Shape Analysis of Heart Rate Lorenz Plots

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A quantitative geometrical method to analyse heart rate variability is presented. From the heart rate data Lorentz plot was constructed and converted into a grey scale image. To it imaging techniques were applied to determine the outline of the attractor area. Its shape was described in terms of Fourier coefficients. The method was applied to the RR-interval data collected by 15 healthy male subjects (30 ± 4 years) during step test (YMCA protocol) and the consequent 10 minutes relaxation.

1 Introduction

Under normal physiological conditions, heart rate is not a periodic oscillator - the time interval between heart beats is constantly changing due to both the fluctuating inputs to the system and dynamic responses of cardiovascular regulatory mechanisms [1]. Although heart rate variability has been known about for more than a century, its analysis and interpretation is still an active research field, mainly due to new developments in computational and digital signal-processing techniques, as well as due to new understandings of non-linear systems [2]. The standard procedure is to deduce the time intervals between R-peaks from measured electrocardiograms. These intervals may be Fourier analysed, but recently, methods of non-linear dynamics, including the phase space representation, have often been applied [3]. From the heart rate data, a standard Lorenz (or Poincaré) plot is constructed by plotting each RR time interval as a function of the immediately preceding one. These plots give a visual representation of the RR data, but their shapes are also used to classify the data. The shapes of the attractor regions are also determined quantitatively by approximating them by ellipsoids and calculating their principal axes [4]. It was thus of interest to develop a more general method for quantitative representation of the shapes of heart rate attractor regions. Here we describe a method based on computer imaging and determination of Fourier coefficients of the graph outline. This work is based on our previous research in shape analysis of phospholipid vesicles [5] and has been shortly introduced elsewhere [6].

The developed method was applied to the data collected during a standard step test procedure. This is a simple method used to estimate the maximal oxygen capacity and thus physical fitness of subjects with submaximal exercise testing[7]. It consists of subjects performing work at well defined power for long enough time for heart rate to reach the steady state value from which the maximal oxygen consumption may be estimated. In step test the work is done by stepping on a bench at a given pace (usually imposed by a metronome). The work done by subjects was additionally regulated by changing the mass they were carying in a backpack.

2 Methods

Data analysis was done mostly on a Pentium IV computer, with 512 MB memory, running under Linux operating system. For this purpose computer programmes were specially developed - they consisted of routines written in C language and shell procedures.

Heart rate data were collected from 15 healthy male subjects, 30 $\pm$ 4 years old, 83$\pm$ 9 kg, with body mass index 26 $\pm$ 2 kgm^{-2}. They performed the standard YMCA step test procedure: 24 steps per minute on 30 cm high bench for 3 minutes [8]. Each test was repeated four times: normal test and three tests with additional loads of 5, 10 and 15 kg carried by the subjects in a rucksack. Heart RR intervals were measured by Polar Vantage NV (Polar Electro, Oy, Finland) heart rate monitors during the stepping phase as well as during the following 10 minutes relaxation period. Prior to test all subjects signed an informed consent as demanded by the National Committee for Medical Ethics which approved this research.

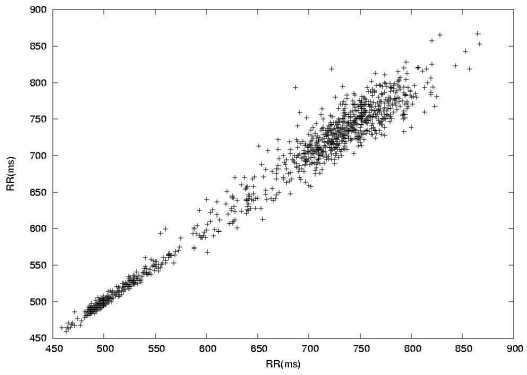

Fig. 1. A typical Lorenz plot for RR-intervals: the values of RR time intervals are plotted as a function of the previous ones.

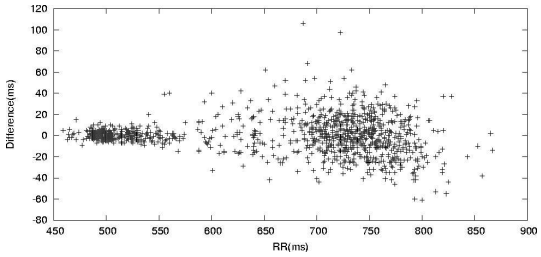

Fig. 2. A typical difference plot for RR-intervals: the values of the differences of RR time intervals are plotted as a function RR intervals.

3 Image Processing

From the RR time interval data, standard Lorenz plot was constructed by plotting each RR time interval as a function of the immediately preceding one (Fig. 1). Beside these standard Lorenz plots, we also considered difference plots. They were constructed in the same way, but the differences between the RR time interval and the preceding one were plotted on the vertical axes (Fig. 2).

All the plots were centred at the average RR value. Data were plotted on a 512x512 array of byte cells where the value in each cell was proportional to the count of graph points corresponding to it. The resulting array was interpreted as an image with 256 grey levels and standard image analysis techniques were applied to it.

First, it was normalised to ensure that the full range of 256 values was used, and then smoothed using $\frac{1}{8}(010/141/010)$ filter. Usually the resulting image consisted of scattered, not connected, points, as a consequence mainly of short measurement time. On these images the normalisation and smoothing cycles were repeated up to hundred times until the compact attractor region was obtained. The image was then binarised by thresholding at half of the maximal height.

The outline of the resulting black region was determined by a contour following algorithm[5]. In the chosen region of interest a point on the image contour was found. Then a maze walking algorithm was used to determine all the remaining points of the attractor outline. At each step it started to investigate the points from the right to the left of the path and moved to the first encountered white point. This algorithm always returns to the first point of the outline.

Next, a contour pruning procedure was applied. It was necessary because the maze walking procedure often yielded some one pixel wide threads extending from the contour as a consequence of entering thin closed channels and returning back on its own path. Finally, the centre of the vesicle outline was calculated and all the coordinates were expressed with respect to it and stored for further analysis.

To describe the resulting attractor shape quantitatively, its contour was analysed in terms of Fourier coefficients (a_m and b_m):

$$R(\phi) = R_0\Big(1 + \sum_{m=1}^{m_{max}} [a_m cos(m\phi) + b_m sin(m\phi)]\Big), \quad (1)$$

where $R(\phi)$ is the distance from the chosen origin of the coordinate system to the contour point at a given polar angle ϕ. In the above equation, the coefficients a_m and b_m have been defined relatively to (in the units of) the average contour radius R_0. Thus, the coefficients depend only on the contour shape and not on its size.

In such a way defined Fourier coefficients are similar to the Fourier descriptors usually employed in shape recognition [9, 10, 11]. The difference is that our contour points are function of the angle rather than the distance along the contour path. Although other shape description measures, such as moments or even simple compactness, were sometimes equivalent to Fourier descriptors [12] our choice was motivated by the ease of interpretation of the results.

In analysing the experimental data only the shape of the attractor region is of interest, not its orientation. It was thus more convenient to use, instead of Fourier coefficients a_m and b_m, their squares (u_m^2) defined as:

$$u_m^2 = \frac{1}{2}[a_m^2 + b_m^2]. \quad (2)$$

There are various methods to obtain the Fourier coefficients from the outline coordinates. Since our points were not equidistant and computational time was not crucial, we used the most straightforward method - least square fitting of Eq.1 to the experimentally determined contour points. The sum of the squares of the differences between the measured and the calculated vesicle outline points was minimised. The resulting normal equations gave a linear system that could be easily solved. For this purpose the method of LU decomposition [13] was used. It decomposes the matrix into the product of a lower and an upper triangular one from which the solutions can be calculated by a simple substitution.

4 Results

To test the experimental procedure four sessions of 15 heart rate measurements recorded during 3 minute step test and the following 10 minutes relaxation were analysed. Considering two missing measurements this resulted in 58 heart rate data series. At the beginning of the test the RR intervals quickly decreased and in less than two minutes settled to nearly steady state value. After 3 minutes, when exercising was finished and the subject lay down, the RR interval quickly increased. Since the heart rate attractor regions were expected to be different during the exercising and resting period, the two activities were analysed separately.

Because the measuring time was quite short the resulting graphs were not compact on the 256×256 grid. About 100 smoothing and normalising cycles were usually required to obtain graphs with compact central region. These were then analysed, as described above. It was found that no more than the first ten Fourier coefficients were needed to sufficiently describe the shape of the obtained smoothed

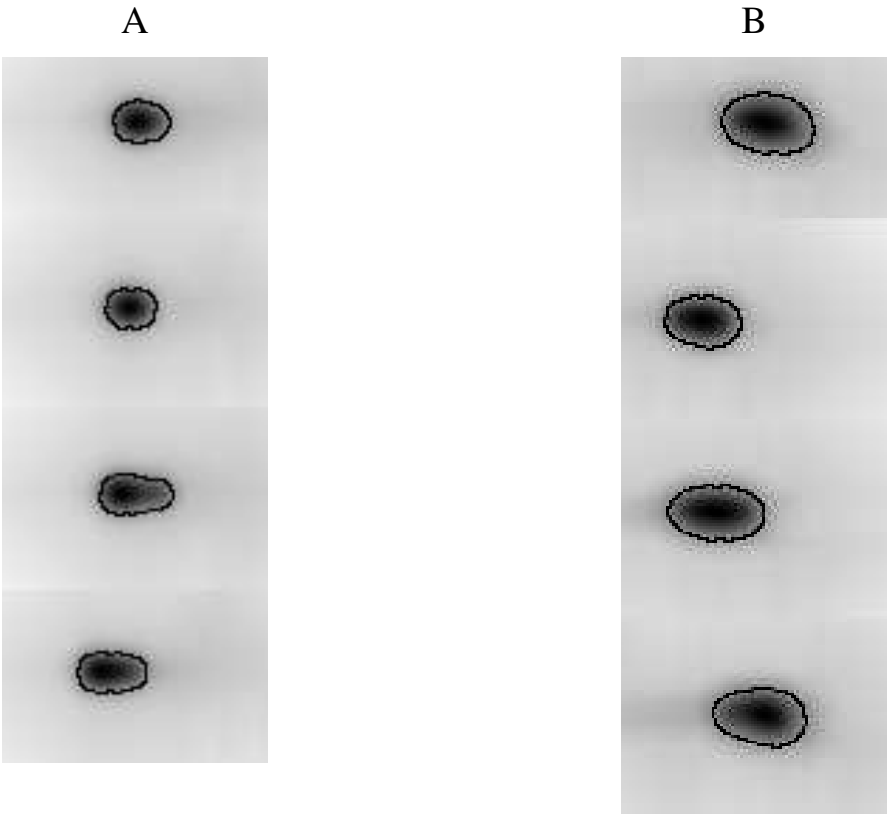

Fig. 3. Samples of difference plots for the step test (A) and the following relaxation (B). Graphs represent measurements with 0 kg, 5 kg , 10 kg and 15 kg external loads from top to bottom, respectively.

attractor region. The quality of fit was also monitored by plotting the contours, as calculated from the resulting Fourier coefficients, over the attractor image (Fig. 3).

5 Discussion

The main purpose of this study was to develop a new method to quantitatively characterise the shapes of the heart rate attractor. The method was tested on data from healthy subjects during exertion and the following relaxation. The reported procedure proved to be efficient at describing heart rate variability data. Visual inspection of the resulting images indicated the quality of the recorded data. The ones with multiple regions were mainly related to changing heart rate regimes during the experiment or to recording problems. But most of the standard Lorenz plots were of the well-known ellipsoidal or club-like shapes, centred along the image diagonal. Although Lorenz plots are more generally accepted to represent the heart rate phase

space, the difference plots were preferred, since their interpretation was much more straightforward - they reflect typical variations of HR at any given heart rate value. For shape analysis, the difference plots also proved to be more convenient, as they usually consisted of a symmetric horizontally-extended attractor region. Their shape could be quantitatively determined by the first few Fourier coefficients of the region outline.

This method enables us to qualitatively describe the shapes of heart rate attractors. Due to the problems with eventual small number of data points and the resulting averaging, it is believed that this method is useful mainly with the long period measurements. And the physiological interpretations of the resulting heart rate attractor shapes are also still an open issue.

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