Biological Systems: Stochastic, Deterministic or Both

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Many systems in nature, including biological systems, have very complex dynamics which generate random-looking time series. To better understand a particular dynamical system, it is often of interest to determine whether the system is caused by deterministic subsystems (e.g. chaotic systems), stochastic subsystems, or both. Although there are now several different approaches to determine this from time series data (e.g. correlation dimension and Lyapunov exponent calculations), these methods often require large amounts of stationary data (biological data is frequently nonstationary for long time scales), can often mis-identify certain systems, and can be subject to other technical problems. Alternatively, one can use methods that measure the complexity in a particular system which seldom make assumptions about a particular system, such as assuming the presence of stationarity. Additionally, mathematical and computational modeling techniques can be used to test different hypothesis about the dynamics of biological systems.

1 Introduction

Given a biological system which generates random-looking time series, one may want to determine if the system is a caused by: 1) a purely random process, 2) deterministic chaos or 3) a chaotic system with noise. Thus far, the methods for this kind of determination often require a large amount of data, are not straightforward to carry out, and can give spurious results. The phase space plot analyses, though very helpful in characterizing a particular system, cannot in and of themselves always distinguish one type of nonlinear system from another. Furthermore, the calculation of the correlation dimension by the Grassberger-Proccacia algorithm, also an important
tool in nonlinear dynamical system analyses, can sometimes identify random systems as being chaotic. In addition, data from biological systems frequently do not meet the criteria necessary to use many existing methods of nonlinear dynamical systems identification.

Mechanistic models of biological systems can give insight into identifying the system nonlinear dynamics type and the nature of the biological system dynamical behaviour under various conditions. A model which has dynamics that fits experimental data generated by a biological system can strongly suggest what type of nonlinear process (e.g. chaos or chaos with noise) the system is. This kind of mechanistic approach to modeling and system identification was carried out with the baroreceptor reflex heart rate control system. Standard deterministic equations for cardiac mechanics and neural control (neural network) were used with and without added Gaussian white noise. Time series, power spectra and phase space plots for the purely deterministic case and the mixed deterministic/stochastic case were compared to plots from experimental data and it was found that the deterministic/stochastic model generated plots which most resemble the experimental plots. Once an accurate model of biological system is developed one can use the model to test different hypotheses about the dynamics of the system or any of its subsystems.

Nonlinear system identification of biological systems in many cases remains an elusive task. Theoretical modeling of biological systems can aid in identifying its nonlinear system type, can give new insights into the dynamics of the biological system, and can enable one to make predictions about future behaviour of the system.

2 Studying Dynamical Systems in Biology by Analyzing Time Series

Nonlinear dynamics have recently been used by several different groups in characterizing biological time series [1–3]. Much effort has been spent recently trying to search for low-dimensional deterministic chaos in biological systems, using techniques such as correlation dimension measurement and the calculation of Lyapunov exponents. These approaches require the analysis of long time series generated by systems which observe stationarity (i.e. systems whose parameters and phase-space attractors do not change). Unfortunately, biological systems are often characterized as being non-stationary. When using the Grassberger-Proccacia algorithmic approach to calculate the correlation dimension, it has been shown that, for a calculation to be valid, the estimated dimension cannot exceed \(2 \log N\), where \(N\) is the number of points of the time series [4]. Furthermore, to accurately estimate Lyapunov exponents one needs approximately the square of the number of points needed to estimate the dimension [4]. The measurement of the correlation dimension, in addition, has been shown to mis-identify the presence of low-dimensional chaos in a time series generated by filtering random noise [5].