20 BioSig: An Open-Source Software Library for BCI Research

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20.1 Abstract

BioSig is an open-source software library for biomedical signal processing. Besides several other application areas, BioSig also has been developed for BCI research. It provides a common interface to many different dataformats, it supports artifact processing and quality control, it provides adaptive signal processing and feature extraction methods that are very suitable for online and real-time processing, it supports handling of missing values, and it includes several classification methods for single-trial classification of EEG.

This chapter provides an overview of the current status and an outline of future possibilities. BioSig is licensed with the GNU General Public License; it provides an open development platform unencumbered from legal restrictions. Therefore, it is also an ideal tool for research and development.

20.2 Overview

Besides several proprietary software packages, several open-source software tools are available in the field of EEG processing. Currently, we know of the the following packages: EEGLAB by Makeig and Delourme, BioSig by Schlögl et al., OpenEEG, Bioelectromagnetism toolbox by Weber et al, EMEGS, FieldTrip, LORETA by Pascual-Marqui, and BCI2000 by Schalk et al (see also table 20.1). The first five are licensed with the GNU General Public License (GPL); thus, the user has the freedom to *run, copy, distribute study, change, and improve* the software. EEGLAB, Bioelectromagnetism toolbox, EMEGS, FieldTrip, and LORETA are designed for classical offline EEG analysis. The

Table 20.1 Software packages for EEG analysis.

Package	License	Language	Requirements
BCI2000	?	C++	Windows
Bioelectromagnetism	GPL	Matlab	Matlab
BioSig	GPL	Octave, Matlab, Simulink, C/C++, Qt, Java, Python	various
EEGLAB	GPL	Matlab	Matlab (5+)
EMEGS	GPL	Matlab	Matlab (6+)
FieldTrip	GPL	Matlab	Matlab
LORETA	?	unknown	Windows
OpenEEG	GPL	various	various

Table 20.2 The library of m-functions is organized along the following subtasks or topics.

(i)	Data acquisition
(ii)	Data formats and storage
(iii)	Preprocessing
(iv)	Signal processing and feature extraction
(v)	Classification and statistics
(vi)	Evaluation criteria
(vii)	Visualization
(viii)	Interactive viewer and scoring

packages BioSig and BCI2000 are dedicated to BCI research. BCI2000 is described in detail in chapter 21, while the BioSig project is discussed here.

A major aim of BioSig is to provide an open-source software library for BCI research; it is available from http://biosig.sf.net. In the following chapter, we outline the general structure of BioSig and highlight some important components.

20.3 BioSig for Octave and MATLAB

The BioSig project was started as a library for MATLAB with an attempt to be compatible with Octave by Eaton. The first toolbox already contained several subtasks (see table 20.2). With the advent of other subprojects (rtsBCI, C/C++, SigViewer, etc.) this part was renamed “Biosig for Octave and MATLAB”.

20.3.1 Data Formats and Storage

The “data format module” implements a common interface to various data formats; currently, more than fourty different data formats are supported. This is more than any other project in the field of biomedical signal processing.

Automated detection of the file format is supported. The range of supported formats includes data formats of equipment providers (e.g., ACQ from BIOPAC or CNT from NeuroScan), specific research projects (e.g., Physiobank format from MIT, or the BCI2000 format), and standards and quasi-standards (e.,g., EDF, SCP, or MFER formats), and also supports several audio and sound formats.

The various data formats contain many encoding schemes using different bit depths, allowing single or multiple sampling rates, and they contain different header information. With the common interface implemented in BioSig, the users do not need to care which data format is actually used or how the proper scaling of the amplitude values is obtained or from where to obtain the sampling rate. The interface also supports simple preprocessing like the selection of specific data channels and overflow detection (if supported by the underlying data format). If an overflow is detected, the corresponding sample value is replaced by *not-a-number* (NaN) (IEEE754). This feature of automated overflow detection can be turned off, but by default it is on.

However, none of these data formats contains all the features needed for BCI research. Therefore, the advantages of various data formats were used to construct the general data format (GDF) for biomedical signal processing (by Schlögl). Besides several other improvements, an encoding scheme for events and annotations is part of the GDF definition (see table 20.3). The codes are grouped according to different application areas, for example, EEG artifacts have the code range 0x0100–0x010f, while the range of 0x0300–0x3ff is reserved for BCI experiments.

The GDF format has been used already in several BCI studies, for example, the datasets IIIa and IIIb of the BCI competition 2005 have been exchanged in the GDF format. Also, the "rtsBCI" and the "biofeedpro" (see sections 20.4 and 20.6) are using GDF as the standard data format for data recording.

20.3.2 Preprocessing

Methods for preproccessing are applied at an intermediate state between data access and feature extraction. Accordingly, this module contains several useful preprocessing routines. One of the most often used functions is probably the function for triggering the data, that is, to extract data segments relative to a given trigger. Also available is a function for extracting the trigger time points from a continuous trigger channel, as well as some simple resampling methods. Some advanced algorithms for artifact processing are also included: a method for quality control using histogram analysis (Schlögl et al. (1999c)), an algorithm for reducing EOG artifacts based on regression analysis, and a method for detecting muscle artifacts based on inverse filtering.

20.3.3 Signal Processing and Feature Extraction

Naturally, signal processing is one of the core components of a biomedical signal processing toolbox. Many signal processing methods are already available elsewhere. Unfortunately, it is rare that any signal processing toolbox supports the handling of missing data. Exceptions are the "time series analysis (TSA) toolbox" (by Schlögl) and the NaN toolbox

Table 20.3 Predefined event codes for BCI experiments. The complete list is available from http://cvs.sourceforge.net/viewcvs.py/*checkout*/biosig/biosig/doc/eventcodes.txt.

###	Table of event codes.
#	
###	table of event codes: lines starting with # are omitted
###	add 0x8000 to indicate end of event
###	0x010_ EEG artifacts
0x0101	artifact:EOG (blinks, fast, large amplitude)
...	
###	0x011_ EEG patterns
0x0111	eeg:Sleep spindles
...	
###	0x012_ Evoked potentials
0x0121	VEP: visual EP
...	
###	0x013_ Steady State Evoked potentials
0x0131	SSVEP
...	
###	0x03__ BCI: Trigger, cues, classlabels,
0x0300	Start of Trial, Trigger at t=0s
0x0301	Left - cue onset (BCI experiment)
0x0302	Right - cue onset (BCI experiment)
0x0303	Foot - cue onset (BCI experiment)
0x0304	Tongue - cue onset (BCI experiment)
0x0306	Down - cue onset (BCI experiment)
0x030C	Up - cue onset (BCI experiment)
0x030D	Feedback (continuous) - onset (BCI experiment)
0x030E	Feedback (discrete) - onset (BCI experiment)
0x030F	cue unknown/undefined (used for BCI competition)
0x0311	Beep (accustic stimulus, BCI experiment)
0x0312	Cross on screen (BCI experiment)
0x0313	Flashing light
0x031B	- 0x037f reserved for ASCII characters #27-#127
0x0381	target hit, task successful, correct classification
0x0382	target missed, task not reached, incorrect classification
0x03ff	Rejection of whole trial
###	0x00__ user specific events
0x0001	condition 1
0x0002	condition 2
...	

(by Schlögl). Both are part of OctaveForge and are distributed with BioSig (by Schlögl et al.).

The NaN toolbox contains methods for statistical analysis that support data with missing values encoded as not-a-number (NaN) according to the IEEE754 standard. The basic functionality of the NaN toolbox is a function called `sumskipnan.m`, which skips all NaNs, and sums and counts all numerical values. The two return values `SUM` and `COUNT` are sufficient to calculate the mean of the data. This principle also can be used to calculate the expectation value of any statistic including covariance matrices and more advanced statistics. Whether or not this principle can be applied to more advanced signal processing methods is being investigated.

The TSA toolbox contains many functions for parametric modeling, that is, autoregressive estimators. It contains the well-known Burg and Levinson-Durbin algorithms for estimating autoregressive (AR) parameters of single-channel stationary processes. Adaptive autoregressive (AAR) estimators (Schlögl (2000a)) like Kalman filtering, and RLS and LMS algorithms are available. Multivariate autoregresssive (MVAR) estimators like the Nuttall-Strand method (multichannel Burg) or the multichannel Levinson algorithm have been included. Furthermore, the adaptive estimation of some standard EEG parameters (e. g., bandpower, Hjorth (1970) and Wackermann (1999) parameters) are also supported. The adaptive estimation does not require downsampling and is still computationally efficient. Accordingly, the features are obtained with the same sampling rate as the input data. All these functions can deal also with missing data encoded as NaN. This represents an efficient way of handling missing data values and can be used easily in combination with artifact detection methods, for example, saturation or muscle artifacts.

20.3.4 Classification

This module has been developed according to the needs of the Graz BCI system (see chapter 4) using the advantage of statistical classifiers (e.g., robustness) like linear and quadratic discriminant analysis. This use allowed the possibility of a continuous feedback (in time as well as magnitude). A classifier combines various features into a single output, and the time lag of classification should be as small as possible. Often, one wants to know how well the classifier is able to separate the training data. To prevent overfitting, cross-validation is required. Finally, the optimal time point for applying the classifier must be identified in BCI research.

To fulfill the various needs, a wrapper function (`findclassifier.m`) has been developed that includes the required functionality. In the first version, a linear discriminant analysis (LDA) for two classes was implemented. Later, quadratic classifiers and an interface to support vector machines (SVM) were added; multiple classes $N > 2$ are supported (using a one-versus-rest scheme). Another important issue was the selection of the proper time segment for estimating a classifier. For this purpose, the data were triggered and separability was calculated for each time segment. The length of each segment can be varied from 1 to N samples; typically, a fixed segment length of a fraction of a second (e.g., 0.2 s or 0.125 s; 8 to 25 samples depending on the sampling rate) is used. For the search step,

the relative separability is sufficient; the cross-validation is omitted in this step. In the next step, a trial-based leave-one-out method (LOOM) is used for cross-validation.

The samples from the chosen segment of all but one trial are used to train the classifier, and this classifier is applied to all samples of the testing trial; this provides a time course of the output for the specific trial. This procedure is repeated until each trial has been used once as test trial. When all permutations are finished, a time course of the output is obtained from each trial. This outcome is then evaluated for different evaluation criteria like error rate, SNR, mutual information, and kappa. An example is shown in section 19.6.

Results have been used in several works (e.g., Blankertz et al. (2004); Schlögl et al. (2002, 2003, 2005). This classifier was also used in the BCI competition 2005 on dataset I (rank 7) and IVa (rank 8). Moreover, the general classifier was obtained from the data of the selected segment. This classifier has been used together with "rtsBCI" in several BCI experiments (Scherer et al. (2004b); Vidaurre et al. (2004a,b)).

20.3.5 Evaluation Criteria

Several different evaluation criteria are used in BCI research (for details, see also chapter 19): Implemented are accuracy (error rate), information transfer (Schlögl et al. (2002, 2003)), Cohen's kappa coefficient (Schlögl et al. (2005)), and several others. Moreover, functions for analyzing the time courses of the different criteria are provided. The implementation of these functions were also used for analyzing results of the BCI competition 2003 (dataset III) (Blankertz et al. (2004)) and BCI competition 2005 (dataset IIIa and IIIb).

20.3.6 Visualization

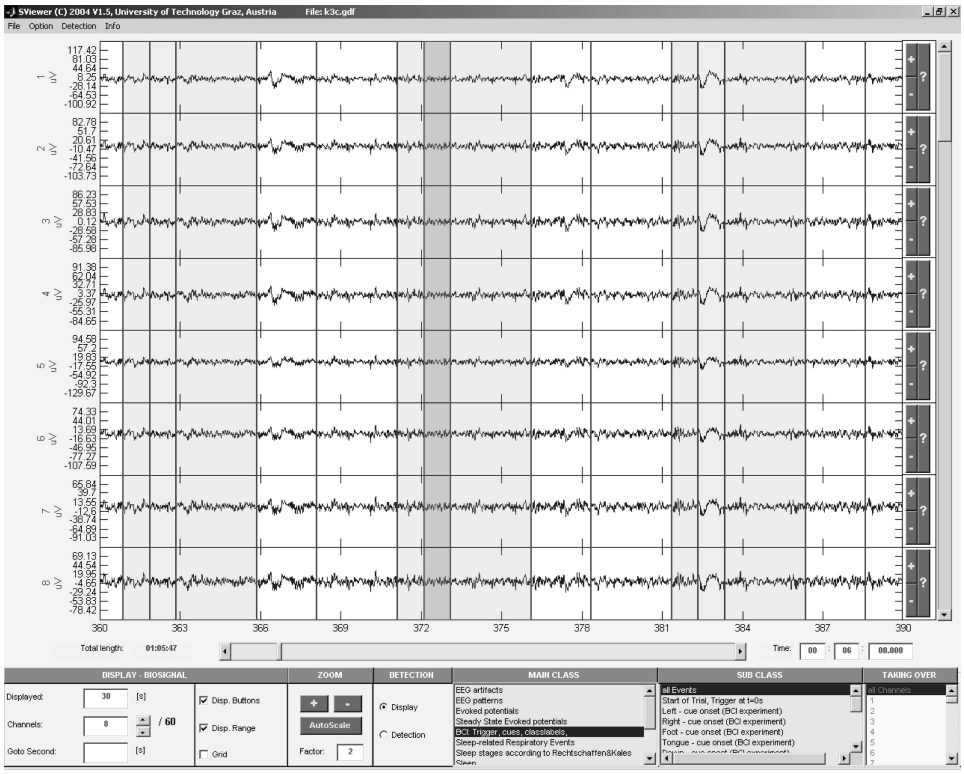
Visualization is always an important issue. Currently, the function `plota.m` is a wrapper function for displaying various results. The presented result depends on the input data and which function has generated a certain result. For example, the outcome of `findclassifier.m` for two classes is presented as time courses of the error rate, SNR, and the mutual information. If the result stems from $N > 2$ classes, the time course of the accuracy and the kappa coefficient are displayed.

Another useful function is `sview`, which is able to present the raw EEG data in a compressed form on a single screen. It also includes any event information (if available). Within MATLAB it is possible to zoom into specific segments. The `sview` function is useful to get an overview of the available data. Another important functionality is the scoring of EEG data. Two packages—SViewer and SigViewer—support the viewing and the scoring of EEG data and are described in more detail in section 20.5.

20.3.7 SViewer – a viewing and scoring software

`SViewer` is written in MATLAB, and it uses the MATLAB GUI functions and the functions for reading the data and for writing event information. Because it is based on the common interface, it can read any data format supported by *Biosig for Octave and*

Figure 20.1 SViewer: a viewing and scoring software based on the graphical user interface of MATLAB.



MATLAB. The annotations, markers, and events can be edited and stored in a separate event file. A screenshot of SViewer is shown in figure 20.1. SViewer must not be confused with SigViewer, which is a stand-alone program and does not require MATLAB; SigViewer is described in section 20.5.

20.4 Real-time BCI System Based on MATLAB/Simulink—rtsBCI

The Graz BCI (see chapter 4) open-source software package rtsBCI provides a framework for the development and rapid prototyping of real-time BCI systems.The software is licensed under the GNU GPL and based on MATLAB/Simulink (The Mathworks, Inc., Natick, MA, USA) running on Microsoft Windows (Microsoft Corporation, Redmond, WA, USA). To enable hard real-time computing on Windows platforms, the Real-Time Windows Target (RTWT) and, for the generation of stand-alone C code, the Real-Time Workshop (RTW) are required. Both toolboxes are extensions of Simulink. Furthermore, BioSig for Octave and MATLAB is required for data format handling, and the TCP/UDP/IP

toolbox (by Rydesäter) is required for network communication support. In addition, to the software requirements, a data acquisition card (DAQ) is needed to sample the biosignals.

After installation, all rtsBCI modules are listed in the Simulink Library Browser and can be used to design (model) the BCI system (figure 20.2). Several MATLAB functions and Simulink blocks are available for (1) data acquisition and conversion; (2) storage (using the open data format GDF (by Schlögl)); (3) digital signal processing (e.g. bandpower feature estimation, adaptive autoregressive parameters (AAR) estimated with Kalman filtering (by Schlögl (2000a)), or linear discriminant analysis (LDA)); (4) visualization (e.g. signal scope, presentation of cue information, or feedback of a moving bar); (5) paradigm control (synchronous and asynchronous operation mode); and (6) network support (e.g., remote monitoring).

Tunable parameters as well as other information relevant for the experiment (e.g., subject information, amplifier settings, electrode setup, and paradigm timing) are stored in an individual configuration file (INI file). Before a model is executed, the configuration is transferred to the model and stored altogether with the biosignals for further analysis. The division of model and parameters makes it very easy to deal with changes: For example, a new classifier requires only the replacement of the classification block. A new subject requires only the modification of the related data in the configuration file.

Most of the online BCI feedback experiments reported from the Graz research group (see chapter 4) in the past few years are based on rtsBCI and come along with the package: the standard Graz BCI training without feedback (Pfurtscheller and Neuper (2001)), the standard two-class Graz BCI training with feedback (Pfurtscheller and Neuper (2001)), and the two-class basket paradigm (Krausz et al. (2003)). Generally, the first paradigm is used to collect data for analysis and setup of the classifier. The second provides a simple feedback in the form of a bar moving either toward the left or right side of the screen. The third paradigm provides feedback in the form of a ball falling from the top to the bottom of the screen at a constant speed with the task of hitting the correct target at the bottom of the screen by moving the ball either to the left or right side (figure 20.2).

20.5 SigViewer

SigViewer is a viewing and scoring program for biosignals, originally designed to process electroencephalogram (EEG) signals. SigViewer can load multichannel signals, such as EEG, ECG, EMG, and EOG recordings, and display these in various scales. For example, figure 20.3 shows the viewer displaying five EEG channels simultaneously. Besides the viewing functions of SigViewer, the other major application is the scoring of biosignals, which permits the user to make annotations to the signals (e.g., mark segments as artifact or mark specific events) and save this information to a file (either in the original data file, a copy of the data file, or in a file that contains only these annotations). In the example in figure 20.3, an EOG artifact is marked inside the left light grey area. The right light and dark grey rectangles label two overlapping events; for instance, the light grey area might denote an EEG trial and the dark one might indicate the period where an arrow (a cue) is displayed to the subject.

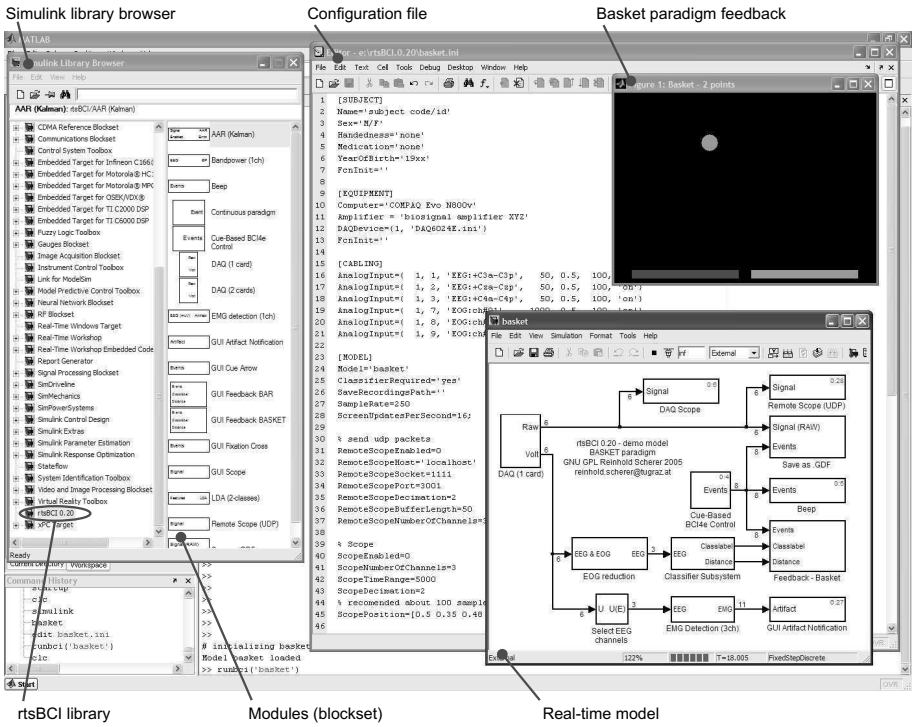


Figure 20.2 The screenshot shows the development environment: the basic platform MATLAB, Simulink with rtsBCI, an editor with configuration file, and a real-time model of the Basket paradigm with feedback window.

It is also possible to view basic information about a specific file (e.g., number of channels, sampling frequency, number of events, time of recording). In addition to graphically scoring the data, a list-based widget is available for viewing and deleting all events (annotations) manually. In the future, adding new events that way will also be possible.

Currently, the software supports only GDF files as input and output signals, but thanks to its modular structure it can be extended to support other file formats. In principle, any kind of signal data (including audio files) is a candidate to be displayed. The availability of new import and export filters is planned for in the separate subproject called "BioSig for C++" (or biosig4c++ for short), which can be used not only by SigViewer but also by other programs.

SigViewer is written in C++ using the platform-independent graphical user interface (GUI) toolkit QT4. One major design specification was that SigViewer be able to run under many different operating systems such as Linux, Windows, and MacOS and thus be designed as platform-independent. Moreover, SigViewer does not depend on any proprietary software, making it a truly free program.

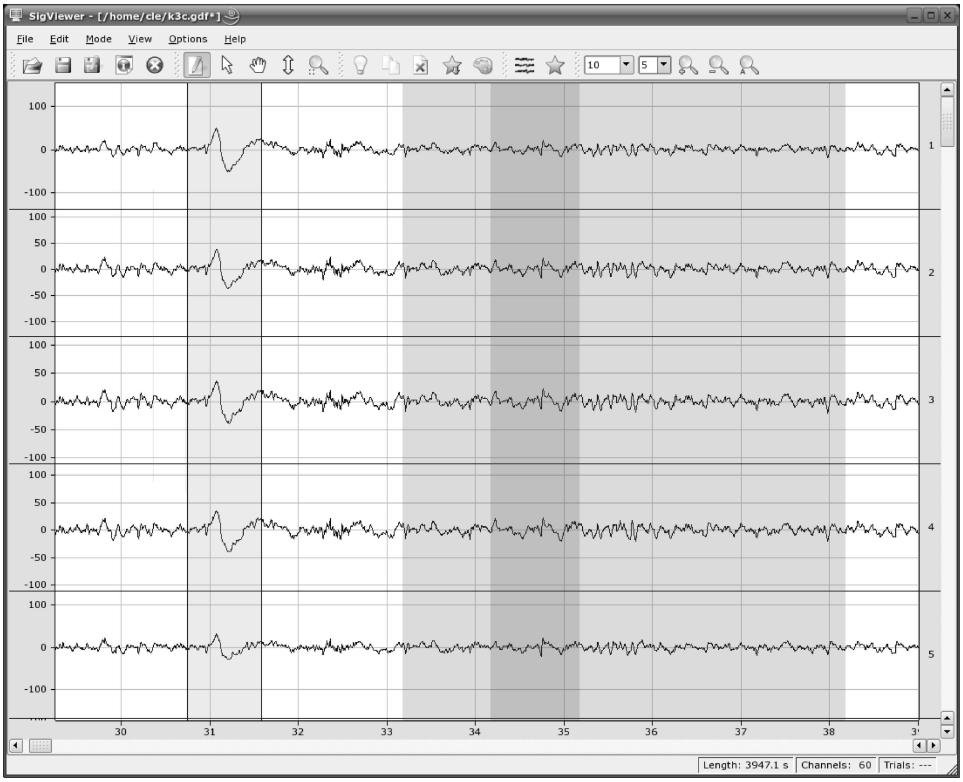


Figure 20.3 Screenshot of SigViewer.

20.6 BioProFeed

BioProFeed is a data acquisition module based on the real-time application interface (RTAI) (by Mantegazza et al). Currently, BioProFeed can be used with the following data acquisition hardware:

(1) g.mobilab from g.tec
(2) NI-6024e PCMCIA from National Instruments
(3) ModularEEG from OpenEEG

Support for further hardware modules is in preparation.

The name *BioProFeed* stands for Portable **Bio**signal acquisition, real-time **Pro**cessing and **Feed**back generation framework. The biosignal acquisition chain consists of one or more transducers, a biosignal amplifier, an ADC and a processing and storage unit. BioProFeed is a software framework for the processing and storage unit that is often a standard personal computer. It is licensed under the GPL and is a part of the Biosig project.

BioProFeed was written with the following specifications in mind:

(1) it should be platform independent
(2) it should be modular to support different data aquisition hardware

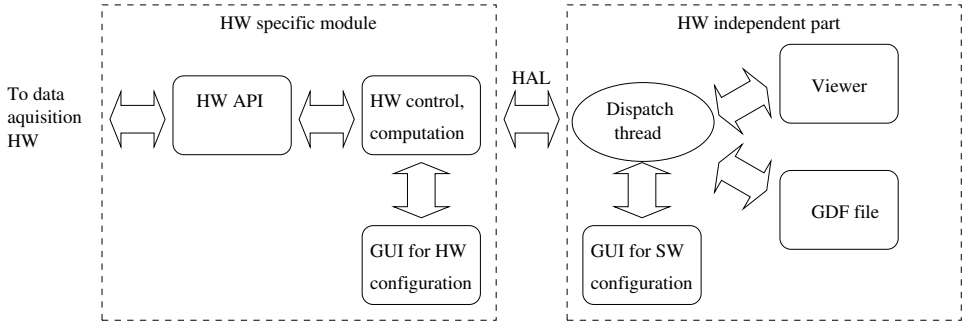


Figure 20.4 Software structure of BioProFeed.

(3) real-time data processing should be possible
(4) storage of the data in GDF format (by Schlögl) should be possible

Currently, BioProFeed runs on Linux (i386, ppc, arm), MacOS, and Windows XP with Cygwin. Autotools (by Vaughan et al), like autoheader, autoconf, and automake, are used to build software framework. These help to build the software by ensuring correct byte ordering for the different hardware platforms. The byte ordering is important when storing the data in GDF format (by Schlögl).

Gimp-Toolkit (GTK) has been used to write the user interface of the software. It can be integrated into any C/C++ program and is also highly portable. In fact, many GLib (glib) functions have been used to make BioProFeed more portable. In addition to the gLib functions, standard POSIX functions have been used.

The main structure of BioProFeed can be seen in figure 20.4. BioProFeed consists of two parts: the main part where data can be processed, displayed and stored, and the module part that controls and gets samples from the data acquisition hardware. The interface between the main part and the module part is called HAL (hardware abstraction layer). The modules supporting the data aquisition hardware are present in the CVS Tree of BioProFeed.

BioProFeed is a tool for data acquisition, processing, storage, and feedback generation. It is not restricted to specific data acquisition hardware or to specific data processing and storage hardware, and can store the data in GDF format (by Schlögl) for further offline data processing.

20.7 Summary

There are plans to improve almost every part of BioSig. The common interface to access different file formats will be translated into the languages C/C++, Java, and Python. Improvements in artifact processing and quality control should be evaluated offline, and, if successful, implemented online. Support for additional signal processing and feature extraction methods needs to be developed including the ability to handle missing values. Further data formats in SigViewer should be supported. The next version of a common data format (e.g. GDF 2.0?) will be finalized. Although each component of BioSig can be improved, it provides a working environment that has been used already in several

BCI projects. BioSig contains modules for data acquistion, for BCI experiments with online feedback, viewing and scoring software for reviewing the raw data, functions for offline analysis of BCI data, and for obtaining a classifier that can be applied in online experiments, and many more. It contains everything for running BCI experiments, analyzing the data, and obtaining classifiers.

Almost all components can be used with free software; the M-code is also compatible with Octave (by Eaton). Exceptions are the SViewer (which requires the graphical user interface of MATLAB) and rtsBCI (which requires the MATLAB, Simulink, and the Real-Time Workshop from Mathworks). SigViewer is a viewing and scoring software that can be used to replace SViewer as it requires only open-source software. Despite this deviations, the overall commitment to the open source philosophy is substantiated through the GNU General Public License (GPL).

Notes

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