ATINER CONFERENCE PAPER SERIES No: COM2013-0596

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ATINER's Conference Paper Series
COM2013-0596

A Mathematical Information Algorithm for the Analysis of ECG Complexity

Dovile Karaliene
PhD Student
Kaunas University of Technology
Lithuania

Zenonas Navickas
Professor
Kaunas University of Technology
Lithuania

Agne Slapsinskaite
Master's Student
Lithuanian University of Health Sciences
Lithuania

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Athens Institute for Education and Research
8 Valaoritou Street, Kolonaki, 10671 Athens, Greece
Tel: + 30 210 3634210 Fax: + 30 210 3634209
Email: info@atiner.gr URL: www.atiner.gr
URL Conference Papers Series: www.atiner.gr/papers.htm

ISSN **2241-2891**
1/10/2013

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This paper should be cited as follows:

Karaliene, D., Navickas, Z. and Slapsinskaite, A. (2013) **"A Mathematical Information Algorithm for the Analysis of ECG Complexity"** Athens: ATINER'S Conference Paper Series, No: COM2013-0596.

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Dovile Karaliene
PhD Student
Kaunas University of Technology
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Master's Student
Lithuanian University of Health Sciences
Lithuania

Abstract

The last years studies showed that the complexity in human body functioning is important area of research. The complexity of ECG signals is an important characterization of a process and might be used as a diagnostic tool. ECG parameters have different duration and could show the complexity in different fractal levels. A number of methods have been used for the analysis of ECG complexity. These methods evaluates global features of processes but are not able to detect local features of dynamical processes.

In this paper is presented the mathematical information algorithm based on the concept of the rank of a sequence. The task of the presented algorithm is to develop strategy for finding algebraic progression to each segment of time series of the ECG parameters. This algorithm was integrated into software for the analysis of ECG complexity. This software was applied for the analysis of physiological processes in a bicycle ergometry test. The practical experience has shown that this software can be effectively used for the analysis of ECG parameters although ECG signals are contaminated with noise.

Keywords: the rank of a sequence, complexity analysis, ECG parameters

Corresponding Author:

Introduction

According to the available statistics each year cardiovascular disease causes over 4 million deaths in Europe, its about 47% of all deaths in Europe and 40% in the European Union (European Cardiovascular Disease Statistics, 2012). So timely diagnosis of cardiovascular diseases is one of the most important problems not only in medical but also in social terms. The main feature of the physiological systems – their complexity "hidden" in the biomedical signals (Berskiene K. 2010). The processing of these signals in terms of complex systems provides the possibilities to perceive the system components and dynamic interrelationships. The basic cardiovascular research, widely used in clinical practice is an electrocardiogram (ECG) recording and its parameters analysis. ECG parameters have different duration (larger structures could be associated with longer time scales) and could show the complexity in different fractal levels (Vainoras A. 2009; Venskaityte E. 2011)

A number of various mathematical methods, algorithms and computerized ECG analysis systems have been proposed for the analysis of ECG complexity, for example, entropy-based algorithms (Pincus M. S. et al. 1991; Pincus M. S. et al. 2006; Costa M. et al. 2006), spectral analysis (Yeragani V. et al. 2005), chaos-based algorithms (Sliupaite A. et al. 2009; Ubeyli E. D. 2009), hidden Markov chains (Cohen A. 1998), Lempel-Ziv method (Zhou S. et al. 2011) and other methods. Most of these analysis algorithms are heuristic and evaluate global features of processes and are not able to detect local features of dynamical processes.

The main objective of this paper is to present the algorithm of a new mathematical method (Karaliene D. et al. 2012) for ECG complexity analysis. This method is based on the concept of the rank of a sequence (Navickas Z. et al. 2006). The concept of the rank of a sequence have been successfully used to express solutions of nonlinear differential equations in forms comprising ratios of finite sums of standard functions (Navickas Z. et al. 2010; Navickas Z. et al. 2011; Ragulskis M., Navickas Z. et al. 2011), for time series forecasting (Ragulskis M., Lukoseviciute K. et al. 2011), logistic-matrix representation (Navickas Z. et al. 2012) and research of chaos (Ragulskis M., Navickas Z. 2011; Ragulskis M., Navickas Z. et al. 2012).

The proposed algorithm was integrated into MATLAB Toolbox for the analysis of ECG complexity and was tested using experimental data performed during an bicycle ergometry test. An experimental result has shown that this software can be effectively used for the analysis of ECG parameters although ECG signals are contaminated with noise.

This paper is organized as follows. In Section 2, we present the concept of the rank of a sequence and its application for the reconstruction of a given sequence. Then is Section 3, we present a mathematical information algorithm based on the concept of the rank of a sequence. Finally, developed software for the analysis of ECG complexity and some ECG analysis examples are presented in Section 4.

Preliminaries

Let us consider a sequence: $p_0, p_1, ... := (p_j; j \in Z_0)$ where elements p_j can be real or complex numbers. Then, a sequence of Hankel matrixes reads:

$$H_n := (p_{i+j-2})_{1 \le i,j \le n} = \begin{bmatrix} p_0 & p_1 & \cdots & p_{n-1} \\ p_1 & p_2 & \cdots & p_n \\ & & \cdots & \\ p_{n-1} & p_n & \cdots & p_{2n-2} \end{bmatrix}, \quad n = 1,2,... \tag{1}$$

The Hankel transform (the sequence of determinants of Hankel matrixes) $(d_n; n \in N)$ reads:

$$d_n := \det H_n \tag{2}$$

Definition 1. The sequence $(p_j; j \in Z_0)$ has a rank $m \in Z_0; m < +\infty$:

$$Hr(p_j; j \in Z_0) = m \tag{3}$$

if the sequence of determinants of Hankel matrixes has the following structure:

$$(d_1, d_2, ..., d_m, 0, 0, ...) \tag{4}$$

where $d_m \neq 0$ and $d_{m+1} = d_{m+2} = ... = 0$.

Example 1. Let $p_j := j^2$, $j \in Z_0$. Then, $Hr\left(j^2; j \in Z_0\right) = 3$ because the sequence of determinants of Hankel matrices reads $(0,-1,-8,0,0,\ldots)$.

Definition 2. Let $Hr\left(p_j; j \in Z_0\right) = m$. Then the characteristic Hankel determinant for the sequence $(p_j; j \in Z_0)$ is defined as (Navickas Z. et al. 2006):

$$\hat{d}_m := \det \hat{H}_m := \begin{vmatrix} p_0 & p_1 & \cdots & p_m \\ p_1 & p_2 & \cdots & p_{m+1} \\ \cdots & \cdots & \cdots & \cdots \\ p_{m-1} & p_m & \cdots & p_{2m-1} \\ 1 & \rho & \cdots & \rho^m \end{vmatrix} = 0. \tag{5}$$

The expansion of the determinant in Eq. (5) yields an *m*-th order algebraic equation for the determination of roots of the characteristic equation:

$$A_m \rho^m + A_{m-1} \rho^{m-1} + ... + A_1 \rho + A_0 = 0 \tag{6}$$

where $A_m \neq 0$ because $A_m = d_m \neq 0$.

We have assume, that $\mu_{rg} \binom{j}{g} \rho_r^{j-g} = 0$ if $\binom{j}{g} = 0$ what is true when $0 \le j < g$. Moreover, $0^0 = 1$; $0^1 = 0^2 = ... = 0$. Then the following theorem holds.

Theorem 1. Let $Hr\left(p_j;\, j \in Z_0\right) = m$ and the recurrence indexes of roots $\rho_1, \rho_2, \rho_3, ..., \rho_c$ of the characteristic equation (Eq. (6)) are $m_1, m_2, ..., m_c$ $(c = 1,2,3,...)$ accordingly; $\sum_{r=1}^{c} m_r = m$. Then the following equality holds true:

$$p_j = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \mu_{rg} \binom{j}{g} \rho_r^{j-g} \tag{7}$$

where $\mu_{rg}, \rho_r \in C$; $\mu_{rm_r-1} \neq 0$.

Rigorous proof of this theorem is given in (Navickas Z. et al. 2006).

Definition 3. A sequence $(p_j;\, j \in Z_0)$ is an algebraic progression if elements of that sequence can be expressed in the form of Eq. (7).

Corollary 1. Eq. (7) can be rewritten in the following form:

$$\sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \mu_{rg} \binom{j}{g} \rho_r^{j-g} = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \frac{\mu_{rg}}{\rho_r^g} \frac{j!}{g!(j-g)!} \rho_r^j = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \hat{\mu}_{rg} j^g \rho_r^j \tag{8}$$

where $\rho_1, \rho_2, ..., \rho_c \neq 0$; $\mu_{rm_r-1} \neq 0$ and $\hat{\mu}_{rg}$ do not depend on *j*.

Corollary 2. In case when all roots of the characteristic equation are different, Eq. (7) obtains a more simple form:

$$p_j = \sum_{r=1}^{m} \mu_r \rho_r^j \tag{9}$$

It can be also noted that coefficients μ_{rg} (or just μ_r) can be found solving the linear algebraic system of equations ($\rho_1, \rho_2, ..., \rho_c$ are determined beforehand):

$$\sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \binom{j}{g} \rho_r^{j-g} \mu_{rg} = p_j,\ j = 0,1,...,m-1 \tag{10}$$

This linear system of algebraic equations has one and the only one solution (Navickas Z. et al. 2006).

Corollary 3. Let $Hr(p_j;\, j \in Z_0) = m$ and the first *2m* elements of that series are known. Then it is possible to use Eq. (6), Eq. (10) and Eq. (7) to calculate all elements of that sequence.

Corollary 4. Let Eq. (3) holds true. Then can be noted that accordingly to Eq. (8) the following equality holds true:

$$\begin{aligned} q_j = q_j(k,h) = p_{k+hj} = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \hat{\mu}_{rg} (k+hj)^g \rho_r^{k+hj} = \\ = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \tilde{\mu}_{rg} \rho_r^k \cdot j^g \cdot \left(\rho_r^h\right)^j = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \tilde{\mu}_{rg} \tilde{\rho}_r^k \cdot j^g \cdot \tilde{\rho}_r^j, . \end{aligned} \tag{11}$$

where $j \in Z_0$, $k = 0,1,2,...$, $h = 1,2,3,...$, $\rho_1, \rho_2, ..., \rho_c \neq 0$; $\mu_{rm_r-1} \neq 0$; $\tilde{\mu}_{rg} \rho_r^k$ do not depend on *j* and

$$\tilde{\rho}_r = \rho_r^h. \tag{12}$$

Then the rank of a subsequence $(q_j; j \in Z_0)$ with all $k \in Z_0$, $h \in N$ is equal to:

$$Hr(q_j; j \in Z_0) \le m. \tag{13}$$

Next the inverse task will be needed. It is to obtain the algebraic progression of sequence p_j, $j \in Z_0$ then is known an algebraic progression q_j (Eq. (12)) and parameters *h*, *k*. Then accordingly to Eq.(12) ρ_r can be expressed in the form:

$$(\rho_r)_a = \sqrt[h]{|\tilde{\rho}_r|} \cdot \exp\left(\frac{i(\arg \rho_r + 2\pi a)}{h}\right) \tag{14}$$

where $|\tilde{\rho}_r| \ge 0$, $\sqrt[h]{|\tilde{\rho}_r|} \ge 0$ and $-\pi \le \arg \tilde{\rho}_r < \pi, a = 0,1,...,h-1.$

But values of ρ_r is the only one (it is then $a = a_0$) in the algebraic progression of p_j, $j \in Z_0$:

$$(\hat{p}_j)_{a_0} = \sum_{r=1}^{c} \sum_{g=0}^{m_r-1} \hat{\mu}_{rg} \cdot j^g \cdot (\rho_r)_{a_0}^j \tag{15}$$

where values $(\rho_r)_{a_0}$ can be selected minimizing the root mean square error:

$$R\left((\hat{p}_j)_{a_0}\right) = \min_a \sqrt{\frac{1}{\eta} \sum_{j=0}^{\eta} \left((\hat{p}_j)_a - p_j\right)^2} \tag{16}$$

where $\eta \in N$ which allows estimating a value of a_0.

It can be noted that coefficients $\hat{\mu}_{rg}$ (Eq. (15)) can be found solving the linear algebraic system of equations.

Algorithm for the Analysis of ECG Complexity

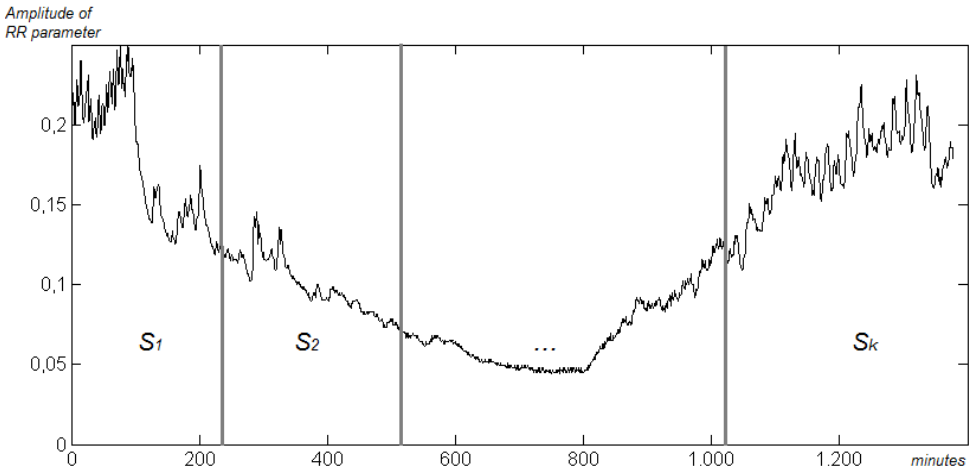
Let $P = (p_0, p_1,..., p_{L-1})$ the time series of ECG parameter of length *L* consisted of several segments of algebraic progressions (Eq. (7)). Then it could be possible to distinguish sequence *P* into non-overlapping contiguous segments by constructing algebraic progressions of each segment (Karaliene D. et al. 2012). Unfortunately, time series of ECG parameters usually are noisy and proposed method (Karaliene D. et al. 2012) can't be applied directly.

Let time series of ECG parameters *P* is segmented manually into *k* non-overlapping contiguous segments (Figure 1):

$$S := \bigcup_l S_l, l = \overline{1,k}$$

where $S_l = S_l(u_l, v_l) = (p_{u_l}, p_{u_l+1},..., p_{v_l})$, $u_l \le v_l$, u_l is the start and v_l - the end position of segment $S_l, l = \overline{1,k}.$

Figure 1. *ECG parameter segmentation*



Below is presented information algorithm (Algorithm 1) based on the proposed metodology (Karaliene D. et al. 2012). The main interactions between steps of a given algorithm are shown in activity diagram (Figure. 2).

The main task of the algorithm is to find an algebraic progression $\hat{p}_j^{(l)}, j=\overline{0,n_l},\ n_l=v_l-u_l+1$ of segment $S_l, l=\overline{1,k}$ with the condition:

$$\sqrt{\frac{1}{n_l}\sum_{j=0}^{n_l}\left(\hat{p}_j^{(l)}-p_j^{(l)}\right)^2}\le\varepsilon_1 \tag{17}$$

and accordingly to the conditions (18) and parameter $\varepsilon_2\ge 0$ to calculate the counts of (a) stationary, (b) stimulant and (c) inhibitory components of the each observed ECG parameter segment $S_l, l=\overline{1,k}$.

$$\begin{aligned}
&\text{a)}\ \omega_{j,0}^{(l)}=\sum_{k:|\hat{\rho}_k|=1\pm\varepsilon_2}\hat{\mu}_k\hat{\rho}_k^j,\ j\in Z_0,\\
&\text{b)}\ \omega_{j,1}^{(l)}=\sum_{k:|\hat{\rho}_k|>1\pm\varepsilon_2}\hat{\mu}_k\hat{\rho}_k^j,\ j\in Z_0,\\
&\text{c)}\ \omega_{j,-1}^{(l)}=\sum_{k:|\hat{\rho}_k|<1\pm\varepsilon_2}\hat{\mu}_k\hat{\rho}_k^j,\ j\in Z_0.
\end{aligned} \tag{18}$$

where $\hat{p}_j^{(l)}=\omega_{j,-1}^{(l)}+\omega_{j,0}^{(l)}+\omega_{j,1}^{(l)},\ j\in Z_0.$

The detailed methodology of the algorithm is given at (Karaliene D. et al. 2013).

Algorithm 1.

Input: $S:=\bigcup_l S_l, l=\overline{1,k},\ S_l=S_l(u_l,v_l), u_l\le v_l,\ 0<\varepsilon_1\le 1,\ \varepsilon_2\ge 0$

Step 1. Get sequence $p_j^{(l)}=(p_{u_l}, p_{u_{l+1}},..., p_{v_{l+1}})\in C,\ j=\overline{0,n_l}, n_l=v_l-u_l+1$ of segment $S_l(u_l,v_l)$

Step 2. Generate all possible combinations of parameters $\left(v_l, u_l, \tilde{k}_l, \tilde{h}_l, \tilde{m}_l\right)$ for a given sequence $p_j^{(l)} \in C,\ j = \overline{0, n_l}$ with conditions: $\tilde{h}_l \geq 2,\ v_l = u_l + 2m_l h_l - h_l$

Step 3. Compute algebraic subsequence $q_j = q_j(\tilde{k}_l, \tilde{h}_l) = p^{(l)}_{\tilde{k}_l + \tilde{h}_l j},\ j = \overline{0, n_l}$ with generated parameters $\left(v_l, u_l, \tilde{k}_l, \tilde{h}_l, \tilde{m}_l\right)$ combination.

Step 4. Construct the characteristic Hankel determinant $\hat{d}_{\tilde{m}_l} := \det \hat{H}_{\tilde{m}_l}$ by using generated subsequence $q_j,\ j = \overline{0, n_l}$.

Step 5. Form the characterizing polynomial Eq. (6) and evaluate all zeros (Eq. (12)) $\tilde{\rho}_r \in C, r = 0,1,..., \tilde{m}_l$.

Step 6. Accordingly Eq. (15) and Eq. (16) compute values $\rho_r \in C, r = 0,1,..., \tilde{m}_l$.

Step 7. Compute $\mu_{rg}, g = 0,1,..., m_r - 1; r = 1,..., c,\ \sum_{r=1}^{c} m_r = \tilde{m}_l$ as the solution of the linear algebraic system of equations Eq. (10).

Step 8. Construct algebraic progression $\hat{p}_j^{(l)}$ (Eq. (10)) using computed parameters ρ_r and $\mu_{rg}, g = 0,1,..., m_r - 1; r = 1,..., c.$

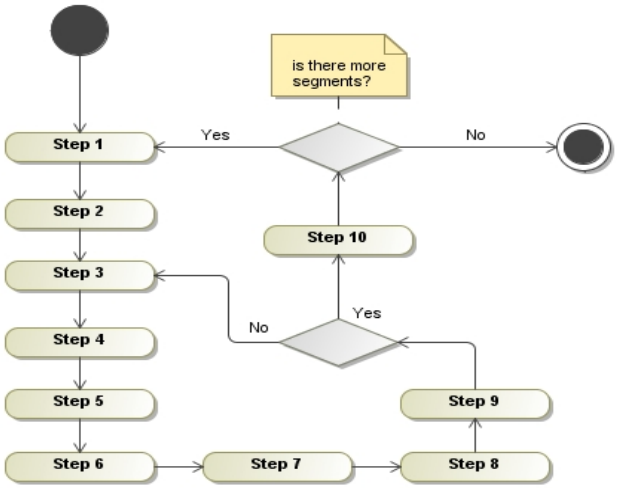
Step 9. If condition Eq. (17) is true then output parameters: $\rho_r, r = 1,..., c$ else repeat *Step 3* to the new subsequence $q_j = q_j(\tilde{k}_l, \tilde{h}_l) = p^{(l)}_{\tilde{k}_l + \tilde{h}_l j},\ j = \overline{0, n_l}$ with other parameters $\left(v_l, u_l, \tilde{k}_l, \tilde{h}_l, \tilde{m}_l\right)$ combination.

Step 10. Distinguish (using Eq. (18)) and count stationary, stimulant and inhibitory components with given $\varepsilon_2 \geq 0$ of the segment $S_l(u_l, v_l)$.

Repeat *Step 1* for a new $S_l(u_l, v_l)$ segment.

Output: Counts of stationary, stimulant and inhibitory components of the each segment $S_l = S_l(u_l, v_l),\ u_l \leq v_l,\ S := \bigcup_l S_l, l = \overline{1, k}$.

Figure 2. *Activity diagram for the Algorithm 1*



Software & Experiment

Given above algorithm was integrated in to MATLAB Toolbox for the analysis of ECG complexity. Toolbox consists of two modules: data preparing (Figure. 3) and data analysis (Figure. 4).

For the experiment were selected ECG data of healthy participants (20,1±2,23 years age). Data were performed during an bicycle ergometry test (Karaliene D. et al. 2013). The aim of this experiment was to explore the local changes of different ECG parameters in dynamic.

In finding a starting point to explain the pattern of results it is necessary to remind that ECG parameters that are examined reveal different complexity levels e.g. *RR* interval helps to characterize the state of organism in regulatory level, *JT* interval represents the metabolic reactions of the systems and *QRS* reflect the intrinsic regulatory state of the organ.

Each time series of ECG parameter were segmented into 11 non-overlapping segments where 1 segment represented the rest, 2-6 - the load and 6-11 - the recovery interval (Figure 3). In the toolbox complexity analysis could be made for one or for all ECG parameters of the same person or for all input data (it is for group of persons) (Figure 4). In the last case there are calculating the normalized values of inhibitory, stationary and stimulant processes dividing the counts of each process components to the total number of all counted components at each segment. For example, the normalized values of inhibitory (a), stationary (b) and stimulant (c) processes of *RR* parameters are shown at Figure 4.

Given results showed that the beginning of the physical load starts the inhibitory process begin to lead and is mostly expressed at the last segment of the load in this case it is 5 to 6 segments (Figure. 4 (a)). As expected, the influence of the stimulant process decreases (Figure. 4(c)) especially in the last segment of the load. This phenomenon can be explained physiologically - working muscles try to satisfy the expanded energetic demand during the physical load while other organs of the human body have to adapt to lowered supply. The next interesting finding related to complexity of ECG intervals *RR*, *JT* and *QRS* is the delay in recovery processes. For example, in the first segment of recovery *RR* interval shows contrary situation of influencing process - stimulant processes rapidly increase (Figure. 4(c) from 6-th to 7-th segment) while inhibitory process reacts to opposite direction. It can illustrate that recovery processes are not synchronous in different human body systems More about experimental results can be found at (Karaliene D. et al. 2013).

Results & Discussion

Changes of ECG parameters could be very quick and application of statistical technologies or Fourier transform analysis is not always possible. It is important to separate time series of ECG parameters into intervals where similar physiological situations could be observed.

In this paper we presented an information algorithm for the proposed technology (Karaliene D. et al. 2013) based on the identification of algebraic progression of each segment of ECG data. Presented algorithm was integrated into Matlab Toolbox for ECG complexity analysis.

Given experiment has shown that this software can help in analysis of short intervals of data which allows revealing of intervals with stable or unstable physiological features and can be effectively used for the analysis of ECG parameters although ECG signals are contaminated with noise.

Figure 3. *Graphical user interface for the ECG data preparing module*

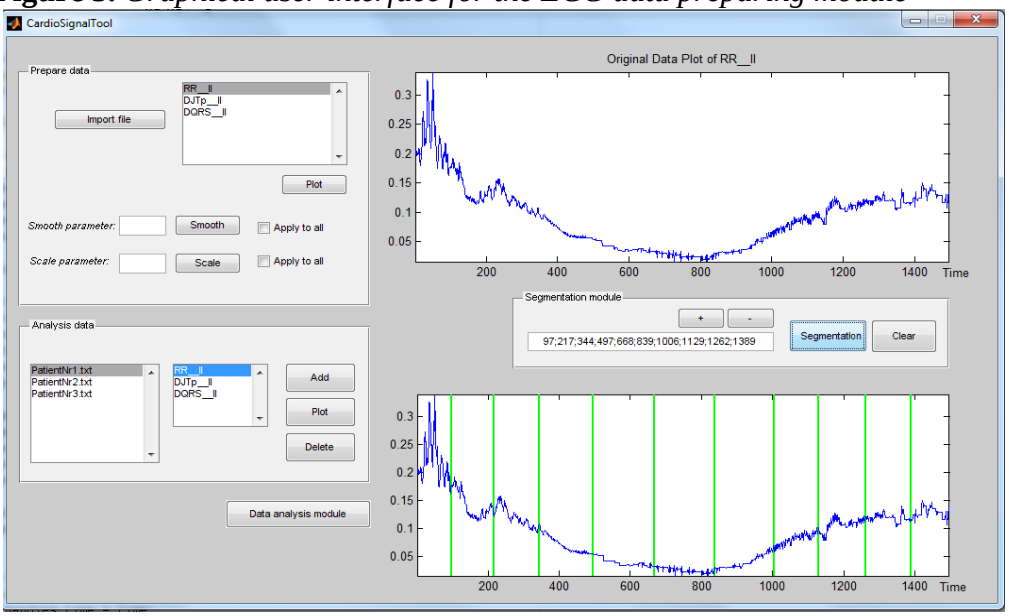
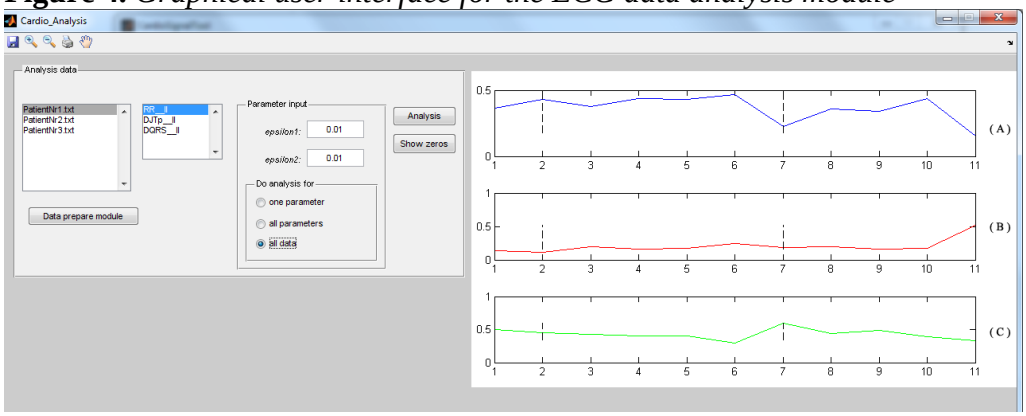


Figure 4. *Graphical user interface for the ECG data analysis module*



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