Non-Linear Analysis of Heart Rate Variability

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Abstract—HRV signals can be viewed as discrete time series and treated as well through accepted mathematical procedures in order to find specific properties. These mathematical procedures can be linear or non-linear. Lately, non-linear analysis methods brought new and valuable results in HRV analysis and prediction. This paper deals with approximate entropy and sample entropy calculations in order to find unrevealed properties of these signals. The used signals are obtained from the MIT-BIH Long-term ECG database. The aim of this paper is to measure information theory based parameters as different entropies for different signals to emphasize non-linear dynamics in HRV in order to help cardiology specialists.

Keywords—HRV, nonlinear dynamics, approximate entropy, sample entropy.

I. INTRODUCTION

From over hundred years electrocardiogram (ECG) plays an important role in the analysis of human heart activity and the identification of different cardio-diseases. In an attempt to obtain a better understanding of the mechanisms of ECGs, procedures based on different theories such as information theory, chaos and fractal theory have been used to extract linear and nonlinear information from these signals.

Heart rate variability (HRV) analysis is a relatively new method for measuring the effects of interactions with the environment of human body. It is measured as the time difference between heart beats (named R peaks on regular ECGs) and its variations are correlated to health status. High HRV is an indication of healthy autonomic and cardiovascular response. Low HRV may indicate that the sympathetic and parasympathetic nervous systems aren’t properly coordinating to provide an appropriate heart rate response [8].

In 1996 a Task Force of the European Society of Cardiology (ESC) and the North American Society of Pacing and Electrophysiology (NASPE) defined and established standards of measurement, physiological interpretation and clinical use of HRV. Time domain indices, geometric measures and frequency domain indices nowadays constitute the standard clinically used parameters [15].

Electrophysiological time series (as HRV) are usually stochastic; lately using different new theories these have been identified as fractal-like and as being generated by scaling phenomena [14], [6].

There are many methods to study and analyze HRV signals; these are usually grouped under linear and non-linear methods. The linear methods are defined in time-domain (based on the beat-to-beat or NN (normal in sinus rhythm) intervals, which are analyzed through parameters as standard deviation of different intervals or differences, root mean square of successive differences, the number or proportion of different pairs of successive NNs that differ by more than a fixed time interval [15]) and frequency-domain (power spectral density computation by several parametric or non-parametric methods in different frequency bands of interest, which are typically high frequency (HF) from 0.15 to 0.4 Hz, low frequency (LF) from 0.04 to 0.15 Hz, and the very low frequency (VLF) from 0.0033 to 0.04 Hz) [1].

The most commonly used non-linear method of analyzing HRV is the Poincaré plot which quantifies by fitting mathematically defined geometric shapes to the data represented as a pair of successive beats. The graphical representation means that on x-axis is represented the current RR interval, while on the y-axis is the previous RR interval [2].

In this paper an information theory approach to supporting the analysis of HRV signal is proposed. Information theory parameters as sample entropy and approximate entropy of R-R intervals extracted from regular ECG signal were calculated and analyzed [9]. These parameters of R-R interval dynamics can exhibit different patterns. This paper presents approximate entropy and sample entropy computation applied to three different long term ECG signals obtained from MIT-BIH database.

II. NONLINEAR METHODS IN HRV ANALYSIS

A. Heart Rate Variability

The HRV recorded as time duration between two heartbeats or as a distance R-R (R being the peak of QRS complex) on a surface electrocardiogram (ECG) is strongly related to the activity of autonomic nervous system. This is irregular if measured in milliseconds. This variation is significant and is related to physiological (controlled by the autonomous nervous system) conditions. A reduction of HRV has been reported in several diseases.
Moreover, HRV also may have a prognostic value and is therefore very important in risk stratification [12]. Previous studies demonstrated a fractal-like complexity pattern in the variability of heart rate (HRV) which is possible to be measured, evaluated and quantified [9]. Fast variations (fluctuation) of HRV can reflect changes of sympathetic and parasympathetic activity; in other words, HRV is a noninvasive index of the autonomic nervous system’s control on the heart. Many studies suggested that mechanisms involved in the regulation of cardiovascular system interact with each other in a nonlinear way and that it is possible to study these mechanisms with several algorithms for non-linear signals and systems [10], [11]. Recent data suggest that non-linear mechanisms with several algorithms for non-linear signals other in a nonlinear way and that it is possible to study these heart. Many studies suggested that mechanisms involved in the fabrication of regularity and the unpredictability of fluctuations over time-series data. This entropic measure was first proposed on the chaotic systems measures used to quantify the degree of regularity and the unpredictability of fluctuations over time-series data. This entropic measure was first proposed by Pincus [2], and it exhibits a good performance in the characterization of randomness even when the data sequences are not very long. In order to compute the approximate entropy, the embedded dimension m, that is, the number of previous values for each vector is formed, where

\[ \phi^m(r) = \frac{1}{N-m+1} \sum_{i=1}^{N-m+1} \ln c^m_i(r) \]  

Parameter selection as length of data m and noise filter threshold r hardly depends on the chosen application. Approximate Entropy reflects the likelihood that similar shapes of observations will not be followed by additional similar observations [5].

b) Sample Entropy:

The sample entropy is the negative natural logarithm of the conditional probability that two sequences similar for m points remain similar for m + 1 points, where self-matches are not included in calculating the probability. Thus, a lower value of sample entropy also indicates more self-similarity in the time series. To be defined, sample entropy requires only that two templates similar for m samples remain similar for m + 1 samples. Distance between every pair of vectors \( x_i \) and \( x_j \) is computed as before (equation (3)). Then, for given \( x_i \), a probability function is computed as:

\[ C_i^m(r) = \frac{1}{N-m+1} \sum_{j=1,x\neq i}^{N} \mathcal{H}(r - d_{ij}) \]  

Where \( \mathcal{H} \) is the Heaviside function, defined as

\[ \mathcal{H}(z) = \begin{cases} 1 & \text{if } z > 0 \\ 0 & \text{if } z \leq 0 \end{cases} \]  

The probability that two sequences match for m points

\[ \Phi^m(r) = \frac{1}{N-m+1} \sum_{i=1}^{N-m+1} c^m_i(r) \]  

For \( m + 1 \), \( c^m_i(r) \) and \( \Phi^m(r) \) are calculated. Finally, sample entropy is:

\[ SE(n,r) = -\log \frac{\Phi_{m+1}(r)}{\Phi_m(r)} \]  

It is clear from the definition that \( \Phi_{m+1}(r) \) will always have a value smaller or equal to \( \Phi_m(r) \). Therefore, \( SE(n,r) \) will be always either be zero or positive value. A smaller value of \( SE(n,r) \) also indicates more self-similarity in data set or less noise.