New Nonlinear Methods of Heart Rate Variability Analysis in Diagnostics of Atrial Fibrillation

Michal Pierzchalski, Robert A. Stepien, Pawel Stepien

***Abstract*—** Detection of atrial fibrillation in HRV signals needs analysis of irregular time series. Standard time domain and spectral method are not sufficient. We applied three new methods of time series analysis – symbolic method, fractal method, and empirical mode decomposition. Our method enables distinguishing atrial fibrillation, atrial flutter, and sinus rhythm, and are helpfull in tracking irregular heart rate activity.

***Keywords*—** HRV, RR intervals, sinus rhythm, atrial fibrillation, atrial fluttter, time series analysis, symbolic methods, Higuchi's fractal dimension, empirical mode decomposition

I. Introduction

Typical diagnosis of *atrial fibrillation*, AF, is based on 12-leads ECG. AF usually narrow QRS complexes and causes irregular RR intervals. The last feature allows the use of heart rate variability, HRV, for the diagnosis of atrial fibrillation and then for assessing the progress of treatment. However, statistical and spectral methods, which are commonly used to analyze the HRV signal can not cope with irregularity of RR series [1], [2]. We propose three new methods of HRV analysis for diagnosis of AF – symbolic method, method based on Higuchi's fractal dimension, and method applying empirical mode decomposition.

The calculations was based on the data from PhysioNet [3] and the data received from G.Varoneckas from Klaipedia Hospital in Lithuania (NHL) (cf. [4]).

II. New Method of Symbolic Analysis of Heart Rate Variability in Atrial Fibrillation

A. Method

The symbolic methods proposed in this work and modified spectral methods are based on the same idea of tracking trends in acceleration and de-acceleration of heart rate. Those trends are non-symmetric [5], [6]. When the rhythm is abnormal asymmetry between these trends is disappearing.

Manuscript received August 24, 2011. This work was supported in part by Nalecz IBBE PAS statutory activity 4.4/st/11.

M.Pierzchalski, R.A.Stepien. P.Stepien are with the Lab of Biosignal Analysis Fundamentals, Nalecz Institute of Biocybernetics and Biomedical Engineering, Polish Academy of Sciences, Warsaw, Poland, e-mail: mpierzchalski@ibib.waw.pl, step@ibib.waw.pl, stepienp@ibib.waw.pl

The time series of RR intervals is encoded into a series of symbols. For the series of RR intervals *x(i)* we calculate the first range differences and represent them by the symbols from the two-elements set {0,1}:

$$s(i)=\begin{cases}1 \text{ if } [x(i+1)-x(i)]\geq 0\\ 0 \text{ if } [x(i+1)-x(i)]<0\end{cases}, \quad i=1,\ldots,(I-1) \qquad (1)$$

As a result of signal's encoding we obtain a series of symbols, P, for example

[1,1,1,0,0,1,1,1,1,0,0,1,1,1,0,0,0,0,1,1,1,1,11,1,0,0,0,0,0,0,0]

In such a series symbol "0" represents acceleration of the heart rhythm - negative value of the first range difference corresponds to shortening of the successive RR intervals, while symbol "1" represents de-acceleration of the heart rhythm.

Symbolic series P contains tuples consisted of identical symbols - *mono-sequences*. They correspond to periods of heart rate acceleration (these composed of "0"'s) or to periods where heart rhythm de-accelerates or does not change (these composed of "1"'s). By calculating the *cardinalities*, *L*, of such mono-sequences in P we obtain a pattern of rhythm changes in the analyzed signal.

In our approach we calculate cardinality only of mono-sequences of length two - *[*00*]* and *[*11*]***.** These mono-sequences dominate the distributions of mono-sequences, so called *seq-spectra* [7], both for atrial fibrillation (Fig. 1.) and for sinus rhythm (Fig. 2.).

Due to non-stationarity of the analyzed signals cardinality calculation is done using technique of double windowing. The string of symbols P is divided into windows of chosen length. In order to improve the resolution the consecutive windows are overlapped. Each of these windows is divided into sub windows of two symbols each and cardinalities of tuples *[00]* and *[11]* are calculated. This method of calculation allows to take into account the contribution of long mono-sequences to the calculated cardinality. For example, mono-sequence of length 4 is represented by two mono-sequences of length 2, mono-sequence of length 6 by the three mono-sequences of length 2, etc.

The cardinality *L*[00] is the characteristic of acceleration trend in HRV and the cardinality *L*[11] is the characteristic of de-acceleration (slowing down) trend in HRV.

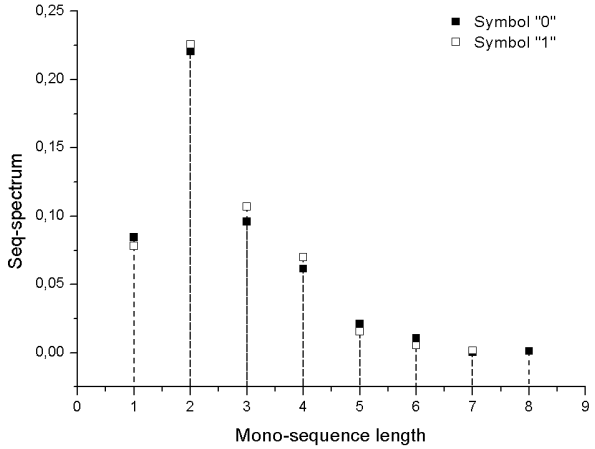

Fig. 1. The *seq-spectrum* of RR series of atrial fibrillation activity (data from NHL).

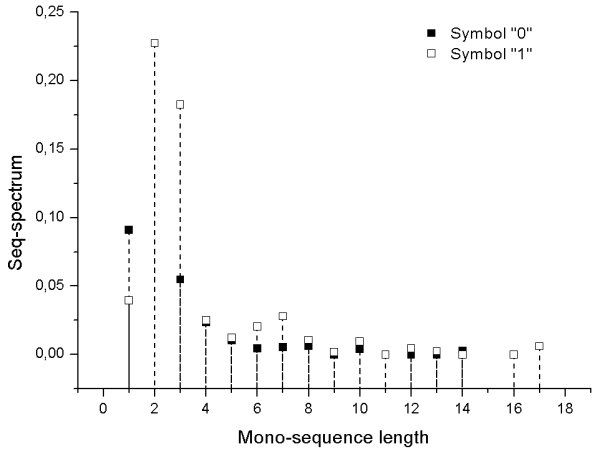

Fig. 2. The *seq-spectrum* of RR series of sinus rhythm (data from NHL).

For assessing asymmetry of these trends we define point-to-point distance, *D*, between curves of cardinalities *L[00]* and *L[11]*:

$$D_i = |L_i[00] - L_i[11]| \qquad (2)$$

B. Results

We studied 12 cases of HRV with atrial fibrillation from NHL, 6 with restored sinus rhythm, 5 mixed cases with AF, SR end AFL. The quinidine was used to restore sinus rhythm in six cases. HRV records for five cases contains sinus rhythm, atrial fibrillation and atrial flutter. The data were analyzed using moving window 200 samples (RR intervals) width that was shifted by 10 samples in each consecutive step.

For atrial fibrillation activity difference between sec-spectrums of symbol “0” and seq-spectrum of symbol “1” is small (Fig.1). The curves of cardinalities *L[00]* and *L[11]* are also close to one another (Fig. 3.). The point-to-point distances are less then 10. The asymmetry between the trends is weak for atrial fibrillation. The average distance *D* for 12 cases of AF is 3.31±0.35.

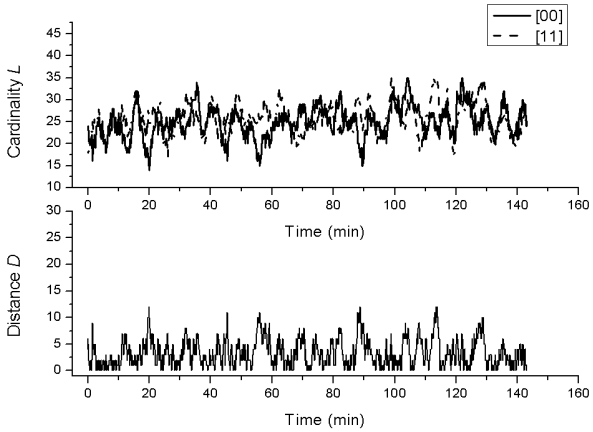

Fig. 3. The atrial fibrillation in pictures of cardinalities, *L*[00] and *L*[11] (upper) and point-to-point distance, *D*, between *L*[00] and *L*[11] (bottom).

The seq-spectra of symbols “0” and “1” differ significantly for the sinus rhythm (Fig. 2). The cardinality characteristics *L[00]* and *L[11]* for SR are clearly separated (Fig. 4.). The distance *D* varies from 1 to 25. The average distance *D* for 6 cases of restored sinus rhythm is 9.89±2.45.

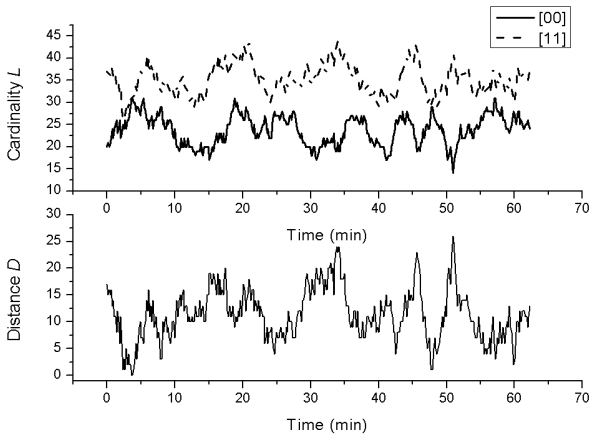

Fig. 4. The restored sinus rhythm. The cardinalities *L*[00] and *L*[11] (upper) and distance *D* (bottom).

Fig. 5. shows results for HRV containing atrial fibrillation activity and sinus rhythm onset after 75 minutes of recording. The mixed HRV studied by us contained sinus rhythm, atrial fibrillation activity and atrial flutter. The average distance, *D*, for 5 cases of mixed activity is 5.38±0.57.

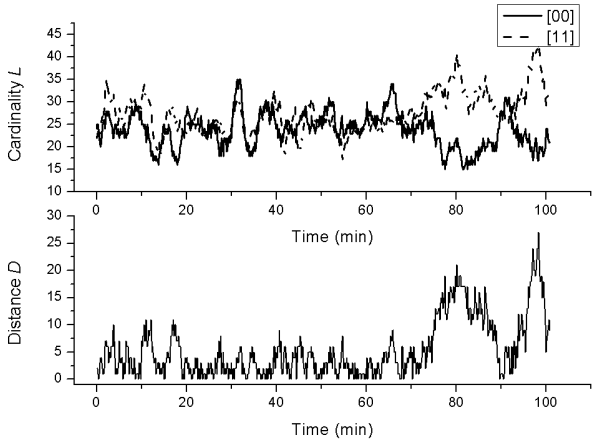

Fig. 5. Atrial fibrillation and onset of sinus rhythm. The cardinalities $L[00]$ and $L[11]$ (upper) and distance D (bottom).

III. Assessing Cardiovascular Reaction to Antiarrhythmic Drugs Using Higuchi's Fractal Dimension

A. Method

The algorithm to calculate fractal dimension of a time series directly in time domain was proposed by T.Higuchi [8]. It is a fast and easy method for fractal dimension calculation. This methods is widely used in the analysis of biomedical signals[(cf. [9], [10]). Here we investigate whether Higuchi's fractal dimension, D_f , of HRV signal can be used to evaluate system response to cardiovascular pharmacological treatments in patients with cardiac arrhythmia.

We analyzed HRV signals of patients with cardiac arrhythmias who at the time of the signal recording, has intravenously administered antiarrhythmic drug (isuprel or adenosine). When there was no body's response to the drug administered at the moment *t1* it was administered again at *t2*. Arrhythmias were classified as atrial fibrillation (AF) or atrial flutter (AFL). For each case Higuchi's fractal dimension was calculated with *window*=100 and *window*=50 samples. Other input parameters of method were the same for both cases, *window shift* = 1, k_{max} = 10. The size of the window used for analysis has an impact on further results interpretation. For evaluation of cardiovascular effects of antiarrhythmic drugs only patients with sinus rhythm and patients exclusively with atrial fibrillation were considered. Statistical analysis of the average fractal dimension to determine the variability in these groups was performed. The minimum average value of D_f in the group with atrial fibrillation has been taken as the threshold for response assessment of the cardiovascular system. If the fractal dimension dropped below this value, it was considered to be the reaction to the antiarrhythmic drug. Otherwise it was just as a distortion, or as a result of atrial fibrillation.

B. Results

Data from three groups of patients were used for analysis. The first group consisted of patients with cardiac arrhythmias, the second of patients with sinus rhythm and the third of patients with atrial fibrillation. We analyzed the data from PhysioNet and from NHL.. From the PhysioNet web page we got Normal Sinus Rhythm RR Interval Database (NSRRRID) and Atrial Fibrillation and Intracardiac Database (IAFD). The first one includes the beat annotation files for 54 long-term ECG recordings of subjects in normal sinus rhythm (30 men, aged 28.5 to 76, and 24 women, aged 58 to 73). The original ECG recordings (not available) were digitized at 128 samples per second. The second database consists of endocardial recordings from the right atria of 8 Patients in atrial fibrillation (6 Patients) or flutter (2 Patients). One record contains both atrial fibrillation and atrial flutter. Each record contained eight signals from different electrodes (intracardiac: CS12 - CS90, or ECG: I, II, V1, aVF). Each signal was sampled at 1 kHz with 14-bit resolution. Record from the electrode aVF was selected for further analysis. During these records, patients iaf1, iaf2, iaf6, and iaf8 received adenosine, and patients iaf3, iaf4, iaf5, and iaf7 received isuprel. The case iaf4 was excluded fromanalysis due to adverse drug effect. The length of RR segments were calculated as the distance between the normal heart beats and corrected using *ecgpuwave* and *wave* software from PhysioNet. Ectopic beats were treated as normal. Data from NHL include already calculated RRs of 14 patients with atrial fibrillation.

The average fractal dimension calculated with *window* = 100 for all cases of a group of patients who received antiarrhythmic drugs varied from 1.935 to 1.988 (Table 1). Healthy patients have an average D_f in the range from 1.568 to 1.888. The threshold of response assessment of the cardiovascular system was adopted at the level of 1.95. This is due to the variability of average fractal dimension for a group of NHL. For these data the average fractal dimension is in the range from 1.947 to 1.996. Evaluation threshold is used to eliminate the interference effect and the typical dynamics of fractal dimension for the arrhythmia. In all analyzed cases, D_f decreases below the threshold following administration of the drug. Then reaches a minimum value of D_f (Table 2.).. Differences in the time between drug administration and D_f falling below the threshold ($t1 - D_f\,react$ or $t2 - D_f\,react$) if the medication was given for the second time) range from 24 s to 621 s (Table 2.). The longest time differences are for cases when isuprel was administered (from 120 s to 621 s). However, visual analysis of HRV signal shows clear and quick response of the cardiovascular system to the applied drug - increase of heart rate (Fig. 6.). The differences are smaller for the cases when adenosine is administered (from 24. sec. to 54. sec.). Reducing the window for fractal dimension calculation to 50 resulted only in small changes of the results, like e.g. performance for the case No. 7 response time is not 395 but 320 s (Fig. 7.), for the case No. 8 there is a slight decrease in D_f in the wake of the first injection (Fig. 8.).

Table 1: Fractal dimension statistics for each group

Name	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
NSRRRID	1.568	1.651	1.711	1.715	1.780	1.888
IAFD	1.935	1.956	1.970	1.966	1.980	1.988
KHL	1.947	1.985	1.989	1.985	1.990	1.996

Table 2: Specification of IAFD data

No.	Diag.	Drug	$t1[s] \mid t2[s]$	$D_f react[s]$	D_f min
1	AF	adenosine	70	110	1.86
2	AF	adenosine	123	160	1.93
3	AF	isuprel	69	690	1.91
4	AF	isuprel	343|547	-	-
5	AFL	isuprel	94|214	530	1.83
6	AF	adenosine	146	200	1.92
7	AF/AFL	isuprel	341	395	1.82
8	AFL	adenosine	120|261	285	1.70

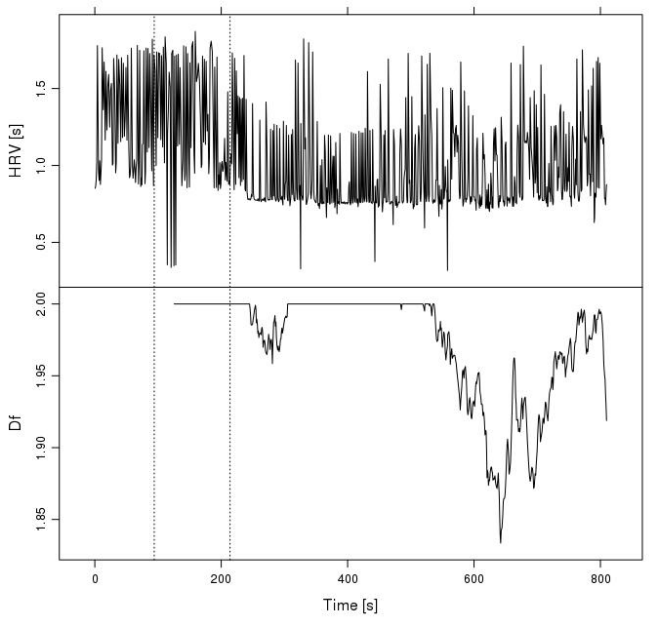

Fig. 6. Isuprel injected at 94. and 214. sec. (vertical lines); top - HRV of the patient with atrial flutter; bottom - D_f calculated with *window* = 100

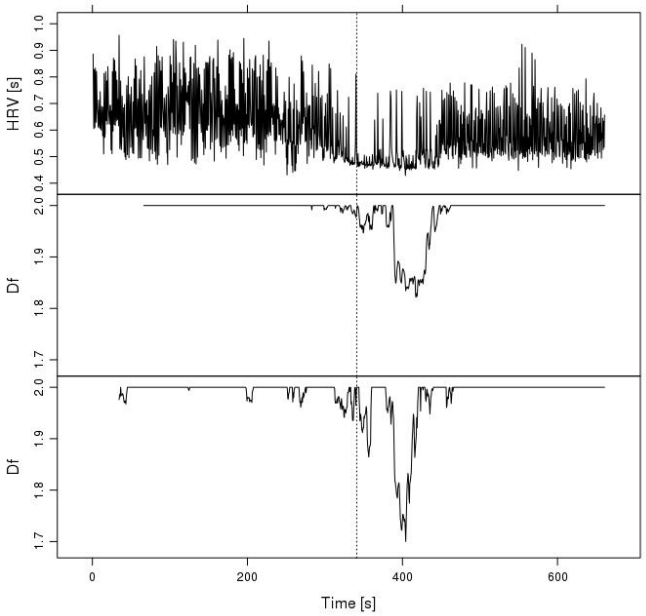

Fig. 7. Isuprel injected at 341 sec. (vertical line); top - HRV of the patient with atrial fibrillation and atrial flutter diagnosis; middle - D_f calculated with *window* = 100; bottom - D_f calculated with *window* = 50

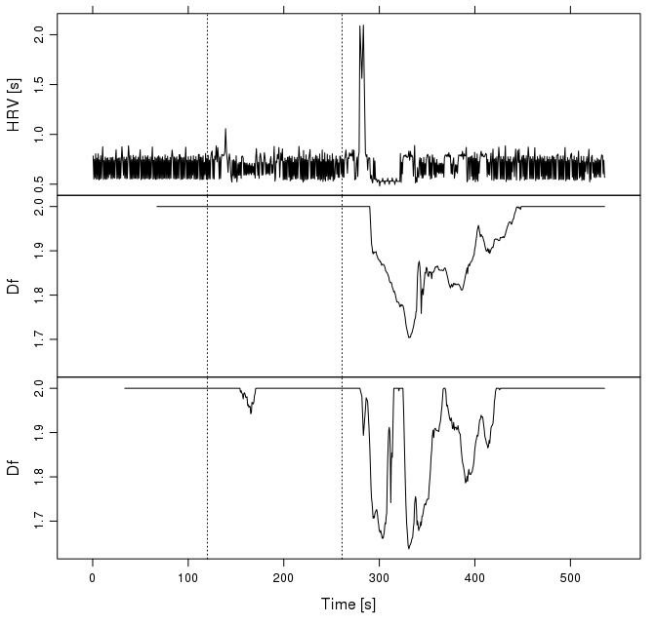

Fig. 8. Adenosine injected at 120. and 261. sec (vertical lines); top - HRV of the patient with atrial flutter diagnosis; middle - D_f calculated with *window* = 100; bottom - D_f calculated with *window* = 50

We have shown that D_f is very close to 2 in the cases of HRV signal disturbance caused by arrhythmias. In all analyzed cases D_f decreases below the adopted threshold following an assessment of antiarrhythmic drug administration to the patient. The dose proved ineffective, the weaker reaction of fractal dimension to the drug. D_f is reduced if the heart rhythm is back to sinus rhythm. For healthy persons D_f is much smaller. Intravenous drug administration induces rapid response of the cardiovascular system that may be seen in HRV signal and is reflected in fractal dimension of the signal, namely in decrease of D_f . Sensitivity to changes in the HRV signal can be adjusted by changing window length - the smaller is the window the more sensitive to change in HRV signal the method is. However, use of small window makes the method more sensitive to interference.

IV. Distinguish atrial fibrillation or flutter from normal sinus rhythm using Sliding Window Empirical Mode Decomposition

A. Method

Empirical Mode Decomposition (*EMD*) is a new method of breaking down a nonstationary, multicomponent signal into its monocomponents, method developed by Norden E. Huang [11]. *EMD* is an entirely data-driven algorithm and it does not depend on any predefined basis function. Such monocomponents are called *Intrinsic Mode Functions (IMFs)*; HRV signals are usually very large data sets. Using *EMD* algorithm for analyzing such signals is time consuming or even impossible in a reasonable time. We modified *EMD* algorithm by using small sliding window (*Sliding Window EMD, SWEMD*). Since it is a new method we explain it below.

1) Intrinsic mode functions

EMD decomposes signal into, so called, intrinsic mode functions (*IMFs*). *IMF* is a signal that fulfills the following conditions:

- the number of extrema and the number of zero crossings of *IMF* are the same or their difference is at most 1,
- the signal has ``zero mean" - the mean value of the envelope determined by maxima and the envelope defined by minima is equal 0 at every point.

Above conditions give us an idea of *EMD*: non-stationary signal is decomposed into stationary, symmetric signals which are quite easy to analyze.

2) EMD Algorithm

EMD algorithm [11], [12] is shown as a block diagram in Fig. 9. The main step (Fig. 10) of *EMD* is extraction of extrema from original signal *x(t)* end creation of the upper envelope e_{max} by cubic spline interpolation of maxima and of the lower envelope e_{min} by interpolation of minima. Then the mean value of two envelopes is calculated:

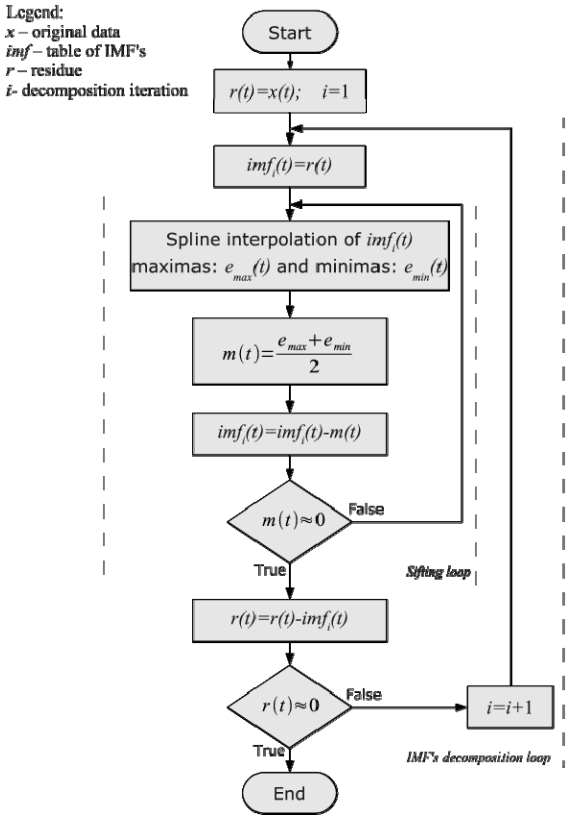

Fig. 9. Block diagram of *EMD* algorithm

$$m(t) = \frac{e_{max} + e_{min}}{2}.$$

This mean value is subtracted from the original data:

$$imf_1(t) = x(t) - m(t).$$

This procedure is named *sifting process*.

In ideal case $imf_1(t)$ could be *IMF*, but usually it is still asymmetric signal. In such a case we need to repeat above procedure with $imf_1(t)$ treated as input data for next sifting process, so mean value m(t) of envelopes of $imf_1(t)$ is calculated and this value is subtracted from $imf_1(t)$:

$$imf_1(t) := imf_1(t) - m(t),$$

where ':=' means ' *becomes equal'* i.e. the right-hand side is substituted for what has been the left-hand side.

This procedure is repeated till $imf_1(t)$ satisfies conditions of *IMF* signal ($m(t) \approx 0$). After extraction of the first *IMF* original data is reduced by $imf_1(t)$:

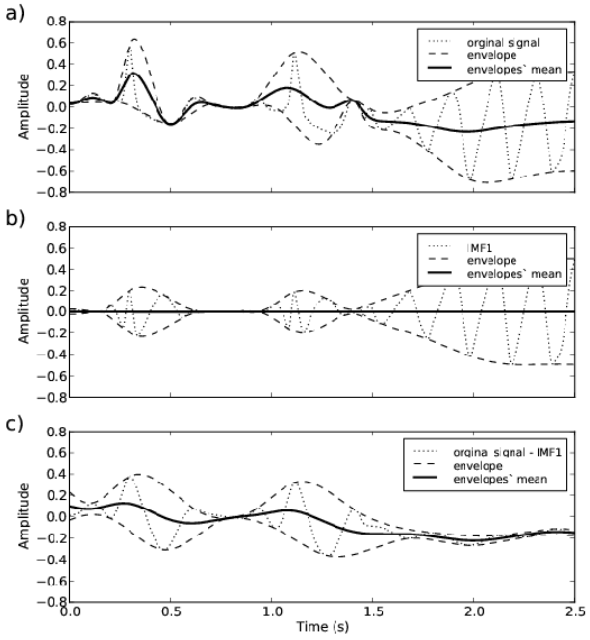

Fig. 10. Main steps of *EMD:* a) start of decomposition, b) end of decomposition of first IMF, c) start of second IMF decomposition.

$$r(t) = x(t) - imf_1(t).$$

The residue $r(t)$ is treated as input data for extraction of the next *IMF* (next sifting loop). Procedure is looped to obtain all *IMFs.* Decomposition is finished when the residue:

$$r_i(t) = r_{i-1}(t) - imf_i(t) \quad i - current mode$$

has less than three extrema or all its points are equal zero.

Summing of all *IMF* components and the residue gives back the original analyzed signal:

$$r_n + \sum_{i=1}^{n} imf_i(t) = x(t) \;\; n - number of\ modes$$

3) Hilbert-Huang spectrum

Signal decomposed into *IMFs* can be easily displayed as time-frequency characteristic by obtaining Hilbert-Huang spectrum. First step is to create *analytic signal* for each decomposition mode:

$$imf_{a_k}(t) = imf_k(t) + iH(imf_k(t))$$

where $H(imf_k(t))$ is the Hilbert transform of the *k-th IMF*. From analytic signal we can obtain instantaneous amplitude as a module of this signal:

$$a_k(t) = \left| imf_{a_k}(t) \right|$$

and instantaneous frequency as a differential of argument of this signal:

$$f_k(t) = \frac{1}{2\pi} \frac{d \arg(imf_{a_k}(t))}{dt}.$$

The instantaneous frequencies and amplitudes of all modes give so called *Hilbert-Huang spectrum, HHS*:

$$HHS(f_k, t) = Re\left[\sum_{k=1}^{N} a_k(t)^{\,j \int f_k(t) dt} \right].$$

With *HHS*, we can calculate the *marginal Hilbert-Huang spectrum*. It gives information about the contribution of the spectrum to the total amplitude (energy) and is defined as follows:

$$hhs(f_k) = \int_{-\infty}^{\infty} HHS(f_k, t) dt.$$

4) Sliding Window Empirical Mode Decomposition

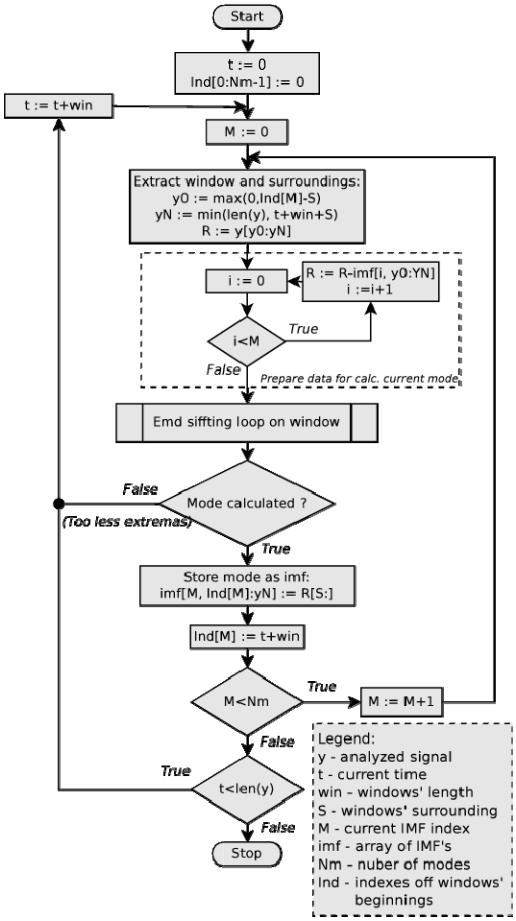

Fig. 11. Block diagram of *SWEMD* algorithm

Sliding Window Empirical Mode Decomposition, SWEMD (cf. Fig. 11.) is based on calculation of *EMD* in a small sliding window. Size of the window depends on frequency of the signal - there must be at least 5 maxima and 5 minima in the window for correct spline interpolation. In such case either number of *IMF's* and sifting steps must be set a priori to prevent possible discontinues between windows [2]. Number of modes depends on nonstationarity of the signal, in this case we decomposed HRV signal into 5 *IMF's.* The number of sifting steps is determined automatically by the decomposition of the first few windows of the signal by classic algorithm and counting the average number of sifting steps for each mod.

To eliminate possible boundary effects surroundings points are added to the beginning and end of the window and *SWEMD* sifting process is done on the window and surroundings part of the data. After obtaining the mode in current iteration, data corresponding to the window are extracted and stored in the *IMF's* array with proper time index. It may occur (especially for modes containing low frequencies) that the window size is too small for spline interpolation (not enough extremas) so there is need to set different window sizes for each mode. In our algorithm it is done automatically, only 'default' window size is set. The array *Ind* (Fig. 11.) stores time indexes of the window's beginning in current iteration. If the mode was extracted successfully this index is increased and the window for this mode is moved forward in the next iteration. If there was not enough extremas, the sifting process is canceled and the index of the window's beginning for current mode does not changed so in the next iteration the window is enlarged two times.

B. Results

We analyzed data from NHL - 10 cases of sinus rhythm, 12 cases of atrial fibrillation and 3 cases of atrial flutter.

.In order to calculate the frequency characteristics using *SWEMD* the HRV signal must be transformed: on the x-axis we mark the time of the heartbeats, on the y-axis - length of subsequent RRs. Such transformed signal is interpolated with spline functions. Marginal Hilbert-Huang spectra computed for three group using *SWEMD* are shown on Fig. 12. There are clear differences in the shape and in the amplitude between these spectra. Therefore, as the parameters characterizing each group we propose to use the following factors:

- Low-Frequency factor, *LF* , determining low-frequency contribution (0-0.025 Hz) to the whole spectrum (0-0.5 Hz):

$$LF = \frac{\int_{0}^{0.025} hhs(f)df}{\int_{0}^{0.5} hhs(f)df},$$

where *hhs(f)* denotes the *marginal Hilbert-Huang spectrum*,

- Mid-Frequency factor, *MF* , determining mid-frequency contribution (0.025-0.1 Hz) to the whole spectrum (0-0.5 Hz):

$$MF = \frac{\int_{0.025}^{0.1} hhs(f)df}{\int_{0}^{0.5} hhs(f)df}.$$

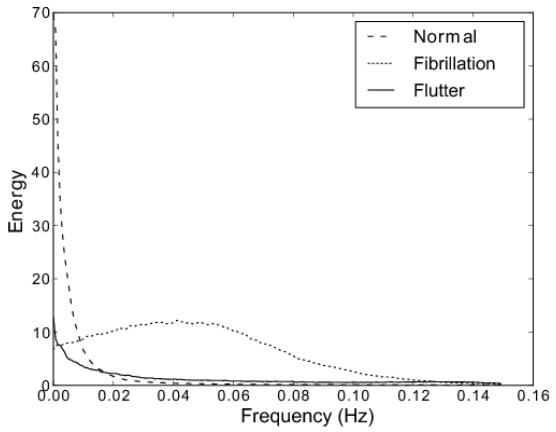

Fig. 12. Marginal Hilbert-Huang spectrum for a normal rhythm, atrial fibrillation, and atrial flutter.groups.

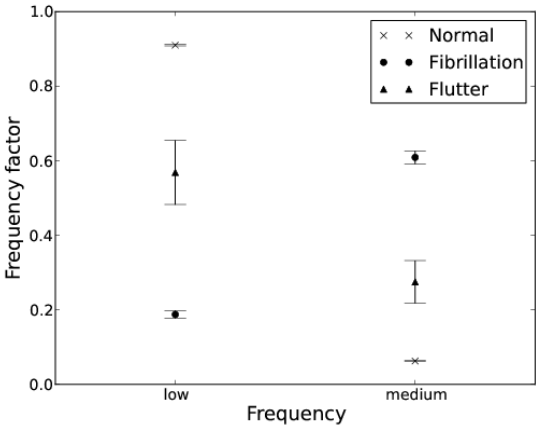

Fig. 13. Mean values and standard errors of the frequency coefficients for normal heart rhythm, atrial fibrillation, and atrial flutter

Fig. 13. shows statistically significant differences in the values of these coefficient between the analyzed groups. Frequency coefficients correctly classify analyzed groups (Fig. 14.). Cases of normal heart rhythm and atrial fibrillation are at opposite areas of the chart, and the cases of atrial flutter fall in between..

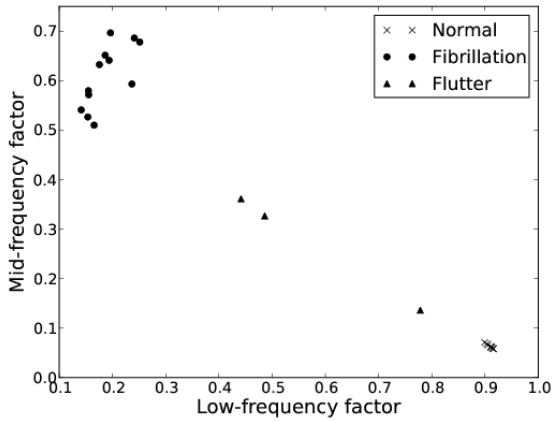

Fig. 14. Classification of arrhythmia using the coefficients *LF* and *MF*.

V. Conclusions

We described a new symbolic method of analysis of HRV signals based on cardinalities of two types of mono-sequences, that correspond to accelerating and de-accelerating trends in heart rate. The lack of asymmetry between these trends indicates atrial fibrillation activity. It is manifested by similarity of the characteristics *L[00]* and *L[11]* and their mean values. Presented method may be very helpful in distinguishing atrial fibrillation activity and sinus rhythm and it allows to track irregular heart rate activity.

Our study also shows that Higuchi's fractal dimension can quantitatively assess reaction of cardiovascular system to antiarrhythmic drug therapy. Effective dose of intravenous antiarrhythmic drug induces rapid response of cardiovascular system that may be observe in fractal dimension of HRV signal. Calibration capabilities of this method are presented.

Our results also indicate that proposed *Sliding Window Empirical Mode Decomposition* method is a promising method for distinguishing atrial fibrillation or flutter from the normal sinus rhythm. Significant difference is noticed in value of low-frequency and mid-frequency factors between analyzed groups. Unfortunately, a small amount of subjects (in particular cases, atrial flutter) can not definitively confirm the effectiveness of the method, however, presented results are very promising.

Summarizing, the proposed new nonlinear methods of heart rate variability analysis may be quite helpful in diagnostics of atrial fibrillation. They may also find other clinical applications in Cardiology and in other fields of Medicine.

Acknowledgment

The authors thank Prof. Wlodzimierz Klonowski for his scientific guidance.

References

[1] Task Force of the European Society of Cardiology the North American Society of Pacing Electrophysiology. "Heart Rate Variability: Standards of Measurement, Physiological Interpretation, and Clinical Use", *Circulation*. 1996, vol. 93 pp. 1043-1065. Available : http://circ.ahajournals.org/content/93/5/1043.full.

[2] D.T.Kaplan, "The analysis of variability". *J Cardiovasc Electrophysiol*. vol. 5, pp. 16-19, 1994

[3] A. L. Goldberger, L. A. N. Amaral, L. Glass. J. M. Hausdorff, P. Ch. Ivanov, R. G. Mark, J. E. Mietus, G. B. Moody, C.-K. Peng and H. E. Stanley: "PhysioBank, PhysioToolkit, and PhysioNet: Components of a New Research Resource for Complex Physiologic Signals" *Circulation* 101(23), pp. 215--220, 2000 (June 13). and Circulation Electronic Pages http://circ.ahajournals.org/cgi/content/full/101/23/e215 .

[4] W.Klonowski, E.Olejarczyk, R.Stepien, G.Voroneckas, A.Alonderis, D.Zemaityte: "Fractal and Symbolic Analysis of Heart Rate Variability and Sleep Staging", 3rd European Medical & Biological Engineering Conference EMBEC´05, Prague, Czech Republic, 20-25 November *IFMBE Proceedings*, vol. 11, 2005, #1944F;

[5] P.G.Katona, F.Jih, "Respiratory sinus arrhythmia: a noninvasive measure of parasympathetic cardiac control", *J Appl Physiol*. vol. 39, pp. 801-805, 1975.

[6] D.L.Eckberg, "Human sinus arrhythmia as an index of vagal cardiac outflow", *J Appl Physiol*. vol. 54, pp.961-966, 1983.

[7] R.A.Stepien, "New method for analysis of nonstationary signals", (2011, June) *Nonlinear Biomedical Physics*. 5:3, July 2011. Avaiable: http://www.nonlinearbiomedphys.com/content/pdf/1753-4631-5-3.pdf

[8] T. Higuchi. Approach to an irregular time series on the basis of the fractal theory. 1988.

[9] W. Klonowski, "From conformons to human brains: Informal overview of nonlinear dynamics and its applications in biomedicine," *Nonlinear Biomedical Physics* 2007, 1:5 [online, open access]. Available http://www.nonlinearbiomedphys.com/content/pdf/1753-4631-1-5.pdf

[10] W.Klonowski,"Personalized Neurological Diagnostics from Biomedical Physicist's Point of View and Application of New Non-Linear Dynamics Methods in Biosignal Analysis", **another paper just submitted**

[11] Norden E. Huang and Zheng Shen and Steven R. Long and Manli C. Wu and Hsing H. Shih and Quanan Zheng and Nai-Chyuan Yen and Chi Chao Tung and Henry H. Liu. The empirical mode decomposition and the Hilbert spectrum for nonlinear and non-stationary time series analysis. *Proceedings of the Royal Society of London. Series A: Mathematical, Physical and Engineering Sciences*, 454(1971):903--995, 1998.

[12] G. Rilling and P. Flandrin and P. Gonçalvès. On empirical mode decomposition and its algorithms. *IEEE-EURASIP workshop on nonlinear signal and image processing NSIP-03, Grado (I)*, 2003.