

Classification of Biological Signals Based on Nonlinear Features

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Abstract—The problem of patient disorder classification and prediction from biological signals is addressed. We approach the problem from the perspective of nonlinear dynamical systems. Explored signals are ECG and EEG. We propose a combination of linear and nonlinear features for classification of four different types of heart rhythms through heart rate variability analysis. Classification accuracy is evaluated by three well-known machine learning algorithms: C4.5, support vector machines and random forest. The algorithms' success rates are compared. The method of combining linear and nonlinear measures shows promising results in heart rate variability modeling. Random forest method has exhibited 99.6% classification accuracy.

I. INTRODUCTION

Biological systems belong to a group of complex systems. As opposed to complicated systems which can be divided into parts, analyzed piece by piece and reconstructed back together based on the principle of superposition, the complex ones are more than the sum of their parts. They are nonlinear to a degree and can never be fully understood [1]. The best effort to understand complex systems is to describe them with a complicated model.

Physiological functions assessment of a particular biological system is based on a variety of clinical tests and measurements. Brain, heart, lungs, nervous and muscular systems are some of the most important physiological systems in human body that are analyzed in hospital environments daily. Noninvasive measurements are preferred in most cases, and invasive ones only when needed. Biological systems emit electrical currents that are the result of electrolytic activity in tissue cells. These currents are measured by positioning electrodes either on the skin of a patient or inserting them deeply into tissue.

The purpose of this work is to present a brief overview of nonlinear properties of electrocardiogram (ECG), more specifically, heart rate variability (HRV) signal. We also briefly mention the application of nonlinear methods in electroencephalogram (EEG) analysis. The concept of nonlinear deterministic system and the extraction of nonlinear features are elaborated. As an example of application of nonlinear analysis, a classification of several types of cardiac rhythms based on heart rate variability information was performed. The classification is based on a combination of linear and nonlinear features. Several well-known classifiers were used: C4.5, support vector machines and random forest.

The paper is organized as follows. In section II, some of the properties of nonlinear deterministic systems are presented. Also, the application of nonlinear dynamics to the study of ECG and EEG is elaborated. In section III, the methodology of heart rate variability analysis of cardiac rhythms is given. In section IV, we present the results. Section V is reserved for discussion, and in section VI we give a conclusion.

II. BACKGROUND

A. Nonlinear dynamics

Nonlinear analysis of complex biological signals does not have a long history. It can be verified that the early attempts to describe the nonlinear properties of ECG and EEG started as soon as it was realized that the signals themselves measure nonlinear biological processes. The development of Wolf algorithm for Lyapunov exponents, Grassberger-Procaccia method for correlation dimension and Takens embedding theorem in the 1980s led to a growing interest in nonlinear methods [2].

A nonlinear dynamical system is a system possessing memory of its previous states. Also, at least some of the equations that describe it are nonlinear. Any real biological system has nonlinear qualities. It is also dissipative, which means that it exchanges energy with its surroundings. Because of the fact that biological rhythms are generally not describable by a system of linear equations, they are considered to be nonlinear. Physiological systems have proven fractal complexity [3].

First attempt to assess the degree of nonlinearity, one can also say the level of deterministic chaos, in a signal is to draw its state space. Herein, an attraction to a position is usually observed. The object consisting of the system trajectory that converges to certain points is called an attractor. Depending on the underlying dynamics, one can obtain several kinds of attractors in state space, as shown in Fig. 1 [2].

When analyzing biological signals, it is however more probable that the type of attractor will be masked by noise and artifacts. Thus, it will not be clear to which general type of system does the signal belong, e.g. Fig. 2. This fact implicates that it may not be prudent to rely on nonlinear features only, because the linear ones might provide us with more information. Hence, a combined approach is usually preferred.

Two parameters are typically specified and modified when extracting nonlinear features: embedding (reconstruction)

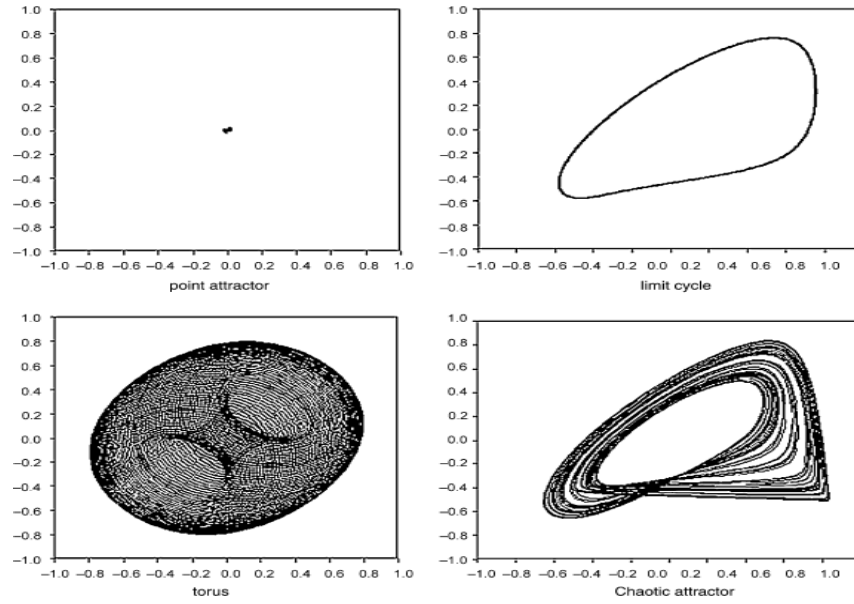


Fig. 1. State space for four basic types of attractors (units of X and Y axis are arbitrary): (top-left) Point attractor is the attractor of a linear dissipative system. Such a system converges to a single steady state; (top-right) Limit cycle is the attractor of a periodic system. Periodic dynamics creates a closed loop in state space; (bottom-left) Torus attractor is a more complex attractor that corresponds to quasi periodic dynamics of a system. It is a superposition of different periodic dynamics with incommensurable frequencies; (bottom-right) Chaotic or strange attractor is a highly complex object with fractal geometry. Its dynamics is deterministic chaos.

dimension (E or m) and interval (lag) (T or l). Embedding dimension is the dimension of the state space, i.e. the number of states that are monitored at a particular moment in time. Interval is the time span between each of these states. In a process where only significant events are recorded (point process), e.g. HRV, interval is the number of events between two observed events. A point in state space of dimension E , interval T , and at time point t is given by:

$$\vec{X}(t) = [x(t), x(t+T), \dots, x(t+(E-1)T)] \quad (1)$$

and the trajectory of k states of the system is:

$$\left\{ \vec{X}(n) \right\}, n = t, t+T, \dots, t+(k-1)T \quad (2)$$

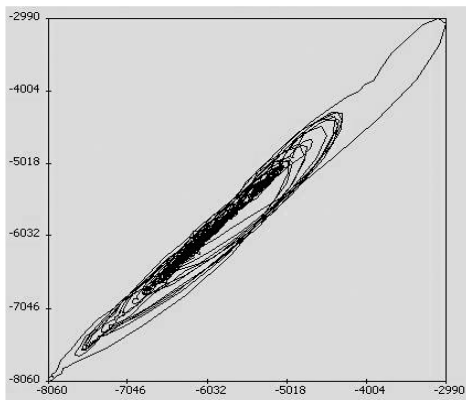


Fig. 2. State space of an ECG arrhythmia record with noise

There are several types of numerical nonlinear features that can be extracted from the state space of a system. The most common ones are: Lyapunov exponents [4], correlation dimension D_2 [5] and various kinds of entropy measures: approximate entropy [6], sample entropy [7], spectral entropy [8], multiscale entropy [7], and fuzzy entropy [9]. Additionally, a number of density measures exist that describe the morphology of the attractor, e.g. spatial filling index [10], central tendency measure [11]. Some of the aforementioned features are described more thoroughly in section III. More information on nonlinear dynamics can be found in [4].

B. Electrocardiogram and electroencephalogram analysis

A pioneer work of author [1] introduced the concept of non-linear dynamics into the field of cardiology. It is the non-linearity of the heart rhythm that is a good descriptor of a patient's overall health. ECG analysis has been perfected in recent years by increasingly sophisticated instruments and powerful computer tools. However, there is still an open question whether there is some additional important information contained within the signal, which has not yet been revealed. It is the goal of ECG analysis to successfully classify patient conditions based on the available signal features. If the condition can be successfully classified, there is a chance that its predictor model can also be constructed.

Although entire ECG signal can be studied using many known and explored methods e.g. time domain analysis, frequency analysis, and PCA, it is the nonlinear nature of the signal that poses a challenge for further research. It can be argued that HRV is more appropriate for nonlinear analysis than the whole signal itself, due to its high resistance to noise.

The work done by [12] clearly demonstrated the existence of non-linear components in HRV. Author [12] also pointed out that linear analysis using time and frequency is inadequate for obtaining complete information about HRV. The observation of the decrease in HRV in patients is often a predictor of coronary problems. The variability decrease has been associated with aging and is the result of progressive autonomic system dysfunction.

HRV analysis presents gratifying method for patient health assessment, because of the relative simplicity of obtaining the information and also because of its predictive potential [13]. Although the question of the prediction capabilities of using only HRV analysis of the heart rhythm has been addressed by many authors, there are very few studies that use real clinical data [14]. There is also a general sense of liberty as to the choice of the employed HRV measures. Hence, no conclusion was reached about the best choice of HRV features.

Today, most of the research done in the field of ECG analysis, particularly classification problems, includes the HRV analysis with at least some nonlinear features. It is the purpose of this work to demonstrate the efficacy of a combined linear and nonlinear approach, as further elaborated in section III.

The first observation of nonlinear properties of a sleep EEG in humans was reported by Babloyantz et al. in 1985 [2]. Afterwards, several research topics that included nonlinear features were investigated. Some of the research topics include: normal resting state (alpha rhythm), sleep, coma and anesthesia, epilepsy, psychopharmacology, perceptual and emotional states, depression and schizophrenia.

One of the most explored topics in nonlinear EEG analysis is epilepsy. It has been shown that nonlinear analysis techniques allow for an improved characterization of epileptic brain states and help to gain deeper insights into the spatial and temporal dynamics of the epileptic process. Univariate nonlinear techniques achieve a successful localization (in retrospective) of epileptogenic zone in roughly 90% of cases. Multivariate nonlinear techniques are used in evaluating interdependencies between brain regions, allowing the assessment of the range of seizure interactions. Current state-of-the-art is an unequivocal identification of precursors to seizures. Thus, nonlinear analysis is of great value in the development of seizure warnings and preventive measures [15].

III. METHODS

A. System description

First part of the analysis was to obtain relevant ECG HRV records. For this purpose, we used several databases from the PhysioBank collection of databases [16]. A total of 100 patient annotation records were prepared as an input to the extraction process. Annotation records contain the times and types of heart beat. Four types of heart conditions were inspected: normal rhythm, any arrhythmia, supraventricular arrhythmia, and congestive heart failure. Each heart condition was represented by 25 annotation records of five minutes duration.

A combination of 11 linear and nonlinear features was extracted from patient data. HRV guidelines [13] recommend the use of four standard linear HRV features: three statistical measures and one geometric measure. This recommendation was respected and pursued in this work. In addition, seven nonlinear features were also extracted from cardiac rhythms. HRV linear features extracted are as follows: SDNN, RMSSD, pNN20, and HRV triangular index (HTI). HRV nonlinear features include: spatial filling index (SFI), central tendency measure (CTM), correlation dimension D2, and four features for approximate entropy (ApEn1–ApEn4).

B. Features

1) *SDNN*: standard deviation of the NN (or beat-to-beat) interval is one of the simplest HRV linear features to calculate. It reflects all the cyclic components responsible for variability in the period of recording. It can be calculated for long-term or short-term recordings [13]. In our case, the feature was extracted from short-term, five minutes recording of NN intervals.

2) *RMSSD*: RMSSD is the square root of the mean squared differences of N successive NN intervals. It can be calculated using the expression [13]:

$$RMSSD = \frac{\sqrt{\sum_{i=1}^{N-1} (x_{i+1} - x_i)^2}}{N} \quad (3)$$

where x_i denotes the length of an NN interval with index i .

3) *pNN20*: pNN20 is the ratio of the number of interval differences of successive NN intervals that are greater than 20 ms and the total number of NN intervals. pNN20 is advocated as a measure better suited than the standard pNN50 [13], [17].

4) *HRV triangular index*: HRV triangular index (HTI) is a geometric measure of HRV. It measures the integral of the density distribution. In discrete scale it is approximated as a total number of all NN intervals divided with the number of NN intervals in the modal bin. HTI is dependent on the length of the bin, i.e. sampling frequency of the ECG record. Because the examined records had different sampling frequencies, smallest time difference between two observed NN intervals was used as the length of the bin.

5) *Spatial filling index*: Spatial filling index is a quantitative description of the density of points of an attractor. It is defined by the expression:

$$\eta = \frac{s}{n^2} \quad (4)$$

where n^2 is the total number of squares used in state space division, and s is the sum of the point distribution in state space:

$$s = \sum_{i=1}^n \sum_{j=1}^n \left(\frac{c_{ij}}{m} \right)^2, \quad m = \sum_{i=1}^n \sum_{j=1}^n c_{ij} \quad (5)$$

c_{ij} is the number of points falling into a specific square (i,j) in state space. The order of magnitude for η is 10^{-3} and it rises with greater concentration of points to a certain region in an attractor [10].

6) *Central tendency measure*: Central tendency measure (CTM) is a quantitative measure of variability for second-order difference plot [11]. Its idea is similar to SFI, because it is also a nonlinear measure that shows the concentration of points in a diagram. However, it is used on the second-order difference diagram, i.e. $[x(t+2) - x(t+1)]/[x(t+1) - x(t)]$ diagram. A point in the second-order difference plot in E dimensions is given by

$$\vec{X}(t) = [x(t+T) - x(t), \dots, x(t+ET) - x(t+(E-1)T)] \quad (6)$$

Usually only two dimensions are examined in literature. CTM can be generalized into E dimensions as:

$$CTM = \sum_{i=1}^{N-E} \delta(d(t)) \quad (7)$$

where

$$\delta(d(t)) = \begin{cases} 1, & \sqrt{(x(t+T) - x(t))^2 + \dots + (x(t+ET) - x(t+(E-1)T))^2} < r \\ 0, & \text{otherwise} \end{cases} \quad (8)$$

N is the number of analyzed NN intervals, T is the number between two measured NN intervals and r is the central area radius, dependent on data.

7) *Correlation dimension*: Definition of the correlation dimension D_2 of an attractor is given as:

$$D_2 = \lim_{l \rightarrow 0} \frac{\log \left(\sum_{i=1}^{M(l)} p_i^2 \right)}{\log l} \quad (9)$$

The second order of probability $p_i = \frac{c_i}{m}$, $m = \sum_{i=1}^{M(l)} c_i$ (c_i is the number of points in i -th cell of length l), is a good estimate of the attractor. D_2 is practically determined by calculating the correlation integral $C(N, l)$, which shows the mean probability that the points in the phase space at two different times points are close to each other [5]:

$$C(N, l) = \lim_{N \rightarrow \infty} \frac{1}{N^2} \sum_{i=1}^{N-1} \sum_{j=i+1}^N \Theta \left[l - \left| \vec{x}_i - \vec{x}_j \right| \right] \quad (10)$$

where $\Theta[\cdot]$ is the Heaviside step function: $\Theta(x) = \begin{cases} 1, & x > 0 \\ 0, & x \leq 0 \end{cases}$.

Once the correlation integral has been determined, correlation dimension is calculated according to the slope in the diagram $\frac{\log_2 C(N, l)}{\log_2 l}$. Correlation dimension enables the estimation of

the smallest possible embedding dimension of an attractor, thus revealing the degree of determinism in the system.

8) *Approximate entropy*: Approximate entropy (ApEn) is a measure used to quantify the regularities in data without *a priori* knowledge of the problem. In essence, it shows the probability that similar observational patterns do not repeat. If a time series demonstrates complex, irregular behavior, it will have a high ApEn measure. The algorithm for determining ApEn is given in [6]. Final expression for ApEn is:

$$ApEn(m, r, N) = \phi^m(r) - \phi^{m+1}(r) \quad (11)$$

Parameters m and r are determined based on the specific problem.

$$\phi^m(r) = \frac{1}{N-m+1} \sum_{i=1}^{N-m+1} \ln \frac{N^m(i)}{N-m+1} \quad (12)$$

where $N^m(i)$ is the number of $\vec{X}(i)$ that compare to $\vec{X}(j)$, $j=1, \dots, N-m+1$, $j \neq i$, in a way that distance between the points satisfies relation:

$$\max_{k=1,2,\dots,m} |x(i+k-1) - x(j+k-1)| \leq r \quad (13)$$

In this work, we took $m=1$ and four values for r . Thus ApEn1 is calculated for $r=0.1\sigma$, ApEn2 for $r=0.15\sigma$, ApEn3 for $r=0.2\sigma$, and ApEn4 for $r=0.25\sigma$, where σ is the time series' standard deviation.

C. Classification algorithms

In order to evaluate the efficiency of the proposed combination of features, a classification of patient records was performed using three well-known classifiers in Weka system: C4.5, support vector machines and random forest. Here we give a brief explanation of the employed classifiers. More information can be found in [18], [19].

1) *C4.5*: C4.5 is the landmark decision tree algorithm developed by Quinlan. C4.5 was used with a minimum amount of six instances per leaf. Six instances per leaf were used instead of the standard two in order to ensure that only relevant leaves are taken into consideration. We used C4.5 method for pruning trees with subtree raising option enabled.

2) *Support vector machines*: Support vector machines (SVM) belong to a general field of kernel-based machine learning methods and are used to efficiently classify both linearly separable and linearly inseparable data. Support vector machines have been successfully used in HRV analysis [20]. Weka platform implements a standard algorithm for the resolution of quadratic programming optimization problem

that arises when determining the maximum margin hyperplane of the support vector machine classifier. This algorithm is called Sequential Minimal Optimization algorithm (SMO). In our work, we used both linear SVM and squared polynomial SVM, varying parameters until an optimal setting was found ($c=4.0$, exponent=1.0 or exponent=2.0, no data normalization).

3) *Random forest*: Random forest (RF) is the state-of-the-art classifier developed by [19]. The forest contains a number of decision trees that choose their splitting attributes from a random subset of k attributes at each internal node and vote for the majority class. The trees are built without pruning, as opposed to C4.5. Because of the combination of bootstrap sampling procedure and random attribute subset, RF ensures at the same time the smallest obtainable bias and very low data variance. In this work, a forest consisting of seven trees was adequate for the classification task.

IV. RESULTS

Three types of analyses were performed. First, we used classification algorithms on all four patient record types. The number of feature vectors per record type is 125 because five feature vectors per record were used. These five feature vectors contain features for representative intervals $T = \{1, 2, 5, 10, 20\}$.

Second, we evaluated the features in two-class classification case. Herein, one class of patients has a normal heart rhythm and the other class contains records with a heart disorder. Analysis was performed on the following combinations: normal-arrhythmia, normal-supraventricular arrhythmia, normal-congestive heart failure.

Third, the extracted features themselves were evaluated. Statistical measures used in the analyses were: total classification accuracy for four patient classes and total classification accuracy (positive prediction), sensitivity and specificity for two patient classes' case. A 10*10-fold cross-validation technique was used in order to randomize the input samples and obtain representative classification accuracy.

A. Classification of four patient classes

Classification results for four patient classes are presented in Table I. The classification performed shows some interesting results. The best classification accuracy was achieved by RF and squared SVM algorithms. There were no significant differences observed between the results of these two methods. C4.5 also gave high results (above 90%), but lower compared to the other two algorithms. Linear SVM gave the least satisfactory results.

TABLE I

CLASSIFICATION RESULTS FOR FOUR PATIENT CLASSES

Classifier	Total classification accuracy, %
C4.5	92.2
SVM (linear)	73.5
SVM (squared)	98.4
RF	99.6

B. Classification of two patient classes

Classification results for two patient classes are given in Table II. It can be observed that two classes' case shows an increase in classification accuracy compared to the four classes' case, as was expected. Best results are obtained when discerning normal heart rhythm from any arrhythmia. Nevertheless, the results for the other two pairs follow close behind.

RF demonstrated very high classification accuracy; squared SVM gave second best results and C4.5 third. Again, the results from linear SVM were the worst.

C. Feature evaluation

It is important to determine which of the extracted 11 features contribute in the greatest extent to the quality of the obtained results. Because of the difficulty in establishing objective contribution of a particular feature to the classification accuracy, we opted for a rather simple, but justified approach. As a test bench, we use feature vectors obtained from four classes of patients, the same as in the classification process presented in subsection A. We classified patient records using only one feature at the time. For this purpose, we employ a simple 1-Rule algorithm [18] with the bucket size of 15 vectors. The classification results are presented in Fig. 3.

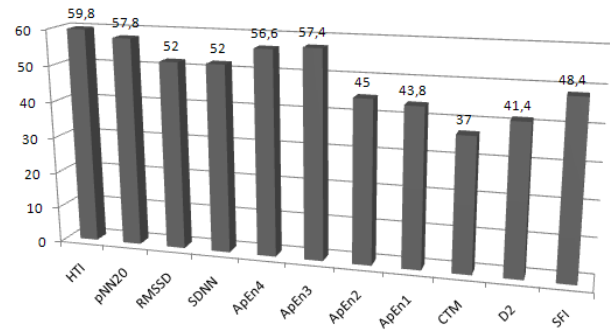


Fig. 3. Classification results for four patient classes using a single feature

HRV triangular index (HTI) was shown to be the most prominent feature, followed by pNN20, ApEn3, ApEn4, SDNN and RMSSD. The least satisfactory classification results were obtained for D₂ and CTM features. It can be observed that both linear and nonlinear features contribute significantly to the model, although the influence of linear measures is somewhat greater.

V. DISCUSSION

The application of nonlinear measures assumes the existence of deterministic chaos. However, the records themselves have not been analyzed in order to reject other options, such as nonlinear randomness or linear determinism. Thus, the HRV of patients used in this study does not necessarily behave in a nonlinear deterministic way, but the methods themselves were nevertheless applied for their

TABLE II
CLASSIFICATION RESULTS FOR TWO PATIENT CLASSES

Two classes		C4.5	SVM (linear)	SVM (squared)	RF
Normal and Arrhythmia	Total classification accuracy, %	99.6	96.4	100.0	100.0
	Sensitivity, %	99.2	96.0	100.0	100.0
	Specificity, %	100.0	96.8	100.0	100.0
Normal and Supraventricular Arrhythmia	Total classification accuracy, %	93.2	74	97.6	99.5
	Sensitivity, %	94.4	73.6	97.6	99.8
	Specificity, %	92.0	74.4	97.6	99.2
Normal and Congestive heart failure	Total classification accuracy, %	98.8	81.5	99.2	99.7
	Sensitivity, %	99.2	77.2	100.0	99.9
	Specificity, %	98.4	87.4	98.4	99.5

analysis. In any hospital system, the prerequisite of nonlinear determinism would have to be established prior to the analysis. Nevertheless, it was our goal to show that any record, regardless of its linear or nonlinear behaviour can be classified efficiently using the combined 11 features.

The calculation of correlation dimension and other nonlinear features was performed in two-dimensional embedding space. Because of the low-dimensionality, it is possible that the influence of nonlinear features was underrated. Because of the very nature of HRV, it is possible that true potential of nonlinear methods lays hidden in higher dimensions, which should be examined in more detail in further work.

We also have to mention that there is a larger number of different arrhythmia types existing in the records from the MIT-BIH Arrhythmia Database, which was used for obtaining records of type any arrhythmia. We recommend assessing different arrhythmia categories as separate heart disorders using the features employed in this work as a topic of further research. However, one should bear in mind that some disorders are not covered with a significant number of patient records to allow reliable estimation of classification results.

VI. CONCLUSION

We have reviewed the widespread use of features from nonlinear dynamics. The apparent complexity of biological signals suggests the use of a combined linear and nonlinear approach for obtaining high quality model of the underlying phenomena. Classification of several cardiac rhythms shows promising results. Linear and nonlinear features both seem to contribute to the acquired model. More thorough analyses need to be performed in order to establish enough evidence for successful implementation of the nonlinear methods in hospital environments.

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