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BIOSIG – an open source software package for biomedical signal processing for use with Octave and Matlab.

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1.   Introduction

Do you work in the field of biomedical signal processing and did you ever have one or more of the following problems?

- Standard algorithms can not be applied because no software is available
- People/colleagues were reinventing the same algorithm
- Various user-specific versions of the same function
- Data/project specific properties of some software prevent compatibility
- Reproducibility is limited due to unknown or badly documented pre-processing
- Converting an old software package to a new platform?
- Data with unknown/unsupported format

If you are working on biomedical signals, the answer is probably, yes. This paper describes how we addressed these issues.

2.   The approach

In another area of software development, a paradigm shift in software development can be observed. This shift has been most prominently described by Eric Raymond's "the cathedral and the bazaar" [1] and is manifested in the success of the Linux operating system. We had already some experiences on open source [2] development from other projects [3,4,6,7] and expect that publishing of software (as opposed to publishing papers) will become more important in the field of biomedical signal processing. Based on the existing experience, it was obvious that a possible solution must have the following cornerstones: (1) supporting tools for concurrent software development; (2) little overhead and management costs; (3) provide tools such that "reinventing the wheel" is not necessary.

3.   The solution

3.1   The project outline

The outline of the current (and first) design is shown in Table 1.

Table 1: Categories of the BIOSIG project.

	Description
T100	Data Acquisition
T200	Data Formats
T250	Quality Control and Artefact Processing
T300	Signal Processing and Feature extraction
T400	Classification, Single Trial Analysis, Statistics,
T490	Evaluation criteria
T500	Presentation, Output
T550	Topographic Mapping, 3-dimensional display
T600	Interactive Viewer and Scoring

The following components are currently available and in use: (a) A common interface is provided for accessing different data formats. The interface consists of function calls SOPEN, SREAD, SEOF, SCLOSE, SSEEK, SREWIND, STELL and SWRITE. These functions allow random data access to data blocks. In case, a whole file should be read, the function SLOAD reads the header information and the data, at once. Currently, over 50

data formats are recognised. Read support is implemented for 15, write support is available for 7 data formats [4]. (b) Basic functions for triggering of data, artefact detection, quality control, etc. are implemented. Furthermore, a concept for handling missing values, which are encoded as Not-A-number (NaN), is implemented. (c) For the signal processing, mainly the TSA-toolbox [3] with its routines for (adaptive) autoregressive model estimation is used. Currently also a simple QRS detector is included. (d) The classification part contains mainly linear and quadratic classifier, cross-validation and tools for analyzing data from Brain computer interface (BCI) experiments [9]. (e) The data presentation is organized in a single display function, which can handle different "datatypes". Examples for such datatypes are: histograms, coherence, partial directed coherence, directed transfer function, scatterplot etc.

3.2   Sourceforge:

Sourceforge was choosen for hosting the repository. Sourceforge provides Concurrent Versions System (CVS), a tool for concurrent software development and version tracking, it provides facilities for hosting the WWW project pages, and Sourceforge is well known [8].

3.3   The License:

The GNU General Public License (GPL) [5] was chosen. GPL is one of the most successful and powerful opensource licenses so far. GPL is an open source license, one of its background is the motivation of the "gift culture" [1]. Also we are working in academia and it is not a primary aim "to make money" but to generate "knowledge".

4.   Conclusion

The BIOSIG has started ca. one ago. The download statistics of sourceforge is currently in the range of 200 per month. This points out the interest in the project. The known user-base consists mostly from the colleagues in our lab and the partners in the research projects (e.g. [10,11]).
In future, we expect that this project provides a repository of standard methods for biomedical signal processing. It will become easier for PhD-students to get into the field, it will be easier for reviewers to evaluate manuscripts, BIOSIG will support projects to fulfil its goals. Overall, the BIOSIG project can improve the development of the whole field of biomedical signal processing.

Acknowledgements

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