Fitting ACT-R Models with Trial-by-Trial Maximum Likelihood

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Fitting models

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Fitting models

- We all do. That's part for the job!
- But what do we **fit for**?
- In most cases, we **minimize** *RMSE* or R^2
- Suggestion: We should use Maximum Likelihood (MLE)
- In linear models, minimizing RMSE and maximizing log-likelihood are the same
  - … and they both maximize R^2
- When we use **non-linear** models, however, things are different
- And ACT-R has several non-linear equations

What is MLE?

Find parameters θ of a model that maximize likelihood $\mathcal{L}$

$$\mathcal{L}(\underbrace{m}_{\text{model}}, \underbrace{\theta}_{\text{parameters}} \mid \underbrace{x}_{\text{data}}) = P(x \mid m, \theta)$$

In practice, you use **log**-likelihood, because probs become vanishingly small when there are series of products

$$\log \mathcal{L}(m, \theta \mid x) = \log P(x \mid m, \theta)$$

Why would you use log-likelihood?

Intuitively, that is what you are trying to do: Finding the most probable model. But, also:

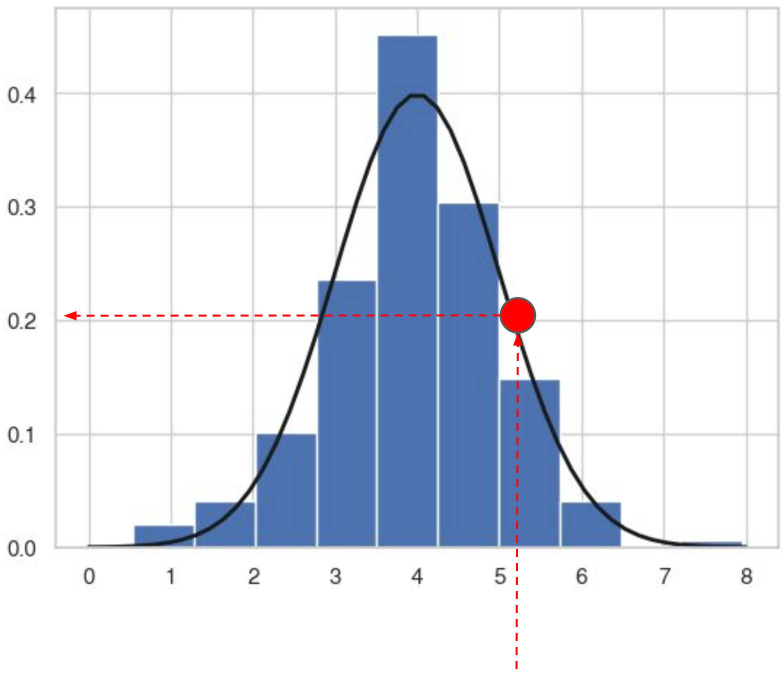
- It allows **comparison** across models with different complexity
  - BIC and AIC are expressed as a function of log likelihood:

$$\textbf{BIC} = k \log(n) - 2 \log \mathscr{L} \qquad \textbf{AIC} = 2k - 2 \log \mathscr{L}$$

- It allows fitting to **individuals** as well as **group** data
  - Group-level log likelihoods are the **sum** of individual log likelihoods!

How to do it – easy way

- Set your values for *m* and θ
- Run many simulations
- Calculate mean and standard deviation
- Compare to subject data point **x**



Participant data

Limits

ACT-R models often takes a long time to run

Necessary to run model many times to get stable data

Aggregated data often contains very few data points

Trial by trial

Trial by trial likelihood

$$\mathcal{L}(m, \theta \mid \mathbf{x}) = P\,(\mathbf{x} \mid m, \theta); \qquad \mathbf{x} = \{x_1, x_2, \ldots\, x_N\}$$

$$P(\mathbf{x}|m, \theta) = P(x_1|m, \theta) \cdot P(x_2|m, \theta, x_1) \cdot \ldots \cdot P(x_N|m, \theta, x_1, x_2 \ldots x_N)$$

ACT-R is a Markov model, and every choice is determined only by the current state.

So, if we force the model to follow the choices:

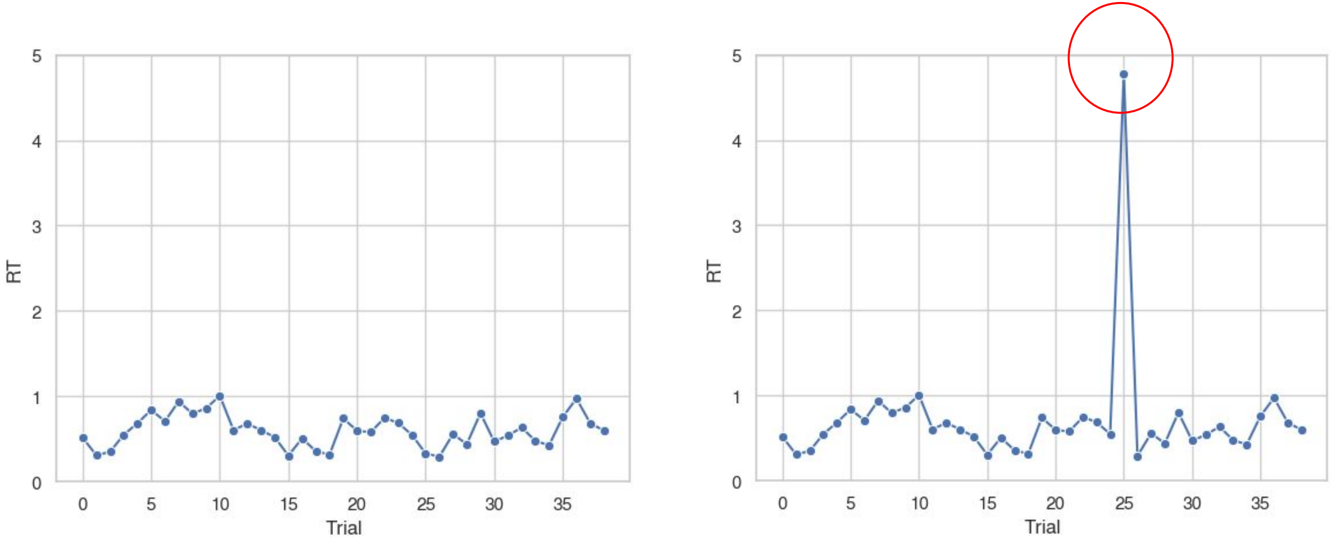
$$P(\mathbf{x}|m, \theta) = P(x_1|m, \theta) \cdot P(x_2|m, \theta) \cdot \ldots \cdot P(x_N|m, \theta)$$

$$\log \mathcal{L} = \textstyle\sum_i \log P(x_i|m, \theta)$$

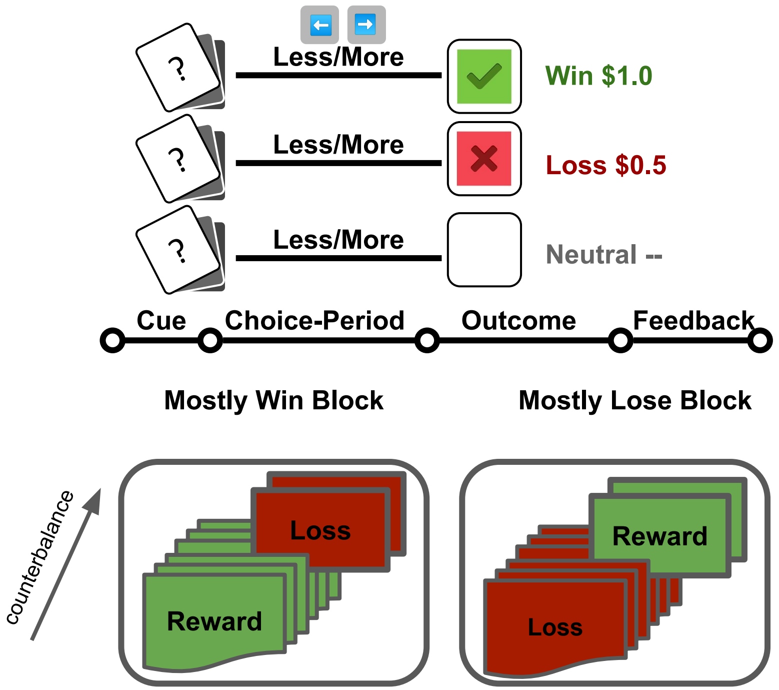
This is just **model tracing**! (Koediger & Anderson, 1993)

Advantages of trial by trial data

- You get **more data points** for every individual
- Aggregated data can be deceiving:



Example: Incentive Processing Task

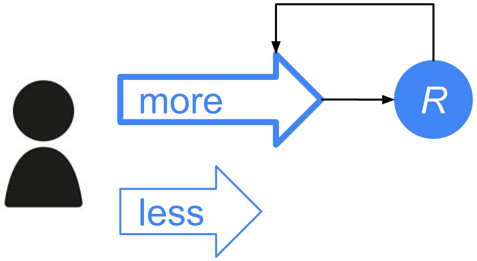


CONNECTOME COORDINATION FACILITY

- *N* = 199 participants
- **2 runs** for each participant
- **4 blocks** per run (2 Win, 2 Loss)
- **8 choices** per block
- **64 trials** total

Two ways to approach the task

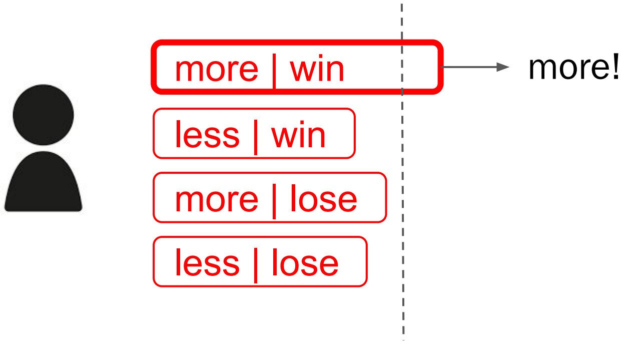
Procedural Memory



$$U_t(p) = U_{t\text{-}1}(p) + \alpha[R - U_{t\text{-}1}(p)]$$

$$P(more) = e^{U(more)/T} \;/\; e^{U(more)/T} + e^{U(less)/T}$$

Declarative Memory



$$A_t(c) = \Sigma_i\,(t - t_i)^{-d}$$

$$P(more) = e^{A(more)/s} \;/\; \Sigma_{chunk} e^{A(chunk)}$$

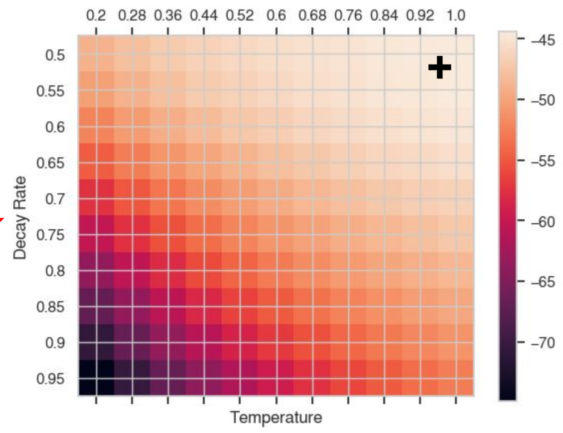
Model-Based Group Assignment

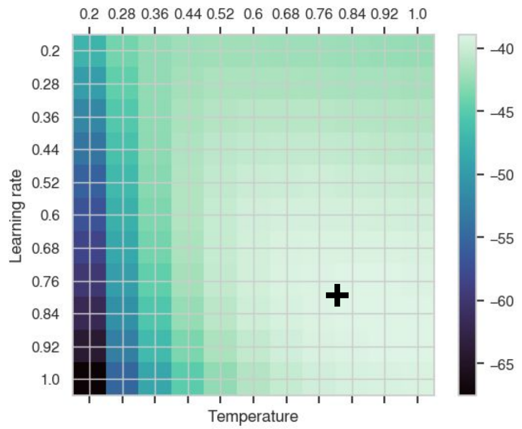
Implemented equations in Python

For every participant:

- Use Powell's method to maximize **Declarative** log-likelihood across parameters (θ)
- Repeat for **Procedural**
- Assign participant to the model with greater likelihood

Total runtime: ~ 20 mins!

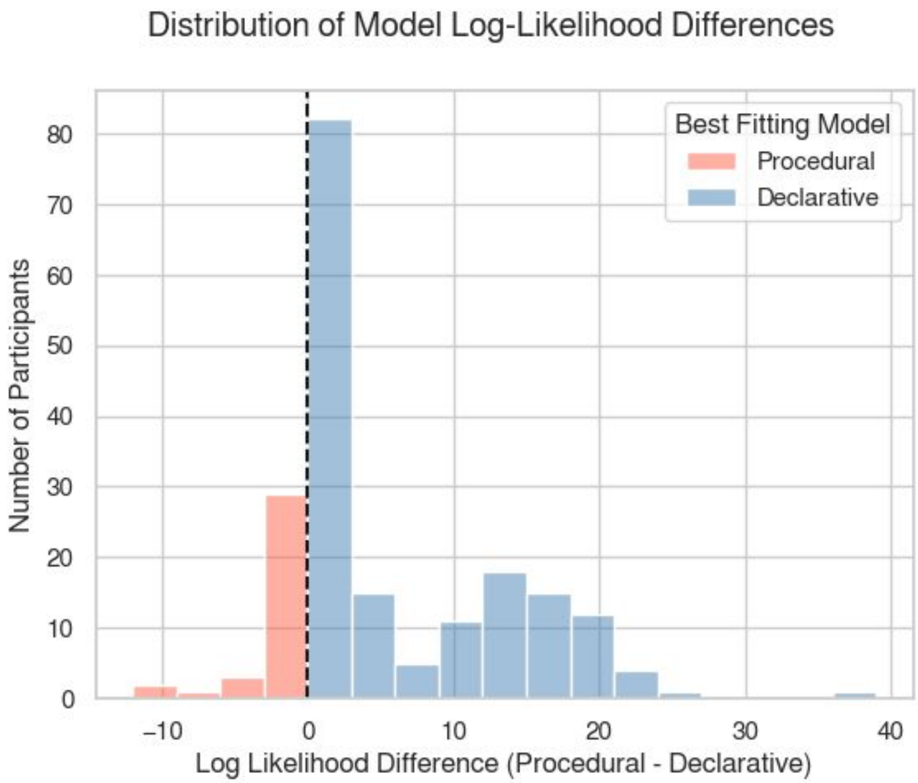




https://github.com/UWCCDL/ProcVsDecl/

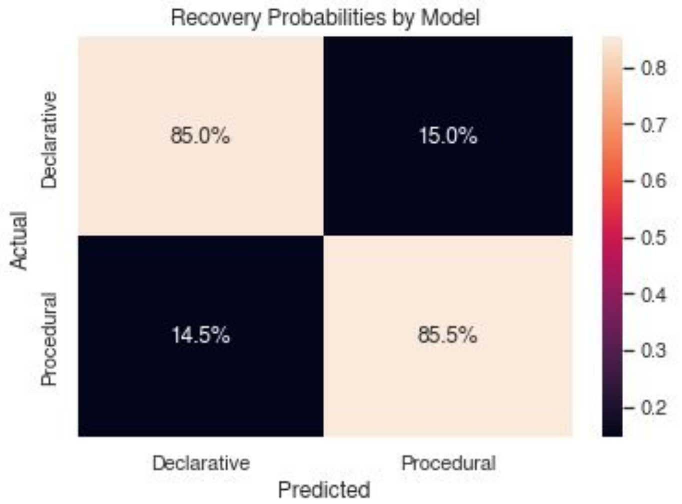
Yang et al, *BioArXiv*

Participant assignments

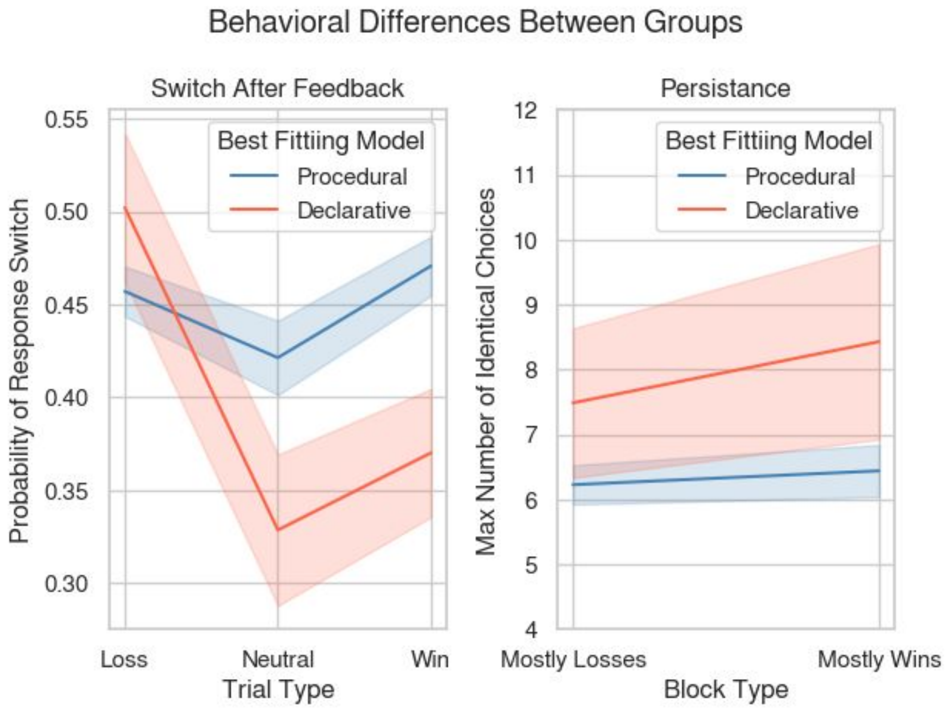


How Reliable are our Models?

- Generated 20,000 simulated runs for each model
  - with random initial params
- Applied trial-by trial MLE to recover model



Differences btw Declarative and Procedural groups



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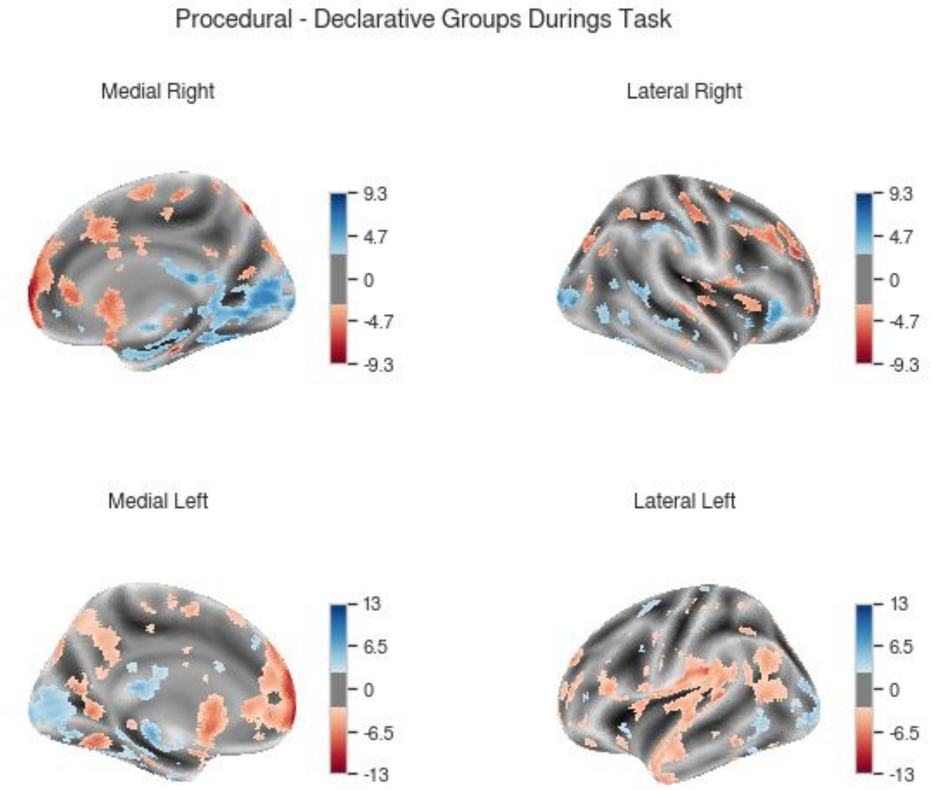
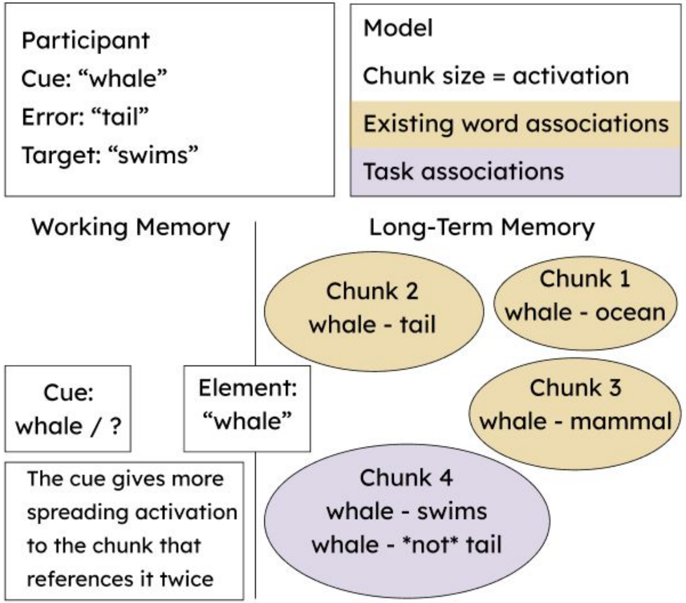


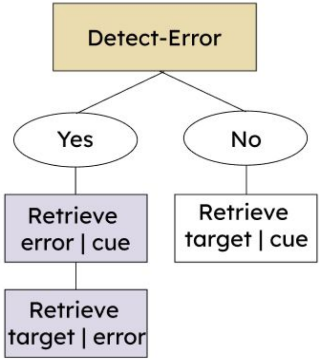
Mixing different measures

Better memory after errors

Elaborative Hypothesis



Mediator Hypothesis



Mediator predicts longer RTs!

Leonard et al., 2022 *CogSci*

Mixing different measures

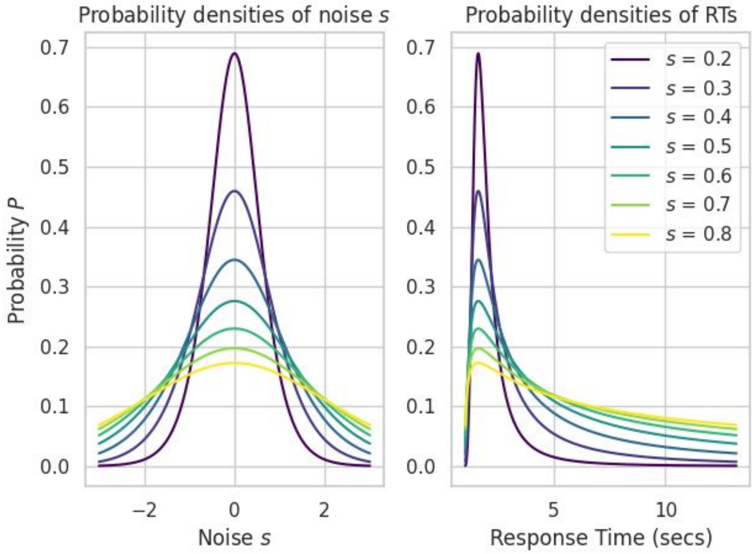
$$A_t(c) = \sum_i (t - t_i)^{-d} + s$$

$$P(c) = e^{A(c)/s} \,/\, \sum_i e^{A(i)/s}$$

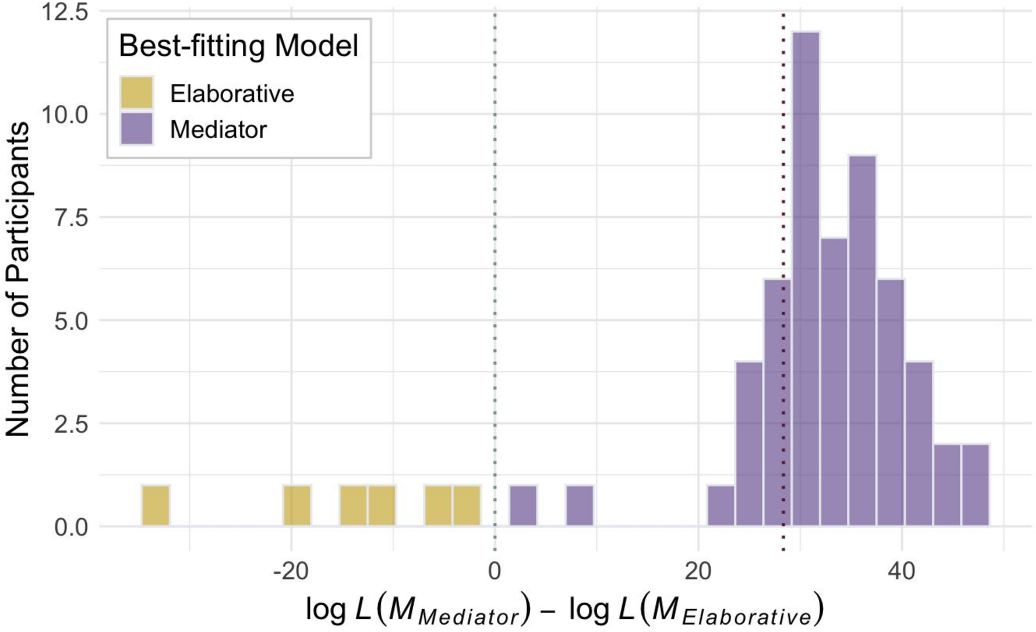
But ACT-R also makes **predictions about RTs:**

$$rt = t_0 + F\,\mathrm{e}^{A(c)}$$

$$P(\mathbf{x}_i|m, \theta) = P(c_i|m, \theta) \cdot P(rt_i|m, \theta)$$



Mediator vs Elaborative



Evidence for Mediator = sum of individual ΔLL = 1,728. **Mediator is $e^{1{,}728}$ more likely**

Accurate Parameter Recovery

Accurate parameter recovery

In my lab, we make a big deal about understanding individuals using parameters

But to make sense, these parameters need to be **accurate**

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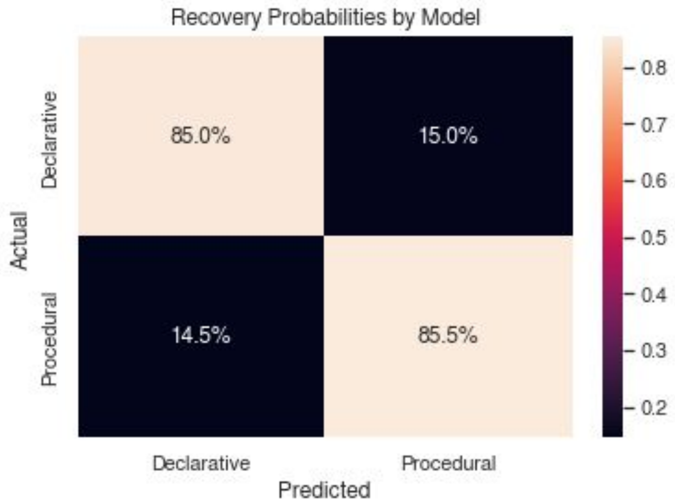

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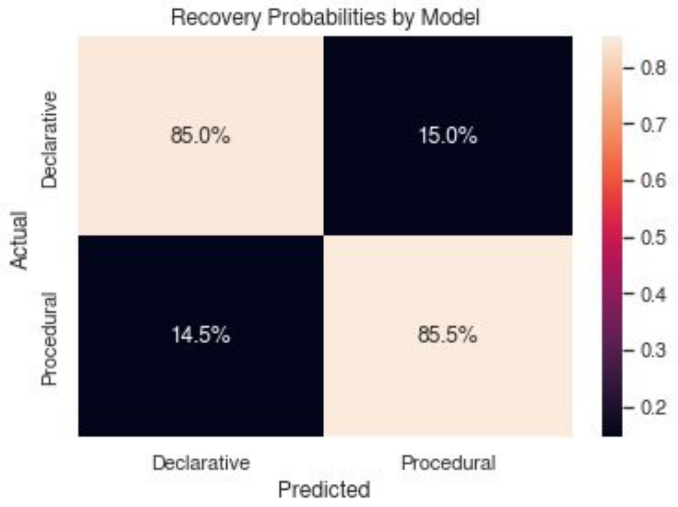
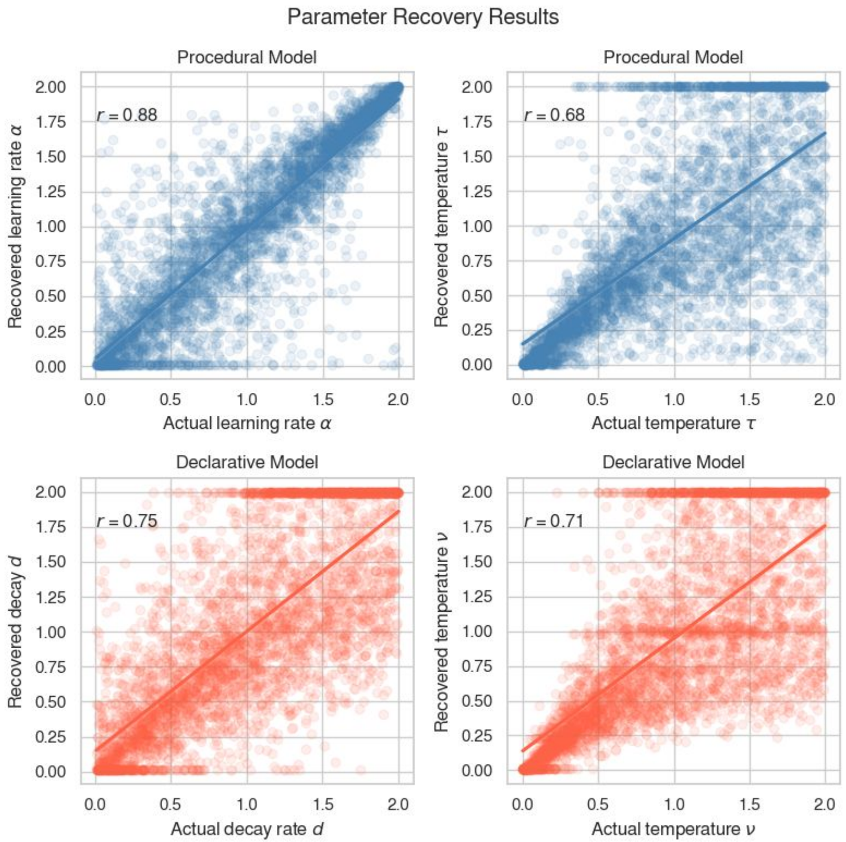
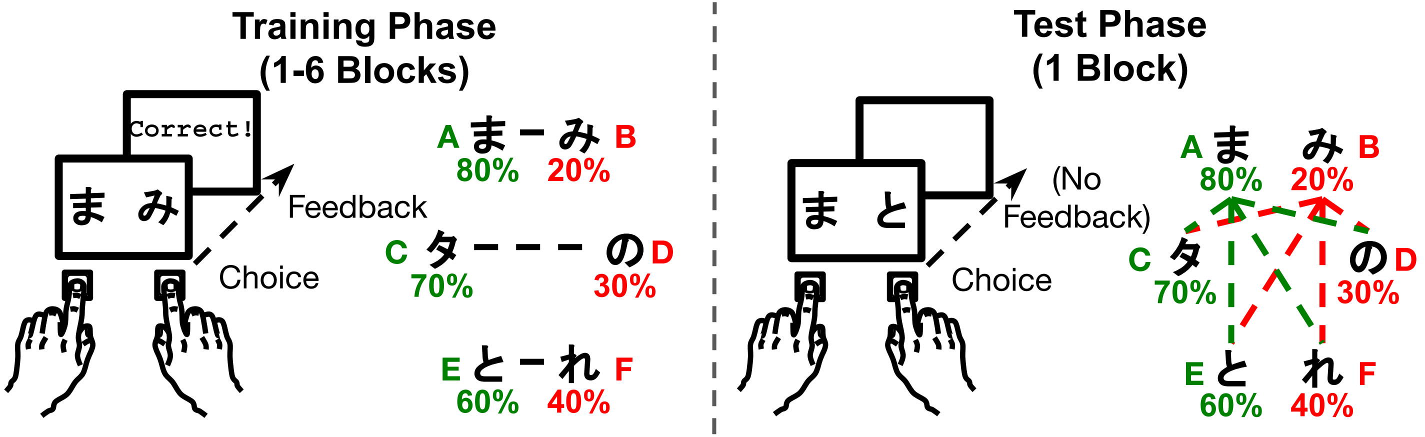


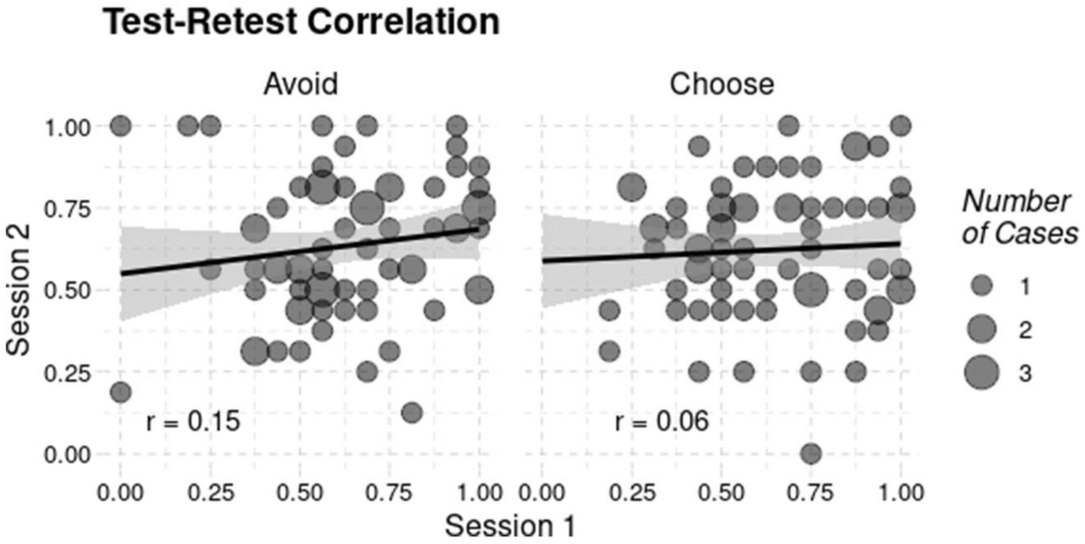


PSS Task (Frank et al., 2004)



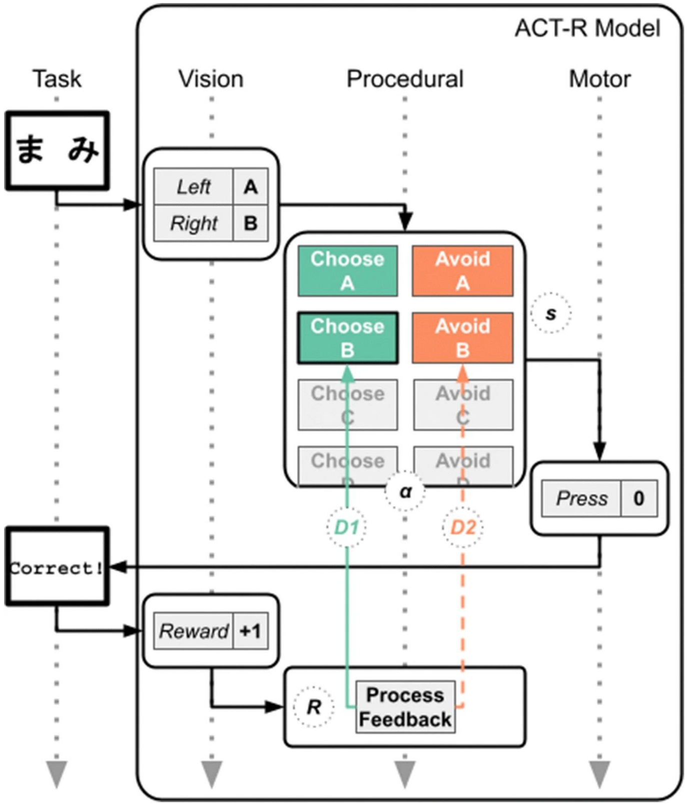
ChooseA and AvoidB are proxies for D1/D2 dopamine receptors

Poor reliability

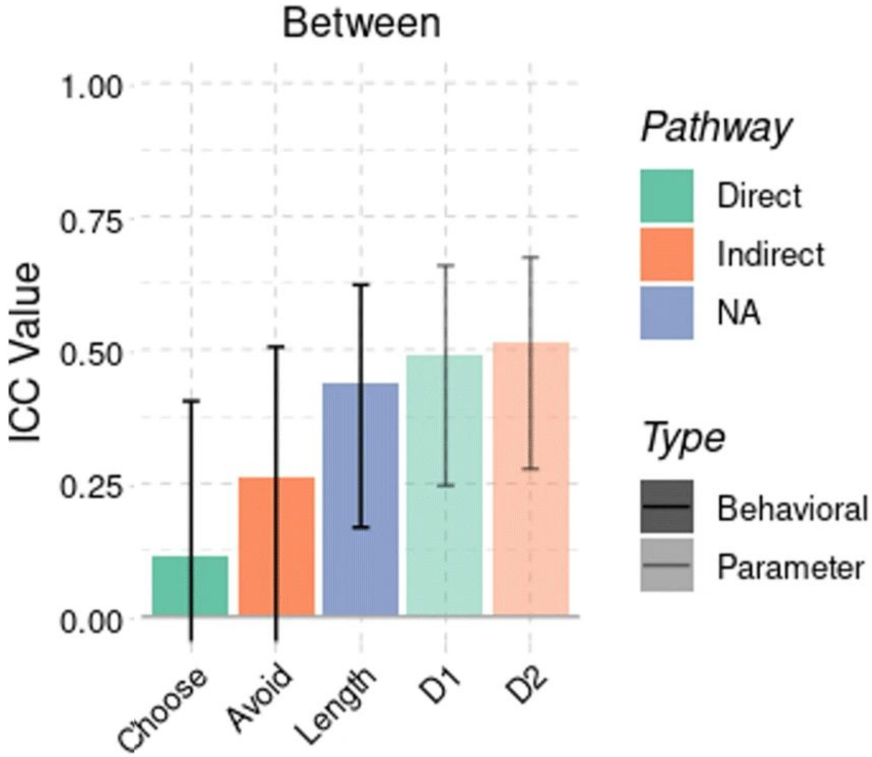


Xu & Stocco, 2021, *Comp. Brain Behav.*

Including D1/D2 parameters in ACT-R model



Parameters have greater reliability!



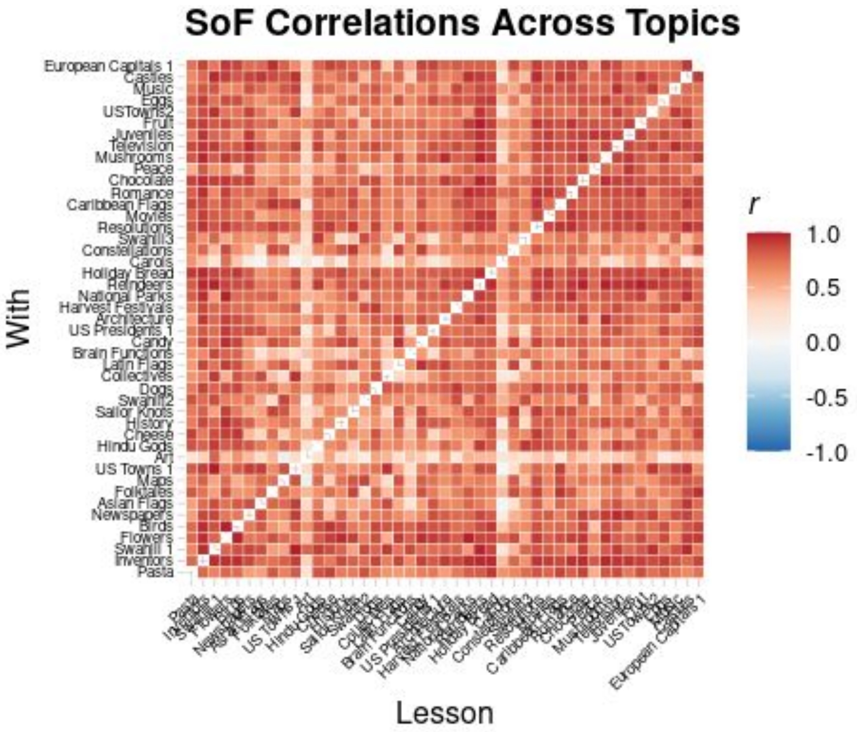
Tracking memory decline

Long-running study to track memory decay in 47 elderly individuals

Really, **α** param in Pavlik & Anderson ("Speed of forgetting", **SOF**)

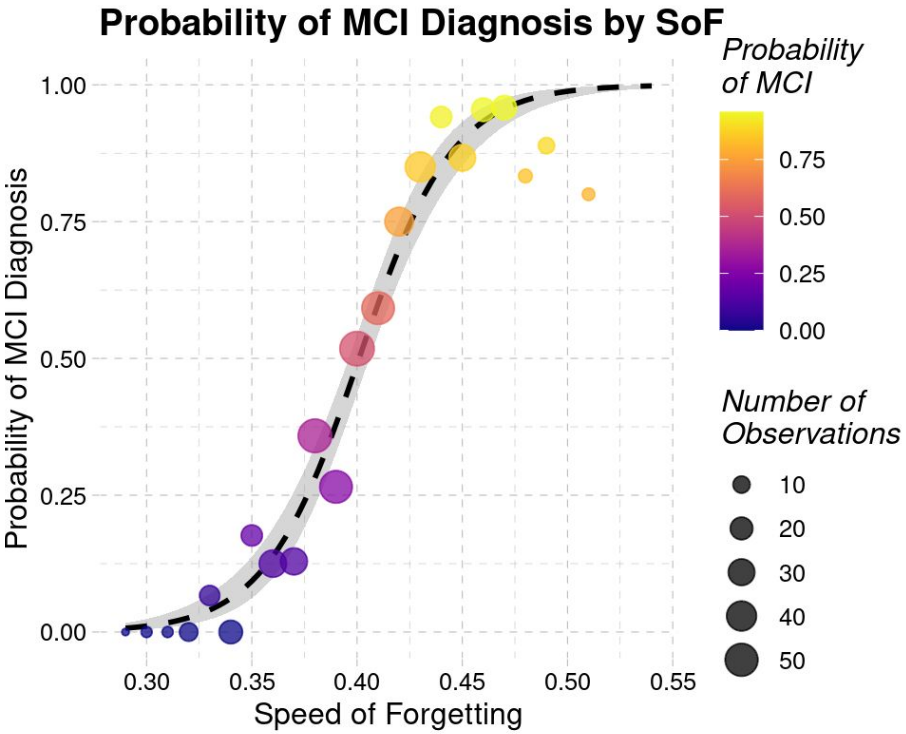
Weekly tests over **one year**

Mean correlation $\boldsymbol{r = 0.72}$



Hake et al, 2023, *CogSci* ♕ Applied Modeling Award

Differences in memory predict cognitive impairment



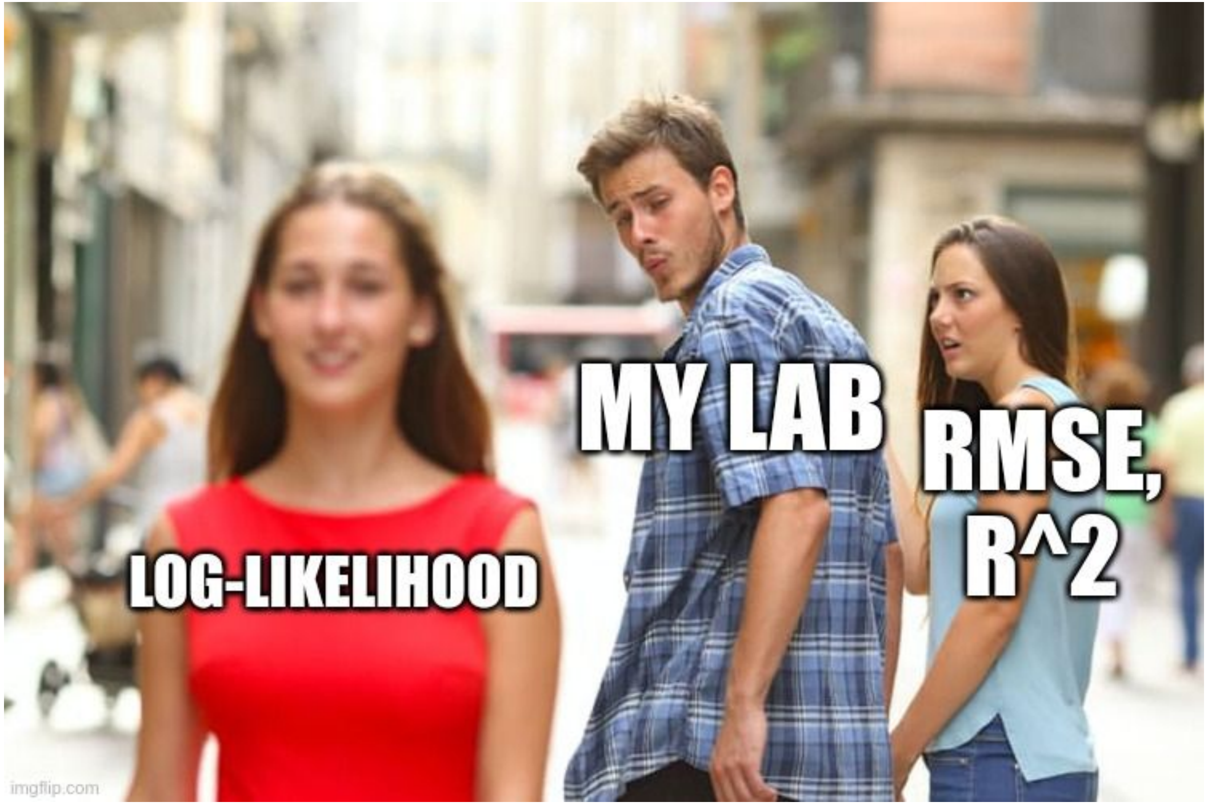
Adjusted $r^2 = 0.38$

Summary

Reasons to use Maximum Likelihood (especially trial-by-trial)

- Clear **interpretation**
- Comparisons between models of **different complexity**
- Can mix **multiple measures**
- Reliable **individual differences**

Even shorter summary



Super special thanks to...