Korea University Conditioning Simulator v1.3

GUI-based easy to use association learning model simulation script.

* The concept

The main purpose of this script is to easily compare existing association learning models. Starting from three major models (Rescorla & Wager, 1972; Mackintosh, 1975; Pearce & Hall, 1980), I included three more recent models for comparison (Schmajuk & Moore, 1985; Esber & Haselgrove, 2011; Sutton & Barto, 1987). Although this collection does not include some of influential models such as SOP model, this script will serve as a good starting point of differentiating learning models.

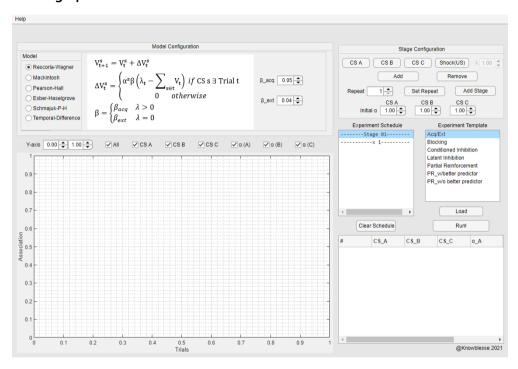
Originally, I wrote this script for my personal purpose and maybe for student homework when I get a chance to manage a semester-length course on associative learning. By the point of writing this documentation, I'm not sure if anyone could use this script, because the learning model is an old topic and it seems no one is interested in it while busy doing their optogenetic experiments. However, I'm writing this doc for those who are fascinated by this field and hoping to find a nice simulator for all those models.

If you ever read this doc or use the simulator that I wrote, any kind of response, reply, email, Github star, criticism, questions, etc..., are always welcome.

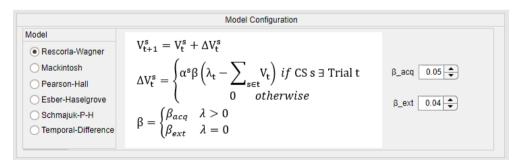
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* Windows

Korea University Conditioning Simulator (KUCS) has 5 areas in its GUI: **Model configuration, Stage configuration, Experiment section, Result table,** and **Result graph**.



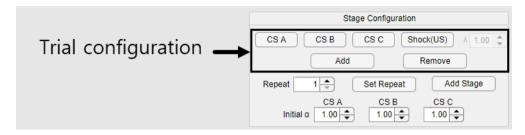
* Model Configuration



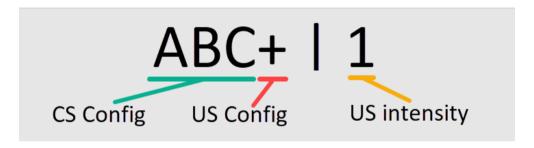
The **Model Configuration** window manages which associative learning model to use in the simulation. By clicking the left side radio button, you can switch between six models. Each model section is filled with model's equation box and changeable parameter GUI. Default values are carefully selected to simulate most of the learning phenomena, but you can always change manually. Keep in mind that some

of the parameters has minimum and maximum values.

* Stage Configuration



The **Stage Configuration** manages the experiment schedule. There are four buttons at the top which can toggled on/off, each representing the presence of CSs and US. When you choose to give the US, you can change the lambda value (the intensity of the US) manually. After selecting the proper configuration of a single trial, you can click **Add** button to add the trial in the experiment schedule. Each added trials will be appeared in the bottom Experiment Schedule section with a short notation.



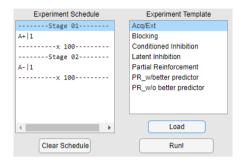
The purpose of "Stage" is to repeatedly present the same trial. After adding trial(s) in the stage you can set the amount of Repeat and click the **Set Repeat** button. You can always add more stages by clicking the **Add Stage** button.

To remove a trial or a stage, click the target text in the Experiment schedule, and click the **Remove** button. If you want to remove a stage, you can either select the Stage XX line or the corresponding ending line of the target stage.

Since **Add**, **Remove**, **Set Repeat**, **Add Stage** buttons are linked with the current selection in the Experiment schedule box, so beware when you add or delete element in experiment schedule.

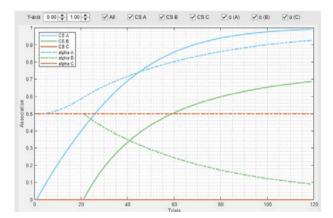
* Experiment Template

I included some of the basic Experiment schedules in the **Experiment Template** box. Click the desire schedule template and click the **Load** button. Caution is needed, because this will overwrite the current experiment schedule.



* Running the simulation

After configuring the experiment schedule, click the **Run!** button to show the simulation result. You can change the current model using the radio button in the **Model Configuration** box, and press the **Run!** button again to see the result with the newly selected model.



After running the simulation, the result will appear in the left graph panel. The table at the right side shows the raw data used to plot the graph. You can turn on/off the current graph line with the check box button at the top. This is extremely usefully when two values are overlapped with each other.

If the simulation result goes over the current range, especially when you do the conditioned inhibition simulation, you can always manually select the current display range by changing the value in the Y-axis up-down box at the top-left corner of the graph.

* Equations used for the simulation

During the implementation of each learning models, I found that exact mathematical formalization was absent for some models. For example, Mackintosh model only mentions when to increase or decrease the stimulus specific saliency α , not specifying how much to change. I added and fixed original models to implement in a working program and this alternation is colored in green. Although I preserved the most important concept in each model (colored in red) while the implementation, please beware that the green parts are not originated from the original works.

* Notations

Subscript: (usually) time or trial

Superscript: corresponding CS

 V_t^s : Strength of association between CS $\,s\,$ and US at time $\,t\,$

 $\alpha_t^s\,$: Stimulus specific learning rate. Usually referred as acquired saliency or attention.

 λ : Strength of US. US saliency

If any variable has s or t in the sub/superscript, then it is stimulus/trial specific. If not, it is constant across stimulus/trial.

* Rescorla-Wagner Model

$$\begin{split} & V_{t+1}^s = V_t^s + \Delta V_t^s \\ & \Delta V_t^s = \begin{cases} \alpha^s \beta_t \left(\lambda_t - \sum_{s' \in t} V_t^{s'} \right) \text{ if CS s \exists Trial t} \\ & 0 \text{ otherwise} \end{cases} \\ & \beta_t = \begin{cases} \beta_{acq} & \lambda_t > 0 \\ \beta_{ext} & \lambda_t = 0 \end{cases} \end{split}$$

 α^s : saliency of CS s

 $\begin{array}{l} \beta_t \; : \text{learning rate at Trial t} \\ \lambda_t \; : \text{US saliency in the Trial t} \end{array}$

 $\textbf{A}_t:$ US saliency in the Trial t $\sum_{s'\in t}V_t^{s'}:$ sum of ~V~ of all CSs exist in the Trial ~t~

* Mackintosh Model (Explainability)

$$\begin{split} & V_{t+1}^s = V_t^s + \Delta V_t^s \\ & \Delta V_t^s = \left\{ \begin{matrix} \alpha_t^s \beta_t (\lambda_t - V_t^s) & \text{if CS s } \exists \text{ Trial } t \\ & 0 & \text{otherwise} \end{matrix} \right. \\ & \beta_t = \left\{ \begin{matrix} \beta_{acq} & \lambda_t > 0 \\ \beta_{ext} & \lambda_t = 0 \end{matrix} \right. \\ & \alpha_{t+1}^s = \alpha_t^s + \Delta \alpha_t^s \end{split} \\ & D_t^s = \left. |\lambda_t - V_t^s|, \qquad D_t^{X_s} = \left| \lambda_t - \left(\left(\sum_{s' \in t} V_t^{s'} \right) - V_t^s \right) \right| \\ & \Delta \alpha_t^s = \left\{ \begin{matrix} D_t^s < D_t^{X_s} & k \cdot (1 - \alpha_t^s) \cdot (D_t^{X_s} - D_t^s)/2 \\ D_t^s = D_t^{X_s} & k \cdot \alpha_t^s \cdot (D_t^{X_s} - D_t^s)/2 \end{matrix} \right. \end{split}$$

 $k : proportional parameter (0 \le k)$

 $\varepsilon\,$: small value to make $\,\Delta\alpha_t^s\,$ negative when $\,D_s=D_X\,$

This implementation is similar to the Moore & Stickney (1980), but added ϵ for the latent inhibition. Read the article to know how they explain the latent inhibition without the ϵ .

* Pearson-Hall Model (Uncertainty)

$$\begin{split} \dot{V}^s_t &= V^s_t - \overline{V}^s_t \\ V^s_{t+1} &= V^s_t + \Delta V^s_t \quad \Delta V^s_t = \left\{ \begin{matrix} S^s \alpha^s_t \lambda_t & \text{if CS s \exists Trial t} \\ 0 & \text{otherwise} \end{matrix} \right. \\ \overline{V}^s_{t+1} &= \overline{V}^s_t + \Delta \overline{V}^s_t \quad \Delta \overline{V}^s_t = \left\{ \begin{matrix} S^s \alpha^s_t \overline{\lambda}_t & \text{if CS s \exists Trial t} \\ 0 & \text{otherwise} \end{matrix} \right. \\ \overline{\lambda}_t &= \left(\sum_{s' \in t} (V^{s'}_t) - \sum_{s' \in t} \left(\overline{V}^{s'}_t \right) \right) - \lambda_t \\ \alpha_{t+1} &= \left| \lambda_t - \left(\sum_{s' \in t} (V^{s'}_t) - \sum_{s' \in t} \left(\overline{V}^{s'}_t \right) \right) \right| \end{split}$$

 $\begin{array}{l} \dot{V}^s_t \ : \text{net prediction of US (=CR strength)} \\ \overline{V}^s_t \ : \text{association strength between CS} \ s \ \text{and no US in trial} \ t \\ \end{array}$

In the Pearce-Hall model, the α is not stimulus specific or, to put it precisely, remains constant across all CSs. Moreover, the α is bound to the drifting λ value, so this value tend to be fluctuate easily.

* Schmajuk-Pearson-Hall Model

$$\begin{split} \dot{V}_{t}^{s} &= V_{t}^{s} - \overline{V}_{t}^{s} \\ V_{t+1}^{s} &= V_{t}^{s} + \Delta V_{t}^{s} \quad \Delta V_{t}^{s} = \begin{cases} S^{s} \alpha_{t}^{s} \beta_{ext} \lambda_{t} & \lambda_{t} - \sum_{s' \in t} \dot{V}_{t}^{s'} > 0 \\ 0 & \text{otherwise} \end{cases} \\ \overline{V}_{t+1}^{s} &= \overline{V}_{t}^{s} + \Delta \overline{V}_{t}^{s} \quad \Delta \overline{V}_{t}^{s} = \begin{cases} S^{s} \alpha_{t}^{s} \beta_{inh} \overline{\lambda}_{t} & \lambda_{t} - \sum_{s' \in t} \dot{V}_{t}^{s'} \leq 0 \\ 0 & \text{otherwise} \end{cases} \\ \overline{\lambda}_{t} &= \left(\sum_{s \in t} \dot{V}_{t} \right) - \lambda_{t} \\ \alpha_{t}^{s} &= \begin{cases} \gamma \left| \lambda_{t} - \sum_{s' \in t} \dot{V}_{t-1}^{s'} \right| + (1 - \gamma) \alpha_{t-1}^{s} & \text{if CS s } \exists \text{ Trial t} \\ \alpha_{t-1}^{s} & \text{otherwise} \end{cases} \end{split}$$

γ : proportional parameter

 β_{ext}, β_{inh} : excitatory/inhibitory rate parameter $\beta_{inh} < \beta_{ext} \le 1$

Schmajuk-Pearce-Hall model is an advanced version of the PH model and by introducing the recurrence relationship to the α , the fluctuation is dampened.

* Esber-Haselgrove Model (Uncertainty)

$$\begin{split} \dot{V}_{t}^{s} &= V_{t}^{s} - \overline{V}_{t}^{s} \\ V_{t+1}^{s} &= V_{t}^{s} + \Delta V_{t}^{s} \quad \Delta V_{t}^{s} = \begin{cases} \alpha_{t}^{s} \beta_{1} \left(\lambda_{t} - \left(\sum_{s' \in t} V_{t}^{s'} - \sum_{s' \in t} \overline{V}_{t}^{s'} \right) \right) & \text{if CS s } \exists \text{ Trial } t \\ 0 & \text{otherwise} \end{cases} \\ \overline{V}_{t+1}^{s} &= \overline{V}_{t}^{s} + \Delta \overline{V}_{t}^{s} \quad \Delta \overline{V}_{t}^{s} = \begin{cases} \alpha_{t}^{s} \beta_{2} \left(\left(\sum_{s' \in t} V_{t}^{s'} - \sum_{s' \in t} \overline{V}_{t}^{s'} \right) - \lambda_{t} \right) & \text{if CS s } \exists \text{ Trial } t \\ 0 & \text{otherwise} \end{cases} \\ V_{t+1}^{pre \to s} &= V_{t}^{pre \to s} + \Delta V_{t}^{pre \to s} \quad \Delta V_{t}^{pre \to s} = \begin{cases} \beta_{t}^{pre \to s} \left(1 - V_{t}^{pre \to s} \right) & \text{if CS s } \exists \text{ Trial } t \\ \beta_{t}^{pre \to s} \left(- V_{t}^{pre \to s} \right) & \text{otherwise} \end{cases} \\ \alpha_{t}^{s} &= \varphi^{s} + \varepsilon_{t}^{s} - k V_{t}^{pre \to s} \\ \varepsilon_{t}^{s} &= f \left(V_{t}^{s} + \overline{V}_{t}^{s} \right), \quad f(x) = x \end{cases} \\ \beta_{1} &= \begin{cases} \beta_{1}_{acq} & \Delta V_{t}^{s} \geq 0 \\ \beta_{1}_{ext} & \Delta V_{t}^{s} < 0 \end{cases} \quad \beta_{2} = \begin{cases} \beta_{2}_{acq} & \Delta \overline{V}_{t}^{s} \geq 0 \\ \beta_{2}_{ext} & \Delta \overline{V}_{t}^{s} < 0 \end{cases} \end{cases}$$

$$0 \leq V, \overline{V}, \alpha \cdot \beta \leq 1, \quad \beta_{1acq} \cdot \beta_{2acq} > \beta_{1ext} \cdot \beta_{2ext}, 0 \leq k \leq 1$$

 ϕ : unacquired properties of the cue (0 $\leq \phi \leq 1$)

 ϵ : acquired salience of the cue

Esber-Haselgrove model clearly described how each component is updated and changed throughout the experiment. And also, they mentioned conditions of parameters which result successful simulation. However, the original work refrained the formalization of the $\Delta V_t^{\mathrm{pre} \to \mathrm{s}}$, and I used the most basic form, RW model, to fill the blank.

* Temporal Difference Model

$$\begin{aligned} & w_{t+1}^S = w_t^S + \Delta w_t^S \\ & \Delta w_t^S = c(\lambda_t + \gamma \max(\boldsymbol{w_t^T}\boldsymbol{x_t}, 0) - \max(\boldsymbol{w_t^T}\boldsymbol{x_{t-1}}, 0)) \boldsymbol{\bar{x}_t^S} \\ & \boldsymbol{\bar{x}_t^S} = \beta \boldsymbol{\bar{x}_{t-1}^S} + (1 - \beta) \boldsymbol{x_{t-1}^S} \end{aligned}$$

 \bar{x}_t^s : eligibility trace of CS s in trial t

 w_t^s : weight of CS s in trial t. analogue of V_t^s

 \mathbf{w}_{t} : weight vector of all CS in trial t

 \mathbf{x}_t : CS vector of all CS in trial t

c: learning rate

 β : eligibility trace parameter

 $\gamma\,$: relative importance between presence and onset/offset of the CS

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Short version: Do whatever you want, but please put my name on it.