CENTRE FOR COMPUTATIONAL AND ANIMAL LEARNING RESEARCH

CAL Simulation Guides

PEARCE MODEL SIMULATOR

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Alexandru Gheorghescu, Esther Mondragón, and Eduardo Alonso

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Pearce Model Simulator ©

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Alexandru Gheorghescu, Esther Mondragón & Eduardo Alonso

Centre for Computational and Animal Learning Research

St. Albans, United Kingdom

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1 Introduction

This document describes the steps required for downloading and utilizing the *Pearce Model Simulator © V. 1 (2017)*. The simulator is available for multiple platforms - .exe for Windows, .app for macOS, and .jar for Unix/Linux operating systems. It can be downloaded from CAL-R website and no installation is needed, although JRE 1.8 or later is required for its running.

This document does not address the theory behind Pearce's configural model of classical conditioning or any programming details.

2 Downloading

Different versions of *Pearce Model Simulator © V. 1 (2017)* can be found at address https://www.cal-r.org/ according to the operating system on which it will run.

The file is provided for download under the names *"Pearce_Simulator.exe"*, *"Pearce_Simulator.dmg"* and *"Pearce_Simulator.jar"* for Windows, macOS and Unix/Linux operating systems, respectively.

3 Running the simulator

3.1 Launching

NOTE: the following launching method and images corresponds to Windows environment and may vary slightly for different platforms, but the steps in operating the simulator are the same on all environments.

After download is completed the application can be launched by double click on file's icon (provided that JRE 1.8 or later is installed) and the simulator's main interface will appear in the centre of the screen (Figure 1). The interface is organised into five areas: *the menu bar* which contains the menus "File", "Settings" and "Help", *the toolbar* which contains the "New", "Open", "Save", "Export" icons and displays the current date and time, *the trials panel* where experimental sequences can be entered by group and phase, *the parameters panel* where the parameters can be entered and set through "Set parameters" button and the *bottom area* which contains the buttons "Clear All", "RUN" and "Display figures".
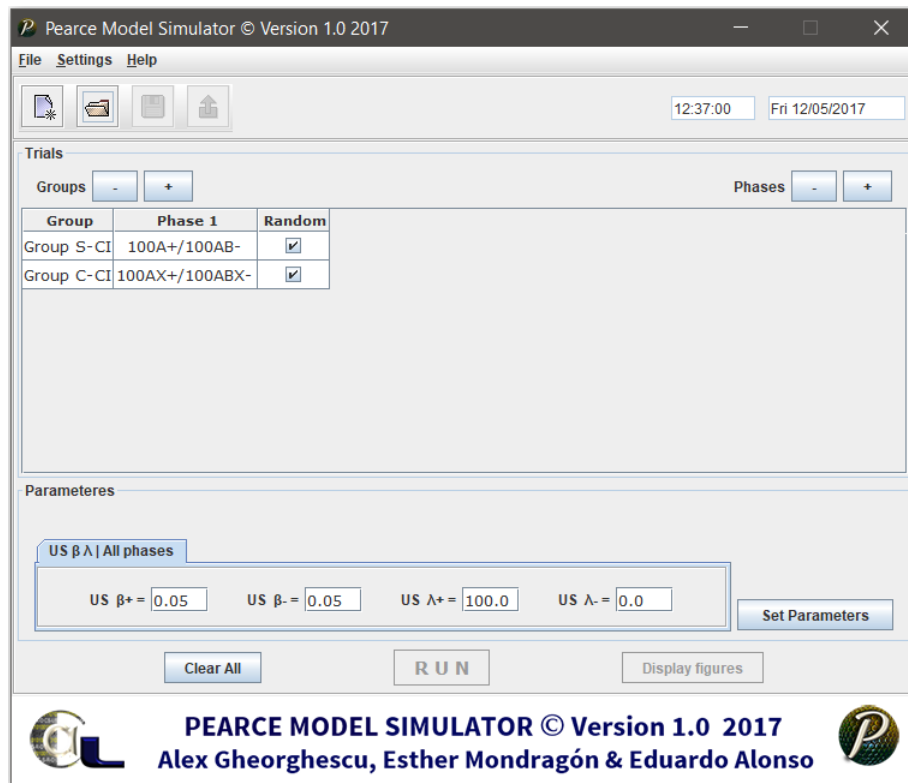
Figure 1 – Main interface

3.2 Simulating

The trials panel allows the number of groups and phases to be specified by the corresponding "-" / "+" buttons. The name of the groups can be specified in the column headed by "Group" and the experimental sequence can be introduced in the columns headed by "Phase". An experimental sequence can be composed of multiple **trial designs** separated by "/" (forward slash) symbol. **A trial design** must be of the form: number of stimuli followed by conditional stimulus, or CS, (an alphabetical value between [a-z] or [A-Z]) followed by reinforcer, or US, ("-" or "+" symbols). A single stimulus is represented by one letter whereas a compound of stimuli by a series of letters (e.g. **100A+/100AB-**, **100AX+/100ABX-**). Optionally a hat function can accompany a CS by entering "^" symbol in the trial design. The simulator takes a snapshot of the conditional stimuli which have a hat associated and outputs their prediction values separately (e.g. **100A^+/100AB^-**, **100AX^+/100ABX^-**).

When the checkbox for "Random" column is selected, the associated experimental sequence will be intermixed by a random number of times, which by default this is 1000. Random can have values between 1 and 10 000 and this value can be specified into simulator through "Settings -> Number of Random Trial Combinations" (Figure 2) or by pressing "Control + 1" keys simultaneously, and the "Random" dialog will appear (Figure 3).
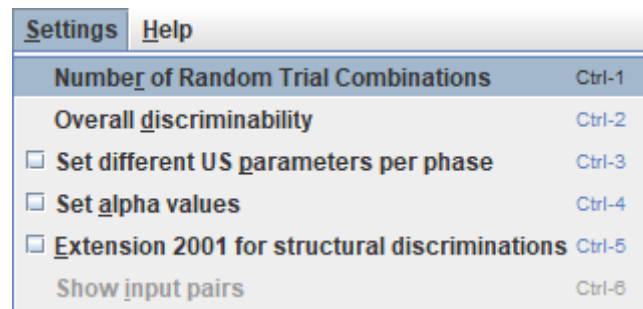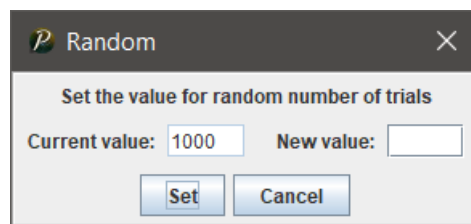
Figure 2 – Random menu item

Figure 3 – Random dialog

If the value of random is not in the range of 1 to 10 000, or is not a numeric value an error message will pop up (Figure 4).
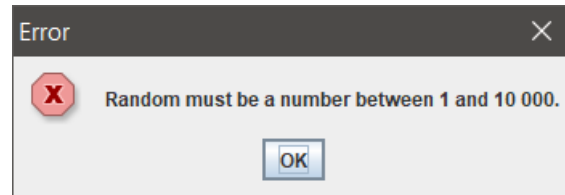

Figure 4 – Random dialog error message

The overall discriminability by default has the value 2, but this can be changed through "Settings -> Overall discriminability" (Figure 5) or by pressing "Control + 2" keys simultaneously, and the "Discriminability" dialog will appear (Figure 6).
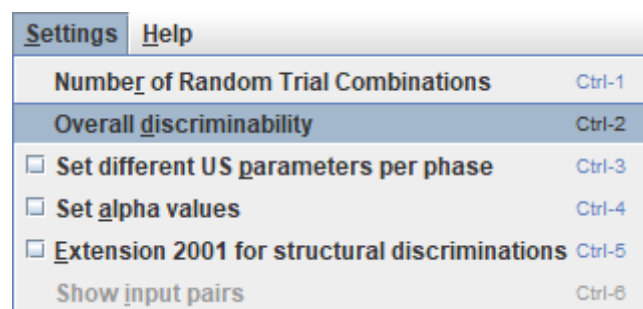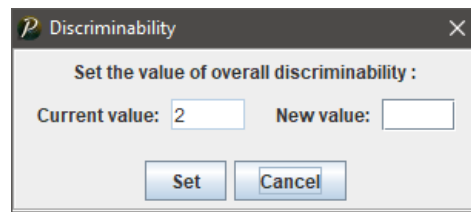

Figure 5 – Random menu item

Figure 6 – Discriminability dialog

The discriminability value has to be in the range of 1 to 100 and be a numeric value, otherwise an error message will pop up (Figure 7).
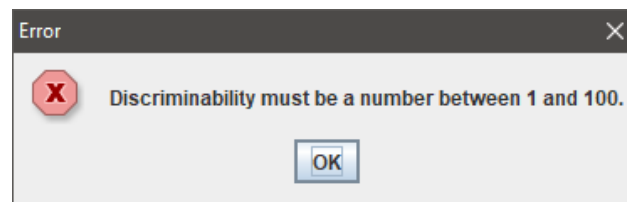

Figure 7 – Discriminability dialog error message

After the experimental sequences have been introduced in *the trials panel*'s table, the parameters for the reinforcer (or unconditional stimulus or US) can be specified in *the parameters panel*. The default values for these are β+ = 0.05, β- = 0.05, λ+ = 100, λ- = 0, as displayed, and apply for all phases in the matrix. If different US parameters values need to be specified per phase, this can be achieved by selecting item menu checkbox "Set different US parameters per phase" from "Settings" (Figure 8) menu or by pressing "Control + 3" keys simultaneously.
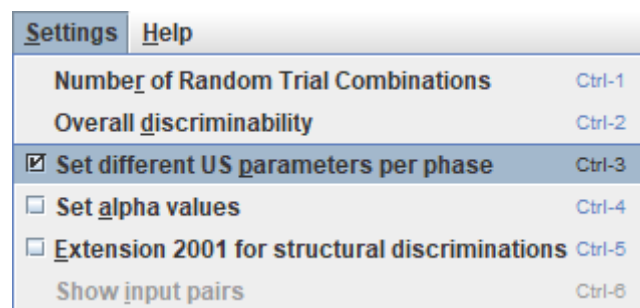

Figure 8 – Set different US parameters per phase

After checkbox "Set different US parameters per phase" has been selected, according to the number of phases present in *the trials panel* a number of tabbed panes will be created in *the parameters panel* which can be easily navigated per phase (Figure 9).

Figure 9 – US parameters per phase

The simulator is an extension of the Pearce's configural model which allows to specify the value of alpha parameter (by default α = 1) for all stimuli (conditional stimulus or CS) present in *the trials panel*. By navigating to "Settings" and selecting the checkbox "Set alpha values" (Figure 10) or by pressing "Control + 4" keys simultaneously, in *the parameters panel* will appear a new panel dedicated to alpha values (Figure 11). The "Get Stimuli" button will display the alpha values associated to each stimulus present in *the trials panel*.

Figure 10 – Set alpha values

Figure 11 – CS parameters panel

For the simulator to compute correctly structural discrimations of the form "100AXR+/100BXR-/100AYR-/100BYR+/100AXS-/100BXS+/100AYS+/100BYS-", "Extension 2001 for structural discriminations" menu item has to be checked from "Settings" or by pressing "Control + 5" keys simultaneously (Figure 12).

Figure 12 – Extension 2001 for structural discriminations

The input pairs formed for structural discriminations can be displayed (Figure 13) by navigating to "Settings -> Show input pairs" menu item or by pressing simultaneously "Control + 6" keys (Figure 14). "Show input pairs" menu item will become available only if "Extension 2001 for structural discriminations" menu item is selected and "Set Parameters" button has been clicked (for checking the correctness of data introduced).
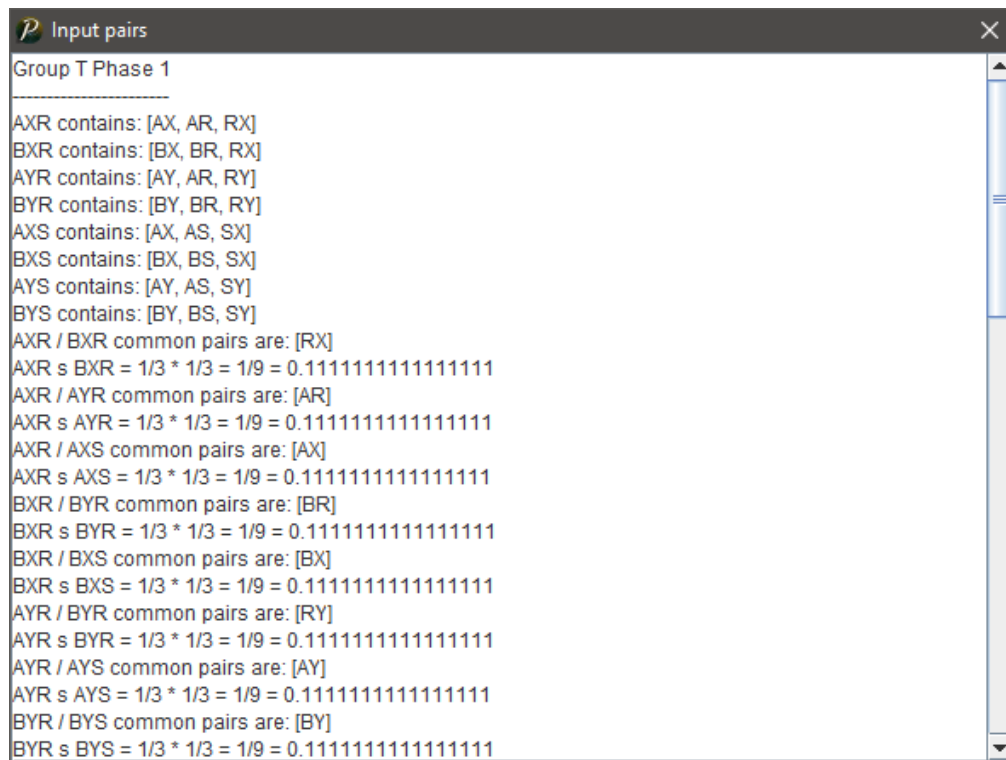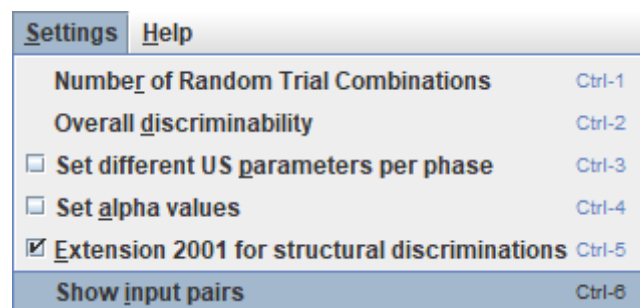

Figure 13 – Input pairs dialog

Figure 14 – Show input pairs

Each *cell* in *the trials panel* and each *input field* in the simulator can be edited with the basic functions such as "Select All", "Copy", "Paste", "Cut" which can be accessed by the keyboard through the combination of keys "Control + A", "Control + C", "Control + V", "Control + X", respectively. The same editing functions can be accessed by right click of the mouse in a *cell/input field* which will pop up an editing menu (Figure 15). Apart from basic

editing functions, the menu contains an extra "Clear" function which will clear the respective *cell/input field*.
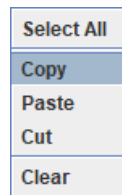
Figure 15 – Edit popup menu

After the group names have been specified, experimental sequences have been entered and the parameters have been set, the "Set Parameters" can be clicked. At this point the simulator performs the checks needed for the correctness of introduced data. The simulator does not allow a group to have the same name as an existing group's name by showing an error message (Figure 16).
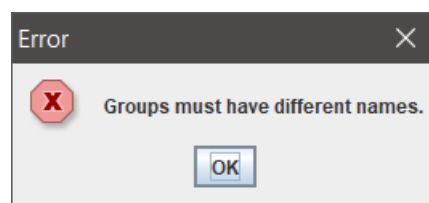
Figure 16 – Group name dialog error message

If an experimental sequence is in wrong format or contains spaces, or a *cell* from *trials panel* has been left empty an error message will appear (Figure 17, Figure 18 and Figure 19 respectively).

Figure 17 – Experiment sequence in wrong format dialog error message
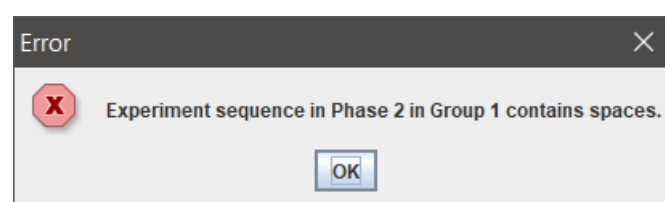
Figure 18 – Experiment sequence contains space dialog error message
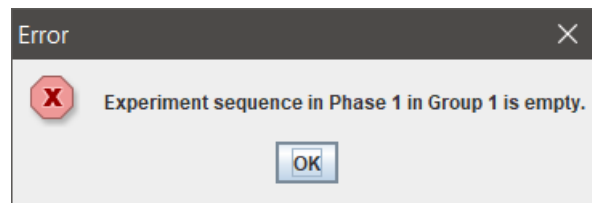
Figure 19 – Empty sequence dialog error message

The parameters must be a numeric value and respect different ranges. The range of alpha(α) must be between 0 and 1, the range of beta(β) must be between 0 and 1 and the range of lambda(λ) must be between -100 and 100. If these conditions are not respected, warning messages will appear accordingly (Figure 20, Figure 21, Figure 22 and Figure 23, respectively).
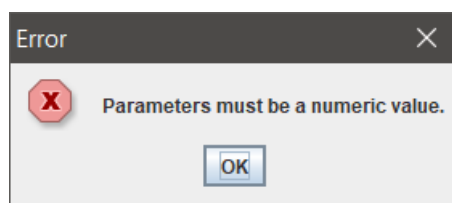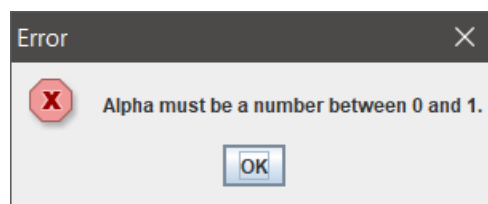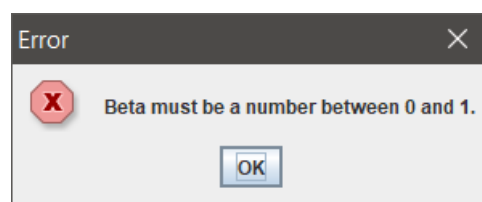

Figure 20 – Parameters dialog error message

Figure 21 – Alpha dialog error message

Figure 22 – Beta dialog error message
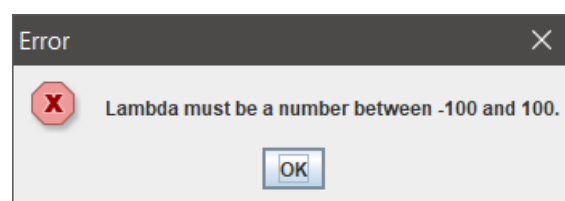
Figure 23 – Lambda dialog error message

If the data entered is correct, after "Set parameters" has been clicked, the "RUN" button will become available. By clicking it, the simulator will process the data. If the experimental sequences are to complex, a loading bar will be shown which indicates the progress of the computation (Figure 24).
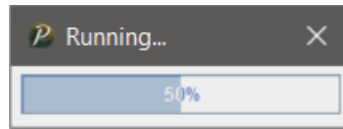

Figure 24 – Loading bar dialog

By closing the loading bar dialog, the calculation will be cancelled.

3.3 Displaying figures

After the simulator has finished computing the data entered, the "Display figures" button will become available. By clicking it, the results are displayed as graphical outputs (Figure 25).
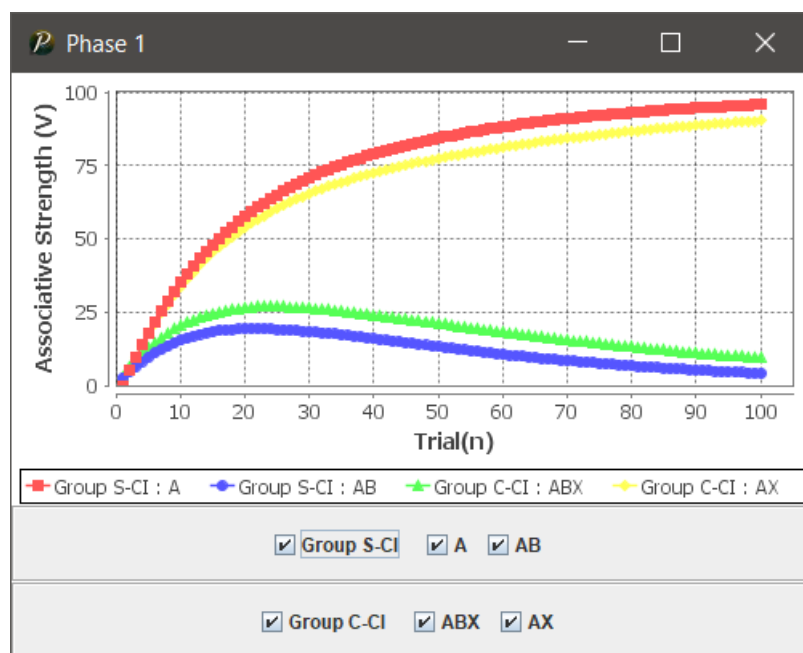
Figure 25 – Display figures frame

For a phase containing two groups, Group S-CI with experimental design 100A+/100AB- and "Random" box checked, and Group C-CI with experimental design 100AX+/100ABX- and "Random" box checked, the displayed figures are as in Figure 20. The bottom of the frame displays a panel for each group which contains the name of the group and the stimuli in the

group as checkboxes. By selecting/deselecting these checkboxes the corresponding data will be displayed/hidden.

3.4 Exporting data

The data computed can be exported as a spreadsheet file through "File -> Export", "Export" icon or be pressing "Control + E" keys simultaneously (Figure 26 and Figure 27).
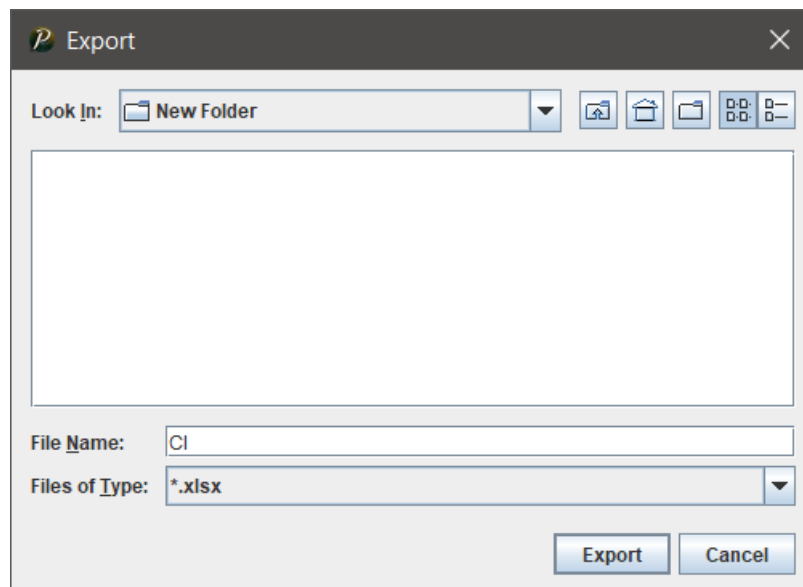

Figure 26 – Export data dialog

Figure 27 – Spreadsheet file

If a ".xlsx" file has been chosen for the data to be exported, the simulator will ask to confirm overwriting (Figure 28).
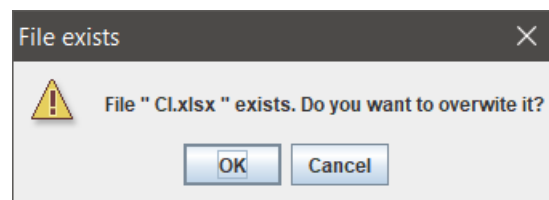

Figure 28 – Export file exists warning dialog

If a file with different file format than ".xlsx" has been chosen for the data to be exported, an error message will appear (Figure 29).
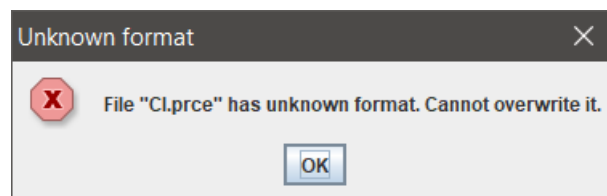

Figure 29 – Export unknown format error dialog

3.5 Save

Experimental sequences with corresponding parameters, random and discriminability values can be saved through "File -> Save", "Save" icon or be pressing "Control + S" keys simultaneously as ".prce" file (Figure 30).
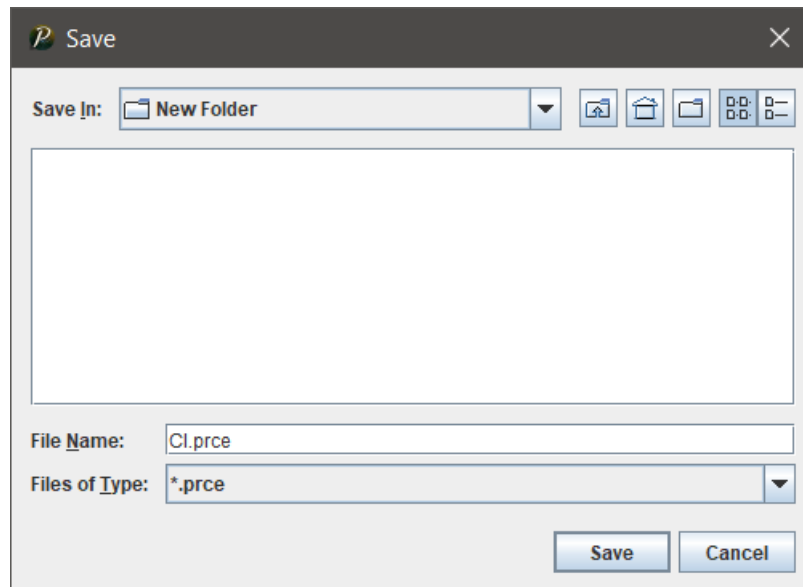

Figure 30 – Save dialog

If a ".prce" file has been chosen for the data to be saved, the simulator will ask to confirm overwriting (Figure 31).
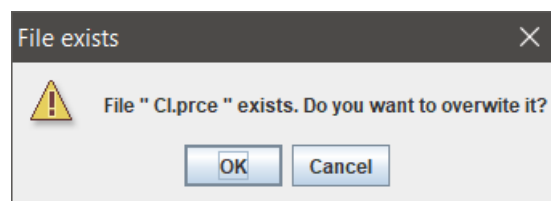

Figure 31 – Save file exists warning dialog

If a file with different file format than ".prce" has been chosen for the data to be saved, an error message will appear (Figure 32).

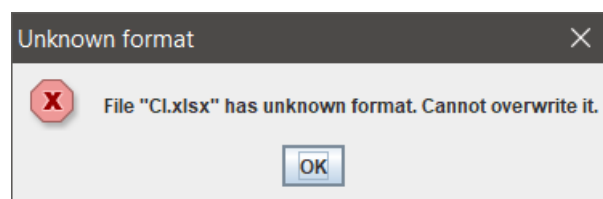Figure 32 – Save unknown format error dialog

3.6 Open

An existing ".prce" file can be opened through "File -> Open", "Open" icon or be pressing "Control + O" keys simultaneously (Figure 33) and the experimental sequences will be loaded in *the trials panel* alongside with the corresponding parameters values. If a specific random value has been pre-set in the ".prce" file, this value will be loaded as well.
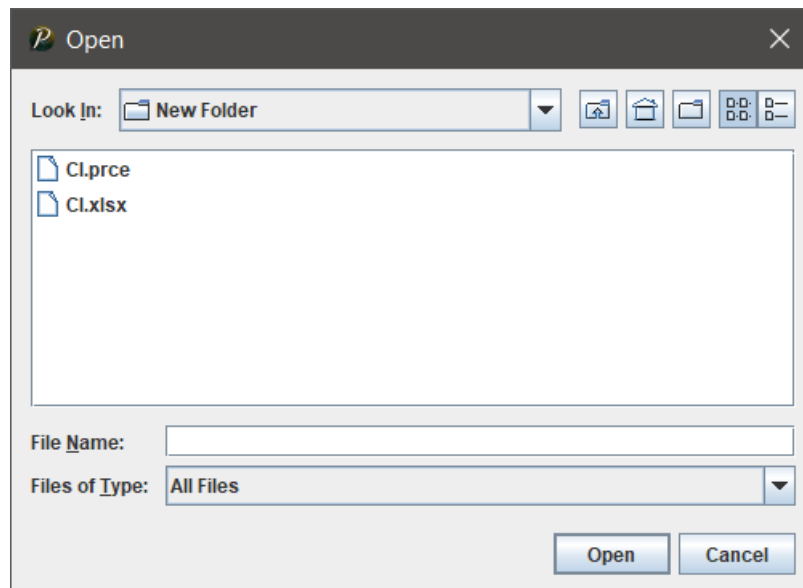

Figure 33 – Open dialog

If a file with different file format than ".prce" has been chosen to be opened, an error message will appear (Figure 34).

Figure 34 – Open unknown format error dialog

4. Terms of use

Please, read carefully the following license agreement. If you don't accept the terms of the agreement, please delete immediately the software from your computer.

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5. Feedback

If you have any questions or comments about the application or this document, please feel free to email Esther Mondragón, at e.mondragon@cal-r.org. We welcome any suggestions or criticisms. If there is an inaccuracy somewhere, please let us know where it occurred and what values were used. It would be very helpful if a saved file from the simulator, which contains the values, is sent as an attachment.

6. References

Mondragón, E., Alonso, E., Fernández, A. and Gray, J (2012). Rescorla & Wagner Simulator © Version 4.0 2012.

Pearce, J.M. (2002). Evaluation and development of a connectionist theory of configural learning. *Animal Learning & Behavior*, 30 (2): 73-95.

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