Handbook of Time Series Analysis

Recent Theoretical Developments and Applications

Edited by
Björn Schelter, Matthias Winterhalder,
and Jens Timmer

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Preface

Reiterated measurements of an experimentally accessible quantity of a dynamical system result in a time series, and one may wonder, what this information can tell about the system on which the measurements are done. Time series analysis is, thus, a very obvious way of an attempt to understand nature—already Kepler did it when studying the observations of Tycho Brahe. He came up with a very simple synopsis formulated in his famous laws and Newton could ascribe these to a single law by postulating a fundamental gravitational force. This marks the beginning of modern science and then, in exploring the nature, fundamental laws or equations motivated by first principles played a dominant role.

Turning to more and more complex systems guidance by first principles became less fruitful for finding a mathematical model. Thus, observations cannot serve any more as indication or pointer to some fundamental underlay but have to be regarded only as a fingerprint of the system. First tasks in analyzing these fingerprints then are e.g. characterization or establishing a relation or correlation to other observations. Time series analysis in this sense, thus, has already a long history in fields where the systems to be studied are very complex such as meteorology or medical science. Sophisticated mathematical methods appeared first in late 19th century and during the last decades these methods have been utilized also by many scientists working in applied fields. This has led to many successes in understanding complex systems.

This handbook comprises a wide range of current topics in the field of time series analysis. The editors are well-known for both their theoretical work on time series analysis techniques and their applications. Therefore, the editors attached great importance to both theoretical work and applications. Especially, the interplay of theory and practice is included in this Handbook of Time Series Analysis. The editors brought together contributions of worldwide accepted experts of different branches, e.g. from Physics, Mathematics, Biology, Medicine, Neuroscience, and Engineering. With respect to the theory this Handbook covers a broad variety of presently used methodologies in different disciplines, ranging from linear stochastic systems to Nonlinear Dynamics, from univariate to multivariate time series analysis.

The Handbook of Time Series Analysis will provide guidance for all those working on time series analysis, from students to experienced investigators. I hope that it develops into a standard textbook and that the editors find time to keep it up-to-date in future.

Josef Honerkamp July 26, 2006

Chair for “Stochastic Dynamical Systems” at the Physics Department of the University of Freiburg, and founder of the “Freiburg Center for Data Analysis and Modeling”

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1 Handbook of Time Series Analysis: Introduction and Overview

Björn Schelter, M. Winterhalder, and J. Timmer

Mathematics, Physics, and Engineering are very successful in understanding phenomena of the natural world and building technology upon this based on the first principle modeling. However, for complex systems like those appearing in the fields of biology and medicine, this approach is not feasible and an understanding of the behavior can only be based upon the analysis of the measured data of the dynamics, the so-called time series.

Time series analysis has different roots in Mathematics, Physics, and Engineering. The approaches differ by their basic assumptions. While in Mathematics linear stochastic systems were one of the centers of interest, in Physics nonlinear deterministic systems were investigated. While the different strains of the methodological developments and concepts evolved independently in different disciplines for many years, during the past decade, enhanced cross-fertilization between the different disciplines took place, for instance, by the development of methods for nonlinear stochastic systems.

This handbook written by leading experts in their fields provides an up-to-date survey of current research topics and applications of time series analysis. It covers univariate as well as bivariate and multivariate time series analysis techniques. The latter came into the focus of research when recording devices enabled more-dimensional simultaneous recordings. Even though bivariate analysis is basically multivariate analysis, there are some phenomena which can occur only in three or more dimensions, for instance, indirect interdependences between two processes.

The aim of this handbook is to present both theoretical concepts of various analysis techniques and the application of these techniques to real-world data. The applications cover a large variety of research areas ranging from electronic circuits to human electroencephalography. The interplay between challenges posed by empirical data and the possibilities offered by new analysis methods has been proven to be successful and stimulating.

In the first chapter, Henry D. I. Abarbanel and Ulrich Parlitz present different approaches to nonlinear systems. By means of a real-world example of a recording from a single neuron, they discuss how to analyze these data. Concepts such as the Lyapunov exponent, i.e., a measure for chaos, prediction, and modeling in nonlinear systems, are introduced with a critical focus on their limitations. Ready to apply procedures are given allowing an immediate application to one's own data.

Local modeling is being dealt with by David Engster and Ulrich Parlitz. Local models are amongst the most precise methods for time series prediction. This chapter describes the basic parameters of local modeling. To show the efficiency of this procedure, several artificial and real-world data, for instance experimental friction data sets, are predicted using local models. As an alternative to strict local modeling, cluster weighted modeling is also discussed using an expectation-maximization (EM) algorithm as a parameter optimization procedure.

Holger Kantz and Eckehard Olbrich present concepts, methods, and algorithms for predicting time series from the knowledge of the past. Thereby, they especially concentrate on nonlinear stochastic processes which have to be dealt with by probabilistic predictions. They calculate a certain prediction range in which future values are going to fall. They complete their chapter by discussing verification techniques for their forecasted values, which is very important when dealing with real-world data.

Noise and randomness in biological systems have often been treated as an unwelcome byproduct. Patrick Celka and co-workers identify different noise sources and their impact on dynamical systems. This contribution discusses the concept of randomness and how to best access the information one wants to retrieve. Different time series analysis techniques are presented. The applications govern speech enhancement, evoked potentials, cardiovascular system, and brain–machine interface.

The chapter of Ursula Gather and co-workers is dedicated to robust filtering procedures for signal extraction from noisy time series. The authors present various filter techniques with their specific properties and extensions in order to process noisy data or data contaminated with outliers. They point to the variety of different approaches and compare the advantages and disadvantages. By means of simulated data they demonstrate the different conceptual properties.

Dealing with bivariate time series analysis techniques, the chapter of Michael Rosenblum and co-workers is dedicated to the phenomenon of phase synchronization and the detection of coupling in nonlinear dynamical systems. The authors discuss the usage of model-based and nonmodel-based techniques and introduce novel ideas to detect weak interactions between two processes, together with the corresponding strength and direction of interactions. They illustrate their analysis techniques by application to data characterizing the cardiorespiratory interaction.

An approach to detect directional coupling between oscillatory systems from short time series based on empirical modeling of their phase dynamics is introduced by Dmitry Smirnov and Boris Petrovich Bezruchko. This time series analysis technique is utilized to analyze electroencephalography recordings with the purpose of epileptic focus localization and climatic data representing the dynamics of the North Atlantic Oscillation and El Niño/Southern Oscillation processes.

Phase synchronization analysis of brain signals, for instance intracranial electroencephalography data recorded from epilepsy patients, has come into the focus of neuroscience research. Mario Chavez and co-workers suggest a data-driven time series analysis technique to select the important contents in a signal with multiple frequencies, the empirical mode decomposition. They summarize this concept and demonstrate its applicability to model systems and apply it to the analysis of human epilepsy data.

For cases where the definition of the phase used by common approaches is impossible, Mamen Romano and co-workers present a way to detect and quantify phase synchronization using the concept of recurrences. Furthermore, to test for phase synchronization, an algorithm to generate surrogate time series based on recurrences is discussed. An application to fixational eye movement data complements the results for model systems.

Theoden I. Netoff and co-workers dedicated their work to infer coupling and interaction in weakly coupled systems, especially in the presence of noise and nonlinearity. To this end, they applied several analysis techniques to model data and to data obtained from an electronic circuit. They explored advantages and disadvantages of the methods in specific cases. The conclusion of their chapter is that nonlinear methods are more sensitive to detect coupling under ideal conditions. However, in the presence of noise, linear techniques are more robust.

Dealing with multivariate systems, the chapter of Manfred Deistler is dedicated to state space and autoregressive moving average models. He summarizes the basic ideas about state space models and autoregressive moving average models including external influence. He focuses on the mathematics and discusses approaches to parameter estimation. Lower dimensional parameterizations of these state space models are described to cope with high-dimensional time series.

David S. Stoffer and Myron J. Katzoff introduce an extension to spatio-temporal state space models. They concentrate on the concept of spatially constrained state-space models presenting ideas and mathematical aspects. Their application is dedicated to real-time disease surveillance by analyzing weekly influenza and pneumonia mortality collected in the northeastern United States that is essential in helping to detect the presence of a disease outbreak and in supporting the characterization of that outbreak by public health officials.

Graphical models are introduced in the chapter by Michael Eichler. He introduces the mathematical basis for a graphical representation of the interaction schemes obtained by multivariate analysis techniques. Moreover, the inference in these graphs is discussed and illustrated by means of model systems. Novel multivariate analysis techniques that allow distinction not only of direct and indirect interactions but also of the direction of interactions leading to such graphs are summarized and applied to neurophysiological and fMRI data.

The directed transfer function allows detection of directed influences in multivariate systems. Katarzyna J. Blinowska and Maciej Kamiñski introduce the directed transfer function, extend the concept to nonstationary data, and discuss approaches to decide its statistical significance. In their application, they analyze human electroencephalography data using the directed transfer function. They complement this work by comparisons of different multivariate analysis techniques.

Luiz A. Baccalá and co-workers are working on a multivariate analysis technique called partial directed coherence. Besides several applications of this technique, one of the challenges when applying this technique to real-world data is that a significance level is mandatory. Several approaches to evaluate statistical significance in practice are presented and discussed in their chapter. Moreover, they compare their technique to other techniques suggested for a similar purpose. The techniques are applied to electroencephalography data during and immediately before an epileptic seizure.

Another multivariate analysis technique to detect the directions of interactions between processes is discussed by Mingzhou Ding and co-workers. Bivariate Granger causality and conditional Granger causality are presented with particular emphasis on their spectral representations. Following a discussion of the theoretical properties and characteristics, the time series analysis technique is applied to model systems and to multichannel local field potentials recorded from monkeys performing a visuomotor task.

Pedro A. Valdés-Sosa and co-workers focus in their chapter on multivariate autoregressive models (MAR) based on a Bayesian formulation that combines several components of different types of penalizations as well as spatial *a priori* covariance matrices. This approach is shown to be practical by simulations and an application to concurrent EEG and fMRI time series gathered in order to analyze the origin of resting brain rhythms.

Ranging from univariate to multivariate analysis techniques, ranging from applications of physics to life sciences, covering an exceptionally broad spectrum of topics, beginners, experts as well as practitioners in linear and nonlinear time series analysis who seek to understand the actual developments will take advantage of this handbook.

2 Nonlinear Analysis of Time Series Data

Henry D. I. Abarbanel and Ulrich Parlitz

Nonlinear dynamical systems pose challenges in the analysis of observed time series. The required time-domain methods require more care than linear frequency-domain techniques, yet they are mature enough to answer important questions about the system producing the time series data. We review a set of standard methods for this analysis with an eye toward how they may be used in a practical sense and with a critical focus on their limitations. The key question in any such analysis is what aspect of the physical or biological system is of importance.

2.1 Introduction

Nonlinear dynamics plays an essential role in the behavior of physical and biological systems actually observed in experiments. Chaotic oscillations of moons orbiting heavy planets as well as action potential generation by neurons arise from nonlinear processes in those settings. This means one must step beyond the classical set of time series tools, such as Fourier analysis, utilized widely in the extraction of information from observed time series. Indeed, Fourier analysis is precisely suited for the simplification of linear time invariant dynamics. This method transforms and simplifies such dynamics from differential equations to algebraic problems since the transform kernel $e^{i\omega t}$ is the eigenfunction of the time translation operator. However, even the presence of a quadratic term in the dynamical variable leads to a convolution of the Fourier transform of that variable with itself, thus significantly complicating the analysis rather than simplifying it.

The methods for analyzing time series from nonlinear systems have thus been developed in time domain. We review here some methods in the analysis of such time series concentrating on those which have proven valuable over time and accepting that this chapter will thus miss recent developments which may prove valuable as they are critically used.

Our discussion will start with the embedding methods utilized to reconstruct a "proxy" phase space (or state space) for the observed system based on the geometric theorem of Whitney and brought to nonlinear dynamics by Takens [1] and the Santa Cruz "dynamics collective" [2] around 1980. Within that framework we will address how to determine the key quantities within the embedding process: time delays and dimensions [3–5]. This in itself gives substantial clues to the dynamical system leading to the measurements. To classify that system we require some invariants of the dynamics, and we discuss dimensions and Lyapunov exponents. The latter also give us insight into the predictability of the system. From there, we discuss the job of predicting within the reconstructed phase space. At that stage we turn to estimating the parameters in models of the system producing the time series measurements.

Through this chapter we use an example from the Laboratory of Al Selverston at University of California, San Diego (UCSD) [6]. These are measurements of the cross membrane voltage in an isolated neuron of a small circuit, the pyloric central pattern generator of crustaceans. This neuron, called LP, when in the intact circuit produces quite regular voltage bursts which are coordinated with bursts of two other circuit neurons leading to an important three-phase functional outcome for the crustacean digestive system. While model equations of motion of the Hodgkin–Huxley form are known for this neuron [7], tests for the quality of those models relied in the past on visual, subjective aspects of the time series of voltage. The analysis here is both illustrative of how one uses the tools of nonlinear time series analysis and has important implications for the understanding of the entire neural circuit.

2.2 Unfolding the Data: Embedding Theorem in Practice

We will primarily focus on the usual and simplest case of time series measurements of a single signal $s(t)$. If more than a single measurement is available, there are additional questions one may ask and answer. The signal is observed with some accuracy, usually specified by an estimate of the "noise" level associated with interference of the measurement by other processes. The signal is also measured in discrete time, starting at an initial time t_0 and then typically at a uniform time interval τ_s we call the sampling time. $s(t)$ is thus the set of N measurements $s(t_0 + n\tau_s)$, $n = 1, 2, \ldots, N$.

The dynamical system from which the signal comes is usually unknown in detail. In the case of the LP neuron $s(t)$ is the membrane voltage ranging from about $-70\,\text{mV}$ to $+50\,\text{mV}$, and while one has conductance-based Hodgkin–Huxley models for the dynamics [8], one does not know how many dynamical variables are needed nor does one know with any specificity the many parameters which enter such models. We are certain, however, that there is more than one dynamical variable and the system state space is not one dimensional even though the measurement is. To describe the state of the system we need more than amplitude and phase which is where linear analyses dwell.

The first task is to ask how many variables we will need to describe the system. If the dynamical system has a state space trajectory lying on an attractor of dimension d_A, then our observation is the projection of the multidimensional

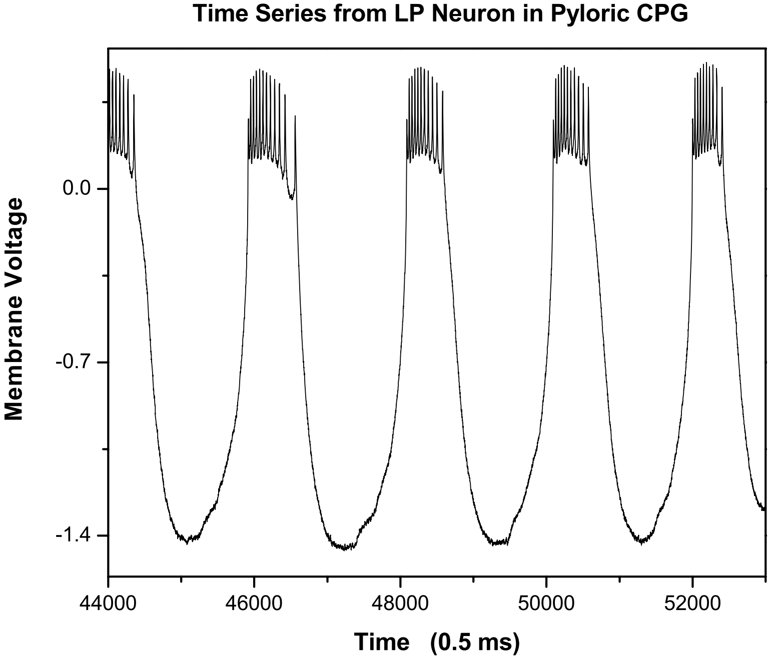

Fig. 2.1: Membrane voltage across the cell membrane of an isolated LP neuron from the crustacean pyloric central pattern generator. The amplitude on the y-axis is in scaled, arbitrary units. The time series is shown as a solid line, but the voltages were measured at 2 kHz or $\tau_s = 0.5$ ms. Altogether 200 000 data points or 100 s of data were recorded.

orbit in a space of integer dimension larger than d_A onto the measurement axis where we observe $s(t)$. If the dynamical system producing $s(t)$ is autonomous, then the orbit does not intersect itself in a high enough dimensional space capturing all the dynamical variables. In a space of integer dimension D a set of points with dimension d_A intersects itself in a set of points of dimension $d_A + d_A - D$. If D is large enough, this is negative, indicating no intersections at all. This tells us that if $D > 2d_A$, we are guaranteed that the space we use to describe the dynamics will have unfolded the projection made by the measurement. This is a sufficient condition. It could be that a dimension smaller than this unfolds the measurement projection, but we need another tool to determine that [3, 9–16].

It was probably David Ruelle's idea in the late 1970s that coordinates for the space of dimension D could be made out of the observations and their time delays. Takens proved a theorem [1] implying that the observed variable and any independent set of $D-1$ other variables made from $s(t)$ would be acceptable coordinates for this space. The simplest set of variables, though not always the very best, is taken from the measurements themselves. One seeks a D-dimensional vector made from $s(t)$ and its time delays by forming

$$\begin{aligned} y(t = t_0 + n\tau_s) \\ &= [s(t_0 + n\tau_s), s(t_0 + (n - T)\tau_s), \ldots, s(t_0 + (n - (D - 1)T)\tau_s)] \,. \end{aligned} \tag{2.1}$$

This D-dimensional vector is composed of the observation $s(t_0 + n\tau_s)$ and the $j = 1, 2, \ldots, D - 1$ earlier observations at $t_0 + (n - jT)\tau_s$. If $T = 1$, the components are selected at each sampling time.

To use this vector as a "proxy" for the degrees of freedom actually specifying the state of the system (unknown to us, of course) we need to determine values for D and T. To simplify the notation we will drop the initial time t_0 and the sampling time τ_s and write $s(n) = s(t_0 + n\tau_s)$ as well as

$$y(n) = [s(n), s(n - T), \ldots, s(n - (D - 1)T)] \,. \tag{2.2}$$

How do we know that the sampling time τ_s is small enough to capture significant variations of the dynamical signal $s(t)$? If we know nothing about the source of the observations $s(t)$, we cannot answer this question with any certainty. We will indicate how one can test this, but that comes in a moment. If we know that the source of the signal is an oscillating neuron, then we might know that the typical time scale of neural activity is in milliseconds, so if τ_s is 1 s, we probably have undersampled data. If τ_s is 1 μs, the data are probably oversampled. One always prefers the latter situation as selecting a subset of the data to describe that the system can be reliable. For now, let us assume that the system is properly sampled or possibly slightly oversampled.

2.2.1 Choosing T: Average Mutual Information

The goal of replacing the original signal $s(n)$ with a vector $y(n)$ is to provide independent coordinates in a D-dimensional space to replace the unknown coordinates of the observed system. The components of the vector $y(n)$ should thus be independent looks at the system itself, so all of the needed dynamical variations in the system are captured. If the time delay between the components $s(n - jT)$ and $s(n - (j - 1)T)$ is too small for some T, then the components are not really independent and we require a larger T. If T is too large, then the two measurements $s(n-jT)$ and $s(n-(j-1)T)$ are so far apart in time that the typical instabilities of nonlinear systems will render them essentially uncorrelated. We need some criterion which retains the connection between these measurements yet does not make them essentially identical.

While it is easy to evaluate the linear autocorrelation between measurements as a function of T, the usual criterion of seeking a zero in that quantity only leads to a value of T where the measurements are linearly independent. The dynamical interest of this is rather small. A much more motivated criterion, though harder to evaluate, was suggested by Fraser and Swinney in 1986: evaluate the average mutual information between measurements at time n and time $n - T$;

look for the first minimum in this quantity. This tells us when the two measurements are nonlinearly relatively independent, and this may provide a useful choice for T [17–21].

To evaluate the average mutual information, we need the distribution of the measurements $s(n)$ over the time series. This means we need to bin the amplitudes $s(n)$, $n = 1, 2, \dots, N$, into a normalized histogram using the whole data set. This gives the frequency of occurrence $P(s(n))$. We also need to do the same for the time-delayed data $s(n-T)$, and we need the normalized histogram of the joint occurrence of $s(n)$ and $s(n-T)$ to find $P(s(n), s(n-T))$. The average mutual information

$$I(T) = \sum_{s(n), s(n-T)} P(s(n), s(n-T)) \log_2 \left[\frac{P(s(n), s(n-T))}{P(s(n))\, P(s(n-T))} \right] \tag{2.3}$$

tells us *in bits* how much, on average over the whole time series or the attractor, we know about the measurement at time n from the measurement at time $n-T$. $I(T) \geqslant 0$, and it acts as a nonlinear correlation function. The sums are over the binned values of the observations. Now the theorem of Takens indicates that (almost)[1] *any* value of T is acceptable, if the data are of infinite precision. Well, that is not likely, so how we choose T is bound to be somewhat arbitrary. In practice, as the goal of this handbook, we recommend that one find the value of T for which $I(T)$ has its first minimum and then evaluate all subsequent quantities we discuss for T, $T \pm 1$, $T \pm 2$, and perhaps $T \pm 3$. If the conclusions from that set of five calculations with different T are the same, then in a practical sense the selection of T is acceptable. Choosing different T is equivalent to selecting different coordinate systems, connected by an unknown nonlinear transformation, in which to view the unfolding of the observations. If the quantities of interest are expected to be independent of the coordinate system, which is usually an important criterion, then this is a simple practical test of that.

Let us look at our LP neuron data now. In Fig. 2.1 we present a selection of the data of scaled membrane voltage from an LP neuron isolated from all other electrophysiological or neurochemical input. The sampling time was $\tau_s = 0.5$ ms. Figure 2.2 shows the average mutual information evaluated using all 200 000 data points. There is a very shallow minimum near $T = 10$, corresponding to 5 ms in time. Note that the data are a collection of spikes riding on top of a slow, large amplitude variation of the membrane potential with a period about 1 s. The T selected by the first minimum of $I(T)$ reflects the variation of the spikes at about 30 Hz.

In the literature there are often suggestions that one should use the first zero of the autocorrelation function of the measured time series as a good choice for the time $T\tau_s$ to use in constructing the data vector $\mathbf{y}(n)$. In the case of the

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[1] Some values of the delay time T may lead to a nonfaithful representation of the dynamics that is not equivalent to the original system. For example, a closed orbit is mapped to a point if T equals exactly the period of the oscillation.

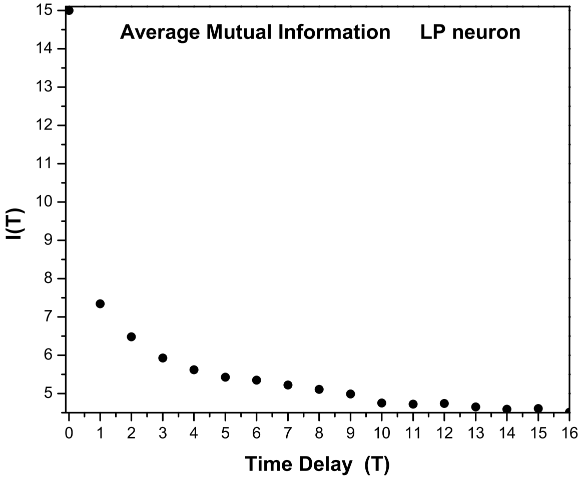

Fig. 2.2: The average mutual information $I(T)$ for the LP neuron membrane voltage time series shown in Fig. 2.1. $I(T)$ has a minimum in the neighborhood of $T = 10$; $T\tau_s \approx 5$ ms. It is a shallow minimum.

isolated LP neuron the Fourier power spectrum of the time series is shown in Fig. 2.3. Its Fourier transform is the autocorrelation function which shows a first zero crossing at 245 ms. This large number reflects the large amplitude oscillations near 1 Hz and washes out the dynamical structure of the spiking activity at each burst. That structure is reflected in the average mutual information choice of $T\tau_s \approx 5$ ms.

Procedure 2.1 (Average mutual information procedure). *From the amplitude range of the observations* $s(n)$ *form* B *bins. Record the frequency with which each bin is occupied by the values of* $s(n)$. *Normalize the frequency of occurrence by the total number of data. This normalized histogram is* $P(s(n))$. *Vary* B *to assure yourself that the amplitudes are properly sampled.*

Do precisely the same with the observations $s(n-T)$. *The corresponding distribution* $P(s(n-T))$ *should be the same as* $P(s(n))$ *if your data are stationary-independent of the origin of time-indicating autonomous oscillations of the signal source.*

From the amplitude range of the observations $s(n)$ *and* $s(n-T)$ *form* B^2 *bins. Record the frequency with which each bin is jointly occupied by the values of* $s(n)$ *and* $s(n-T)$. *Normalize the frequency of occurrence by the total number of data. This normalized histogram is* $P(s(n), s(n-T))$. *Vary* B *to assure yourself that the amplitudes are properly sampled.*

By summing over the bins evaluate

$$I(T) = \sum_{s(n),s(n-T)} P(s(n), s(n-T)) \log_2 \left[\frac{P(s(n), s(n-T))}{P(s(n))\, P(s(n-T))} \right]. \tag{2.4}$$