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PSAAL: A LabVIEW 3 program for data acquisition and analysis in psychophysiological experiments

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PSAAL (Physiological Signals Acquisition and Analysis in LabVIEW language) is a group of seven programs, written in LabVIEW 3.0 language and specialized for acquisition, analysis, reduction, and display of peripheral and central physiological data. The main characteristics of the programs are the wide range of use for most short-duration psychophysiological paradigms and the easy-to-use graphic interface. In addition, two noteworthy features of LabVIEW are included: the portability of the programs on Macintosh, PowerMac, IBM, HP-UX, and SUN computers, and the capability of handling acquisition on many National Instruments A/D boards, including the low-cost ones. PSAAL performs acquisition and simple reduction of peripheral physiological responses with 12- or 16-bit resolution according to the A/D board used. Analysis includes conversion of electrocardiogram into heart rate, the elaboration of the main parameters of skin conductance responses, electromyogram, startle reflex, and averaging of evoked potentials or other event-related physiological responses, under different experimental conditions. The programs allow the user to perform the organization of the data in a spreadsheet ready for most statistical packages and without the use of other spreadsheet applications.

LabVIEW is a general-purpose programming system which also includes libraries of functions designed specifically for data acquisition and instrument control. Some researchers are now beginning to use LabVIEW either to analyze specific parameters of certain physiological functions or to control and handle complex tasks or routines (Reidbord & Redington, 1992; Sherry & Constable, 1992). In many cases, LabVIEW appears suitable when compared with the commercial "turn-key" systems, which not only are more expensive but often lack flexibility. Small laboratories that need custom-made programs and cannot afford professional programmers could take advantage of the easy and flexible LabVIEW 3.0 system.

As pointed out by Bates (1991), LabVIEW (National Instruments, Austin, TX) is an object-oriented language. Whereas traditional languages require translation from the mental picture of the block diagram, LabVIEW comes closer to such an organization, making the programming easy and elastic. With LabVIEW, any researcher can learn quickly to modify or build a program without mastering a professional knowledge of computer languages. In addition, the easy graphic interface between LabVIEW and programmer, including the rich library of virtual instruments (which are subprograms) and functions (e.g., array operators, mathematics, and digital signal processing), is impressive and represents a powerful instrument for psychophysiological research. A further advantage of this language is the speed of execution, comparable with that of C language programs, associated with a very high editing speed, a typical characteristic of the G (graphical) languages.

The latest release of LabVIEW allows the portability of the programs among Microsoft Windows, HP Series 700 workstations, the Sun SPARCstation, and Macintosh platforms, increasing the number of potential users of this programming system. Thanks to LabVIEW's features, PSAAL is able to handle without any modification many different kinds of National Instruments A/D boards. Among these there are PC/AT and Macintosh boards, 12- and 16-bit resolution boards, and low-cost A/D interfaces such as, for example, the models LabNB and LabLC for Macintosh computers. The library of examples (10 Mb of programs) included with LabVIEW 3.0 is useful and well documented; this makes the user autonomous in resolving programming problems. But most of the examples regarding data analysis are applications in the fields of physics and engineering, and therefore they are not very useful for the psychophysiologist.

Beginning with a Macintosh platform, PSAAL has been devised as an integrated group of programs, initially specialized in autonomic nervous system and somatic physiological recordings, that is easily adaptable to most short-duration psychophysiological paradigms. PSAAL was specifically designed for psychophysiological experiments in which stimuli produced by external devices such as slide projectors, other computers, and so forth, are triggered during the acquisition of physiological data. Even though LabVIEW can support a sophisticated stimulus presentation control, in PSAAL this option is not included. It is easier (because it is not necessary to customize and modify PSAAL programs for every specific

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laboratory setup) to handle the computer acquisition and the stimulus delivery by means of an external instrument or computer. This makes PSAAL a general-purpose set of programs. In comparison with most programs for psychophysiological applications, it is very easy to set up the programs with PSAAL, to verify the signals, and to follow the various steps going from acquisition to data analysis. All these features make it a convenient starting point set for conducting experiments in psychophysiology.

HARDWARE REQUIREMENTS

Although PSAAL can be used on SUN and HP-UX computers, it was originally developed on Macintosh computers. We will describe the requirements for this platform and for the popular Windows operating system. Detailed information on other platforms and relative A/D boards may be obtained from National Instruments.

The minimum Macintosh system needed for LabVIEW requires a 68020 computer with a coprocessor and System 6.0.4 with 32-bit QuickDraw. The minimum PC system is a 386/25 with 387 coprocessor. A 486 with floating point capability is strongly recommended by National Instruments. The operating system is Windows 3.1 (or Windows NT 3.1) or later. Both platforms need at least 8 Mb RAM and 25 Mb of disk space. Since LabVIEW 3.0 alone takes 5 Mb of memory, we strongly recommend 12 Mb or 16 Mb RAM memory.

In Macintosh platforms, PSAAL handles either NB-MIO-16 (12-bit resolution) or NB-MIO-16 X (16-bit resolution) A/D boards (National Instruments) with inputs configured in differential mode and a range of ±5 V, but LabNB and LabLC low-cost boards can be used too. To make the programs work with all these boards, the number of channels was limited to eight and the range kept low, ±5 V. In PC platforms, there are A/D boards with features equivalent to the one listed above: AT-MIO-16, AT-MIO-16 X (16-bit resolution), and Lab-PC+, PC-LPM-16 low-cost boards.

PROGRAM OVERVIEW

PSAAL consists of the following seven programs: Acquisition, 1Ch-Analysis, Reduction, 1Ch-Grandave,

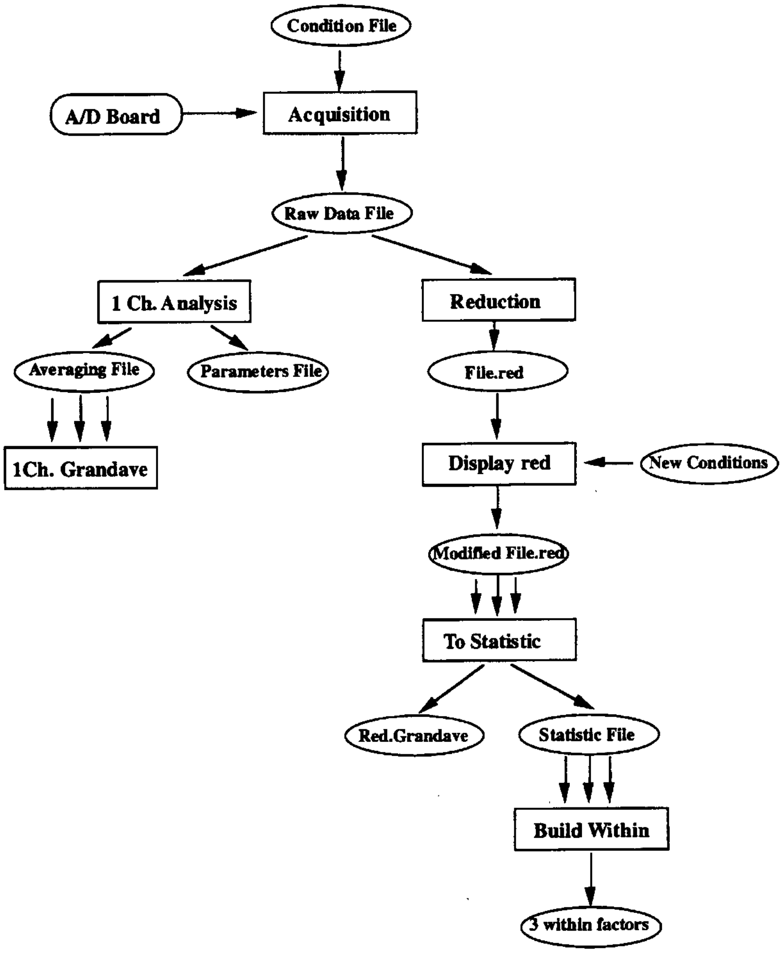


Figure 1. General overview of PSAAL and relationships among the programs. Rectangles represent the programs written in the LabVIEW 3 environment; ovals represent data files (all in ASCII format).

Display Red, To Statistic, and Build Within (see Figure 1).

The file in which the experimental conditions are set may be written by any text program. It simply represents a list of integer numbers (except 0, which is associated with the discarded trials in the following programs), separated by any text character (point and comma excepted). Each number represents the experimental condition associated with the trial in the same sequential position. Before the recording, the Acquisition program asks for the file of conditions and positions it at the head of the raw data file that will be recorded.

The raw data file may be opened and read by two different programs: 1Ch-Analysis and Reduction. 1Ch-Analysis displays only one selected channel and performs the calculation of some useful pattern parameters inside a chosen time window, as well as averages the trials clustered under each condition. It saves two files. One file contains the parameters organized by trial and by condition, ready for statistical analysis. The other file (the averaging file) contains the averaging by condition of the specific channel selected. The program 1Ch-Grandave allows the user to perform the grand averaging of more averaging files (e.g., a group of subjects).

The Reduction program performs a reduction of raw data into summary data or bins, as well as the amplitude conversion of the raw data. Such a program makes it possible to explore all the data inside a selected time window, including the stimulus onset. Display Red shows the file of reduced data and permits the change of single data points and the substitution of the conditions header if it is necessary to cluster the trials under different experimental conditions.

To Statistic is a large program able to work on a group of reduced data files and to create a file in a universal statistical format. It also performs the grand averaging by condition of all the reduced data files. Build Within links more files produced by To Statistic to get a file containing three-within-subject-factors data organization. It is needed in experiments that include more than one experimental session for each subject.

DATA FILE FORMAT

PSAAL is configured to store data in an ASCII file and in a spreadsheet format. In Figure 4 (see the table Record Header on the right side), there is one example of the header[1] of the raw data file.

The header includes, in descending order, notes, number of trials, duration (in milliseconds) of the three acquisition periods (prestimulus, stimulus, and poststimulus), sampling rate, the amplification factor of each channel, and the column of conditions with the trial sequence (in this case there are five different conditions). The header of the reduced data files is almost the same (Figure 5, right): prestimulus, stimulus, and poststimulus durations are updated according to the choices made during reduction. Bin width is put in place of Sampling Rate.

The header, the file of conditions, and the raw and the reduced data can be modified with a word processor or text editor. The advantage given by the column of the conditions recorded in each file header is the use of randomized sequences of conditions. If every randomized sequence is reported into the header, the experimenter does not have to look during data analysis at what sequence was used for every subject and skips a time-consuming step.

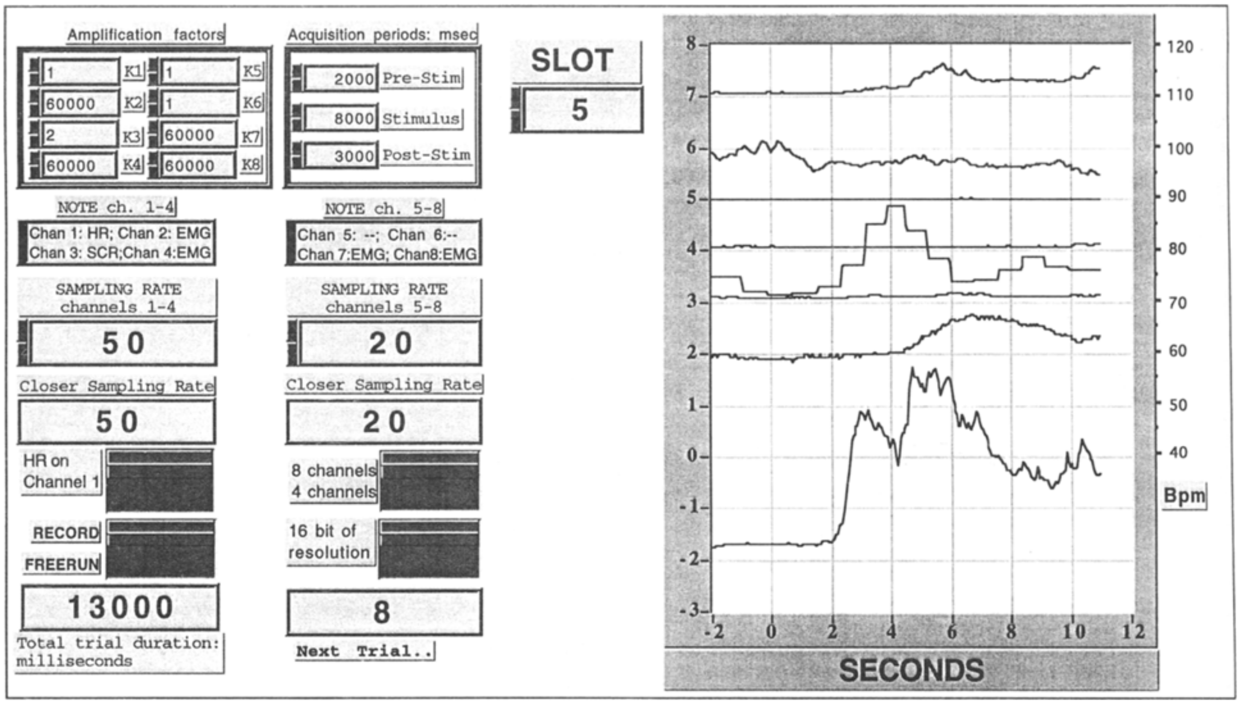
PROGRAM DESCRIPTION

Acquisition

This program (see Figure 2) allows acquisition of four or eight channels. In the eight-channel setting, the program saves two files of four channels each (file name followed by the extension -A for Channels 1–4 and -B for Channels 5–8); this organization makes it possible to have different sampling rates for the two groups of channels. The lower sampling rate is obtained following a decimation[2] of the data collected at the higher sampling rate: this solution is the only one possible for A/D boards (like the NB-MIO-16, LabNB, and LabLC) that do not allow a different sampling rate for each channel. In addition, subsequent steps, such as reduction and analysis, are facilitated by grouping the channels four at a time, because some of them may need a differentiated analysis. The program also is able to perform 16-bit acquisition and display if a high-resolution board (such as the NB-MIO-16 X) is used.

The slot of the A/D board, amplification factors, sampling rate, and prestimulus, stimulus, and poststimulus periods can be set so that the program performs acquisition on four or eight channels. In Free-run mode, data are continuously displayed every 2 sec but are not recorded. In Record mode, the program asks for a file of conditions before starting. The file of conditions and all the other experimental information are recorded inside the header of the raw data file. The start of recording for each trial is externally triggered. During acquisition, data are displayed at the end of each trial. In order not to slow down the computer, displayed data are numerically limited to less than 200 per channel. The HR Acquisition option enables the program to record heart rate (HR) on Channel 1, starting with the electrocardiogram (EKG). The program detects the R-waves by means of a digital trigger and yields a cardiotachometric array of data.[3] Heart rate, together with the other channels, is displayed soon after the acquisition of each trial.

To compute HR with precision, the sampling rate is internally set at 500 Hz. The sampling rate indicated on the front panel is a subsampling such that, after heart rate conversion, the data are decimated to obtain a file with less data. With HR conversion, the sampling rate values allowed by the program are 500, 250, 125, 100, 50, 25, 20, 10, 5, 2, and 1 Hz. Whenever HR is recorded on Channel 1 and/or the sampling rate of Channels 1–4 and 5–8 are different, a decimation is performed. In this case, to achieve a correct decimation, occasionally the sampling rate is forced by the program to a value that is higher than, but as close as possible to, that selected by the experimenter.



Amplification factors
1 K1
60000 K2
2 K3
60000 K4
1 K5
1 K6
60000 K7
60000 K8

Acquisition periods: msec
2000 Pre-Stim
8000 Stimulus
3000 Post-Stim

SLOT
5

NOTE ch. 1-4
Chan 1: HR; Chan 2: EMG
Chan 3: SCR;Chan 4:EMG

NOTE ch. 5-8
Chan 5: --; Chan 6:--
Chan 7:EMG; Chan8:EMG

SAMPLING RATE channels 1-4
50

SAMPLING RATE channels 5-8
20

Closer Sampling Rate
50

Closer Sampling Rate
20

13000
Total trial duration: milliseconds

8

Figure 2. Acquisition program: eight-channel acquisition. The eight channels are recorded in two files of four channels each. Data are recorded and then displayed graphically after each trial: Channel 1 displays the heart rate in beats per minute (bpm) after the cardiotachometric conversion of the EKG; the other channels present SCR and integrated EMG data. Vertical scale is in volts: for display convenience, every channel is shifted by 1 V from the other. Data of the three consecutive periods (prestimulus, stimulus, and poststimulus) are displayed from the beginning until the end of the trial. The prestimulus data are displayed as negative times. Zero represents the stimulus onset.

In Free-run mode, the program displays the EKG to allow the signal quality to be checked.

1Ch-Analysis

The program performs the analysis of one channel at a time (see Figure 3). The channel, the correct amplitude representation (Volt, millivolt, etc.), the resolution of the A/D board used for acquisition (12 bits is the default), HR conversion (if EKG is recorded on Channel 1), and finally the correct vertical scale range on the graph display should be selected before the program is run.

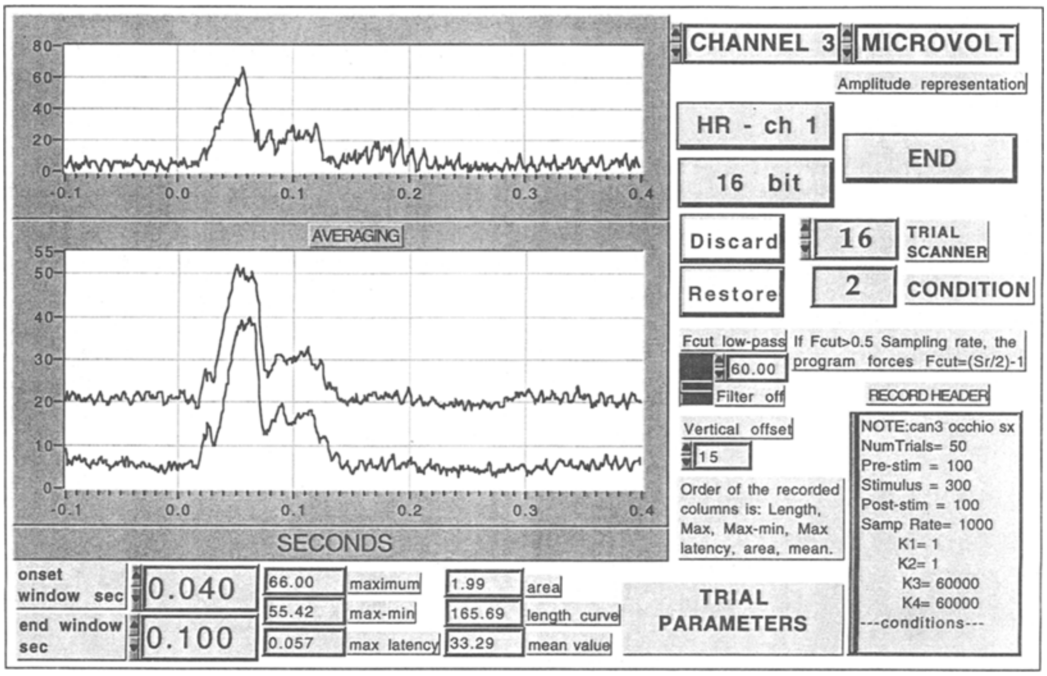
Selection of a time window makes it possible to calculate the following trial parameters: maximum amplitude, maximum/minimum difference, maximum peak latency, area, curve length, and mean amplitude—all inside the specific time window chosen. This allows the computation of the typical parameters of skin conductance responses (SCR), startle reflex (peak amplitude and latency), integrated electromyogram (EMG; area, mean value of a chosen time window) or cardiac responses to stimuli (amplitude of the peak HR acceleration), and evoked potentials (peak amplitude and latency, area of a specific time window). During trial scanning and parameter calculation, the artifact trials can be discarded from the subsequent averaging step. When End is set, the averaging curves are all displayed graphically according to the condition subdivision (one averaging curve for each condition). Each curve may be vertically translated from the preceding one by the Offset amount.

Two files are automatically saved at the end. One file (extension ".n of channel Pa") contains the six parameters computed within the selected window, organized in a spreadsheet by trial and by condition; these data are ready for statistical packages (the organization by trial is useful for correlation or regression analyses). The second file (extension ".n of channel Av") contains the averaging by conditions data.

Two options complete the program. After the cut frequency is set, a fourth-order low-pass Butterworth filter is applied to noisy data (noise due, for instance, to the averaging of a small number of trials). Cursor option, a LabVIEW built-in utility, allows the calculation of peak (or peak-to-peak) latency and amplitude of the displayed averaged waveforms.

1Ch-Grandave

This program performs the grand averaging by condition of the single channel -.nAv data files. It needs the number of the files to be computed, baseline length, and the sampling rate. If requested, it saves the grand averaging data in a spreadsheet file (Save Data option). As in all LabVIEW graphs, the Cursor option is allowed on request (see 1Ch-Analysis); this permits manual computation of waveform's interesting points.



CHANNEL 3 MICROVOLT

Amplitude representation

16 TRIAL SCANNER

2 CONDITION

Fcut low-pass 60.00

If Fcut>0.5 Sampling rate, the program forces Fcut=(Sr/2)-1

Filter off

Vertical offset 15

Order of the recorded columns is: Length, Max, Max-min, Max latency, area, mean.

RECORD HEADER

```
NOTE:can3 occhio sx
NumTrials= 50
Pre-stim = 100
Stimulus = 300
Post-stim = 100
Samp Rate= 1000
     K1= 1
     K2= 1
      K3= 60000
      K4= 60000
---conditions---
```

onset window sec 0.040

end window sec 0.100

66.00 maximum

55.42 max-min

0.057 max latency

1.99 area

165.69 length curve

33.29 mean value

Figure 3. 1CH-Analysis: display of one startle reflex trial (upper graph), and averaging (lower graph), under two experimental conditions, of the startle responses evoked by 50 white noise acoustic bursts. The lower part of the front panel shows six main parameters calculated inside a selected time window of the displayed trial. The waveforms are graphically shifted by 15 μV as reported on the vertical offset indicator. The prestimulus data are displayed as negative times. Zero represents the stimulus onset.

Reduction

Some physiological functions can be usefully reduced into 0.5- or 1-sec bins before the statistical analysis: HR, integrated EMG, SCR, skin conductance level (SCL), respiration activity, and all the slow-change physiological functions. Prestimulus and stimulus (even if it is written as stimulus, setting intervals longer than stimulus duration will include also poststimulus data) windows define a time interval, including stimulus onset, within which all computations and graph representations are made. The program (see Figure 4) reads the file of raw data and the header with all the information about the experiment. Data are reduced into a few bins, each bin being the mean of all the data inside the selected bin width. Each point represented on the graph refers to the next time interval (bin width). Negative times refer to the prestimulus seconds before stimulus onset (time = 0). Data representation of each channel can be selected ("amplitude representation") in volts, millivolts, microvolts, or raw data. In addition a multiplicative constant (V*K) can be selected for those cases in which a gain lower than 1 is obtained by some instruments. A labeled button, "16-bit resolution," allows correct conversion of raw data collected with either 12-bit or 16-bit resolution A/D boards.

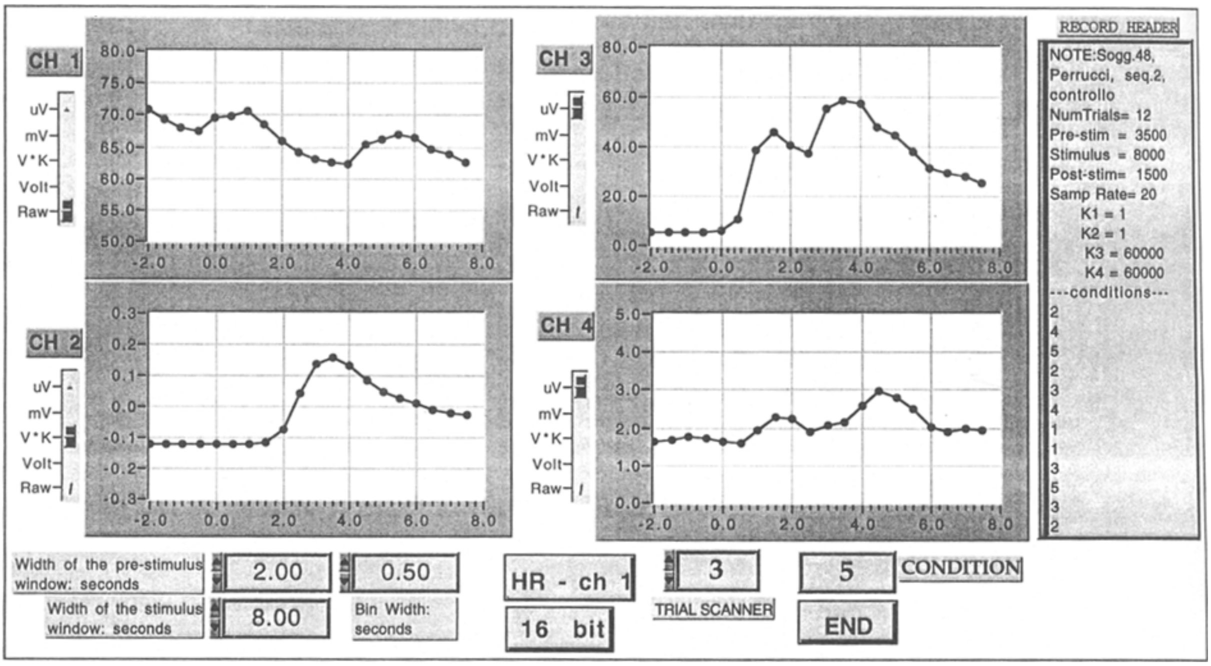
In order to display HR (in beats per minute, bpm) on Channel 1, it is necessary to set the "Amplitude representation" selector to "raw" and press the button labeled "HR on Channel 1." HR reduction into bins is computed according to the criterion of the harmonic mean described by Graham (1978). "Trial scanner" makes it possible to scan up and down the sequence of the trials. The reduced data file, recorded automatically at the end (with the name of the raw data file followed by the extension .Red), is organized into the following spreadsheet format: channel (block), trial (row), bin (column).

Display Red

This program (Figure 5) reads the reduced data files and displays them by means of a trial scanner. It takes less time to display reduced data than the raw data. The program makes it possible to associate a different set of conditions with the same data. When the "new conditions" button is pressed (before running the program), the program asks for the reduced data file and then for the new file of conditions. Trials affected by artifacts can be discarded from the analysis by setting Discard; to retrieve a discarded trial, the Restore option must be selected. If single point artifacts have to be changed, according to a priori specified criteria, it is possible to push the Replace button after inputting the channel selected, the point coordinate in seconds, and the replacing number. All the changes described above will be saved only if, before pushing End, one selects the option Save File. The modified reduced data file will have the extension .Rem.

To Statistic

The program works on a group of reduced (and/or modified) data files to give a file ready for any statistical pack-



```
NOTE:Sogg.48,
Perrucci,  seq.2,
controllo
NumTrials= 12
Pre-stim  =  3500
Stimulus  = 8000
Post-stim=  1500
Samp Rate= 20
      K1 = 1
      K2 = 1
       K3 = 60000
       K4 = 60000
---conditions---
2
4
5
2
3
4
1
1
3
5
3
2
```

Width of the pre-stimulus window: seconds 2.00

Width of the stimulus window: seconds 8.00

Bin Width: seconds 0.50

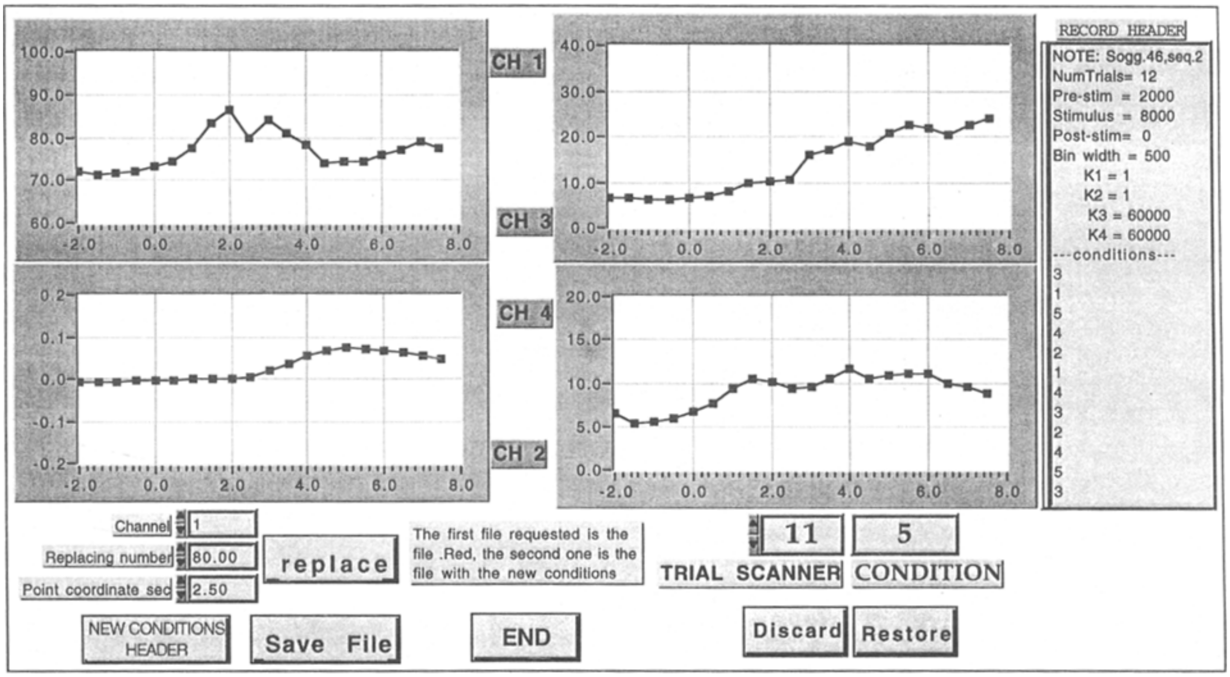
HR - ch 1

16 bit

TRIAL SCANNER 3

CONDITION 5

Figure 4. Reduction program, display of a trial: 2 sec of baseline plus 6 sec of emotional slide projection. The physiological functions are: Channel 1, heart rate; Channel 2, skin conductance response; Channel 3, *Corrugator supercilii* integrated EMG; Channel 4, *Zygomaticus major* integrated EMG. The amplitude scale is in bpm (Channel 1), micromhos (Channel 2), microvolts (Channels 3 and 4). The prestimulus window, displayed with negative times, and the stimulus window can be selected only by including the stimulus onset (0 sec). Bin width was set to 0.5 sec, so each point is the mean of all the raw data inside the subsequent half second. When END is selected, the program saves a reduced data file (filename.Red) automatically. On the right side, the header of the raw data file is displayed.



```
NOTE: Sogg.46,seq.2
NumTrials= 12
Pre-stim  = 2000
Stimulus  = 8000
Post-stim=  0
Bin width = 500
      K1 = 1
      K2 = 1
       K3 = 60000
       K4 = 60000
---conditions---
3
1
5
4
2
1
4
3
2
4
5
3
```

Channel 1

Replacing number 80.00

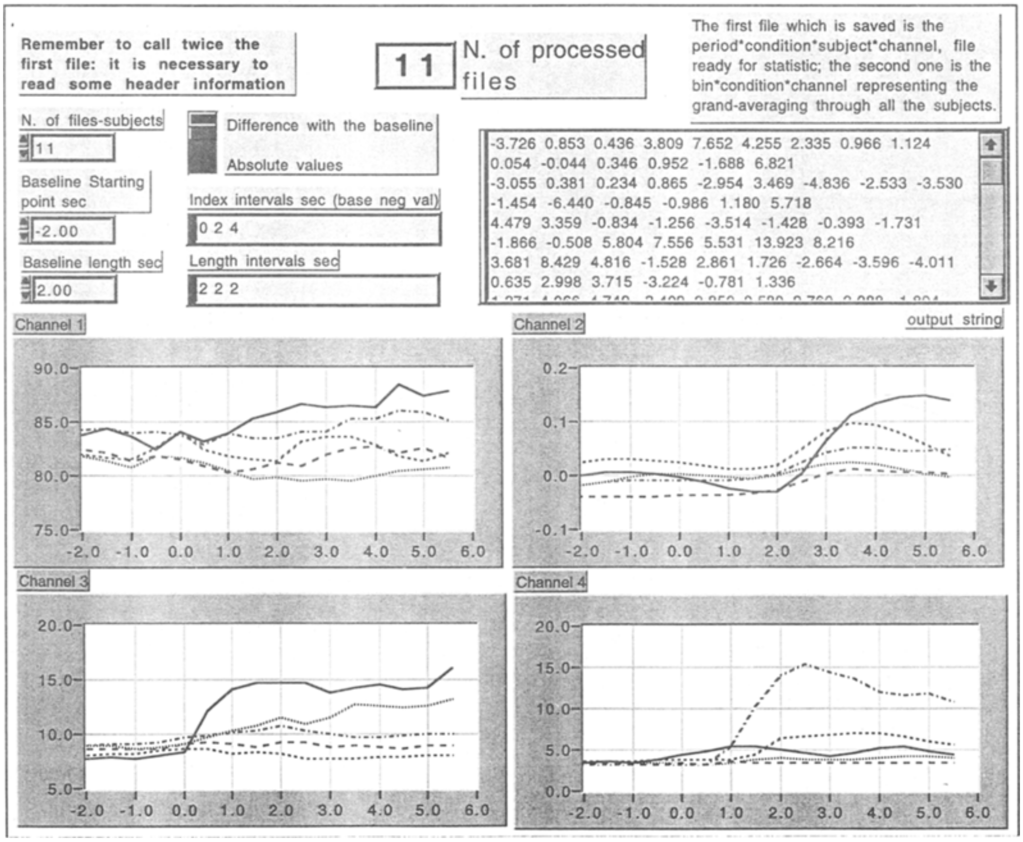
Point coordinate sec 2.50

The first file requested is the file .Red, the second one is the file with the new conditions

TRIAL SCANNER 11

CONDITION 5

Figure 5. Display Red program: physiological functions are the same as in Figure 4. The program allows the user to display the reduced data files or to recode the trials by calling a new condition file. Occasionally it is possible to discard the trials affected by artifacts or change single point values (option replace) according to a priori defined criteria. In this case, one point of Channel 1 was modified to provide an example. The modified file (filename.Rem) will be saved upon request (Save File). On the right side, the record header of the reduced data file is displayed.



Remember to call twice the first file: it is necessary to read some header information

11 N. of processed files

The first file which is saved is the period*condition*subject*channel, file ready for statistic; the second one is the bin*condition*channel representing the grand-averaging through all the subjects.

N. of files-subjects: 11

Difference with the baseline / Absolute values

Baseline Starting point sec: -2.00

Index intervals sec (base neg val): 0 2 4

Baseline length sec: 2.00

Length intervals sec: 2 2 2

output string

```
-3.726 0.853 0.436 3.809 7.652 4.255 2.335 0.966 1.124
0.054 -0.044 0.346 0.952 -1.688 6.821
-3.055 0.381 0.234 0.865 -2.954 3.469 -4.836 -2.533 -3.530
-1.454 -6.440 -0.845 -0.986 1.180 5.718
4.479 3.359 -0.834 -1.256 -3.514 -1.428 -0.393 -1.731
-1.866 -0.508 5.804 7.556 5.531 13.923 8.216
3.681 8.429 4.816 -1.528 2.861 1.726 -2.664 -3.596 -4.011
0.635 2.998 3.715 -3.224 -0.781 1.336
```

Figure 6. To Statistic program: after setting the number of reduced data files that need to be processed, a number of intervals within the trial will be organized as a within-subjects variable. These data are computed as the mean of all the bins included in the interval. In this example, three intervals of 2 sec each are computed by subtracting 2 sec of baseline. The second within-subjects variable has five levels (emotional category slide) and is automatically calculated by means of the conditions listed in the header of each reduced data file. At the end, two files are saved, the statistics file is displayed on the upper right side (four lines of subjects' data are shown here, but it is possible to scroll through all the subjects' and the four channels' data). The grand averaging of all the subjects according to the experimental conditions is displayed graphically too. The four physiological functions are the same as in Figure 4.

age. It allows the reorganization of the data for most complex ANOVA/MANOVA between-/within-subjects mixed experimental designs.

Before running the program (Figure 6), it is necessary to input the number of files (typically a file represents a subject) and select between the options "absolute values" or "difference with the baseline." When the first is set, the average of the points falling within each interval selected will be computed. For each interval, the operator must input the onset point (remembering that stimulus onset coordinate = 0, whereas baseline is represented as negative times preceding the stimulus) and the length, both represented in seconds, into two strings. Inside the strings, the interval values have to be separated by a text character (e.g., the space). If "difference with the baseline" is selected, the baseline is subtracted from the averages of the chosen intervals. The onset point and the length of the baseline interval that the user wishes to consider (sometimes the baseline of interest for the researcher is smaller than the one recorded) must be defined for the baseline also. After the selection of all the .Red files, the program saves two files: one with the data ready for statistics, the other with the grand averaging throughout the subjects and the conditions. The grand averages by condition of each channel are also displayed as waveforms.

The final spreadsheet has the following structure: every block of data represents a channel. Within each block, the rows represent the subjects (each row comes from one file) in the same order as that in which they are called into the program by the user. Therefore, the between-subjects factors are organized as groups of rows. In each row the two main within-subjects factors are nested in the following order: first, the experimental condition under which one or more trials are averaged; second, the intervals of data selected by the user. For example, if the user wishes to divide every stimulus period into three intervals, in every row the first three numbers are the mean values computed within each interval, in the order chosen by the user. These three values are all under Condition 1 (the integer selected for the first experimental condition put into the conditions file), the second group of three values represents the average of the intervals under Condition 2, and so on.

Build Within

This program allows the user to set up a file with a third within-subjects factor ready for statistics. After the user sets both the number of rows-subjects that are to be included in the statistics files and the number of statistics files (which represents the levels of the third factor), the program joins all the data from the four channels. This program is useful in experiments in which the subjects have to perform different tasks in different experimental sessions: in this case, it is necessary to save a file for each session and analyze the files as within-subjects variables. With this program, the nesting of the three within-subjects variables is the following: first, the session; second, the condition (see above); third, the period.

CONCLUSIONS

PSAAL consists of a group of seven programs that perform acquisition, display, reduction, and analysis of physiological data. It is devised specifically for research in psychology and is highly user friendly. It takes advantage of LabVIEW 3 facilities: easy graphic interactive programming, a rich library of primitives, and high flexibility in the field of psychophysiology. In addition, the two programs that organize the data for statistics make it possible to save time by avoiding the use of spreadsheet programs and quitting from LabVIEW. PSAAL has not been specifically designed for event related potentials, but the main analyses of evoked potentials for a few channels are possible (peak amplitude and latency, area of specific time windows, averaging and grand averaging) by working with one channel at a time by means of the 1Ch-Analysis program. This might be very useful for researchers interested in somatic and visceral physiological activity who sometimes want to record also a few EEG channels (e.g., at locations Fz, Cz, and Pz, and ocular activity), together with some peripheral physiological functions.

PSAAL does not perform sophisticated analysis routines or algorithms for psychophysiology research; flexibility and efficiency in data organization are its main features. Furthermore, the portability of the programs to various computer platforms (SUN, Macintosh, AT/PC, HP-UX, and PowerMac) and the capability of handling a large number of drivers make this program unique in psychophysiology.

PSAAL, like LabVIEW, was born and checked in the Macintosh world: even if LabVIEW 3 allows complete portability to the PC, HP-UX, and SUN computers, small adaptations under the supervision of National Instruments might be necessary. Subsequent extensions of the programs will include the overcoming of the limits mentioned above and the expansion of the functions and potentialities of the system in the field of psychophysiology.

Availability. Copies of the programs, together with all the virtual instruments and some data examples, are available from the author upon receipt of a self-addressed mailer and two HD floppy disks (DOS or Mac formatted, with specification of the platform used). A brief description and instructions are associated with every program and virtual instrument, as is usual in LabVIEW.

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NOTES

1. Part of the header structure has been devised by Angrilli and Bettella (1992).

2. For decimation, it is intended that "1 datum out of 2," (or "1 out of 3," "1 out of 4," etc.) is taken. This operation is equivalent to a reduction of the sampling rate by an integer factor such as 2 (half sampling rate), 3 (one third sampling rate), and so forth. This choice has the advantages listed above, but it implies the following distinctions. If HR is not requested on Channel 1, and all the channels are sampled at the same rate, the user can input any desired sampling rate. If the two groups of channels (1–4 and 5–8) are sampled at different rates, the channels with lower rates (in the program necessarily Channels 5–8) have decimated data. Therefore, their sampling rate is forced by the program to the closest as possible correct value, depending on the decimation criterion (in other words, once the user chooses the higher sampling rate for Channels 1–4, the choice of sampling rate for Channels 5–8 is restricted by a decimation rule). If HR is requested on Channel 1, all the channels have decimated data, and the sampling rates allowed for both groups of channels are 500, 250, 125, 100, 50, 25, 20, 10, 5, 2, and 1 Hz. In this case, it is possible to get a lower sampling rate for Channels 1–4 than for Channels 5–8. The user may wish to change the main sampling rate (500 Hz) fixed for HR acquisition selection. It is sufficient to change this number in the block diagram of the Acquisition program.

3. The correct digital computation of the HR is performed by means of the standard limb lead II electrocardiogram configuration and a high-pass filter set at 2–5 Hz. The HR and the cardiotachometric conversions are performed soon after the acquisition of the trial data (real-time processing) and before storing. Every HR value is correctly associated to the R–R interval, and the corresponding cardiotachometric step does not have the typical one-beat delay of the electronic cardiotachometers. Only after HR computation are data numerically reduced; this reduction will not affect the precision of the conversion or that of the following analysis steps.

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