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File Settings Help

Phases − +

Groups − +

Group Name	Phase 1	Random
BICOND	60AX+/60AY-/60BX-/60BY+	☑
SIMPLE	60AX+/60AY-/60BX+/60BY-	☑

Set Parameters

Clear All

CS α	Value
A	.35
B	.35
X	.35
Y	.35

US	Value
β+	0.35
β-	0.35
λ+	1
λ-	0

```
------------------------
BICOND
------------------------
(Phase 1 , Seq: 60AX+/60AY-/60BX-/60BY+ Rand: tr

Cue : A

V1 = 0.0
V2 = 0.059520643
V3 = 0.10577026
```

Run

Display Figures

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Esther Mondragón, Eduardo Alonso & Alberto Fernández

Bicond-Simple-Discrim.

CS alpha:

A	0.35
B	0.35
X	0.35
Y	0.35
c(AX)	0.1225
c(AY)	0.1225
c(BX)	0.1225
c(BY)	0.1225

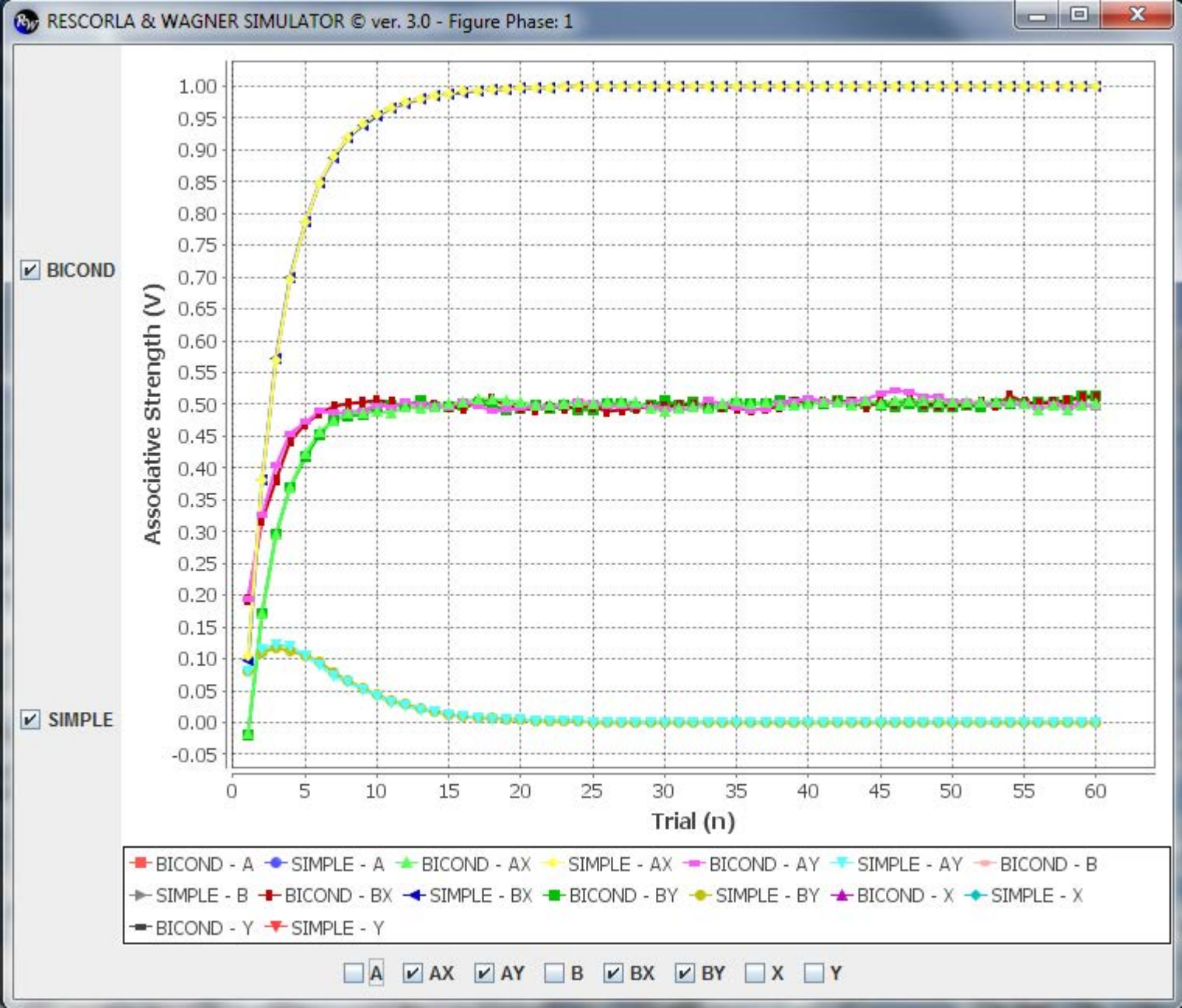
US:

beta+	0.35
beta-	0.35
lambda+	1
lambda-	0

BICOND

Phase 1 Random : true Sequence : 60AX+/60AY-/60BX-/60BY+

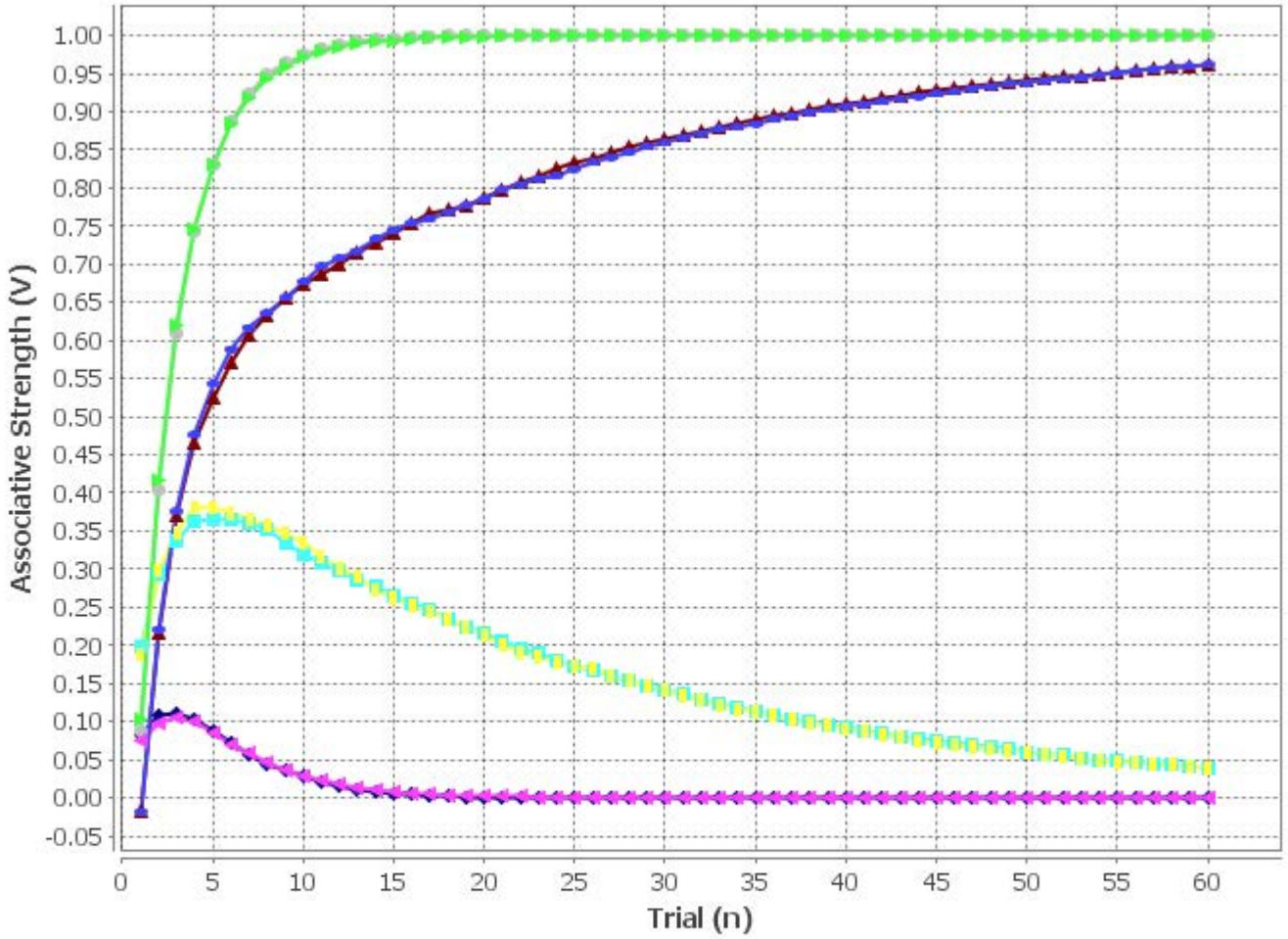
	Trial 1	**Trial 2**	**Trial 3**	**Trial 4**	**Trial 5**	**Trial 6**	**Trial 7**	**Trial 8**	**Trial 9**	**Trial 10**	**Trial 11**	**Trial 12**	**Trial 13**	**Tria**
A	0	0.058475698	0.102336767	0.138011609	0.159818165	0.176949444	0.191733637	0.201554425	0.206461438	0.21067853	0.215818815	0.217604302	0.221936072	0.223
B	0	0.056190673	0.10102235	0.136272811	0.161837435	0.177159148	0.189517629	0.199228716	0.207606998	0.215976446	0.223651078	0.22859338	0.231128649	0.232
X	0	0.060957318	0.100547524	0.130190687	0.155077981	0.174857102	0.188049892	0.195339266	0.207633923	0.212896591	0.218460781	0.220224523	0.220971586	0.222
Y	0	0.060590432	0.106831962	0.140155448	0.165043828	0.18248823	0.193459116	0.203192494	0.211646213	0.215601118	0.219722465	0.22278784	0.22480838	0.226
[AX]	-0.01916165	0.219403222	0.370803924	0.465994429	0.532029177	0.57285627	0.608154806	0.628432983	0.652937215	0.67283747	0.688449903	0.702717476	0.720694207	0.733
[AY]	0.199535388	0.301917943	0.350839349	0.373086249	0.379117667	0.368962849	0.363908499	0.349868857	0.33644358	0.323738646	0.311242006	0.294527944	0.275831311	0.266
[BX]	0.191283929	0.293867017	0.34940071	0.371006669	0.368689837	0.370458898	0.365359107	0.354189284	0.342545465	0.326730085	0.310162178	0.297104086	0.283837284	0.268
[BY]	-0.01706414	0.222382735	0.374029954	0.472302312	0.539772462	0.580827144	0.619131733	0.644997601	0.664123162	0.679424279	0.694771534	0.711549022	0.720588931	0.732
c(AX)	0	0.043696556	0.077164642	0.104141424	0.127036913	0.147101162	0.165414949	0.182215312	0.198146248	0.213026565	0.227053658	0.240411369	0.253157357	0.265
c(AY)	0	-0.00855508	-0.021499812	-0.03654205	-0.05253812	-0.06879279	-0.08461207	-0.10021465	-0.11521528	-0.1296403	-0.14352059	-0.15686509	-0.16949298	-0.18
c(BX)	0	-0.0082013	-0.020800847	-0.0357814	-0.05168831	-0.06749589	-0.08337932	-0.09904409	-0.11422995	-0.12891659	-0.14292514	-0.15622335	-0.16896168	-0.18


RESCORLA & WAGNER SIMULATOR © ver. 3.0 - Figure Phase: 1
BICOND
SIMPLE
Associative Strength (V)
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
-0.05
0
5
10
15
20
25
30
35
40
45
50
55
60
Trial (n)
BICOND - A
SIMPLE - A
BICOND - AX
SIMPLE - AX
BICOND - AY
SIMPLE - AY
BICOND - B
SIMPLE - B
BICOND - BX
SIMPLE - BX
BICOND - BY
SIMPLE - BY
BICOND - X
SIMPLE - X
BICOND - Y
SIMPLE - Y
A
AX
AY
B
BX
BY
X
Y

RESCORLA & WAGNER SIMULATOR © ver. 3.0 - Figure Phase: 1

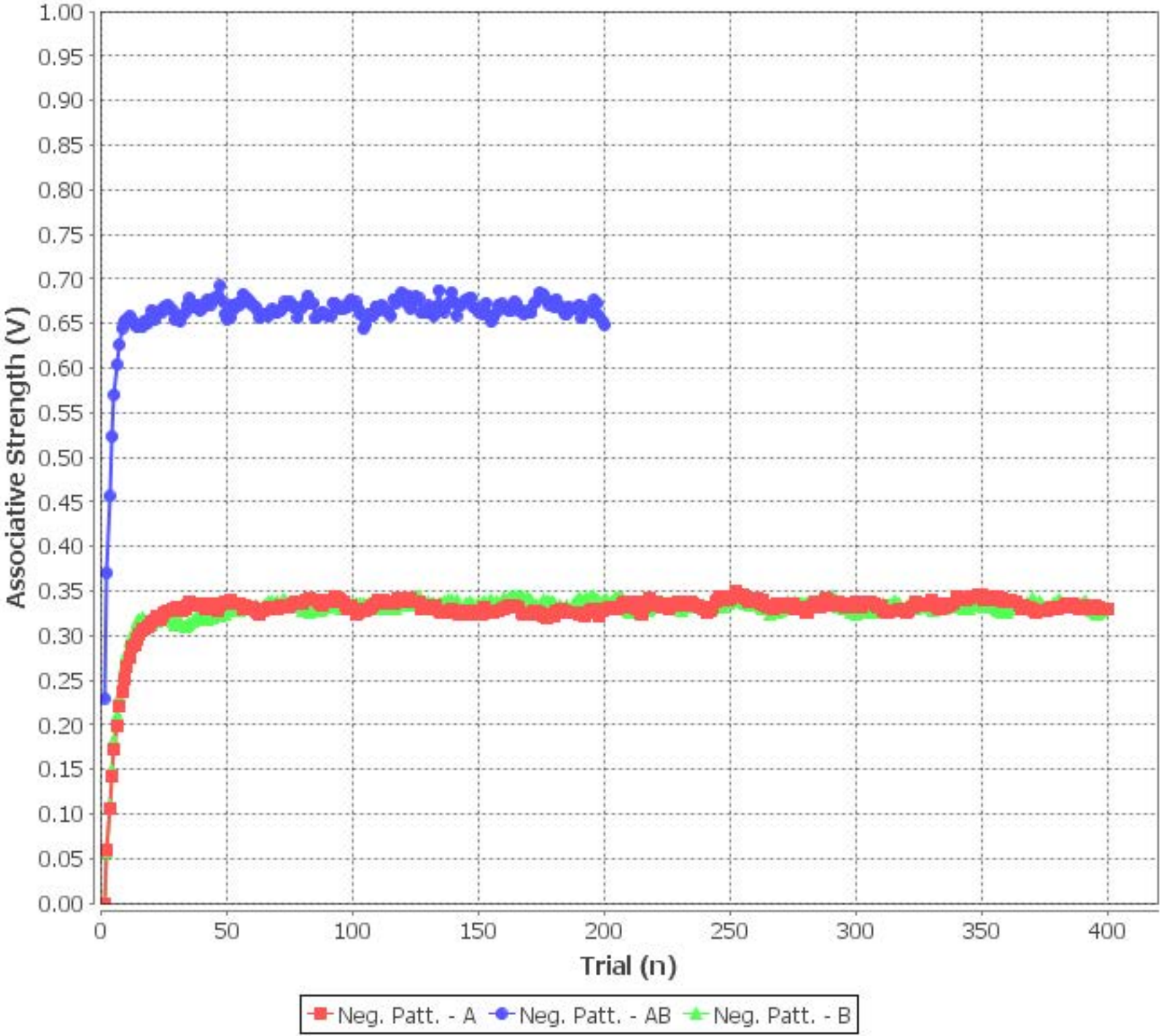
☑ BICOND

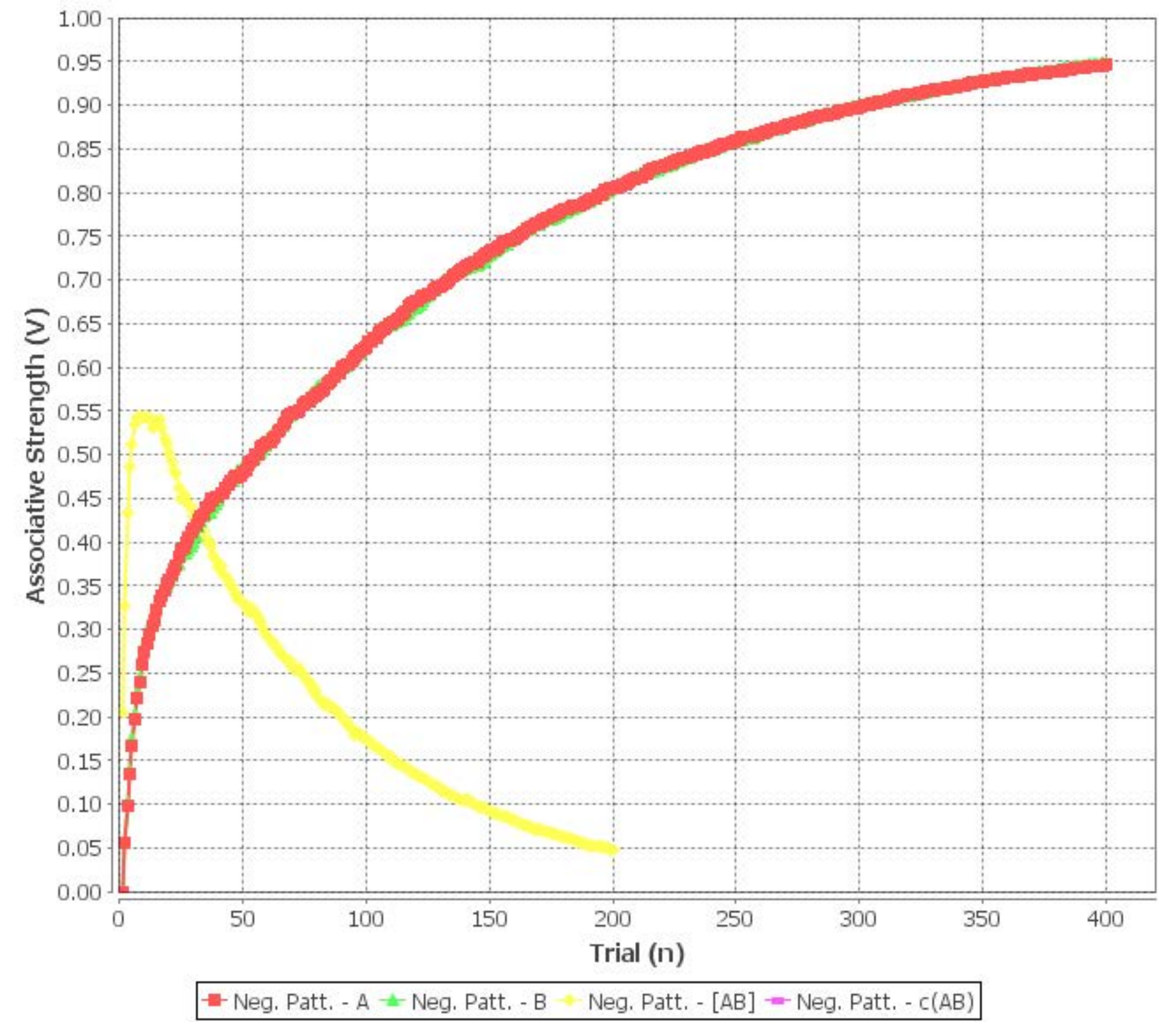
☑ SIMPLE



BICOND - A SIMPLE - A BICOND - B SIMPLE - B BICOND - X SIMPLE - X BICOND - Y
SIMPLE - Y BICOND - [AX] SIMPLE - [AX] BICOND - [AY] SIMPLE - [AY] BICOND - [BX]
SIMPLE - [BX] BICOND - [BY] SIMPLE - [BY] BICOND - c(AX) SIMPLE - c(AX) BICOND - c(AY)
SIMPLE - c(AY) BICOND - c(BX) SIMPLE - c(BX) BICOND - c(BY) SIMPLE - c(BY)

☐ A ☐ B ☐ X ☐ Y ☑ [AX] ☑ [AY] ☑ [BX] ☑ [BY] ☐ c(AX) ☐ c(AY) ☐ c(BX) ☐ c(BY)


1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Associative Strength (V)
0
50
100
150
200
250
300
350
400
Trial (n)
Neg. Patt. - A
Neg. Patt. - AB
Neg. Patt. - B


Associative Strength (V)
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
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0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0
50
100
150
200
250
300
350
400
Trial (n)
Neg. Patt. - A
Neg. Patt. - B
Neg. Patt. - [AB]
Neg. Patt. - c(AB)

A Java simulator of Rescorla and Wagner's prediction error model and configural cue extensions

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Abstract

In this paper we present the "R&W Simulator" (version 3.0), a Java simulator of Rescorla and Wagner's prediction error model of learning. It is able to run whole experimental designs, and compute and display the associative values of elemental and compound stimuli simultaneously, as well as use extra configural cues in generating compound values; it also permits change of the US parameters across phases. The simulator produces both numerical and graphical outputs, and includes a functionality to export the results to a data processor spreadsheet. It is user-friendly, and built with a graphical interface designed to allow neuroscience researchers to input the data in their own "language". It is a cross-platform simulator, so it does not require any special equipment, operative system or support program, and does not need installation. The "R&W Simulator" (version 3.0) is available free.

Keywords: Java simulator; open-source; platform independent; prediction error learning; classical conditioning; compound stimuli; configural cue.

1. The Rescorla and Wagner Model

In natural environments, there is a constant need for organisms to accommodate their behaviour to dynamic surroundings. Learning to predict the regularities in such sensory rich conditions is the key for adaptive behaviour and decision-making. Predictive learning studies in neuroscience have mostly been conducted within the context of associative learning.

One of the basic principles of associative learning is that repeated pairings of two events will allow an individual to predict the occurrence of one of them upon presentation of the other, as consequence of the formation of a link between them.

Typically, classical conditioning, a fundamental associative paradigm, involves the presentation of two stimuli, an originally neutral stimulus (e.g., a tone or a light), and an unconditioned stimulus (US), or *reinforcer*, that has biological relevance (e.g., food). Learning is conceptualized as the formation of an association between the mental representations of these two stimuli. Once the association is formed, presentation of the first stimulus (the conditioned stimulus, or CS) will not only engender activation of its own mental representation, but will also activate the representation of the other stimulus, the US, by means of the link between them. Behaviorally, the CS comes to elicit a conditioned response (CR), indicating that the US is anticipated, and hence predicted by the CS. This simple idea is at the basis of many learning phenomena. Indeed, associative learning has proved to be relevant to human learning both theoretically (judgment of causality and categorization, e.g., [1]) and practically, as the core of a good number of clinical models [2][3].

Rescorla and Wagner's model of classical conditioning [4] is regarded by many as one of the most influential models of learning [5][6][7][8]. As any other model, it has its limitations; but since its publication in 1972 it has become probably the most widely known and cited associative learning model - not only in the field of learning, but also in the many related areas that exploit associative principles. It is still influential to the extent that, even when new models are developed to accommodate phenomena that it cannot explain, they are often based on the same underlying rules (see below). The model assumes that learning occurs only if a US is surprising or, more precisely, unpredicted. The amount of growth in associative strength (V), a concept that represents the weight of the CS-US link on a particular CS-US pairing, is proportional to the degree to which the US is unexpected. With each CS-US pairing (trial) the discrepancy between the expected outcome, the US, and the outcome itself is reduced, increasing the associative strength between the elements, until the CS fully predicts the US, at which point the US is no longer surprising. Thus large error prediction during early conditioning trials produce large increases in associative strength, but these changes decrease in size as learning progresses, and the ability of the CS to predict the US grows, until it approaches asymptotic levels.

Formally, learning on trial n is defined as $\Delta V^n = \alpha\beta\ (\lambda - V^{n-1}(total))$, where α and β represent the salience of the CS and of the US respectively, λ is the maximum amount of learning that can occur for that given US, and $V^{n-1}(total)$ the cumulative amount of learning up to trial $n-1$ −in other words the sum of associative strengths of all CSs that are present on trial n. The associative strength of each of the CSs is determined on the last trial on which each CS occurred, ordinarily trial $(n-1)$. This delta rule is also known as the *error correction rule*: the change in associative strength, learning, is proportional to the prediction error –the difference between the predicted and the actual

reinforcement –and the resultant change in strength reduces the error. Once the increase in associative strength has been computed, it is then used to calculate the new associative strength of the CS using the *update rule* $V^n = V^{n-1} + \Delta V^n$. Obviously, as the prediction improves, the prediction error is reduced until there is nothing left to be learned.

This deceptively simple model (it represents a linear discrete system of the 1st order) predicts a good number of well-established conditioning results. Table 1 shows the full list of phenomena evaluated by Miller, Barnet and Grahame's exhaustive assessment of the Rescorla and Wagner's model [9] classified into 3 categories: Successful predictions, wrong predictions and prediction failures of the model. It is worth noting that this model was not only able to explain most of the conditioning effects known at the time of its publication, but it was able to predict critical and previously undiscovered phenomena, e.g., superconditioning and overexpectation. Some of the model's initial shortcomings are easily dealt with by incorporating minor modifications, as in the case of negative patterning. Other limitations, however, such as the failure to correctly predict the conditions that result in extinction of inhibition, have proved resistant to an explanation in the specific terms of the model. These inadequacies of the Rescorla and Wagner's model have spurred the development of new models that are nonetheless based on the same underlying principles. One critical problem, as Rescorla himself has acknowledged, is the notion that common error value will predict equal associative changes for equally salient stimuli in a given trial - but this is not always the case [10]. Later elemental models of conditioning, such as SGL and its subsequent modifications, make use of a "constrained" error correction-rule to overcome this flaw [11][12]. Other problems related to stimulus generalization have been addressed by the formulation of configural learning models [13]. Moreover, to

overcome the Rescorla Wagner model's inability to account for some temporal phenomena, real-time extensions, notably Temporal Difference [14], have been proposed. Models that incorporate the idea that attention modulates associative strength have also been developed on the basis of Rescorla and Wagner's rule [15][16][17]. Similarly, further elaborations of the model include changes in the associative strength of associatively activated stimuli rather than exclusively of the stimuli physically present on a given trial [18].

Table 1 about here.

In summary, many other classical conditioning models have been advanced since Rescorla and Wagner's in an attempt to conquer its limitations. It is probably safe to say, however, that none of these more recent theories has achieved the universal appeal of their predecessor. For example, predictions based on Rescorla and Wagner's principles are also common in tangential areas of research ranging from drug-reward studies [19] to category learning [20] and geometry learning [21]. Thus, despite its age, the model is far from being obsolete; indeed a significant number of results support the model [22][23][24], others do not [25].

Significantly, the Rescorla and Wagner's model has recently attracted considerable attention in quite a range of brain sciences. There is increasing research that shows that dopaminergic neurons (DA) in several midbrain structures encode reward prediction error [26][27][28]. For instance, DA firing rates in the ventral tegmental area (VTA) parallel CR acquisition in associative learning –as learning

progresses, activation produced by predicted rewards diminishes, while reward-predicting stimuli start generating activation [29]– and stimulus blocking [30].

As an *error correction* model, Rescorla and Wagner's account is central to reward based models of schizophrenia (*e.g.*, [31][32]). These models suggest that patients with schizophrenia show impaired ability to form (or maintain) task-setting information.

Biconditional discriminations are good examples of task-setting procedures and have been used to test these types of cognitive deficiencies in schizotypal populations [33]. In a biconditional discrimination [34] [35] reinforcement is conditional to particular combinations of stimulus, such that two compound stimuli AX and BY signal the US (AX+, BY+) whereas a different combination of the same stimuli, AY and BX, do not (AY−, BX−).

It is well known, though, that the original version of Rescorla and Wagner's model assumes that the associative strength of any compound stimulus is equivalent to the sum of the associative strengths of each component of that compound −the summation assumption. The application of this principle to a biconditional discrimination design would result in each compound stimulus having identical predictive value since individual stimuli are equally associated the US. Therefore, the Rescorla and Wagner model does not predict their discrimination.

To account for the fact that such discriminations can, nonetheless, be solved, one useful adjustment of Rescorla and Wagner's model is to assume that when two stimuli are presented together they create a stimulus compound that consists of the individual elements plus an additional configural cue, a stimulus which is unique to the combination of the elements [36]. This allows a negative patterning discrimination to

be represented as A+, B+, AB*X*−, where *X* represents this configural cue. This assumption results in *X* becoming *inhibitory*, as opposed to excitatory. It can therefore counteract the effect of A and B on compound trials, allowing the discrimination to be solved. A similar representation will allow the model to correctly predict biconditional discriminations. In summary, many current trends in neuroscience take Rescorla and Wagner's predictions as working hypotheses.

In this paper we present a Java simulator of Rescorla and Wagner's model that incorporates configural cues.

2. Why a Java Simulator

A number of simulators of Rescorla and Wagner's model can be found in the literature or on-line. Most of them have become obsolete, because of their system requirements or because the programming languages with which they were developed are outdated, or inaccessible: For instance, [37] [38] [39] [40]. Others are only of limited use as they were designed to fulfill specific tasks [41].

Renner presents a simulator in Excel, a useful tool for teaching undergraduate students the basics of the model [42]; however, Excel is just a spreadsheet application: Even simple programming routines require the definition of VBA macros that are not always intuitive. We have kept Excel for what is effective −to facilitate data processing for statistical analysis, as detailed below.

More recently, Rescorla and Wagner's model has been simulated using MATLAB [43]; indeed, MATLAB is becoming a widespread tool in building simulators of

associative learning models [44] [45] [46].

From the point of view of a programmer, both Java and MATLAB are relatively easy to learn and to use (at least, for simple applications). Speed-wise they are also rather similar, no matter whether they compile or interpret. We believe that the choice between MATLAB and Java is a matter of preference: At the end of the day, having two simulators of Rescorla and Wagner's model at our disposal, one in Java another in MATLAB, can only benefit the associative learning community.

However, as a user, the "R&W Simulator" offers a tool that is already compiled to work in different platforms and does not need any other program to run. The program only requires the user to download and save the executable file ("R&W Simulator.exe" or the "R&W Simulator.app") for their computer platform, PC or Mac respectively. In addition, the Java executable file ("R&W Simulator.jar") is also available and can be run in Linux or any other platform provided that the Java Runtime Environment is installed in the computer. That is, our simulator is a *truly* platform-independent software that can be used in almost any computer and java-based devices.

In short, we have developed our Rescorla and Wagner simulator in Java because it meets the following requirements best: generality, user-friendliness, scalability, fully integrated GUI, Excel export, professional graphical display, free, and platform-independence.

3. The R&W Simulator

The "R&W Simulator" has been built to allow the user to simulate a wide range of procedures, and can compute whole experimental designs at once. It is thus versatile and general. It is not only capable of simulating well-known tasks such as acquisition, extinction, blocking, overshadowing, etc., but it also permits the computation of associative values for elemental stimuli, compound stimuli and configural cue compounds in a single design and display. The user can, moreover, run designs with different US across phases and simulate phenomena such as unblocking [47]. In addition, the simulator allows one to set negative values to non-US λ, that may be useful in simulating categorization experiments in humans involving symmetrical outcomes - that is, for experiments in which outcomes are rated as positive, neutral or negative (e.g., [48]).

The "R&W Simulator" generates both numerical and graphical outputs with a single click. In addition, the user can export the results to a data processor spreadsheet for better manipulation and analysis of data. Its design includes a graphical interface in which the experimental procedure can be entered in a way that resembles standard associative learning designs, so that learning experts can write the program in their own "language".

3.1. Installation

The "R&W Simulator" is available to download at "http://www.cal-r.org/index.php?id=R-Wsim".

Those who *just want to use* the simulator would need to select "PC" or "MAC", depending on which platform they use, and the program will download. Once the file is saved, it is ready to run –it does not require any additional installation. Users of other platforms should select the "JAVA" button to download the "RW_Simulator.jar" file, which will run on any platform provided that the Java Runtime Environment (JRE) is installed in their computer. Most popular Linux distributions such as Fedora, Debian, Ubuntu, Arch, and CentOS already include JRE.

Users who wish to *access the code* should also download the "RW_Simulator.jar" file, and uncompress it. A folder named "R&W Simulator.jar" containing the ".class" files will appear. The content of these files can be accessed using a Java editor such as Eclipse or NetBeans, and the Java Development Kit (JDK).

3.2. Starting the simulator and creating a new experiment[1]

To start the simulator the user needs to navigate to the directory in which the file was stored and double click on the file's icon. The opening screen should look like in Figure 1 (PC version, Mac's GUI differs slightly).

This window is headed by the main menu ("File", "Settings", and "Help"), and consists of two input panels and one output panel. The experimental design is specified in a matrix of groups and phases in the top panel; in the bottom left panel the values of the parameters are entered; the output data is displayed on the right.

[1] Step-by-step instructions to use the simulator are available as a "Guide" in the "Help" menu.

The user can choose to create a new experiment, or to load one that they may have previously saved. Assuming that this is the first time one uses the simulator, we are creating a new experiment: We are using a design similar to the one used by Haddon *et al*. [33] for testing setting-task deficiencies in schizotypal populations. Our design is between groups rather than within subjects to better show the simulator's capabilities. Group BICOND describes a biconditional discrimination (AX+, AY−, BX−, BY+), and Group SIMPLE a compound simple discrimination in which cues A and B are uninformative (AX+, AY−, BX+, BY-).

Figure 1 about here.

The experimental design is entered describing each trial type as follows: Number of trials followed by stimuli followed by reinforcer. Different trials should be separated by a slash symbol without spaces between the characters. Thus the biconditional discrimination depicted above would read “60AX+/60AY−/60BX−/60BY+” in “Group BICOND” and “60AX+/60AY−/60BX+/60BY−” in “Group SIMPLE”. The order of the trials is by default defined by the order in which they are entered in each phase; thus, in the example, 60 AX+ consecutive trials will be followed by 60 AY− trials and so forth. Alternatively, if the design requires that the different types of trial occur in a random order, the user only needs to tick the “Random” box.

To overcome order bias, the simulator runs a number of different random combinations and generates a mean value per stimulus and trial. By default this number

is set to 1,000, but it can be changed in the "Settings/Number of Random Combinations" menu.

The values of the fixed parameters, α, β and λ, are entered by first pressing the "Set Parameters" button. CS α values are entered at the top. The bottom area contains a set of default values given to the US, which the user can modify at will. In addition the user can set different US values per phase using the "Settings/Set Different US per Phase" menu. Ticking this option will allow the user to set different US parameters for each phase in the Set Parameters table.

Pressing the "Run" button will produce a text output on the right hand side. Cue mean stimulus V values per trial will be displayed for each group in each phase; in other words, for each elemental and compound stimulus a list of V_i values will be displayed in which *i* represents the trial number for which V is calculated.

3.3. File menu

Experimental designs can be saved and opened using the "File" menu. These files will have a ".res" extension. The simulator includes the option to export the results in ".xlsx" type spreadsheets, like the ones used by Excel; a workbook is created with a different sheet for every group as shown in Figure 2. For the sake of clarity, each sheet contains the name of the file followed by the CS and US parameters. Each phase is presented on a different table, and the phase tables are preceded by the experiment design. This functionality allows the user to prepare the data as required for analysis. It should be noted that exporting results from designs with a large number of trials may take some

time, and attempting to open the exported file before is fully saved will result in an error message.

Figure 2 above here.

3.4. Figures display

A graphical representation of the output is obtained by pressing the "Display Figures" button. A number of figures will pop up, one per phase. Each figure shows the stimulus mean V values per trial. The stimulus and group to be displayed can be enabled or disabled as required. Figures can also be saved, copied, printed, zoomed and modified by right-clicking (Ctrl+Click in Mac) the graph. The window can remain open while the user chooses to run a new experiment so they can compare the figures.

3.5. Compounds and configural cue compounds

The "R&W Simulator" includes the possibility of computing both standard stimulus compounds and configural cue compounds as proposed by [36].

To calculate standard compound associative values "Show Compound Results" must be selected in the "Settings" menu. Running the simulator will produce individual trial values for each stimulus compound (e.g., AX) described in the design, as well as for each of the elemental stimuli. Likewise, compound data will be shown in the figures and in the exported spreadsheets.

For example, we are running a simulation for the design described above for Group BICOND and Group SIMPLE using the following parameters: 240 trials, 60 of each compound, $\alpha = 0.35$ for each CS, $\beta = 0.35$, $\lambda(+) = 1$, and $\lambda(-) = 0$. This simulation produces the graphical output shown in Figure 3 (we have deselected the stimulus V to show only the more relevant compound stimulus data). The simulation predicts that discrimination should develop quickly in Group SIMPLE. That is, the associative value of the reinforced compound stimuli (AX+ and BX+) should increase promptly and remain higher than the associative value of the non-reinforced compound stimuli (AY− and BY−). In contrast, the Rescorla and Wagner model wrongly predicts that there will be no discrimination in Group BICOND, and that all compound stimuli should acquire equal associative strength value.

Figure 3 about here.

In order to compute configural cues, "Use Configural Cues" must be chosen and the parameters redefined to set α values for the configural cues –by default, the product of the α values of the component elements of the corresponding stimulus compound. Configural cues are represented as "c(AX), c(AY), …". Running with these settings will produce associative values for each configural cue compound [AX], which will be displayed in the output and in the figures instead of the standard compound stimuli values.

Figure 4 shows the results of a simulation of the previous design with identical parameters but using configural cues ($\alpha = 0.12$). As before, the simulation predicts that there would be a good discrimination in Group SIMPLE. Now, however, the introduction of configural cues allows the Rescorla and Wagner model to correctly predict the development of a discrimination between the reinforced (AX+ and BY+) and the non-reinforced (AY− and BX−) compound stimuli in Group BICOND.

Figure 4 about here.

3.6. Test

The simulator has been thoroughly tested against phenomena that the Rescorla and Wagner model successfully accounts for, and also against some it notoriously does not. In this we have followed an exhaustive review of the model by Miller and collaborators [9]. For example, the simulator accurately predicts extinction and acquisition curves, blocking, overshadowing, conditioned inhibition and positive patterning discrimination; and, without choosing the configural cue option, fails to predict biconditional discriminations (Figure 3) −because, as is well-known, the Rescorla and Wagner model can only solve non-linear discriminations by including configural cues (Figure 4). Negative patterning [49] is another prototypical case of non-linear discriminations that are not correctly predicted by the model without assuming configural cues. In negative patterning procedures, two stimuli A and B are reinforced when presented alone, but nonreinforced when presented in compound (i.e., A+, B+, AB−); solution of this discrimination requires the organism to withhold responding to the compound of A and

B while responding to A and B alone. According to the summation assumption, if A and B predict the US individually, a compound of A and B *must* predict the US *even more* –the opposite of what is found. A simulation of a negative patterning discrimination without configural cues is shown in Figure 5. The simulation was run for a total of 600 trials, 200 each type, $\alpha = 0.35$ for each stimulus, $\beta = 0.35$, $\lambda(+) = 1$, $\lambda(-) = 0$.

An inspection of the simulation results clearly shows that the Rescorla and Wagner model wrongly predicts more responding to the compound stimulus AB.

Figure 5 about here.

An identical negative patterning discrimination design was simulated next using the same parameters, but including configural cues ($\alpha = 0.12$). Figure 6 displays the results of this simulation. As can be seen, the model now predicts a correct solution for the negative patterning discrimination: that is, the individual stimuli predict the outcome better than the stimulus compound.

Figure 6 about here.

4. Conclusions

The "R&W Simulator" (version 3.0) provides an easy-to-use yet specialized, fast and free tool to test the predictions of the original Rescorla and Wagner model, as well as modifications involving configural cue compounds. Users will be able to enter whole designs, save figures, and export the data for further analysis and manipulation. The simulator runs in all computer platforms and does not require installation.

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Table and Figures Captions

Table 1. Predictive power of the Rescorla and Wagner's model.

Figure 1. Main GUI of the "R&W Simulator" showing a design with two groups (BICOND and SIMPLE) for a biconditional and a simple discrimination, respectively.

Figure 2. Screenshot of the ".xlsx" spreadsheet containing the experimental data and the design of the biconditional and simple discrimination simulation.

Figure 3. Mean compound stimulus associative strength values across discrimination training for Group BICOND and Group SIMPLE.

Figure 4. Mean configural cue compound associative strength across discrimination training for Group BICOND and Group SIMPLE.

Figure 5. Mean stimulus and compound stimulus associative strength across a negative patterning training discrimination.

Figure 6. Mean stimulus and configural cue compound associative strength across a negative patterning training discrimination.