HeartScope: a Software Tool Addressing Autonomic Nervous System Regulation

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Abstract

The evaluation of cardiovascular control system requires ad-hoc software tools specifically designed to address the complexity of the regulation mechanisms in a multiparametric and multidisciplinary perspective.

We introduce HeartScope a Windows-based C++ tool that brings together the most advanced signal processing methods for the analysis of cardiovascular regulation in a flexible and friendly framework.

1. Introduction

"Dynamical disease" is defined as a pathological status characterized by disorders of the control system that usually precede those of the target organ [1]. At the level of cardiovascular system a "dynamical disease" can be identified trough the monitoring of the sympatho-vagal balance and the evaluation of the gain of reflexes (e.g. baroreflex) and of specific mechanisms (e.g. dynamical properties of the sinus node). The evaluation of the cardiovascular control system requires ad-hoc software tools addressing the complexity of the cardiovascular control mechanisms via a multivariate and multidisciplinary approach [2]. These tools have to be capable of integrating different biological signals and several types of signal processing methods in a friendly framework appropriate to users with different backgrounds.

The aim of the paper is to present HeartScope, a Windows-based computer program written in C++, specifically designed to study the cardiovascular regulation.

2. Program description

HeartScope (version 1.6) works on ECG, arterial pressure (AP), respiratory volume (RESP) and an integrated nerve activity signal (e.g. in humans the sympathetic nerve activity directed to muscle, i.e. MSNA, recorded at the level of the peroneal nerve and integrated with a time constant of 10 s). In this paper we consider an application to MSNA.

2.1. Calibration window

At launch time, HeartScope prompts the user to open a raw signal file or previously saved beat-to-beat series (Fig.1). Input raw signals may not be calibrated (i.e. the sample representation being expressed in quanta values from the A/D board). In this case, a calibration is necessary to extract meaningful AP and respiratory volume values, while it is not necessary on ECG (currently HeartScope assesses only heart period from ECG), and MSNA (all MSNA amplitude parameters are normalized with respect to those derived from a reference period). Fig.2 shows the min-max AP calibration window where the user can calibrate the signal either acting on a single-wave, associating maximum/minimum AP values to a single selected peak/valley pair, or on multiple waves, assigning minimum/maximum AP values to the maximum/minimum averages computed over several peak/valley pairs, (Fig.2, right hand side, the detected peaks and valleys are marked by vertical segments). If necessary, the respiratory volume signal can undergo similar single-wave, max-min calibration. The calibration window allows the visualization of the signals (Fig.2, left hand side). However, a full-screen raw data viewer with capability of excluding one or more traces is also provided.

2.2. Detection of beat-to-beat time series

After closing the calibration window, HeartScope runs detection routines (Fig.1). The following cardiovascular variables are evaluated on a beat-to-beat basis: i) heart period (HP) as the temporal distance between two successive QRS complexes (or two successive diastolic points on AP if ECG is not present); ii) systolic AP (SAP) as the AP maximum inside the current HP; iii) diastolic AP (DAP) as the AP minimum after the current SAP; iv) mean MSNA in the current HP; v) respiratory volume is sampled once per cardiac beat at the beginning of the current HP. MSNA bursts are detected as well and their

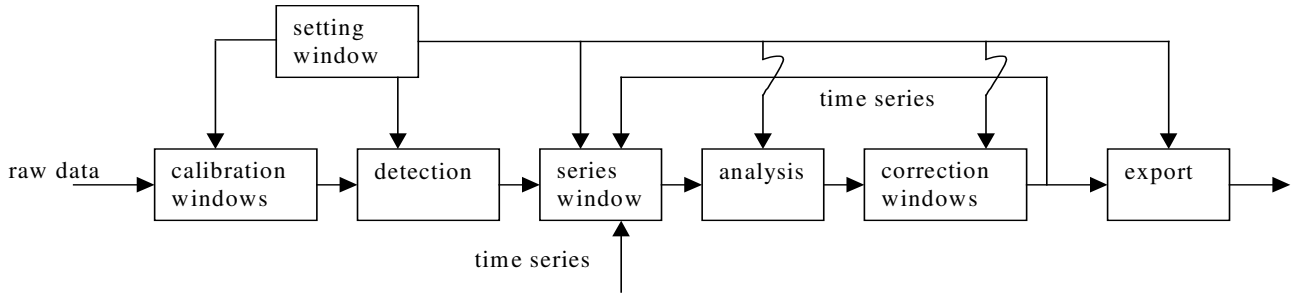

Figure 1. Flowchart of HeartScope

rate, amplitude and area is calculated.

2.3. Time series window

The beat-to-beat variability time series are shown in a dedicated interactive window (Fig.3). User can rescale each series by double-clicking on the y-axis. Segment boundaries (the vertical segments shown in Fig.3) can be controlled (inserted or deleted) by clicking the right mouse button on the graph. Another mouse-driven popup menu can disable/enable the analysis of a given segment. Different background colors help to visualize special meaning associated with each segment, such as its enabled/disabled status or the so-called reference segment (i.e. the segment used in the case it is necessary to normalize indexes derived from the other segments with respect to reference values). In Fig.3, from left to the right, the reference segment, a disabled segment and an enabled segment are shown. Segment boundaries designate the start and the end of multiple sessions during the same recording. These boundaries can be even loaded from an external file (usually generated during recording session). The analysis limits can be different from segment boundaries as it is exemplified in the third segment of Fig.3 (analysis will be carried out only on the grey part of the third segment).

2.4. Analysis of segments

Analysis is performed separately on each enabled segment inside the analysis limits (Fig.1). HeartScope calculates: i) mean and variance; ii) mean burst rate (both expressed in number of bursts per minute and per 60 beats), burst amplitude and area normalized with respect to those calculated in the reference segment; iii) autoregressive (AR) power spectra (Fig.4) and powers in the low and high frequency (LF and HF) bands expressed both in terms of absolute and normalized units [3]; iv) bivariate AR phase spectra and squared coherence between all pairs of series as a function of the frequency and at specific reference frequencies in LF and HF bands [4]; v) the baroreflex gain estimated with several methods (i.e. the square root of the ratio between the HP and SAP powers at LF (or HF) [4], the slope of spontaneous HP-SAP ramp-like sequences lasting 4 beats [5]; the magnitude of the HP-SAP transfer function [6], the slope of the response of the HP-SAP block to a simulated unitary ramp [6] after the identification of an exogenous (X) model with an AR input (XAR model) or of a double X model with an AR input (XXAR, this model involves

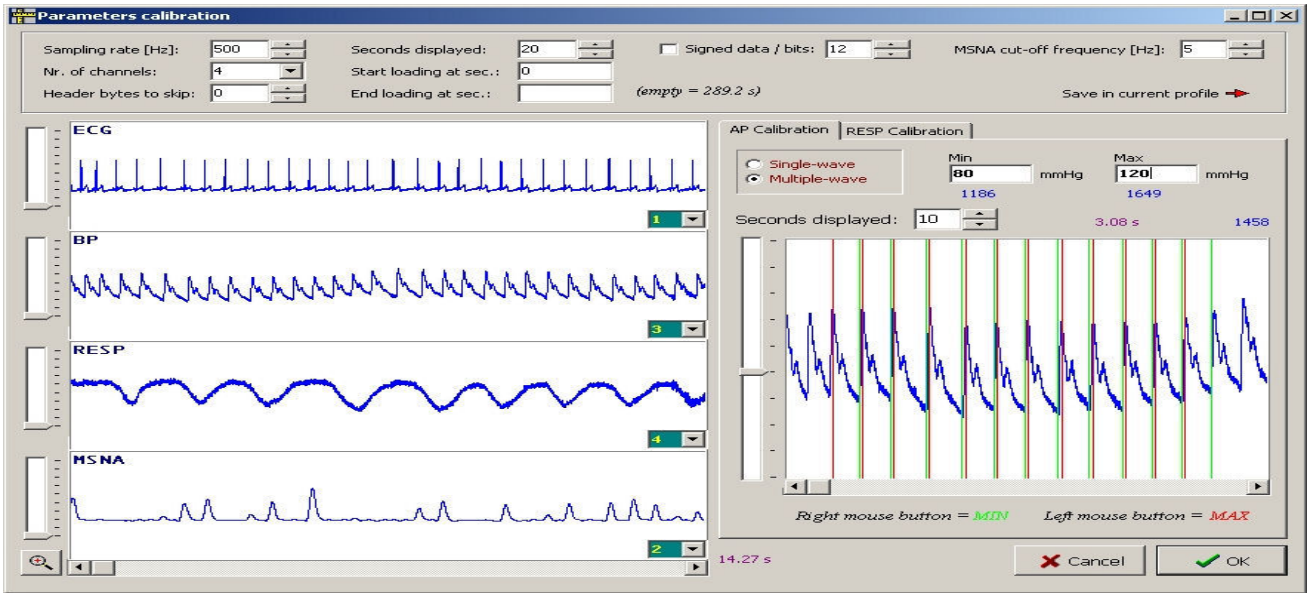

Figure 2. AP calibration window. ECG, arterial blood pressure (BP), respiratory volume (RESP) and MSNA.

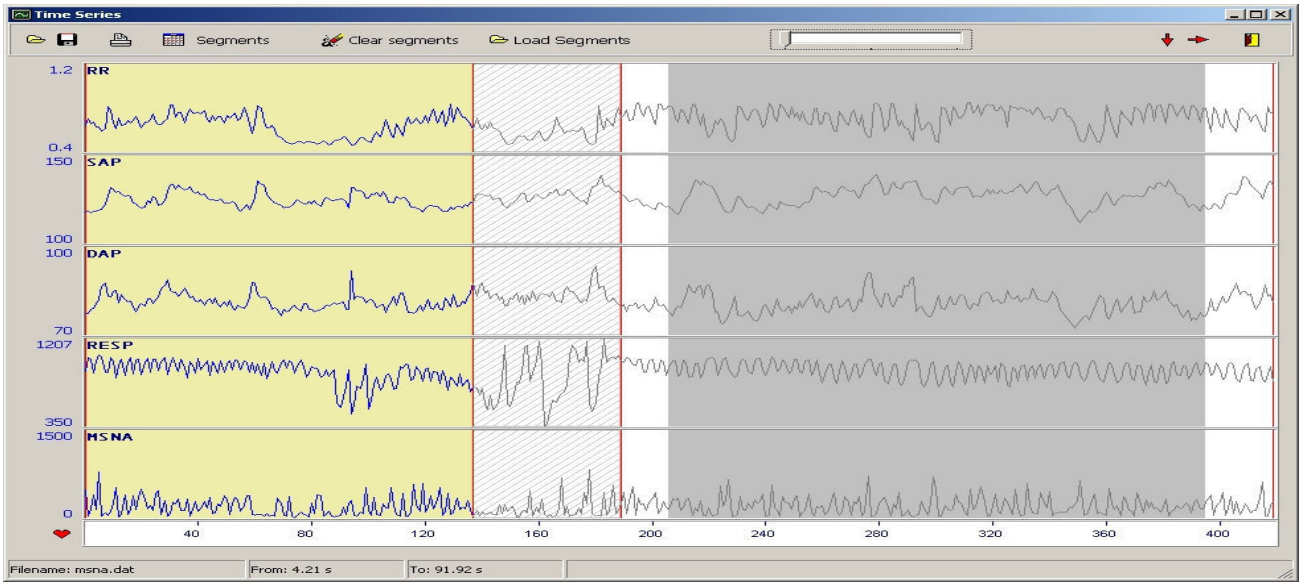

Figure 3. Beat-to-beat variability series window. RR, SAP, DAP, sampled respiration (RESP) and mean MSNA series.

also RESP in addition to HP and SAP); vi) the gain of the SAP-RESP and HP-RESP transfer functions in the HF band; vii) indexes of complexity via a conditional entropy approach [7]; viii) a parameter related to the dynamical properties of the sinus node [8]; ix) parameters from symbolic analysis quantifying the rate of occurrence of patterns lasting 3 cardiac cycles [9].

2.5. Correction windows

The detection of QRS complexes, SAP peaks and MSNA bursts can be assessed using three specific correction windows. HP correction window allows the insertions of missed (under) detections, the removal of erroneous (over) detections and the cubic spline interpolation over several consecutive HP values to smooth several successive outliers. Cubic spline interpolation is also allowed on SAP series. As an example of correction window, Fig.5 shows the MSNA burst correction window. MSNA is depicted over two different time scales (upper and middle panels). The

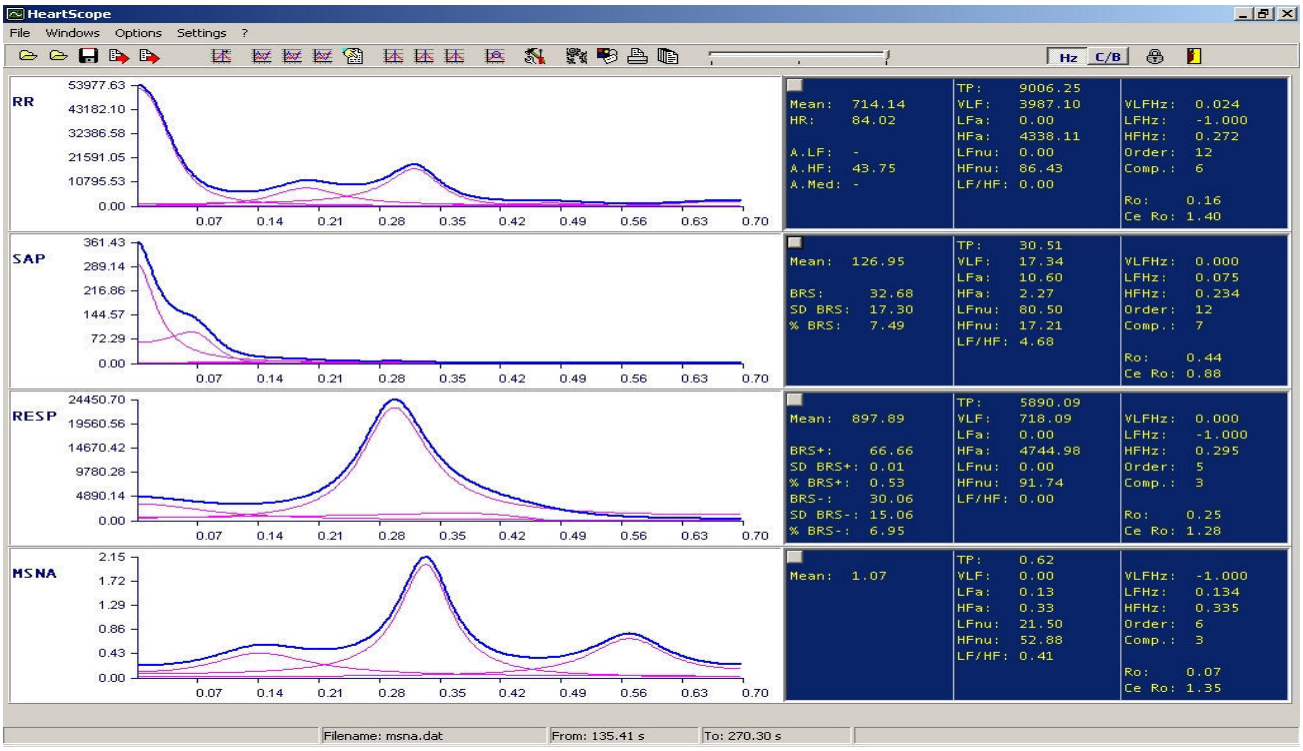

Figure 4. Power spectral analysis window: spectra and spectral components (left) and calculated parameters (right).

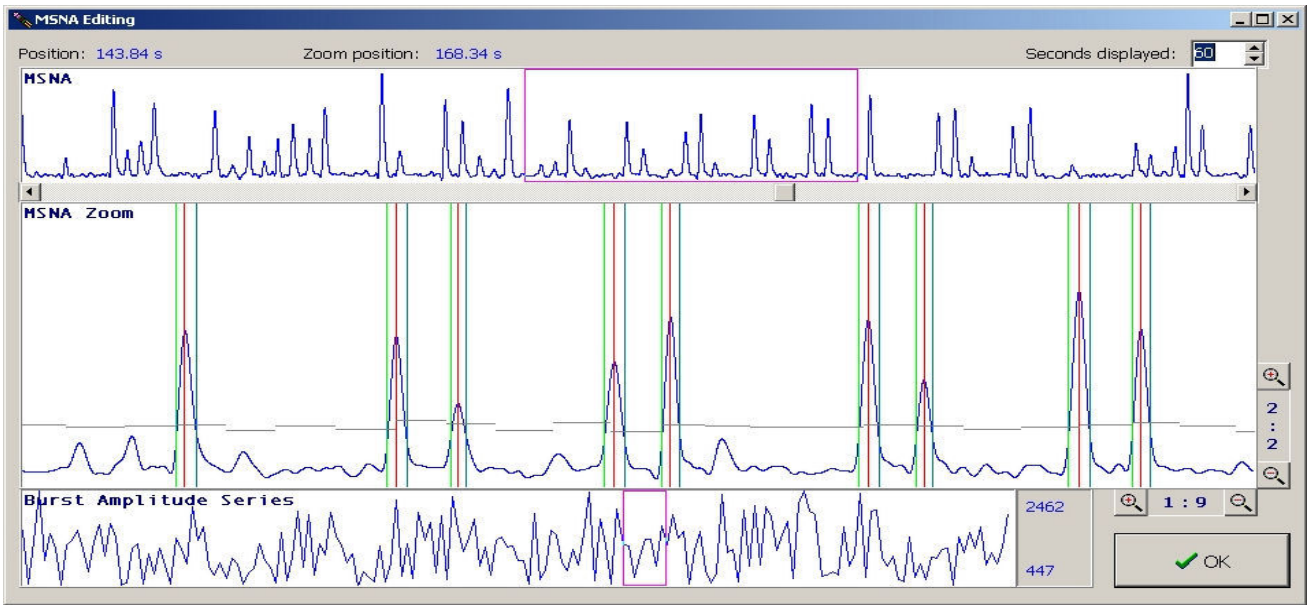

Figure 5. MSNA burst correction window.

upper panel allows the scrolling of the signal. The middle panel displays the selected portion of the MSNA signal from the upper panel. Onsets, peaks and offsets of the detected bursts are marked with vertical segments, while the horizontal lines indicate the running threshold which is updated on a beat-to-beat basis. The manual insertion or cancellation of any detection is carried out by clicking the right mouse button on the middle panel.

2.6. Setting, help and exporting features

Parameters used for the analysis procedures and for customization of the program output are organized in setting folders. The overall analysis profile can be saved and associated to a specific experimental protocol. The application help contains tutorials guiding the user over a complete analysis and explains how to interpret the extracted indexes by providing a list of reference papers. Every data calculated by the software can be exported either as a text file or in an Interbase/Firebird database.

3. Conclusions

By exploiting the contemporaneous presence of cardiovascular signals and several data processing tools, HeartScope may be a fundamental tool in revealing impairments of cardiovascular control.

References

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