

PSYLAB – Documentation

Version 2.1

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1 Introduction

1.1 What is PSYLAB?

'PSYLAB' is a collection of scripts, written in Matlab, for designing and controlling interactive psychoacoustical listening experiments in a uniform and quick manner.

Currently, n -AFC detection and discrimination experiments ($n = 2, 3, 4$) and 2-AFC matching experiments with adaptive control of the stimulus variable according to x -up- y -down algorithms ($x, y \in \{1, 2, 3\}$) are readily supported.

1.2 History of PSYLAB

PSYLAB is based on many ideas of the programs 'SI/SISG' which were written at "Drittes Physikalisches Institut", Universität Göttingen, during the years 1989 to 1991, and distributed under GNU General Public License (GNU GPL). SI ("Signalverarbeitung interaktiv") was programmed in Fortran by Dirk Püschel and René Koch and further colleagues for the purpose of digital signal processing and analysis. SISG, built on SI, was written by Ralf Fassel and was used for development, control and analysis of psychoacoustical experiments. The philosophy and organisation of PSYLAB was inspired by the paradigms of "SISG" in many ways.

PSYLAB has been written by Martin Hansen. It is regularly used for education and research at Institut für Hörtechnik und Audiologie (IHA), Fachhochschule OOW in Oldenburg, Germany, where it has been tested intensively. One aim of PSYLAB has been to provide the students in the psychoacoustic courses with a uniform and simple starting point for designing one's own listening experiments. So far, more than 120 students at IHA have used PSYLAB for their assignments and their experience and comments have nicely contributed to new features and bug fixes of PSYLAB.

1.3 Licence of PSYLAB

PSYLAB is "free software" and is distributed in OpenSource format under the terms of the GNU General Public Licence (GPL). This means, amongst others, that copies of the PSYLAB-software may be distributed, given that the terms of the GNU GPL are obeyed to.

For more details, see <http://www.gnu.org/licenses/gpl> or look at at verbose copy of the GNU GPL on page 23.

1.4 No warranty

PSYLAB is distributed without any kind of warranty. Have a look at the file "NO-WARRANTY" in the root directory of PSYLAB before using it!

The use of PSYLAB for whatever purpose, is under the complete and only responsibility of the user. Special attention is drawn to the fact that PSYLAB does *not* comprise an automatic mechanism to prevent the delivery of too loud sound pressure levels. It is the explicit and sole responsibility of the user of PSYLAB to make sure that the generated stimuli, in combination with any further equipment (sound card, amplifier, headphone or loudspeaker, etc.), will yield the desired sound level.

1.5 Quick start: example experiments

A hands-on explanation of the way how PSYLAB works can be found in the subdirectory 'examples' of the PSYLAB-distribution. It contains several example experiments, ready for giving them a try.

Each experiment is comprised of three scripts with similar name, i.e., with the same first part of the name. The name of the "main script" of an experiment can be chosen freely, e.g. 'myscript.m'. The two accompanying scripts *must* then carry the names 'myscriptset.m' and 'myscriptuser.m'. The main script describes and controls the measurements while the other two scripts are used for stimulus generation during the experiment. For a quick start, run one of the example experiments by running the corresponding main script.

The example in the file 'sam_sincarrier_detect.m' is an experiment which measures the detection threshold of the modulation degree of sinusoidal amplitude modulation ("SAM") as a function of modulation frequency. The measurements are performed for a number of different carrier frequencies of the sinusoidal carrier.

The example in the file `jnd.frequency.m` is an experiment which measures frequency discrimination of pure sinusoids as a function of the reference tone frequency and its sound level.

The example in the file `match_freq_binaural.m` is a matching experiment which measures the frequency for binaural pitch matching between left and right ear for pure tones as a function of the reference frequency.

The example in the file `tone_in_broadbandnoise.m` is an experiment with interleaved tracks for measuring the detection threshold of the level of a sinusoid in broad band noise as a function of the tone frequency.

2 Philosophy of PSYLAB

2.1 Terminology and definitions

This section explains some terms and definitions used inside PSYLAB. In addition, the principal course of psychoacoustical experiments realised with PSYLAB is explained. Some of the terms are illustrated in Fig. 1.

interval, signal, stimulus During an experiment, the human test subject is presented with one or more stimuli. The individual stimuli are also called intervals or signals. In an n -AFC-experiment, n intervals are presented in succession. Most often, these signal intervals will be separated by short pauses (of silence). It is possible to visually mark the individual intervals.

trial A trial is one presentation of the n stimulus intervals that pertain to an n -AFC experiment. After each trial the subject is required to answer respectively respond to a question of the kind “which interval contained the test signal?”.

(stimulus) variable The “variable” inside PSYLAB takes the role of that stimulus dimension/magnitude which is varied adaptively from trial to trial in order to find the subjects threshold. The “variable” carries the reserved name `M.VAR` inside PSYLAB.

(stimulus) step size The step size is the magnitude by which the stimulus variable gets changed from trial to trial during the adaptive experiment. It is measured in the same units of the variable `M.VAR`. The step size is typically larger in the beginning of the experiment and is then progressively reduced until some minimal step size has been reached. The step size carries the reserved name `M.STEP` inside PSYLAB, and the minimal step size carries the name `M.MINSTEP`.

run A run is the succession of all trials that are necessary to reach and determine one threshold of the varying stimulus variable.

(stimulus) parameter The parameter inside PSYLAB has the meaning of the arbitrary (but then fixed) stimulus dimension/magnitude which is usually kept constant during one run until threshold has been established. In the next run the stimulus parameter would then usually be set to another value and the corresponding threshold would again be established, and so on. The “parameter” carries the reserved name `M.PARAM`.

2nd, 3rd, ... (stimulus) parameter If an experiment requires more than only one stimulus parameter, PSYLAB offers the possibility to use (and organise) any number of independent parameters. In that case, `M.PARAM` will just be a vector instead of a scalar, and `M.PARAM(1)` will be the 1st parameter value, `M.PARAM(2)` the 2nd, `M.PARAM(3)` the 3rd, etc.

reference signal In a trial of a n -AFC experiment, n intervals are presented in succession, and in random order. There are $n - 1$ intervals among them which contain the reference signal, i.e. they do *not* contain “the signal” or the “cue” that the subject is required to detect. The reference signal carries the reserved name `m_ref` inside PSYLAB.

test signal The test signal is the signal which *does* contain that special “cue” that the subject is required to detect, contrary to the reference signal which does not. The test signal will be presented at random in one of the n intervals of a n -AFC trial. The test signal carries the reserved name `m_test` inside PSYLAB.

familiarisation phase At the beginning of a new run, the test signal will typically be presented clearly above threshold in order to orient the subject about the kind of the signal respectively the “cue” that is to be detected, and to familiarise the subject with the measurement procedure. The step size will be large during this familiarisation phase so that correct responses of the subject will carry the stimulus variable towards the region of threshold rapidly. At the same time the step size will be reduced progressively until it has reached the minimal step size. The trials up to this point are only used for familiarisation of the subject, and to approach a value of the stimulus variable in the vicinity of the threshold. The trials of the familiarisation phase will however *not* be included in the determination of the threshold.

measurement phase The measurement phase starts at the end of the familiarisation phase. The subject should have approached to a point close to threshold and the stimulus variable changes now only with the minimal step size. The measurement phase lasts until a certain number of reversals (see below) has been reached. This number of reversals needs to be specified by the user. The threshold is then estimated based on all values that the variable had taken on during the measurement phase.

reversal / turning point In a transformed-up-down experiment (Levitt, 1971), the stimulus variable and its direction of change depends on the subjects responses. The direction alternates back and forth between “down” and “up”. In PSYLAB, only the change from an up-phase to the next down-phase is counted as 1 “reversal”. In other words, the occurrence of a local maximum of the stimulus variable $M.VAR$ as a function of the trial number is defined as a reversal. *Note* that this definition inside PSYLAB means that *one* such reversal comprises *two* “turning points”, i.e. two changes of direction: down→up and up→down. In fact, one “reversal” as defined inside PSYLAB will often be counted as two turning point in the literature. The number of reversals serves as a stop criterion for a run. When the number of reversals has reached the maximum number of reversals, as specified by $M.MAXREVERSAL$, that run is terminated.

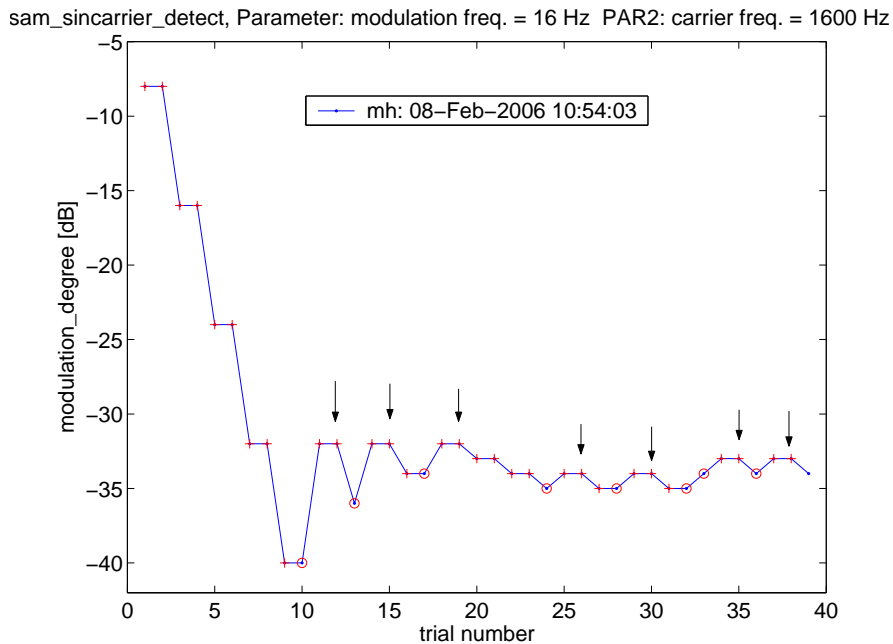


Figure 1: Example of the course of one experimental run with PSYLAB. The plus-signs (+) mark a correct response of the subject, the circles (o) mark a wrong one. The arrows indicate the locations of a reversal. The familiarisation phase lasted from trial 1 up to trial 19. At each reversal, the step size was halved until the minimum step size had been reached. At that point, the measurement phase started (at trial 20) and it lasted for 4 reversals which had been set as the maximum number of reversals. The last reversal was reached in trial 38 and the run terminated there. The very last data point, trial 39, *would* have been presented next with a modulation degree as indicated, hadn't the run stopped.

Figure 1 shows an example run of the experiment `sam_sincarrier_detect.m` which can be found in the subdirectory `examples` of the PSYLAB-distribution. The data show the value of the stimulus variable as a function of the trial number. Except for the arrows, indicating the reversals, the plot can be generated automatically with the PSYLAB-script `mpsy_display_psydat.m`, see section 3.9. The run starts with the familiarisation phase with the settings `M.VAR = -8`; `M.STEP = 8`; . Both values are stated in dB re. 1. The first reversal is reached at trial 12 where the step size is halved to 4 dB. At trial 15 the second reversal is reached and the step size is halved to 2 dB. At trial 19 the third reversal is encountered and step size halved to 1 dB. As this step size had been defined as the minimal step size, the measurement phase starts at that point. From there, the number of reversals starts again counting from scratch. The run terminates when a number of `M.MAXREVERSAL` reversals has been reached. In the example with `M.MAXREVERSAL=4`; this point is reached after trial 38. Note that the plot shows a data point at trial 39 which was *not* presented to the subject. The corresponding stimulus *would* have been presented to the subject, hadn't the run just been terminated. The threshold is calculated as the *median* of all values of `M.VAR` during the measurement phase, a value of -34 dB in the example. The standard deviation of the threshold is calculated from the same data points and amounts to 0.76 dB in the example.

2.2 Conventions in PSYLAB: reserved names for files and variables

An important convention respectively requirement of PSYLAB is that every experiment must be made up of three (Matlab) scripts. These are the “main script”, the “set script”, and the “user script”. These three files must be pure scripts, i.e. they may *not* be Matlab *functions*! As a consequence, the scripts can access all variables of the global Matlab-workspace. The scripts can of course call further scripts or functions. By defining the file name of the main script, the names of the set script and the user script are determined, too: Their names result from concatenating `set` respectively `user` directly after the name of the main script, e.g. `testnameset.m` respectively `testnameuser.m` if the name of the main script is `testname.m`. Note that no single character is allowed between the ‘`set`’ or the ‘`user`’ and the name of the main script.

Another convention applies to the use of certain variables with reserved names, e.g. `M.VAR`, `M.PARAM`, `m_ref`, `m_test`. See sections 3.1, 3.2, 3.3, 4.

2.3 Types of experiments in PSYLAB

PSYLAB offers to perform various kinds of experiments. One class of experiments are detection and discrimination experiments using a N -AFC transformed-up-down method. These experiments can be performed as a sequence of single runs, one at a time, or as a group of interleaved runs. These are described in sections 2.3.1 and 2.3.2.

Slightly different are matching experiments, like for example employed in pitch matching or loudness matching. The difference relative to N -AFC detection experiments is that the answer of the subject can not be judged to be correct or wrong. Matching experiments are described in section 2.3.3.

2.3.1 N -AFC experiments with single runs

The script `mpsy_afc_main.m` is a central part of PSYLAB for controlling adaptive transformed-up-down n -AFC experiments, if you intend to measure one experimental run at a time, i.e. the next run starts only after the completion of the previous run.

It should be unnecessary for the user to change this file. However, in order to work properly, your own experiment scripts need to conform to a number of conventions, see below.

The file `sam_sincarrier_detect.m` in the subdirectory `examples` shows an example for such a 1-up-2-down 3-AFC experiment which measures the modulation detection threshold for sinusoidal amplitude modulation of sinusoidal carriers. Details are explained in section 3.

2.3.2 N -AFC experiments with interleaved tracks

PSYLAB offers the feature to run an N -AFC experiment with “interleaved tracks”, which means that several experimental runs (usually with different sets of parameter values) are running at the same time in an interleaved fashion. Each run is controlled as if it was a single run (see section 2.3.1) but the current trial is chosen randomly from all incomplete runs, i.e. those runs which have not reached threshold.

The script `mpsy_intrlv_afc_main.m` is a central part of PSYLAB for controlling such interleaved-tracks adaptive transformed-up-down n -AFC experiments. It should be unnecessary for the user to change this file, but the same requirements and conventions apply as for single-run experiments (see section 2.3.1).

The file `tone_in_broadbandnoise.m` in the subdirectory `examples` shows an example for a 1-up-2-down 3-AFC experiment with interleaved tracks, which measures the detectability of a sinusoidal tone in broad band noise. In this example, the threshold for tones of different frequencies is measured in an interleaved-tracks fashion. For details see subsection 3.8.

2.3.3 Matching experiments

The script `mpsy_match_main.m` is a central part of PSYLAB for controlling adaptive transformed-up-down matching experiments where two signal intervals are presented per trial and the subject is asked to adjust some stimulus dimension of one of them.

The file `match_freq_binaural.m` in the subdirectory `examples` shows an example for such an experiment where a binaural pitch match is performed for sinusoids presented monaurally left respectively right.

3 Designing your own experiment

This section starts with the description how to use PSYLAB for non-interleaved experiments. Subsection 3.8 explains specific differences that apply for interleaved-tracks experiments.

Designing your own psychoacoustical experiment with PSYLAB is easy: Just write your main script, set script, and user script – and start to listen. This section shows you how to write these scripts. You might also want to take a look at the example experiments in the subdirectory `examples` to get a demonstration, or to use it as a starting point.

3.1 The main script

The purpose of the main script is to assign proper values to a number of principal PSYLAB-variables which define your experiment. These variables are all struct fields of the variable `M` in the global Matlab-workspace. The name `'M'` is *fixed* within PSYLAB, it is a *reserved name* that cannot be used for other purposes (see also section 4).

Your main script should start with the following line

```
mpsy_init;
```

This call of `mpsy_init.m` is mandatory prior to assigning values to further PSYLAB-variables, as `mpsy_init.m` initialises some PSYLAB-variables to their proper start values. The reserved-name variable `M` must reside in the global Matlab-workspace. Then, a number of struct fields of `M` need to be assigned. One important variable is `M.EXPNAME` which carries the name of the experiment, as a string. This name must be identical to the file name of the main script. Therefore, it is good practice to use the following line of code (see the help for `mfilename`) in the main script:

```
M_EXPNAME = mfilename; % important to be set correctly!
```

This implies of course that your main script should bear a good telling name. Next, the following variables need to be set in the main script. The specific values are taken from the example in the file `examples/sam_sincarrier_detect.m`.

```
M.NUM_PARAMS    = 2; % number of parameters
M.PARAMNAME(1)  = {'modulation_frequency'};
M.PARAMUNIT(1)  = {'Hz'};
M.PARAMNAME(2)  = {'carrier_frequency'};
M.PARAMUNIT(2)  = {'Hz'};
M.VARNAME       = 'modulation_degree';
M.VARUNIT       = 'dB';
M.MINSTEP       = 1; % minimum step size, in units of M.VARUNIT
```

```

M.NAFC          = 3 ; % number of forced choice intervals
M.ADAPT_N_UP    = 1 ; % number of successive wrong answers required for "up"
M.ADAPT_N_DOWN  = 2 ; % number of successive correct answers required for "down"
M.MAXREVERSAL  = 4 ; % number of reversals required as stop criterion
M.FEEDBACK     = 1 ; % provide feedback (correct / not correct) to subject
M.INFO         = 1 ; % provide intermediate info for the subject
M.TASK         = 'which interval contained the test signal (1,2,3)? ';

M.FS           = 48000; % sampling frequency
M.EARSIDE     = M_BINAURAL;
M.USE_GUI     = 1;      % use a GUI for user input
M.VISUAL_INDICATOR = 1; % use visual interval indication
M.DEBUG       = 0;      % no verbose debugging

```

You also need to assign the variable `M.SNAME` with the name (or better: initials) of the test subject. This could be achieved by

```
M.SNAME = input('please type your initials (no spaces, please)', 's');
```

It is required by PSYLAB that `M.SNAME` must *not* contain any whitespace characters!

Next, your main script would call the PSYLAB-script `mpsy_afc_main` each time after your stimulus parameter value(s) have been assigned to the PSYLAB-variable `M.PARAM`. The script `mpsy_afc_main.m` then controls one complete experiment run until threshold is established. The principle design of your main script is depicted in Fig. 2.

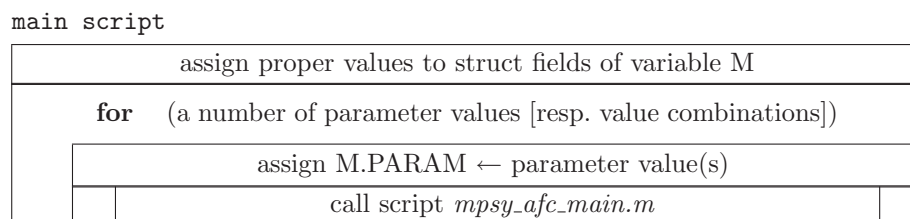


Figure 2: Principle structure of the main script of a PSYLAB experiment.

Assigning parameter values to `M.PARAM` (as a scalar in case of one parameter, or as a vector in case of ≥ 2 parameters) and the subsequent call of `mpsy_afc_main` inside the main script could be achieved in a loop as follows. (The example is taken from the experiment `sam_sincarrier_detect.m`).

```

carrier_freqs = [ 800 1600 3200 ];
mod_freqs     = [ 4 16 64 256 ];

for kk = 1:length(carrier_freqs),
    M.PARAM(2) = carrier_freqs(kk);
    for ll = 1:length(mod_freqs),
        M.PARAM(1) = mod_freqs(ll);
        mpsy_afc_main;
    end
end

```

In this example, the carrier frequency is the second parameter. It will be set to 800, 1600 and 3200 Hz, respectively. The modulation frequency is the first parameter which will be set to 4, 16, 64, and 256 Hz. This way, the experiment consists of all 12 combinations of values of the two parameters. Of course, one could imagine that you would like to measure only 2 or 3 trials today, and continue measuring the remaining parameters the other day. This could be achieved as in the following example:

```

M.PARAM(2) = 1600;
M.PARAM(1) = 4;

```

```

mpsy_afc_main;
M.PARAM(1) = 64;
mpsy_afc_main;

```

As mentioned earlier, the PSYLAB-script `mpsy_afc_main.m` controls one complete run until threshold is reached. The principle flow diagram of the `mpsy_afc_main.m` is depicted in Fig. 3. As can be seen, `mpsy_afc_main` calls the set script of the experiment *once* in the beginning. Then, in a loop running until threshold has been reached, the user script of the experiment will be called once for each trial. The natural purpose of the user script is to generate (new) realisations of the reference signal `m_ref` and the test signal `m_test` which will then be presented to the subject in a *n*-AFC manner. Subsequently, the subjects response will be evaluated and the stimulus variable will be changed according to the adaptive rule.

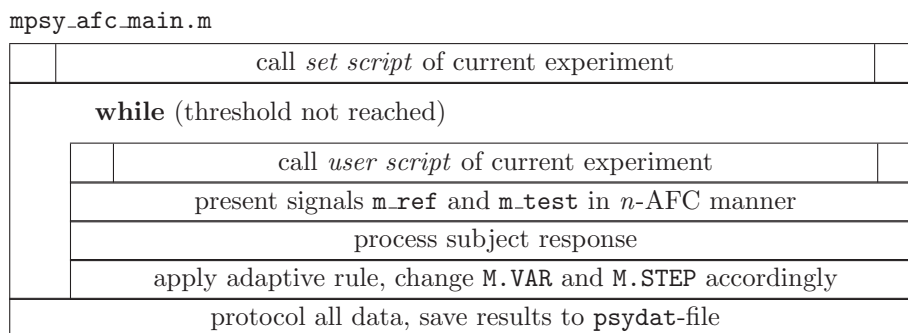


Figure 3: Principle flow diagram of one run, as controlled by the script `mpsy_afc_main.m`.

3.2 The set-script

As already noted in section 3.1, the set script will be called *once at the beginning* of any new run. This will happen before the first trial with stimulus presentation, but after a new parameter value, respectively a set of values, has been assigned to the PSYLAB-variable `M.PARAM` in the main script. The call of the set script is performed automatically by the PSYLAB-script `mpsy_afc_main.m`, or `mpsy_match_main.m`. The user does not need to bother with this.

The purpose of the set script is to set some PSYLAB-variables to a proper start value. At least the variables `M.VAR` and `M.STEP` should be assigned with new start values. Also, any of those calculations that are of high computational load but only need to be performed once, should as well be placed into the set script. Finally, the set script is the appropriate place to pre-generate stimulus signals or parts of signals that will not change during the run. These include, for example, the special signal vectors with reserved names `m_quiet`, `m_presig`, and `m_postsig` which will be placed between, respectively prior, or after the stimulus intervals (see section 3.3).

For an example, see the set script `sam_sincarrier_detectset.m` in the subdirectory `examples`.

3.3 The user script

The user script will be called once prior to each new trial. This is performed automatically by the PSYLAB-script `mpsy_afc_main`, or `mpsy_match_main.m`.

The purpose of the user script is to generate the (new) current stimuli that are to be presented in the current trial. Typically, these stimuli depend on the current value of the stimulus variable `M.VAR`, and most probably also on the value, respectively set of values of `M.PARAM`. The stimuli generated by the user script will then be taken for further use of the calling script, that means `mpsy_afc_main`, or `mpsy_match_main.m`. Therefore, the stimuli are required to have certain *fixed*, reserved names.

The following signal vectors must reside as Matlab variables inside the global Matlab-workspace at the end of the user script:

- `m_test`** The signal vector that contains the stimulus of the test interval. The test interval contains “the signal” to be detected by the subject, respectively the signal deviation to be discriminated, which the reference signal does not.

m_ref The signal vector that contains the stimulus of the reference interval(s). If the variable `m_ref` exists in the Matlab workspace, *this* signal is presented in the $(n - 1)$ reference intervals of an n -AFC experiment, which means that all reference intervals are identical. This is illustrated in the example experiment `jnd_frequency.m`.

m_ref1, m_ref2, ... The $(n - 1)$ signals vectors that contain the reference intervals in case that all reference intervals should be different from each other. This might, for example, be required if independent realisation of a running noise should be used for every reference interval. In this case, the variable `m_ref` must not exist in the workspace. The $(n - 1)$ reference signal vectors `m_ref1`, `m_ref2`, ... will be presented in random order within each trial (on top of the random placement of the test signal within the n intervals).

Additionally, the following signal vectors with reserved names can (but need not) reside in the Matlab-workspace after leaving the user script `PSYLAB` respectively the set script:

m_quiet The signal which is presented between two adjacent stimulus intervals. Most often this will be a quiet pause of silence, i.e. a vector of zeroes. Alternatively the signal could be an empty vector (`m_quiet=[]`) which would mean a direct succession of the n intervals of a n -AFC trial.

m_presig The signal which is presented before the first stimulus interval. This could also be silence, or for example a certain marker stimulus.

m_postsig The signal which is presented after the last of the n stimulus intervals.

If one or more of the three signals `m_quiet`, `m_presig` or `m_postsig` are left unspecified, i.e. nonexistent in the workspace, they default to the empty vector. This is automatically taken care of by the PSYLAB-script `mpsy_check.m`.

3.4 Required type and value of PSYLAB-variables

For the correct functioning of PSYLAB there are certain restrictions imposed on the possible value or type of some PSYLAB-variables. These are:

1. The following PSYLAB-variables must be *numeric* in type:
`M.VAR`, `M.STEP`, `M.NUM_PARAMS`
2. The following PSYLAB-variables must be of type *string* and must *not contain whitespace* characters:
`M.SNAME`, `M.VARNAME`, `M.VARUNIT`
3. The following PSYLAB-variables must be of type “*cell string*” (instead of a string):
`M.PARAMNAME`, `M.PARAMUNIT`

This is mandatory *even in case they only contain one single entry*.

Example: `M.PARAMNAME = {'frequency'}; M.PARAMUNIT = {'Hz'};`

Additionally, the different elements of these variables must *not contain whitespace* characters either.

Not sticking to these rules would let you run your experiment without problems (at first) but would put you into trouble when analysing your data later on, see section 3.7 and 3.9. Therefore, an automatic check of these variables is performed by the PSYLAB-script `mpsy_check.m`.

3.5 Test subject interface

PSYLAB offers a choice of different user interfaces for the test subject. One simple interface is to answer via a keyboard. Another is to provide a graphical user interface to be controlled via a mouse and/or key presses. The former has the advantage that an extra monitor could be omitted. The latter may be more informative for the subject and can provide some extra functionality.

In an n -AFC test, a subject answer of 1, 2, ..., n indicates the subjects decision for interval 1, 2, ..., n . These answers can be indicated by keyboard or by corresponding mouse clicks. Additionally, the following subject answers are possible which carry special meanings: 0 indicates a deliberate wrong answer. It is not possible to give this answer via mouse click. The answer 8 means: terminate the current

run. The answer 9 means: terminate the whole experiment. The last two answers are also available from the “Quit”-menu of PSYLAB’s answer GUI.

The type of interface, including the amount of information and feedback that is provided to the subject is controlled by these variables:

M.FEEDBACK A value of 0 means: do not give feedback to the subject.

A value of 1 means: Give feedback to the subject whether or not the last answer was correct.

A value larger than 1 means: additionally save a plot of the current run’s result after threshold has been reached. The resulting eps-file will always have the same filename, generated as [‘plot_mvars_’ M.SNAME]. It will thus be overwritten after each completed run.

A value larger than 2 means: same as before, but create a new filename including the date/time information for each eps-file.

M.INFO A value of 1 means: Provide additional information to the subject, for example, about parameters of next run, etc.

M.USE_GUI A value of 0 means: use a pure keyboard interface. The subjects answer consists of a keypress, *followed by RET*.

A value of 1 means: use a graphical user interface. This can be controlled via button clicks by a mouse. Alternatively, answering by a single keypress, *without hitting RET*, is possible, too. However, in order for this to work properly the background of the answer GUI must have the focus (rather than, for example, any of the answer buttons). Of course, the keypress needs to be a reasonable subject answer (numbers 1, through n , and 0, 8, 9, see above). Fig. 4 shows the PSYLAB-GUI.

M.VISUAL_INDICATOR This variable only takes effect in case of `M.USE_GUI==1`.

A value of 1 means: mark each stimulus interval visually by highlighting its corresponding answer button. This feature will only work correctly when all n stimulus interval are of the same temporal duration. However, you should be able to achieve this for most experiments.

A value of 0 means: no visual interval indication.

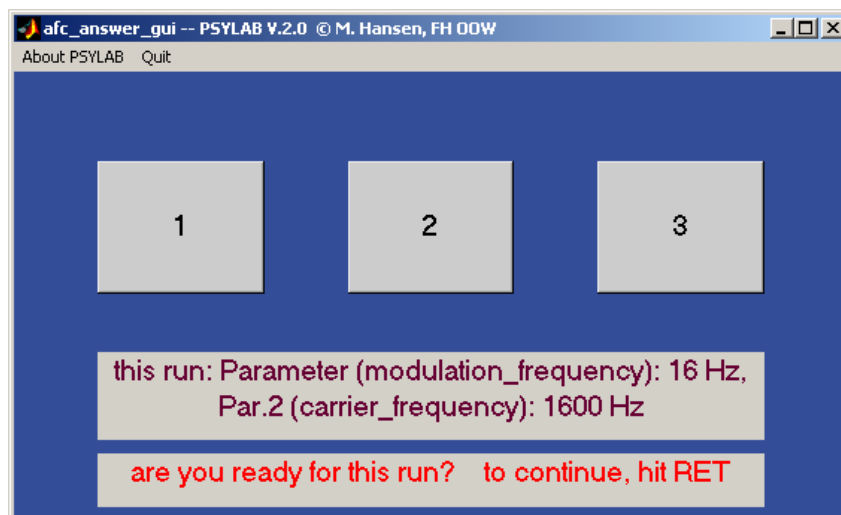


Figure 4: Example of the graphical user interface for the subject.

3.6 Running your experiment

Once you have set up your three experiment files correctly, running your experiment means running your main script. You might want to instruct your subjects to always identify themselves by the identical user ID, for example, their initials, which must not contain any white-spaces. All data gathered from a subject will be saved in a cumulative fashion, on a one-separate-file-per-subject basis, see section 3.7.

The subjects run the experiment at their own pace. They may answer in one of the ways described in section 3.5, as specified by the experimenter.

Analysis of your data can be performed at any later time, independently from the subject performing the measurement.

3.7 Saving your data: the 'psydat' file

Each time when a threshold has been reached, i.e. one run has been completed, the result of that run is saved in a result file in ASCII-format. The name of that file is always formed by the common prefix 'psydat_' followed by the value of `M.SNAME`, i.e. the subject name. It is important for correct functioning of PSYLAB to avoid any whitespace characters in the subject name. Example: `M.SNAME = 'mh'` yields the filename `psydat_mh`.

The psydat-file is written in a special fixed format. One important aspect of this format is the fact that all data entries in the file are delimited by whitespace characters. Consequently, this requires that certain PSYLAB-variables (for example, parameter names or units) *must not contain whitespace characters*. You should not try to change this behaviour, as this would likely interfere with the mechanism for analysis and display of (all) results. It is mandatory that the precise format of the psydat file is maintained. This means that comments, extra lines, or missing lines are not allowed as these would crash the mechanism for automatic data extraction from the psydat file (see section 3.9).

The following data will be saved in the psydat-file after each completion of one run: experiment name; subject name; date and time; number of stimulus parameters; name, value, and unit of each parameter; name of stimulus variable, threshold value, its standard deviation and minimal and maximal value, unit of stimulus variable. The result entry of one run will span across `2+M.NUM_PARAMS` lines in the psydat-file. Have a look into one of the example psydat-files in the `examples` subdirectory. One example entry in the psydat file belonging to the experiment `sam_sincarrier_detect.m` is the following:

```
#### sam_sincarrier_detect mh0 08-Jan-2006__18:46:03 npar 2 ####
%----- PAR1: modulation_frequency 16.000000 Hz
%----- PAR2: carrier_frequency 400.000000 Hz
      modulation_degree -31.000000 1.278275 -34.000000 -29.000000 dB
```

This entry informs you that the subject named 'mh0' performed the experiment 'sam_sincarrier_detect' on the 8th of January 2006 in the early evening. The experiment had 2 parameters which are specified in rows 2 and 3. The result was a threshold value at $m=-31$ dB (median across measurement phase), with a standard deviation of 1.28 dB. The minimal respectively maximal values of the modulation degree during the measurement phase were -34 dB respectively -29 dB.

In addition to the psydat-file in ASCII format, the variables `M` and `M.*` also get saved as a binary mat-file each time a run has been completed. However, this is mainly for rescue and analysis purposes and the binary files may as well be deleted. If you do not need/like this behaviour, look at the end of the file `mpsy_proto.m` and delete the corresponding lines.

3.8 Setting up interleaved-tracks experiments

Designing an interleaved-tracks experiment requires to write a main script, a set script, and a user script as well. Most things are just same as for a single-run non-interleaved experiment, but the following exceptions apply:

1. The variable `M` needs to be an *array*, instead of a scalar variable, the number of elements of `M` being equal to the desired number of simultaneous interleaved tracks of the experiment.

In the main script, it is *not* necessary to copy all fields of the struct variable `M(1)` to those of `M(2)`, `M(3)`, ... for the 2nd, 3rd, ... concurrent run. Instead, it is sufficient to only assign the "relevant" fields of `M(2)`, `M(3)`, When doing this, any fields of `M(2:end)` that are left empty will be assigned with the same values as found in `M(1)` automatically.

2. The script `mpsy_intrlv_afc_main.m` is called to control the whole AFC experiment, instead of `mpsy_afc_main.m`.

The following example code illustrates how to set up an interleaved-tracks experiment. The example shows the main script for the tone-in-broadband-noise experiment (see in the subdirectory `examples`) in

which a sinusoidal tone of different frequencies is to be detected in a running broad band noise of fixed bandwidth and level.

```

mpsy_init;

M.EXPNAME      = mfilename;    % experiment name, very important to be set correctly!
M.NUM_PARAMS   = 2;            % number of parameters
M.PARAMNAME(1) = {'testtone_frequency'};
M.PARAMUNIT(1) = {'Hz'};
M.PARAMNAME(2) = {'noise_level'};
M.PARAMUNIT(2) = {'dB'};
M.VARNAME      = 'testtone_level';
M.VARUNIT      = 'dB';
M.MINSTEP      = 1 ;          % minimum step size, in units of M.VARUNIT
M.NAFC          = 3 ;          % number of forced choice intervals
M.ADAPT_N_UP    = 1 ;          % number of successive wrong answers required for "up"
M.ADAPT_N_DOWN  = 2 ;          % number of successive correct answers required for "down"
M.MAXREVERSAL  = 4 ;          % number of reversals required as stop criterion
M.FEEDBACK      = 1 ;          % 1/0 = yes/no
(...)
M.FS            = 48000;       % sampling frequency
M.USE_GUI       = 1;          % use a GUI for user input

M.SNAME = input('\n\n please type your name (initials, no spaces, press RETURN at end) ','s');

tone_freqs = [ 200 400 800 1600 3200 6400 ];

% assign different parameter sets for interleaved tracks experiment
for kk = 1:length(tone_freqs),
    M(kk).PARAM(1) = tone_freqs(kk);
    M(kk).PARAM(2) = -30;          % use a fixed noise level
end

mpsy_intrlv_afc_main;

```

The first part looks exactly the same as for a single-run experiment. The difference starts in the `for`-loop, where `M(kk).PARAM(1)` and `M(kk).PARAM(2)` are assigned, thereby rendering `M` into an array with `length(bandwidths)` elements (in this case 6 elements). After the `for`-loop, most fields of `M(2:6)` are still empty. These fields will be filled in automatically by way of the script `mpsy_intrlv_init.m` which is called after the end of the `for`-loop.

The script `mpsy_intrlv_afc_main` will start an experiment with a number of 6 interleaved tracks (in this example). It needs to be called only once and it will exit after the last of the concurrent interleaved tracks has finished. The principle organisation of an interleaved-tracks experiment is illustrated by the flow diagram in Fig. 5.

Note that the set script and the user script of an experiment can sometimes stay exactly the same as for a single-run experiment. However, all variables (including signals) that need to be different in the different tracks (i.e. different parameter settings) must become a field variable of the current variable `M`. Then, these fields will be saved into the variable `MI`, as shown in the flow diagram in Fig. 5. For more details, consult the source code of the files `mpsy_intrlv_*.m` dealing with interleaved-tracks experiments.

Currently, only interleaved N -AFC experiments are supported in PSYLAB version 2.1. However, interleaved matching experiments could rapidly be adapted after looking at `mpsy_intrlv_afc_main.m` and `mpsy_match_main.m`.

3.9 Displaying your results

Every time when a subject has completed one run, that run's result is documented in the "psydat" file, see section 3.7. All results can later be analysed and displayed in several ways by using one of the following

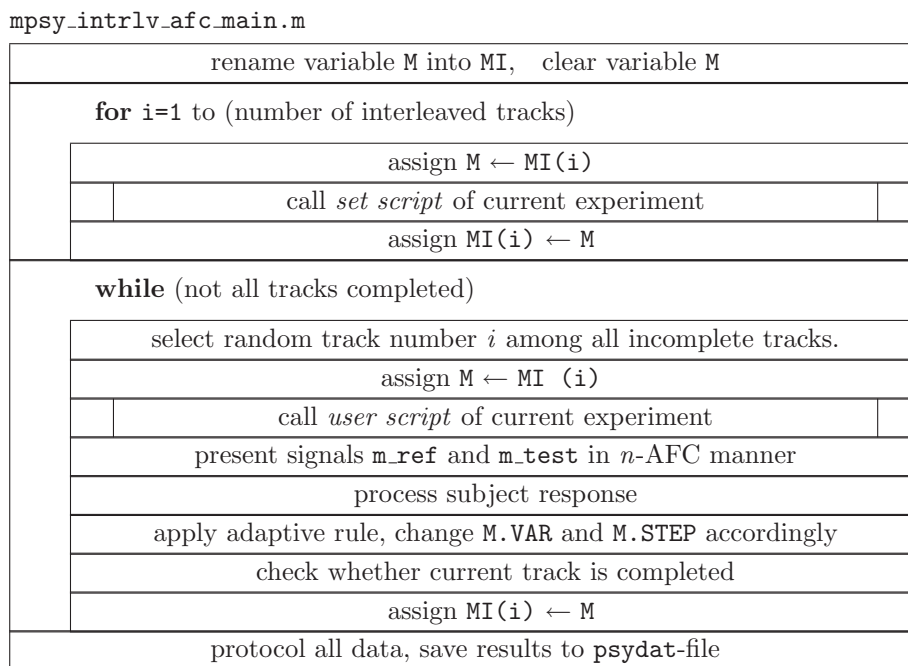


Figure 5: Principle flow diagram of an interleaved-tracks experiment, as controlled by the script `mpsy_intrlv_afc_main.m`

PSYLAB functions:

read_psydat.m Extract from the psydat file all those data points that belong to one subject and one experiment.

display_psydat_raw.m Plot all individual data points for one subject and experiment.

display_psydat.m Plot all threshold results, individually averaged across all repetitions for identical parameter value combinations.

These three functions are explained in the following subsections.

3.9.1 read_psydat.m

The script `read_psydat.m` performs the action to read the corresponding psydat file of the subject and to extract from it all those lines that belong to the given experiment name (and of course subject name). Lines that pertain to a different experiment are simply skipped by `read_psydat`. The extracted data are returned in two different data formats. After the call

```
[x,y] = read_psydat(s_name, exp_name)
```

variable `x` contains a struct variable with all data extracted from the psydat file. Each struct field is a vector or cell string with as many elements as the number of data points in the psydat file. A lot of information contained in `x` is therefore quite redundant. Variable `y` stores only the subset of numerical data of `x`, in a matrix format which is explained in the verbose output of `read_psydat`. See also the following section.

3.9.2 display_psydat_raw.m

You can have a look at all individual data points that were accumulated over time for one subject in an experiment. In order to plot *all* data points *individually*, use the script `display_psydat_raw.m`. This script makes use of `read_psydat.m` internally. Aside from plotting, `display_psydat_raw.m` also returns the data that were extracted from the psydat file in the same way as done by `read_psydat`.

The output from calling `display_psydat_raw.m` might look like this and produce a plot as shown in Fig. 6:

```

>> [x,y] = display_psydat_raw('mh', 'sam_sincarrier_detect')
*** info: found 19 matching entries in psydat_mh
*** info: meaning of the 6 cols of y:
        threshold, thres_sd, thres_min, thres_max, par1, par2
x =
    date: {1x19 cell}
    par: [1x2 struct]
    varname: {1x19 cell}
    threshold: [-31 -35 -48 -34 -29 -50 -31 -32 -32 -32 -34.5 -31 -40 -54 -32 -52 -32 -34 -31]
    thres_sd: [1x19 double]
    thres_min: [-34 -36 -50 -36 -30 -52 -33 -33 -36 -35 -35 -33 -42 -55 -33 -54 -34 -35 -32]
    thres_max: [-29 -32 -47 -32 -27 -49 -30 -28 -24 -29 -33 -30 -37 -53 -31 -51 -31 -33 -30]
    varunit: {1x19 cell}
y =
1.0e+003 *
-0.0310    0.0013   -0.0340   -0.0290    0.0160    0.4000
-0.0350    0.0010   -0.0360   -0.0320    0.0640    0.4000
-0.0480    0.0010   -0.0500   -0.0470    0.2560    0.4000
-0.0340    0.0012   -0.0360   -0.0320    0.0160    1.6000
-0.0290    0.0010   -0.0300   -0.0270    0.0640    1.6000
-0.0500    0.0008   -0.0520   -0.0490    0.2560    1.6000
-0.0310    0.0008   -0.0330   -0.0300    0.0160    3.2000
-0.0320    0.0014   -0.0330   -0.0280    0.0640    3.2000
-0.0320    0.0034   -0.0360   -0.0240    0.2560    3.2000
-0.0320    0.0017   -0.0350   -0.0290    0.0160    0.4000
-0.0345    0.0008   -0.0350   -0.0330    0.0160    1.6000
-0.0310    0.0008   -0.0330   -0.0300    0.0160    0.4000
-0.0400    0.0016   -0.0420   -0.0370    0.0640    0.4000
-0.0540    0.0007   -0.0550   -0.0530    0.2560    0.4000
-0.0320    0.0006   -0.0330   -0.0310    0.0640    1.6000
-0.0520    0.0009   -0.0540   -0.0510    0.2560    1.6000
-0.0320    0.0009   -0.0340   -0.0310    0.0160    3.2000
-0.0340    0.0007   -0.0350   -0.0330    0.0640    3.2000
-0.0310    0.0007   -0.0320   -0.0300    0.2560    3.2000

```

As the experiment of this example comprised two parameters, the output `y` has 4+2 columns. These are: threshold, standard deviation of threshold, the minimal and maximal value of the stimulus variable that occurred during the measurement phase, and the values of parameter 1 and parameter 2. Figure 6 shows an errorbar-plot of the first and second column of `y` as a function of the 5th column (parameter 1), separately for each value of the 6th column (parameter 2), while columns 3 and 4 are not shown in the plot.

3.9.3 display_psydat.m

The normal way to process and take a look at your threshold data results is to use `display_psydat.m`. This script also makes use of `read_psydat.m` to extract all corresponding data from the psydat file. Subsequently, all thresholds that were measured repeatedly are first averaged, individually per each (combination of) different parameter value(s), and then plotted. The first and second argument of `display_psydat` specify the subject name and experiment name.

Calling `display_psydat` with the same input arguments as for `display_psydat_raw` produces four return arguments:

```
[x_all, y_average, y_ave2, hplot] = display_psydat(s_name, exp_name)
```

The output `x_all` contains the same data as described for output `x` from `read_psydat`, see above, but sorted by the value of the 2nd parameter (and 3rd, 4th parameter, if present). Output `y_average` contains the same data as output `y` of `read_psydat`, but *averaged* across repeated measurements with the same set of parameter values. Output `y_ave2` contains the same data as `y_average`, but in a matrix format,

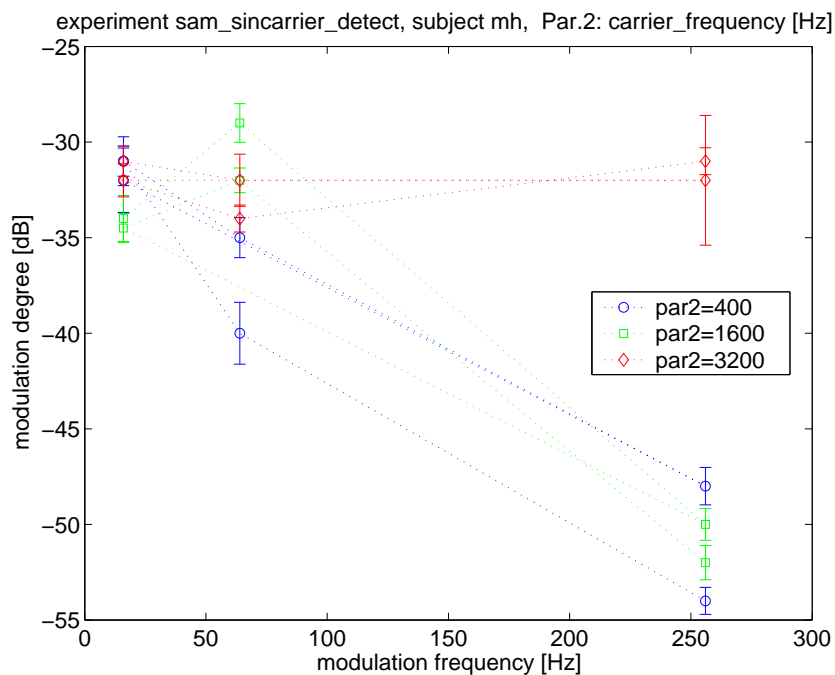


Figure 6: Example plot resulting from a calling `display_psydat_raw`. Every single data point (threshold) obtained by the subject is displayed separately.

where each final data point to be plotted is contained in one row. The last output `hplot` contains an array of handles to all plot lines in the figure.

The output from a calling `display_psydat.m` might look like this and produce a plot as shown in Fig. 7. Compare the output and the data to those output by `display_psydat_raw.m` (see page 13).

```
>> [x_all,y_average,y_ave2] = display_psydat('mh', 'sam_sincarrier_detect')
*** info: found 19 matching entries in psydat_mh
*** info: meaning of the 6 cols of y:
        threshold, thres_sd, thres_min, thres_max, par1, par2

x_all =
1x3 struct array with fields:
    psydata
y_average =
1x3 struct array with fields:
    psydata
y_ave2 =
1.0e+003 *
   -0.0313    0.0006   -0.0340   -0.0293    0.0160    0.4000
   -0.0375    0.0035   -0.0390   -0.0345    0.0640    0.4000
   -0.0510    0.0042   -0.0525   -0.0500    0.2560    0.4000
   -0.0343    0.0004   -0.0355   -0.0325    0.0160    1.6000
   -0.0305    0.0021   -0.0315   -0.0290    0.0640    1.6000
   -0.0510    0.0014   -0.0530   -0.0500    0.2560    1.6000
   -0.0315    0.0007   -0.0335   -0.0305    0.0160    3.2000
   -0.0330    0.0014   -0.0340   -0.0305    0.0640    3.2000
   -0.0315    0.0007   -0.0340   -0.0270    0.2560    3.2000
```

A comparison of `x_all(1).psydata` and `y_average(1).psydata` respectively the first three rows of `y_ave2` illustrate the work of `display_psydat`:

```
>> x_all(1).psydata
```

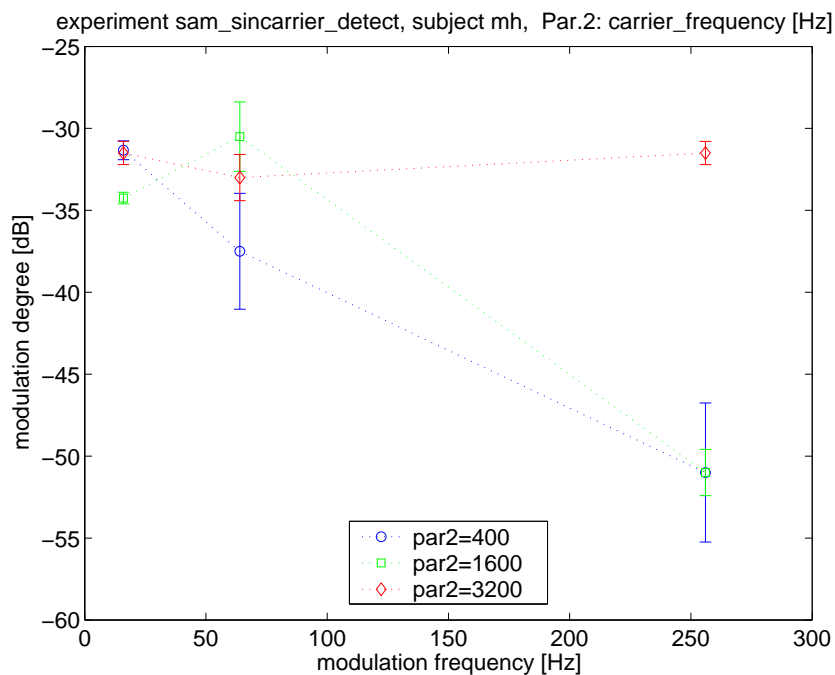


Figure 7: Example plot resulting from a calling `display_psydat` for the same experiment and subject as shown in Fig. 6. All data points (thresholds) pertaining to repeated measurements with the same set of parameter values have been averaged across prior to plotting.

```
ans =
-31.0000    1.2783   -34.0000   -29.0000    16.0000   400.0000
-32.0000    1.6855   -35.0000   -29.0000    16.0000   400.0000
-31.0000    0.7878   -33.0000   -30.0000    16.0000   400.0000
-35.0000    1.0463   -36.0000   -32.0000    64.0000   400.0000
-40.0000    1.6204   -42.0000   -37.0000    64.0000   400.0000
-48.0000    0.9783   -50.0000   -47.0000   256.0000   400.0000
-54.0000    0.7050   -55.0000   -53.0000   256.0000   400.0000
>> y_average(1).psydata
ans =
-31.3333    0.5774   -34.0000   -29.3333    16.0000   400.0000
-37.5000    3.5355   -39.0000   -34.5000    64.0000   400.0000
-51.0000    4.2426   -52.5000   -50.0000   256.0000   400.0000
```

Here, the values -31.3333 and 0.5774 in the first row of `y_average(1).psydata` (or of `y_ave2`) are the mean and the standard deviation across the thresholds that belong to the three repetitions of the experiment with 1st parameter=16 Hz and 2nd parameter=400 Hz. The values -37.5000 and 3.5355 are the mean and the standard deviation of the two repetitions belonging to 1st parameter=64 Hz and 2nd parameter=400 Hz, etc. Note that the standard deviation of each experimental run, appearing in the 2nd column of `x_all(:).psydata`, is neglected in `display_psydat`.

3.9.4 special effects: permute/change the look of your data with `display_psydat.m`

`display_psydat.m` offer an optional third and fourth argument. They only take effect for experiments with more than one parameter: the third argument specifies the “plot style”. A value of 1 means: plot all data into one single figure. A value of 2 means: use a new figure for each value of the 2nd parameter (resp. for each unique combination of values of the 2nd, 3rd, ..., *n*th parameter).

The optional fourth argument of `display_psydat` specifies a permutation of parameters prior to further analysing and plotting them. The meaning of the fourth argument can best be explained by the

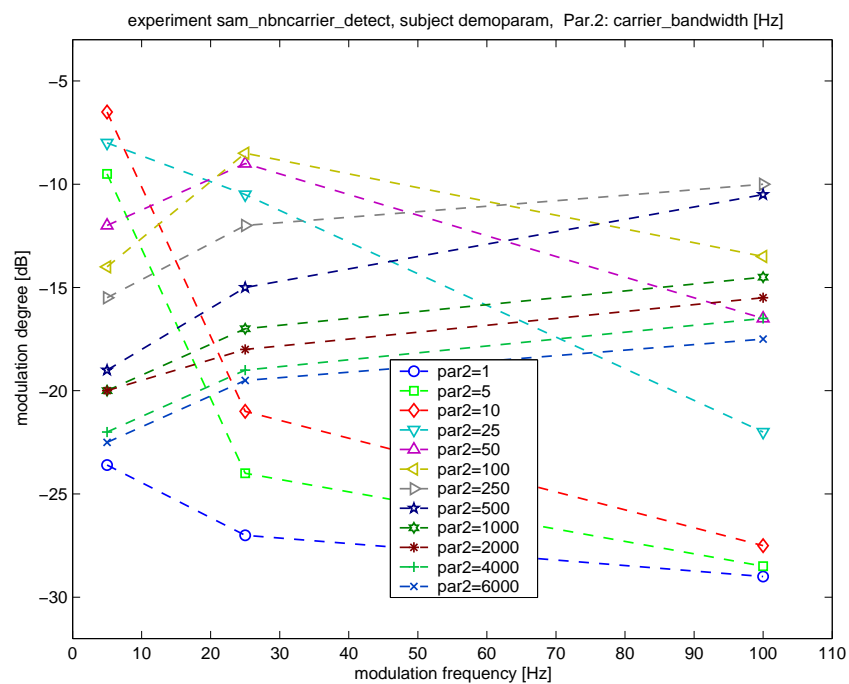


Figure 8: Example data of a modulation detection experiment as described by Dau *et al.* (see text). These data have been taken from Fig. 1 in Dau *et al.*, JASA 106(5), 2752–2760. For clarity, standard deviations have been removed.

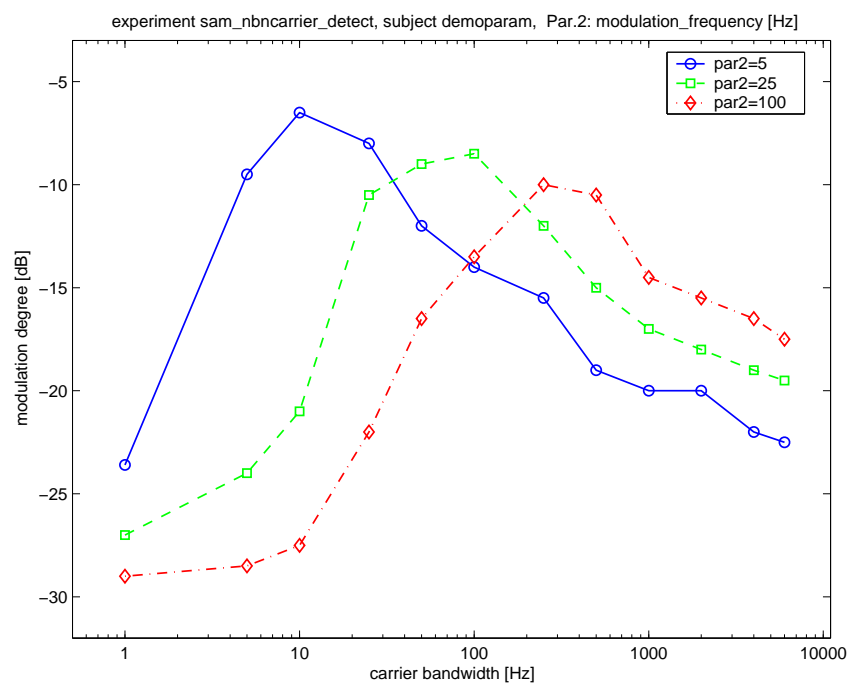


Figure 9: Replot of the same data as shown in Fig. 8 (See also Fig. 2 of Dau *et al.*, JASA 106(5), 2752–2760). This plot was made by `display_psydat` after permuting the order of the two parameters of the PSYLAB-experiment, see text.

following examples. Consider the modulation detection experiment of Dau *et al.* (1999) (JASA 106(5), 2752–2760). The Variables and Parameters could have been defined in the main script as follows:

```
M.EXPNAME      = 'sam_nbncarrier_detect';
M.NUM_PARAMS   = 2;
M.PARAMNAME(1) = {'modulation_frequency'};
M.PARAMUNIT(1) = {'Hz'};
M.PARAMNAME(2) = {'carrier_bandwidth'};
M.PARAMUNIT(2) = {'Hz'};
M.VARNAME      = 'modulation_degree';
M.VARUNIT      = 'dB';
```

You might have measured the same thresholds as Dau *et al.*, and calling `display_psydat` like in

```
display_psydat('demoparam', 'sam_nbncarrier_detect');
```

results in a plot as shown in Fig. 8. Note here that threshold data (values of `M.VAR`) are plotted as a function of the first parameter (values of `M.PARAM(1)`) in Fig. 8, and each value of the second parameter (`M.PARAM(2)`) yields a separate curve. This is the standard behaviour of `display_psydat`. There are 12 curves for the 12 individual values of the 2nd parameter (carrier bandwidth).

If you would like to replot your data so that threshold is plotted as a function of carrier bandwidth, then you would need to permute the numbering of your two parameters, prior to using `display_psydat`. This can in fact be specified by the fourth argument of this function, which must be a permutation of the numbers 1 through n , where n is the number of parameters of your experiment, i.e. `M.NUM_PARAMS`. Calling `display_psydat` like in

```
display_psydat('demoparam', 'sam_nbncarrier_detect', 1, [2 1])
set(gca, 'Xscale', 'log')
```

specifies that the original order of the parameters shall be permuted into `[2 1]`, i.e. the reverse order of the two parameters. The third argument, `'1'`, specifies that all data should go into one single plot figure. The result is a plot like shown in Fig. 9. Note here that only 3 curves are shown, namely one for each value of the (originally first) parameter “modulation frequency”, and each curve is now made of 12 data points. The modulation bandwidth now acts as the first parameter in this plot and its title mentions the modulation frequency as the second parameter. If the third argument (“plot style”) had been changed into 2 instead of 1, then three separate figures would have resulted instead of the single one shown in Fig. 9.

3.10 Debugging your experiment

For purposes of debugging, set the variable `M.DEBUG` to a value larger than zero (1, 2, 3), to get an increasing amount of temporary information and plots. When gathering real data with test subjects you would normally want to set `M.DEBUG=0`;

4 Variables controlling PSYLAB

PSYLAB is controlled by a number of variables with a fixed, reserved name. All of these variables are struct fields of the variable with reserved name `'M'`. Some of these variables are for internal purposes, while others need to be specified by the user according to the needs of the current experiment.

Table 1 contains a list of all PSYLAB-variables, and explains their use. It is important to remember that some variables are required to be of a certain type, for example, a string, a scalar or a cell string, or must not contain white-space characters. This is described in section 3.4. The required type of each variable is mentioned in parentheses in Table 1.

user variables	
Name (type)	Meaning
M.SNAME (s)	subject name, as a string. Preferably only initials. <i>Important:</i> must not contain any white-space characters.
M.EXPNAME (s)	experiment name. The experiment name must be identical to the name of the main script (except for the extension '.m').
M.VAR (n)	The value of the stimulus variable, as a scalar number, which is adaptively changed from trial to trial to find the subjects threshold.
M.VARNAME (s)	Name of the stimulus variable M.VAR, e.g. 'test_tone_level'.
M.VARUNIT (s)	Unit of the stimulus variable M.VAR, e.g. 'dB_SPL'.
M.NUM_PARAMS (n)	The number of stimulus parameters. Must be equal to the length of M.PARAM.
M.PARAM (v)	The value resp. values, as a vector, of the stimulus parameter(s) which is/are kept constant during one run until threshold is reached. In case of only one parameter, M.PARAM is of course a scalar.
M.PARAMNAME (c)	Name(s) of the parameter(s), as cell strings, e.g. 'frequency'.
M.PARAMUNIT (c)	Unit(s) of the parameter(s), e.g. 'Hz'.
M.STEP (n)	Value of the current step size by which M.VAR will be changed adaptively depending on the subjects answer. M.STEP is specified in the same unit as M.VAR.
M.MINSTEP (n)	Minimal value of the step size. As soon as the condition M.STEP == M.MINSTEP has been reached, then M.STEP will not be reduced (halved) any longer and the measurement phase starts. At that time, also the counter M.REVERSAL will be reset to zero.
M.MAXREVERSAL (n)	Number of reversals == criterion for the termination of a run. If the condition M.MAXREVERSAL == M.REVERSALS has been reached after the measurement phase has begun, the run is terminated.
M.NAFC (n)	The number of n of intervals in the n -AFC-task.
M.ADAPT_N_UP (n)	The number of successive wrong answers required for going "up" in the adaptive transformed-up-down rule.
M.ADAPT_N_DOWN (n)	The number of successive correct answers required for going "down" in the adaptive transformed-up-down rule.
M.FS (n)	The sampling frequency, in Hz.
M.CALIB (v)	Calibration constant = RMS level, in dB SPL, of a full-scale square wave. Note that automatic calibration of your equipment is not yet part of PSYLAB.
M.EAR SIDE (n)	Variable specifying the presentation side in case the signals are generated purely mono. Can take one of three predefined values: M_BINAURAL (default value), M_LEFTSIDE, or M_RIGHTSIDE.
M.TASK (s)	Task of the subject, as a string. Typically something like "Which interval contained the test signal?"
M.FEEDBACK (n)	Flag variable (1 or 0), whether or not to provide feedback to the subject (e.g. correct/not correct) after each answer.
M.USE_GUI (n)	Flag variable (1 or 0), whether or not to use a graphical user interface for the subjects answers instead of keyboard input.
M.VISUAL_INDICATOR (n)	Flag variable (1 or 0), whether or not to provide a visual indication of the individual n intervals of each trial by colour-flashing the individual answer buttons. Works only in case that M.USE_GUI has been set, too.
M.INFO (n)	Flag variable to indicate whether or not additional information about the experiment should be provided to the subject.
M.RESULTSTYLE (n)	Flag variable determining the style of resulting data plots directly after new data have been gathered. A value of 1 (default) means: Plot all data into one figure. Value 2 means: use individual figures for each unique combination of parameter values.

M.SAVEMEAN (n)	Flag variable to indicate that the threshold value should be calculated as the <i>mean</i> across M.VAR for trials within the measurement phase, instead of the default behaviour, i.e., calculate their <i>median</i>
M.DEBUG (n)	Flag variable (0, or larger) to indicate the amount of intermediate information presented for debug purposes. Should be set to 0 during real work measurements.

internal variables - not to be manipulated by the user
--

Name (type)	Meaning
M.QUIT (n)	Flag variable indicting a complete termination of the current experiment.
M.ACT_ANSWER (n)	Current answer of the subject (1=correct, 0=wrong).
M.LAST_ANSWER (n)	Previous answer of the subject (1=correct, 0=wrong).
M.REVERSAL (n)	Number of reversals in the current run. Reversals are detected and counted automatically. Counting starts at 0 again upon start of the measurement phase.
M.REV_IDX (v)	Indices (trial numbers of the current run) at which reversals are detected.
M.UA (n)	Current user answer in AFC experiments, i.e. the interval number, or special values requesting a quit of the run or the experiment.
M.UD (n)	Current user answer in up-down experiment like in matching experiments. Value 1 means 'down', value 2 means 'up'.
M.ANSWERS (v)	Vector with all answers of the subjects during the current run.
M.STEPS (v)	Vector with all values of M.STEP during the current run.
M.VARS (v)	Vector with all values of M.VAR during the current run.
M.ALLPARAM (v)	Vector resp. matrix with all values of M.PARAM during the current experiment. Each row of M.ALLPARAM contains the value(s) of M.PARAM pertaining to one run.
M.ALLTHRES_MED (v)	Vector with all threshold values of the current experiment. Each threshold is calculated from the values of M.VARS during each run.
M.ALLTHRES_STD (v)	Vector with all value of the standard deviation of the thresholds during the current experiment. Calculated from the values of M.VARS during each run.
M.DIRECTION (n)	Flag variable for the previous direction of change when applying adaptive up-down-rules. Can take one of the predefined values M.UP, M.DOWN, or M.STAY.

Table 1: List of name and meaning of the PSYLAB-variables, to be specified by the user or for internal use. The character in parentheses indicates the required variable type, i.e. s=string, n=scalar number, v=vector, c=cell string.

5 Helpful scripts in PSYLAB

The PSYLAB distribution contains a few small additional functions that are not needed directly by PSYLAB, but that can come in handy for signal generation etc. The following scripts/functions are also described in their `help`.

rms.m Calculate RMS value of a signal vector.

gensin.m Generate sinusoidal tone.

hanwin.m Perform temporal windowing of a signal with a Hanning window resp. generate Hanning-window-shaped temporal ramps for onset- and offset of a signal.

fft_rect_filt.m Function for very steep bandpass/notch filtering via FFT, by way of setting all Fourier components outside the passband to zero.

6 New contributions to PSYLAB

Starting with version 2.1, a new directory **contrib** has been added to the PSYLAB distribution. It contains newly provided contributions to PSYLAB. These contributions comprise additional features for PSYLAB, like new experimental paradigms, and accompanying example experiments.

The contents of the **contrib** directory should be considered as “experimental” or beta-level-tested. As time goes by and new versions of PSYLAB are released, the new features might migrate to become part of the regular PSYLAB-distribution.

The first two contributions are provided by students of “Institut für Hörtechnik und Audiologie”, Fachhochschule OOW. They implemented two new experimental designs in PSYLAB, namely

1. A procedure to estimate several points on the psychometric function (that means: not only one threshold value) by repeatedly presenting stimuli at several fixed values of the stimulus variable, and recording the corresponding percent correct responses. The accompanying example experiment is a replication of the binaural pitch detection and discrimination experiments by Santurette & Dau (Hear. Res. 223, 2007)
2. A closed-set 1-out-of- n identification procedure. The accompanying example experiment is a replication of the melody recognition experiment by Akeroyd et al. (JASA 110(3), 2001)

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