Chapter 14
Medical and Biological Analysis

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ABSTRACT

Medical and biological analysis refers to the engineering methods of signal processing as applied to measurements from human subjects, with the purpose of defining the differences between normal and pathological signals, in order to detect the presence of a disease process or detect changes in the status of a patient associated with treatment. As such, the focus of this chapter is on the identification of the sources of biomedical signals and their classification. This is followed by a historical background with emphasis on clinical applications and early quantitative and engineering approaches. Subsequently, the chapter presents classical engineering methods addressing signals in one dimension, focusing on traditional signal processing methods. It then describes some contemporary engineering approaches to medical and biological analysis, and concludes by addressing filters and noise removal and signal compensation.

14.1. CHAPTER OBJECTIVES

The focus of this chapter is on the use of engineering tools to describe and characterize biomedical signals for the diagnosis of disease. The objectives of the chapter are:

1. To describe the types of information that can be derived from (one-dimensional) biomedical signals;
2. To introduce quantitative engineering methods for deriving this information from biomedical signals;
3. To provide the theoretical foundation for advanced readings on these topics, and
4. To present examples which show the advantages and limitations of various approaches.

14.2. INTRODUCTION

Disease processes are often diagnosed by assessing apparent deviations from normal in measurements from a patient. Historical approaches in medical practice depended upon those data that the physician could acquire through visual, auditory, or tactile inspection such as average respiratory rate

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or average heart rate, or acoustic or mechanical responses to probing. Early approaches to computerized analyses of medical data signals often replicated what the physician did – e.g., counting, averaging – and in many contemporary situations this approach is sufficient because it provides more precise information, more frequently in time, of a type that the physician is accustomed to using. Advances in biomedical sensors and instrumentation, however, have vastly expanded the data available to the physician to characterize the health of a patient. In addition to an increase in the number and type of measurements that are available, there is recognition that the temporal variations in these signals may contain diagnostic information. These variations are described in terms of their amplitudes, frequencies, and repeatability in time. As a result the physician is increasingly reliant on technical analyses of signals which provide insights well beyond, or at least in finer detail than, those obtainable by traditional means. Furthermore, the physician likely does not have the technical training to fully evaluate the analysis methods and their strengths and weaknesses.

A further complication is that a reliable diagnosis often depends on the merging of information from different signals. Although such merging has always been a part of differential diagnosis in the medical field, the additional information available through sophisticated signal processing necessitates equally sophisticated methods of data merging and an appreciation of possible correlations among signals (because addition of a correlated signal to a data set may provide little novel information). Another practical limitation is that it may be impossible to sense those signals that are most directly related to the pathophysiology of interest, either because appropriate sensors are not available or because such measurement would be too invasive for use on human subjects. In such cases, signals that are correlated with the desired measurements and based on the physiology are sought. The ultimate objective, proving that a given collection of signals or of information derived from these signals is able to diagnose a specific disease process, depends on advanced statistical testing and is beyond the scope of this chapter.

This chapter considers biomedical signals that are functions in one dimension (i.e., time). Through widespread application of Fourier analysis, it is well recognized that most such signals can be represented as a summation of phase-shifted cosine waves having various frequencies; thus, one speaks of the frequency content of a signal, often using a compact representation of the power of each cosine wave in a signal versus its frequency – the power spectrum. Although it is correct that the representations of a signal as a time function (i.e., the time domain) and as a spectrum of power versus frequency (i.e., the frequency domain) contain *"the same"* information, it is sometimes easier to extract desired information from one representation than from the other. Thus, insightful analysis methods may be based in either domain.

Real-world biomedical signals often violate the simplifying assumptions inherent in various methods of signal analysis. Biomedical signals always contain noise components; and, many analysis methods make some assumption regarding the character of noise – e.g., it is additive, white, Gaussian. For some methods standard practice dictates that one should formally evaluate the characteristics of noise to ensure that assumptions are met; however, this evaluation often is not done. Furthermore, this task is complicated by the facts that the noise often is not white (Bruce, 1996), and it is often unclear where to draw the distinction between signal and noise. Typically this distinction must depend on knowledge of medicine/physiology rather than signal processing, although it may be aided by the latter. Another frequent assumption is that the properties of a signal do not change with time (although the chapter will also discuss analysis methods which can account for such changes).