time Series Analysis Tools focus more on the applications in engineering. Time series exist in many application areas, ranging from economics to engineering. Use the Time Series Analysis VIs to analyze or process a time series. Univariate Time Series and Multivariate Time Series You can collect observed values from a single source or simultaneously from two or more sources. 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