BioSigBrowser, biosignal processing interface

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Abstract—**This paper presents a user-friendly interface in *Matlab*® that aims to make easy the use of algorithms in the scene of biomedical signal processing. The platform is called *BioSigBrowser*. It includes methods related with cardiovascular signal processing, including some multimodal analysis. This platform can treat a single signal or work in a batch mode on a given database as it is usually done in research. Furthermore the modular characteristic of the platform allows easy incorporation of new methods.**

I. MOTIVATION

THE Communication Technologies Group (GTC) is a research group who, amount other topic, deals with biomedical signal processing.

For the last 14 years GTC has been involved in the development of automatic systems for measuring and studying clinical relevant electrocardiogram (ECG) parameters. Recently analysis of polysomnographic recordings involved in the study of the childhood sleep apnea or others ongoing projects related with electrogram, arterial blood pressure and respiratory signals are also being developed. General use algorithms have been developed to delineate and characterize ECG waves, sudden death risk indices analysis, characterization of the autonomous nervous system such as heart rhythm variability modeling, etc.

This work has being developed in collaboration with another research groups, which has putted in evidence the need to transfer the technology in an easy way. One of the problems is that researchers usually implement their programs according to the data and specific goal of the study, giving less importance to the generalization of it. Thus, the methods are usually not ready to be easily used by others, and only became an available tool for user in a much latter stage of the research.

The creation of an interface, in which all of those algorithms will be available, is the next step to support them. Researchers will have a biomedical signal processing toolbox with user-friendly interface and clinicians will be provided with an auxiliary diagnostic tool that can be easily used with limited technical knowledge.

This interface, *BioSigBrowser*, is being developed in *Matlab*® language which is used for performing mathematical calculations, analyzing and visualizing data, writing new software programs. Also for those ones demanding task, C or C++ routines can be embedded.

BioSigBrowser modular structure allows an easy incorporation of new methodologies/modules. It is multiplatform software, being able to be used either under *Windows*, *Linux* and *MAC* operating systems and also it has high compatibility with *Octave* (GNU General Public License) allowing future migration with low effort potentiating its distribution.

In clinical practice, *BioSigBrowser* is aimed to be stand-alone executable, not demanding a *Matlab*® installation and being able to reach higher levels of performance and avoiding any kind of license.

II. STRUCTURE

The structure of the software is specially fitted for ECG recordings, but without excluding other biomedical signals. Along biomedical signals, it is very important to retrieve event marks during the recording, called annotations that have a physiological meaning. Therefore, two data types can be available: biomedical signal itself and related

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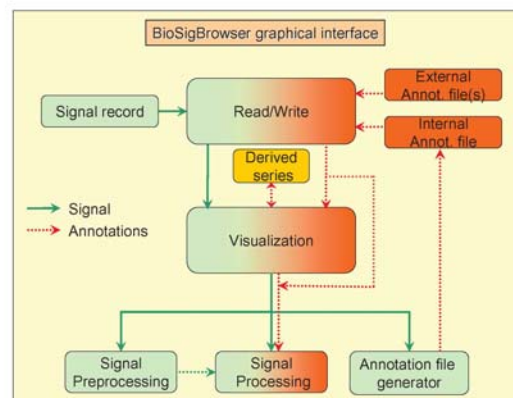
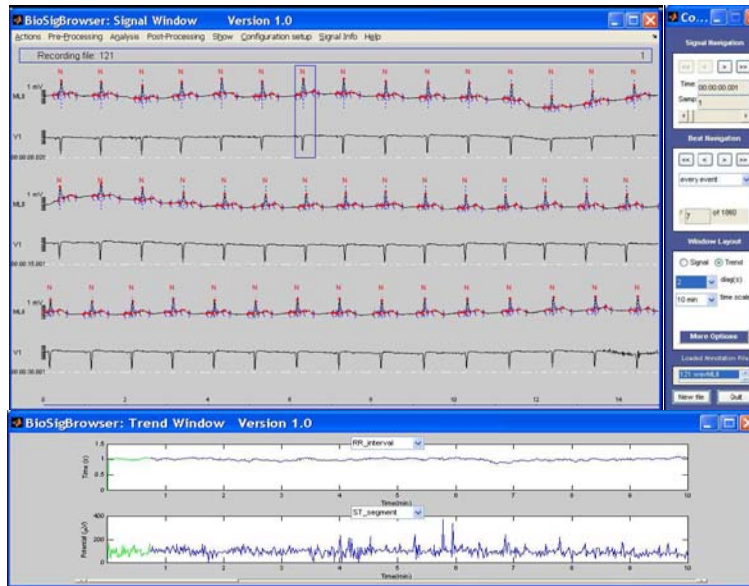Fig. 1. Workflow diagram of the *BioSigBrowser* structure.

Fig. 2. Signal Window (top left) is displayed the signal with interest points from a loaded annotation file. Control Window (top right) has all the browser and zoom tools for signal and event navigation. In the bottom, series of interest associated with annotation points, in this case beat-to-beat series are shown and the number of series can be selected in Control Window.

annotations. These events can be generated manually or automatically making use of implemented applications in the software.

Fig. 1 presents the software structure compounded of modules responsible for specific tasks. There are two input data types: signal and annotations. The signal path shows the available workflows and having only the signal is enough to be able to use all the applications. Annotation file can be created using the proper *annotation file generator* module or can be provided by other applications or manual elaboration. On the other hand, annotation path is optional. Nevertheless signal must be with annotations to use the processing module. Next, we are going to focus in the description of the modules:

A. Read/Write module

The *read/write module* allows loading a single signal file with or without the related annotation file or a whole database in a sequential way and save any final or intermediate results that could be of interest in the analysis as well. The default format data is the MIT-BIH database format [1], and the current version holds compatibility with data acquired with commercial equipment, such as Mortara Instruments® Digital Holter and Biopac® data acquisition MP Systems. The modular characteristic of the software allows the incorporation of other formats on an easy way.

B. Visualization module

This module allows to display data (multilead ECG or multimodal recordings, e.g. arterial blood pressure, electromyograms...), annotations related with the current loaded signal recording and series of interest extracted from those annotations, as the RR intervals series derived from

the ECG beat annotations.

The signal recording is displayed in the *Signal Window* (Fig. 2 top left) and the navigation and zoom tools are available in the *Control Window* (Fig. 2 top right).

Annotation files can be selected to be simultaneously superimposed on the signal and/or make event navigation. Event navigation allows user to browse timing events distinguishing between two types: beats and episodes. Beats are labeled according to one standard annotation code (i.e. MIT-BIH code) and episodes are other type of physiological marks (for example on ECG: *ST* level, rhythm change onset and offset...). The tools for this navigation can also be found in *Control Window*.

Derived series can be defined from annotations, as the *RR* intervals series obtained from the ECG. They have a specific visualization window named *Trend Window* (Fig. 2 bottom). During the event navigation, current event will be marked with a blue square. By right-clicking on it, a submenu will appear displaying the values of the series for that time and the access to a specific graphical interface named *Annotation file manager*. In order to be able to modify those series, it allows to insert new, remove or edit existing annotations and any change will be updated automatically in *Trend Window* and potential saved. Making right-click on the *Signal Window* and *Trend Window* we are able to export the displayed segment or whole signal or series into *Matlab*® workspace.

The visualization module allows user to apply the different software modules over the displayed signals using the menus on the *Signal Window*.

C. Annotation file generators

BioSigBrowser allows generating annotation files manually or automatically. Manually using the *Annotation file manager* or automatically using for instance, the ECG detector/delineator that generates one file including the annotations referred to onset/peak/offset of each QRS complex, T and P waves. This task is carried out by a fully automatic system for ECG waves delineation based on wavelet analysis [2]. The first step of this system is the identification of each QRS complex, taken as the reference for the location of the cardiac beat, for following delineation of the relevant ECG waves.

For the analysis of other biomedical signals besides the ECG, this module can be extended to attend new specificities, e.g. to detect front waves in EMG or to detect and delineate ABP waves.

This generated annotation file can be afterwards loaded in order to make use of *BioSigBrowser* tools, as if an annotation file would be *apriori* loaded and dense trend as RR, etc.

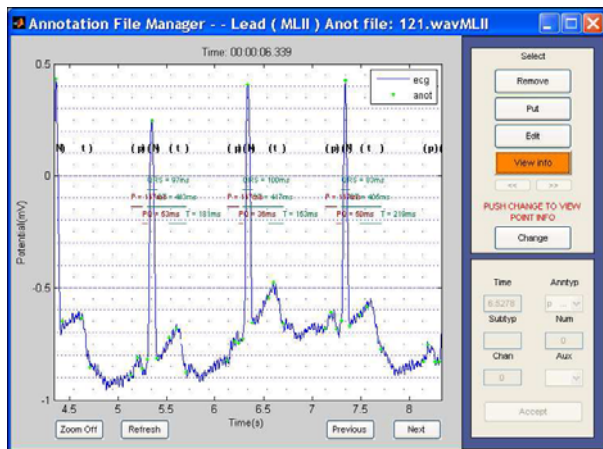

Fig. 3. Annotation file manager to allow the user to insert new and remove or edit existing annotations. The interface shows the signal annotations '*'. If the annotation file contains fiducial points, the onset '(' and offset ')' of the ECG characteristic waves and the corresponding points to those waves are shown, and it is considered the possibility to measure segments of interest inside of a beat

D. Preprocessing module

Biomedical signals are likely contaminated by artifacts. This module is defined to clean and prepare the signal for analysis. Many methods are included, such as subtraction of baseline wander (using cubic splines, time varying or invariant filter or design your own filter) and power line interference (using non linear filter [3-6]).

With respect to ECG signals, tools to derive leads using linear relations were also included: i) to estimate a missing extremity/limb lead from the other two; ii) to estimate augmented leads from limb leads; iii) vectocardiogarphic (VCG) leads estimation by inverse Dower matrix or by Levkov's method from 8 or 9 standard leads or from limb and precordial leads. iv) standard 12-lead estimation from the VCG leads by Dower matrix.

Several frequency domain analysis are included such as fast Fourier transform, cross and power spectral density function by Welch method and magnitude squared coherence estimate function.

E. Processing module

The following analysis methods were developed over previous research projects in the group. Once those are mature and stable tools, they are incorporated into the system.

Currently, the analysis methods included in the software are:

1) *An ischemia detector based on the root mean square (RMS) series of the ST interval with body position cancellation* [7]. Ischemia is a restriction in oxygen supply, generally due to factors in the blood vessels, with resultant damage or dysfunction of tissue. Cardiac ischemia may cause chest pain, known as angina pectoris.

2) *A T-Wave alternans (TWA) detector* [8]. TWA is a phenomenon appearing in the ECG surface as a consistent fluctuation in the repolarization morphology (ST segment and T wave) on an every-other-beat basis and also it is presently regarded as a promising marker of increased risk for ventricular vulnerability and sudden cardiac death.

3) *ECG-based estimation of the respiratory frequency* [9], exploiting the oscillatory pattern of the rotation angles of the heart's electrical axis, as induced by respiration. The series of rotation angles, obtained from least-squares loop alignment, is subject to power spectral analysis and then estimation of the respiratory frequency.

Some of the processing can generate annotation files related to the results as *T-Wave* alternans or ischemic intervals. Therefore those annotations will be available to be loaded afterward and to navigate over them.

All of these methodologies require the initialization of parameters or setup that is available in the menus of the *Signal Window*. Once the analysis method is executed, the results and the setup configuration will be saved in a file associated with the current annotation file and the results will be displayed to be visually checked.

III. FUTURE WORK

In a short term the software will be extended with two new analysis modules. One is related to the *characterization of the Autonomous Nervous System*. It will do an estimation of the heart rate variability [10] and the heart rate turbulence [11]. And the other one is about *sleep apnea detection* from cardiovascular signals (photoplethysmography (PPG) or ECG) [12].

IV. ACKNOWLEDGMENT

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