

A Biosignal Analysis System Applied for Developing an Algorithm Predicting Critical Situations of High Risk Cardiac Patients by Hemodynamic Monitoring

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Abstract

A software system for efficient development of high quality biosignal processing algorithms and its application for the Computers in Cardiology Challenge 2009 – Predicting Acute Hypotensive Episodes is described.

The system is part of a medical research network, and supports import of several standard and non-standard data formats, a modular and therefore extremely flexible signal processing architecture, remote and parallel processing, different data viewers and a framework for annotating signals and for validating and optimizing algorithms.

Already in 2001, 2004 and 2006 the system was used for implementing algorithms that successfully took part in the Challenges, respectively. In 2009 we received a perfect score of 10 out of 10 in event 1 and a score of 33 out of 40 in event 2 of the Challenge.

1. Introduction

Biosignal analysis is a common topic in the field of eHealth and biomedical engineering that has a large application area.

When developing new algorithms for biosignal analysis, several tools are required to help the developer finding the suitable features of the signal, implementing the algorithm, validating the algorithm's results and optimizing existing algorithms in order to achieve a predefined optimal performance. By the use of such tools, it is not only possible to increase the quality of the resulting algorithms, but also to significantly reduce the development time for new algorithms.

In the present paper we describe such a set of tools that are included in our biosignal processing system and by the example of the *Computers in Cardiology Challenge (CinC) 2009 – Predicting Acute Hypotensive Episodes* [1] we demonstrate, which important steps can be facilitated by the use of a powerful biosignal processing system.

2. Methods

2.1. System overview

The biosignal processing system consists of a Matlab (The MathWorks, Inc., Natick, MA, USA) framework that is part of a medical research network [2]. Figure 1 gives an overview of the biosignal processing system and its modules.

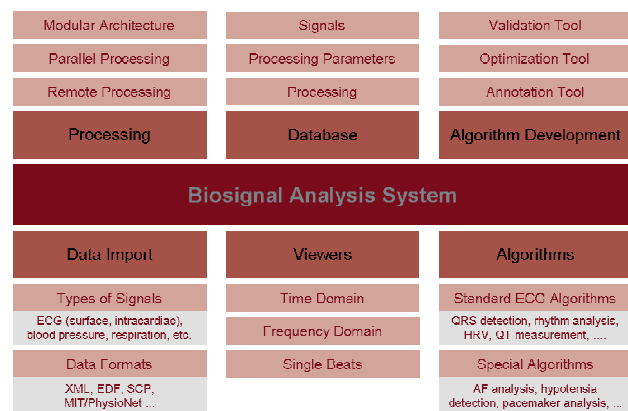


Figure 1: System overview

2.2. Data import

Several standardized data formats (e.g. EDF [3], FDA XML [4], SPC [5], PhysioNet [6]) as well as proprietary data formats for different kinds of biosignals (e.g. ECG, blood pressure, respiration) are supported.

2.3. Biosignal processing algorithms

The system currently includes several standard algorithms – most of them for ECG processing – as well as some several algorithms for special applications (such as the CinC challenges 2001, 2004, 2006 and 2009).

A common set of functions and algorithms used for standard ECG analysis consists of:

- Load meta data from the signal header
- Detect QRS complexes [7]

- Classify QRS complexes according to their morphology [8, 9]
- Analyze the cardiac rhythm [8, 9]
- Detect the characteristic points of the ECG (P, QRS, and T) [10, 11]

Special algorithms implemented so far include:

- Heart rate variability (HRV) analysis
- QT measurement [10, 11]
- Calculation of averaged heart beats [9, 11]
- Removal of ventricular signal portions [9, 12]
- AF initiation prediction [8, 9, 13]
- AF termination prediction [9, 12]
- Pacemaker status check [14]
- Acute hypotensive episode prediction

2.4. Processing

Data processing is implemented using a **modular architecture**, so that different algorithms can be arranged in arbitrary order – depending on the problem intended to be solved. For each algorithm, a set of processing parameters can be defined. New algorithms can easily be added to the system by defining a new algorithm pipeline.

Remote processing is provided by an interface to the medical research network [2]. Via a web-interface biosignals can be uploaded to a medical data centre. As soon as a new biosignal becomes available within the database, the biosignal processing systems picks-up the signal, processes it and sends the results back to the medical research network. The results are again presented to the users via a web-interface (Figure 2).

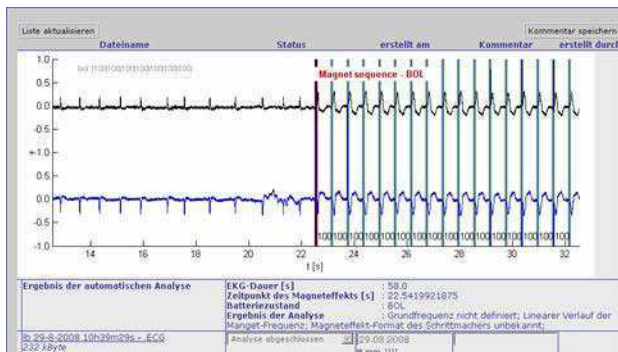


Figure 2: ECG with markers for pacemaker spikes and pacemaker status information as presented to the physician via internet browser [14].

Parallel processing has been developed so as to reduce the time for testing and validating new features and versions during the process of algorithm development. Especially in the case when algorithm development implies to deal with a large number of signals or signals with a long duration or many channels,

a high performance is essential. We use the Matlab Compiler (The MathWorks, Inc., Natick, MA, USA) to generate standalone executables of our biosignal processing system that can be run on an arbitrary number of workstations. Each workstation is connected to the biosignal database and can pick out signals and send back its results.

2.5. Viewers

Depending on the biosignal and the kind of algorithm to be developed, different settings are required from the viewers used to display the biosignals and algorithm results.

Time domain viewer: Usually, the signal is plotted as a function of time. In this common view it is important to display additional information such as expert annotations and calculated results. Hence, this signal-over-time viewer is the most common one that is implemented in almost all biosignal processing systems.

Frequency domain viewer: Many analyses are based on a frequency domain approach, and therefore a frequency domain viewer is another tool often needed during algorithm development. Depending on the signal analyzed, different settings for the time-frequency-transformation are required (e.g. short time Fourier transformation with different time window lengths, wavelet transform, etc.).

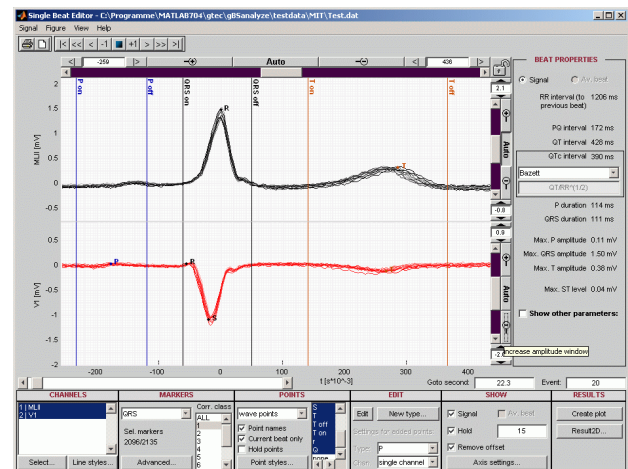


Figure 3: Screen shot of the single beat viewer in a use case for the comparison of the wave onset / offset detection algorithm results for subsequent heart beats.

Single beat viewer: More specifically, when developing algorithms that deal with individual events within biosignals, the viewer should be able to plot e.g. single heart beats. Additionally, there is a need to show several events simultaneously and compare the results

achieved for each of the events with one another (see Figure 3).

2.6. Algorithm development

When developing biosignal processing algorithms it is essential to know which result is intended to be received. Therefore, a gold standard has to be defined that should be reproduced by the algorithm.

The definition of this gold standard can be a) very difficult and b) very time consuming. Often annotations provided by physicians are used as a gold standard. In order to facilitate the process of annotating possible a large number of biosignals, special **annotation tools** are a basic requirement.

As soon as a gold standard and an initial algorithm for solving some kind of problem exist, the algorithm's results can be **validated against the gold standard**.

Finally, optimal values of processing parameters such as filter frequencies, threshold values etc. are initially unknown and therefore have to be guessed by the developer. Finding the optimal value of these parameters can significantly increase the algorithm's accuracy. Therefore, a **tool for optimizing processing parameters** is needed as well.

The system described allows for annotating signals in several different editors and a special optimization and validation tool is provided, too.

2.7. Database

A central database is used for managing parallel and remote processing, versioning, storage of signals etc. All processes, process sets and processing parameters are stored in the database as well.

2.8. CinC Challenge 2009

Our first step concerning the CinC 2009 challenge was to design an import function that allowed us to display the signals of the MIMIC2CDB [15] in our biosignal processing system – including all annotations for medications etc. We then manually inspected the data of the trainings-set – and tried to identify parameters capable to distinguish in between the different groups of data, mainly based on our understanding of physiological and pathological aspects of the human circulatory system and the associated biosignals.

In a previous study for home-monitoring of patients with congestive heart failure provides [16] we used increasing body weight (2 kg weight gain within 2 days) as an early warning sign of fluid retention. This regimen led to an adjustment of medication, resulting in a reduced frequency and duration of heart failure hospitalizations. The data recorded in that study also indicated that the difference in between systolic and diastolic blood

pressure decreases prior to cardiac events.

Since no body weight changes were available in the MIMIC2CDB, the difference in between systolic and diastolic blood pressure was one of our first features analyzed during the CinC Challenge 2009. Other features were achieved from the manual inspection of the signals, especially the mean arterial blood pressure seemed to be lower for patients developing acute hypotensive episodes than in other.

Subsequently, an automated method for predicting acute hypotensive episodes was developed. We detected the QRS complexes in all signals and for each heart beat (i.e. in between all subsequent QRS complexes) we calculated the mean arterial blood pressure for all signals.

In **event 1** the median of all mean arterial blood pressure values achieved for all beats of the last 60 minutes (ABP_{60_0}) of the signal was used as the selection criteria: patients featuring a value lower than 70mmHg were classified as "will exhibit a hypotensive episode" (see criteria 1):

criteria 1 – hypotensive episode will appear, if
 $ABP_{60_0} < 70 \text{ mmHg}$

For **event 2** we also considered the change of the median mean arterial blood pressure within the last 30 minutes (ABP_{30_0}) as compared to the preceding 30 minutes (ABP_{60_30}):

criteria 2 – hypotensive episode will appear, if
 $ABP_{60_0} + (ABP_{30_0} - ABP_{60_30}) < 65 \text{ mmHg}$

3. Results

Apart from several clinical studies [16, 17], the framework was also used for algorithm development during the CinC Challenges 2001 [8], 2004 [12], 2006 [10] and 2009, respectively.

In 2001 the AF initiation prediction algorithm received the best results in both events of the challenge. The AF termination prediction algorithm developed 2004 scored best in event 1 of that year's challenge. In 2006, the QT measurement algorithm was the most precise of all participants taking part in event 2.

With our final entry to the CinC Challenge 2009 we received a perfect score of 10 out of 10 correct classifications. Our initial entry to event 2 of the CinC Challenge 2009 received a score of 34 out of 40 correct classifications. This result could not be improved with our additional three votes.

4. Discussion and conclusions

There are several biosignal processing systems available on the market. However, in a research environment it is essential to guarantee the possibility to update existing and include additional features in an easy way, which is only possible, if the source code of the

software is available. There are even some open source biosignal processing systems available, such as [6, 18]. Some aspects addressed in the present paper are implemented in these projects as well, but no system fulfils all the requirements. Anyway, these open source systems can help accelerating the implementation of biosignal analysis systems as described in the present paper.

One challenge in developing algorithms for biomedical applications is to transfer algorithms from a research framework to clinical routine. Therefore, strict quality management is needed already in the phase of software development and the use of open source software developed for research purposes may sometimes prove unfavourable soon as the software should be transferred to clinical routine.

Since other participants in the challenge 2009 received the perfect score sooner than we did, the first prize was won by another group. However, by achieving the perfect score of ten out of ten, the effectiveness of the biosignal processing system could once more be proven. Concerning event 2 the best result of all participants was 36 out of 40. Therefore, although not the best, our result still is hardly worse.

In conclusion – even though other participants performed better in the CinC Challenge 2009 – the system described in the present paper has proven its value as a tool for the development of high quality biosignal processing algorithms. The description of the tools used within the system may assist other developers to improve their programming environment and thus shorten the development time and enhance the quality of future biosignal processing algorithms.

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