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HDDM Demo

Carney Computational Modeling Workshop
08-19-21
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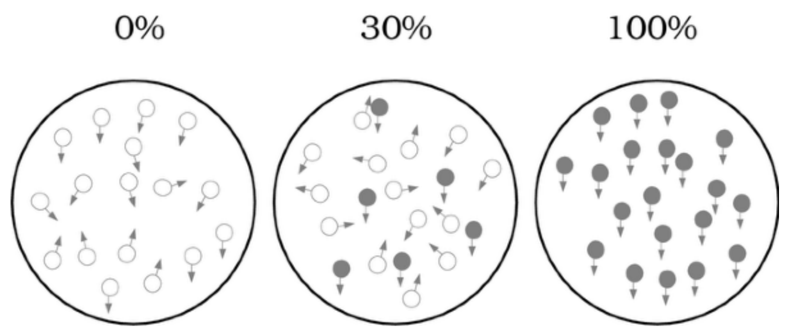
Introduction: using DDM to study social decisions

What has DDM been used to study?

- Traditionally, "simple" types of decision-making
  - Perceptual: random dot motion (Ratcliff & McKoon 2008, Neural Comput)
  - Inhibition: stop-signal (White et al. 2014, J Cogn Neurosci)
  - Response conflict: stroop, flanker, etc (Cavanagh et al. 2011, Nat Neurosci)
- Extensions: value-based decision-making
  - Interplay between reward and attention (Shenhav et al. 2018, Nat Comm)
  - Personal preferences (Krajbich & Rangel 2011, Proc Nat Acad Sci)
- More recently: social and moral preferences
  - Altruistic choice (Hutcherson et al. 2015, Neuron)
  - Food preferences for self vs other person (Harris et al. 2018, J Cogn Neurosci)
  - **Conformity to others' moral values** (Son, Bhandari, & FeldmanHall, 2019)



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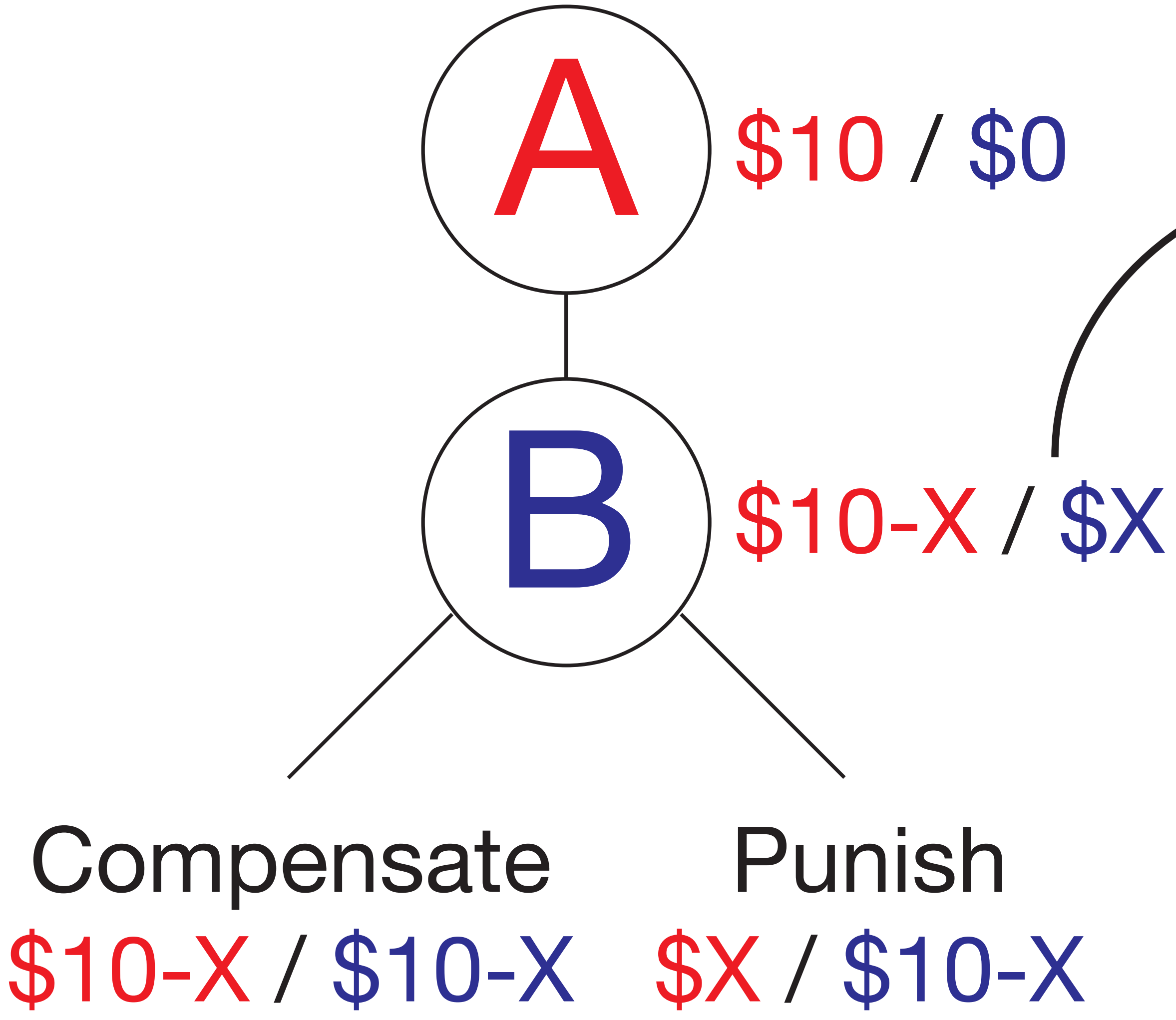
Measuring punitive preferences

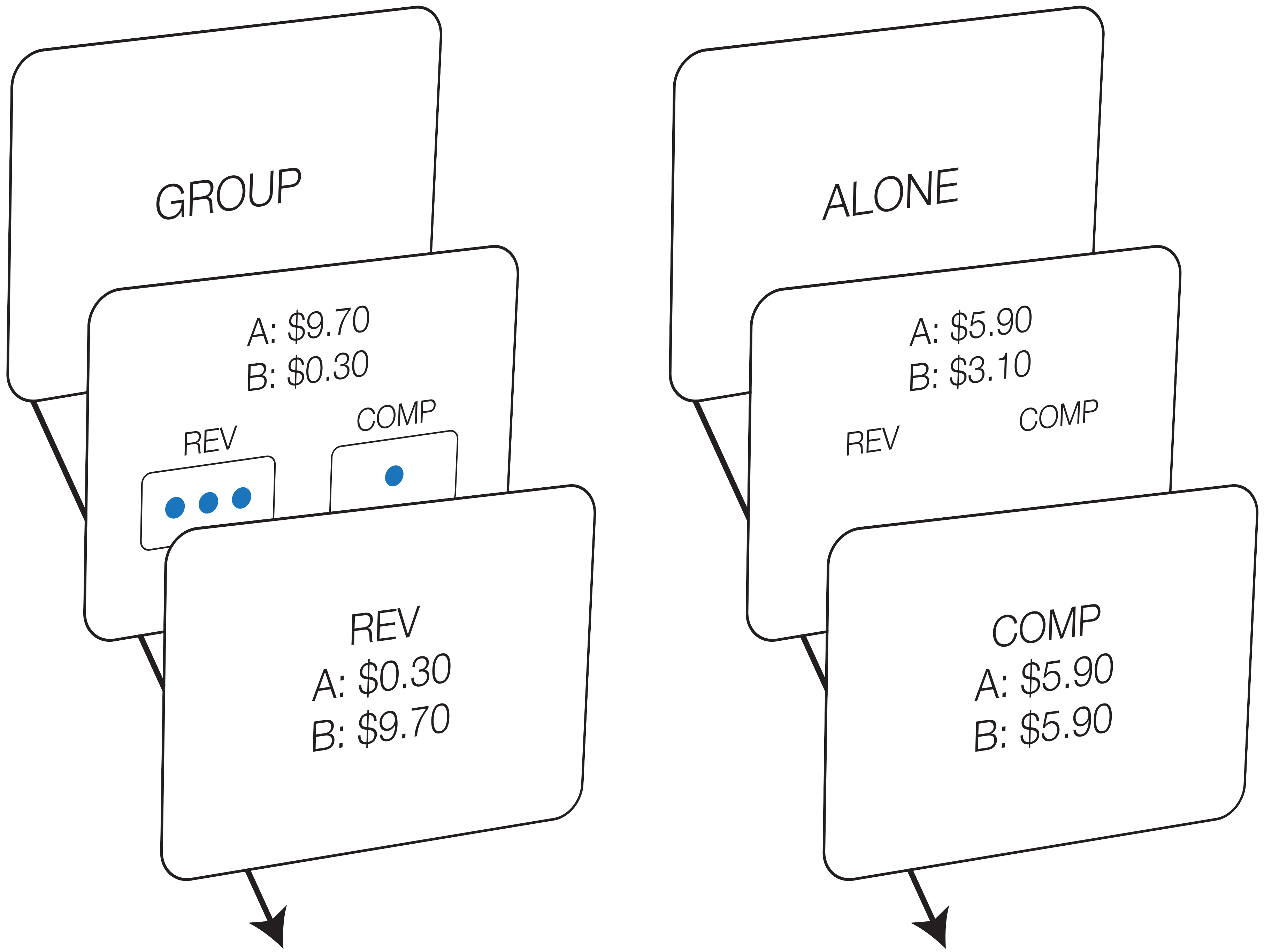


Violation Severity:

Mild: $5.70 / $4.30
Some: $7.50 / $2.50
High: $9.30 / $0.70

All ranges mean ± 60¢

Conformity paradigm



Victim vs Juror

Victim: Was harmed by the perpetrator's moral violation, punishment decision affects how much money they earn

Juror: Makes punishment decision on behalf of a victim; wasn't harmed, won't earn more money based on their choice

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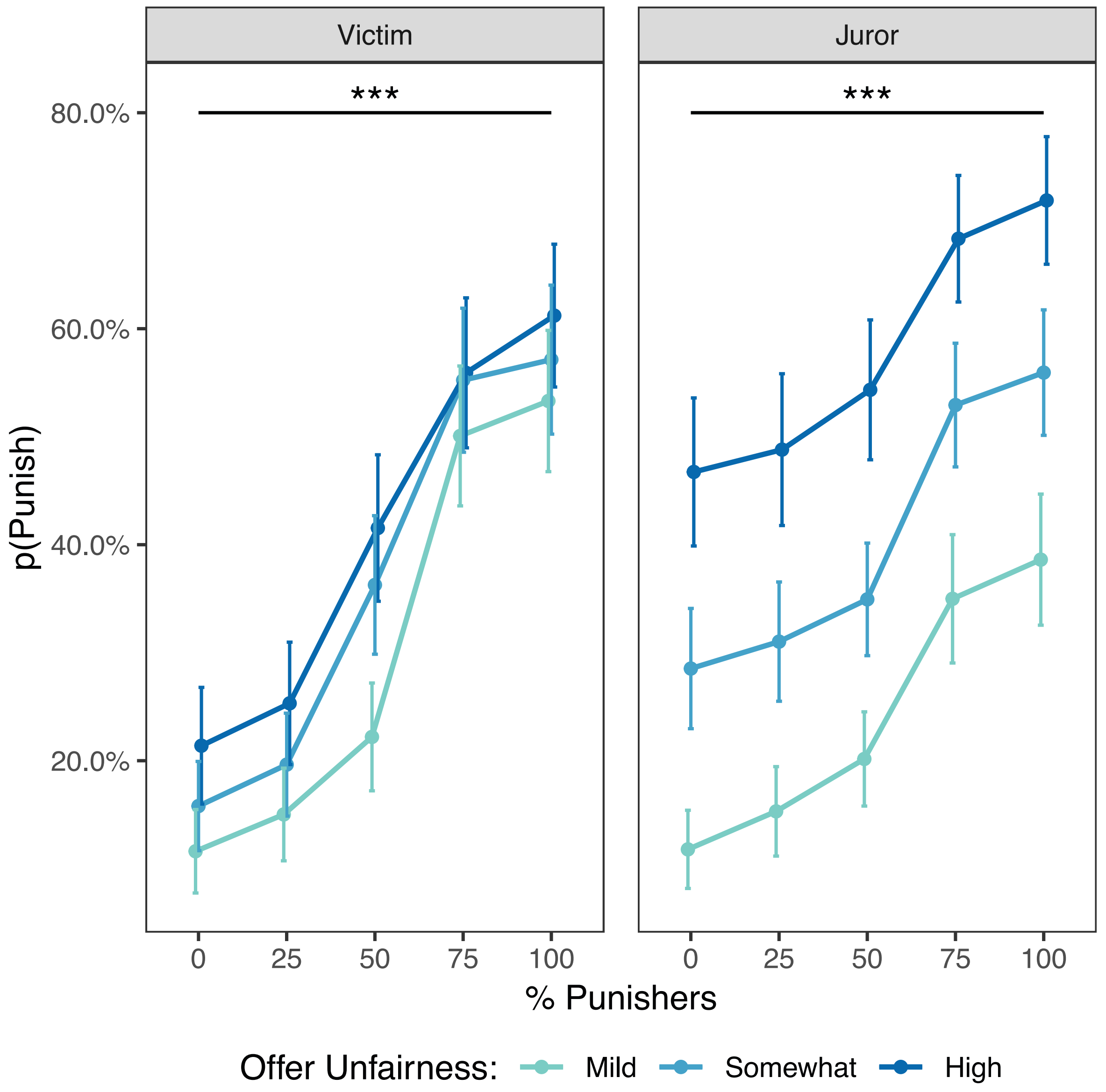
Behavioral results:



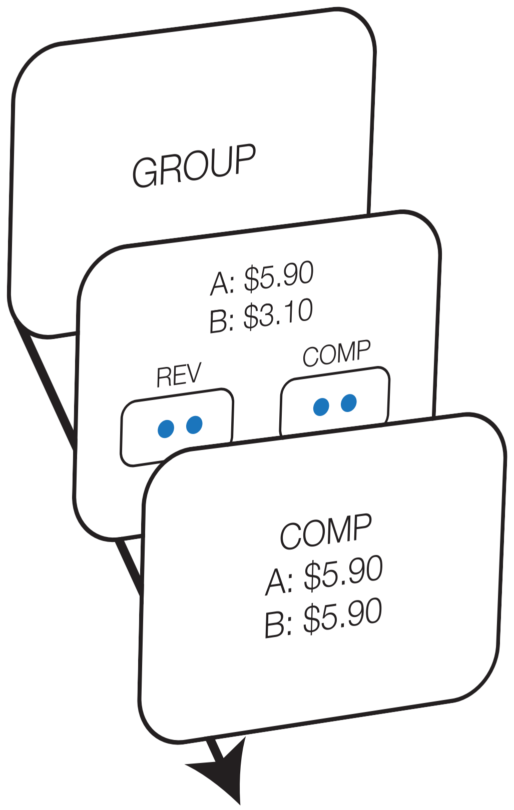
Two longstanding hypotheses about why people conform:

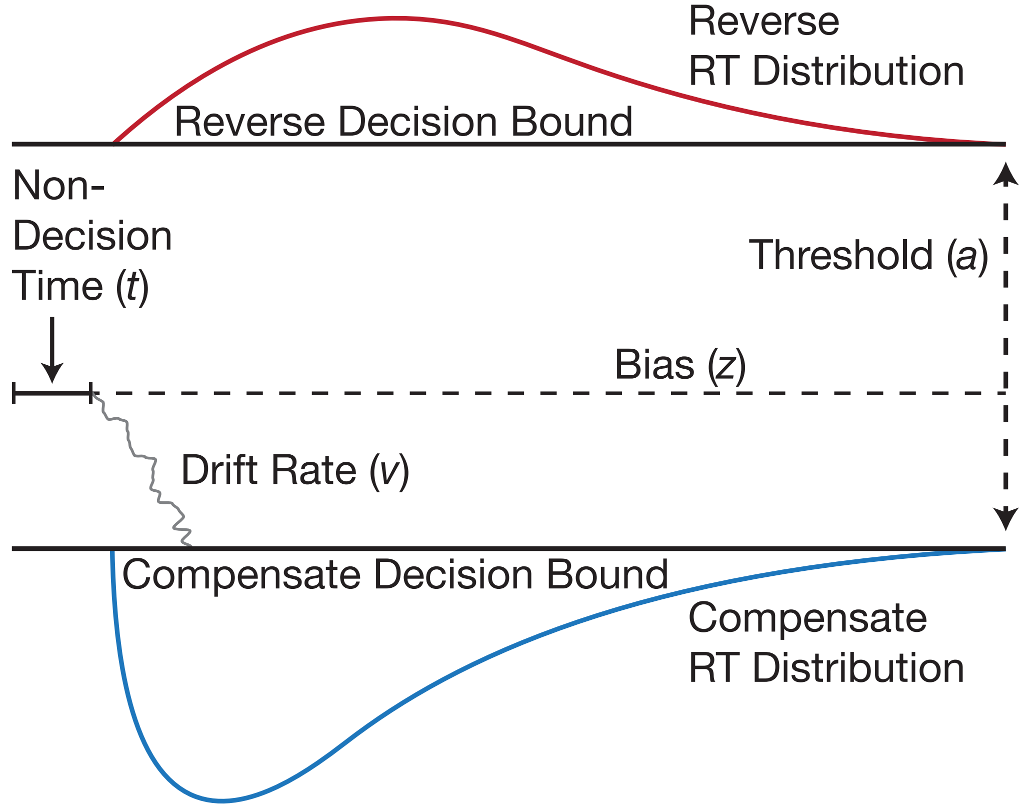
1. Being part of a group makes you less vigilant about your decisions
2. Groups provide evidence about what is (socially) valued

Problem: our behavioral data can't tell us WHY people are conforming to others' punitive preferences!

How does DDM help us?

- Parameters are psychologically interpretable:
  - Bias *z* = how much individuals prefer punishment in the absence of group influence
  - Threshold *a* = the extent to which groups cause individuals to relinquish moral responsibility
  - Drift *v* = the extent to which groups provide evidence that punishment is (socially) valued





Analysis pipeline: how did I use HDDM to test these questions?

Analysis Overview

1. **Fit models**
2. Check model diagnostics
3. Analyze data
4. Posterior predictive check (PPC)
5. Parameter recovery

Fit models

- Define model(s)
  - What's your hypothesis-driven model, and why?
  - What are good alternative models that are approximately matched for model complexity?
- Estimate parameters
- Model selection (tentative until you've checked convergence!)

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Check model diagnostics

- Convergence: who cares?
  - Inferential power of MCMC sampling rests on certain key assumptions
  - If there is evidence of convergence failure, it implies that these assumptions have been violated
  - And if the assumptions do not hold, that means that your parameter estimates are unreliable
- Problem: in theory, there is no way to tell whether your analysis has converged
- Praxis: there are some fairly good heuristics that will help you catch convergence failures

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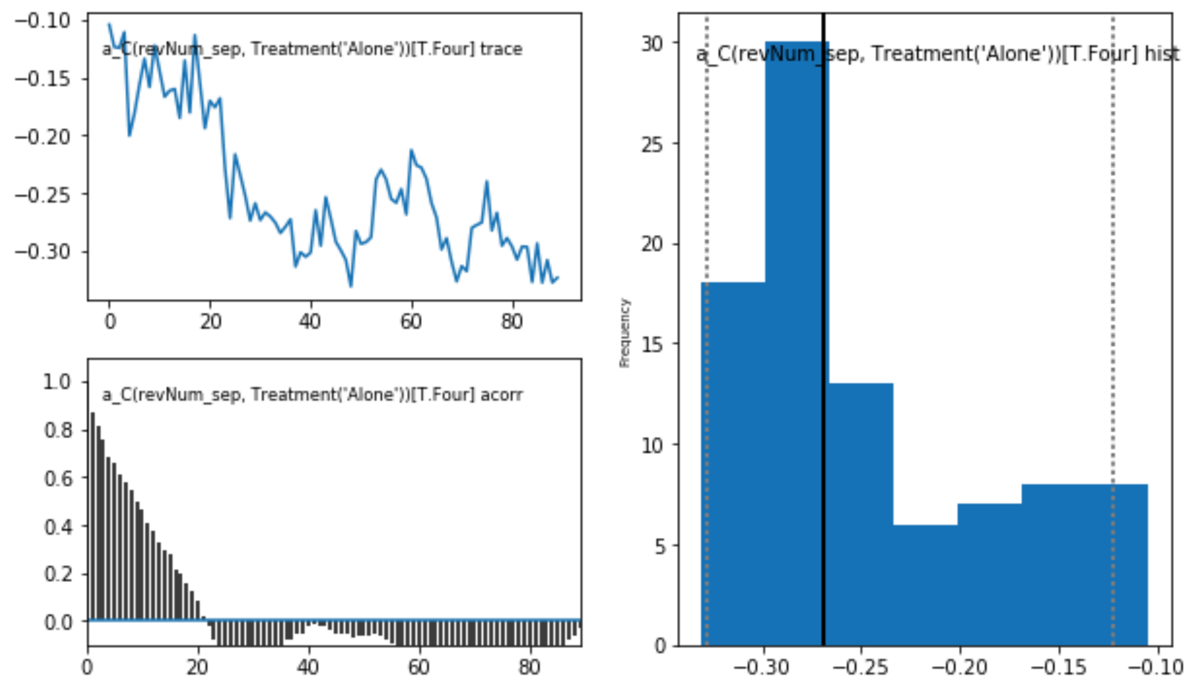
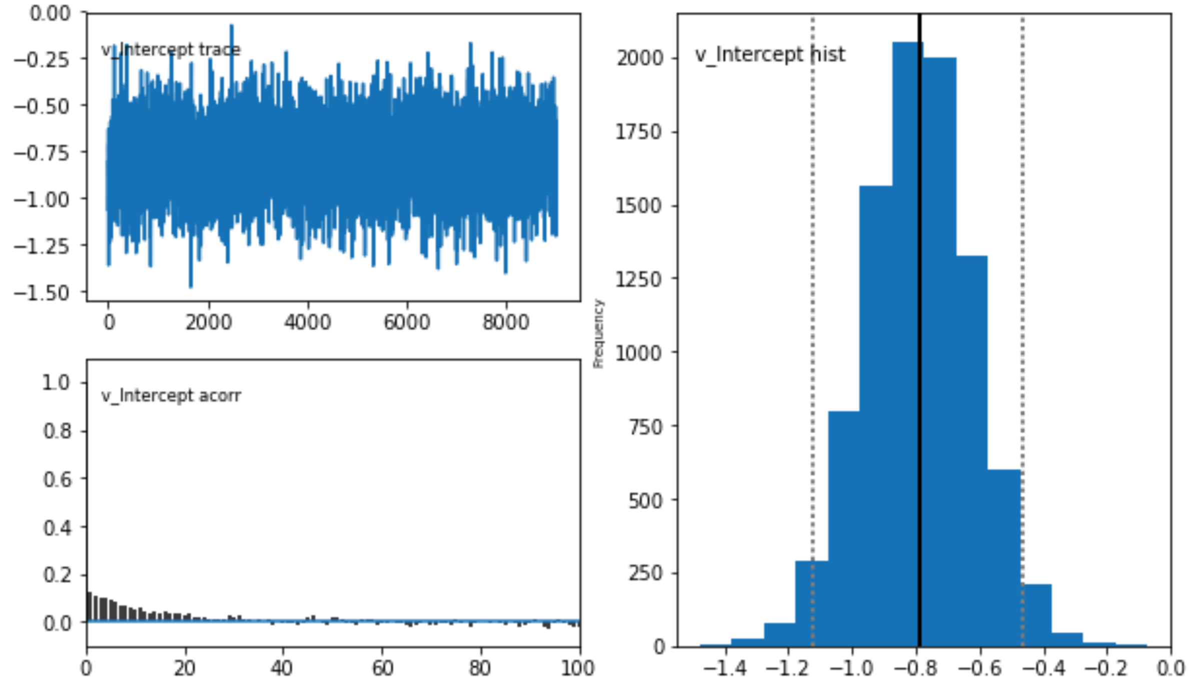
Check model diagnostics

“Weak” convergence check: visual inspection

BAD

GOOD





- Traces jump around, shows trend
- High autocorrelation throughout
- Posterior distribution non-normal

- Traces are stationary (stable)
- Low autocorrelation (except at the beginning – this is why we burn)
- Posterior distribution approx. normal

Check model diagnostics

- Better convergence check: R-hat statistic
- Basic logic
  - If your model is truly capable of sampling the "best" parameter space, it should do so consistently every single time you run it
  - In other words, all of your chains should be *stationary*
  - The R-hat statistic compares the within-chain variance against the between-chain variance
  - This provides a metric for telling whether your chains are stationary (converged) or not (non-converged)

http://ski.clps.brown.edu/hddm_docs/howto.html#assess-model-convergence

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Analyze data

- Bayesian hypothesis testing
  - Read the HDDM documentation
  - Read the BEST paper (Bayesian estimation supersedes the t-test)
- Once you've downloaded the traces (as a CSV file), you can do analyses in other stat software, like R or Python

http://ski.clps.brown.edu/hddm_docs/howto.html#hypothesis-testing

https://jkkweb.sitehost.iu.edu/articles/Kruschke2013JEPG.pdf

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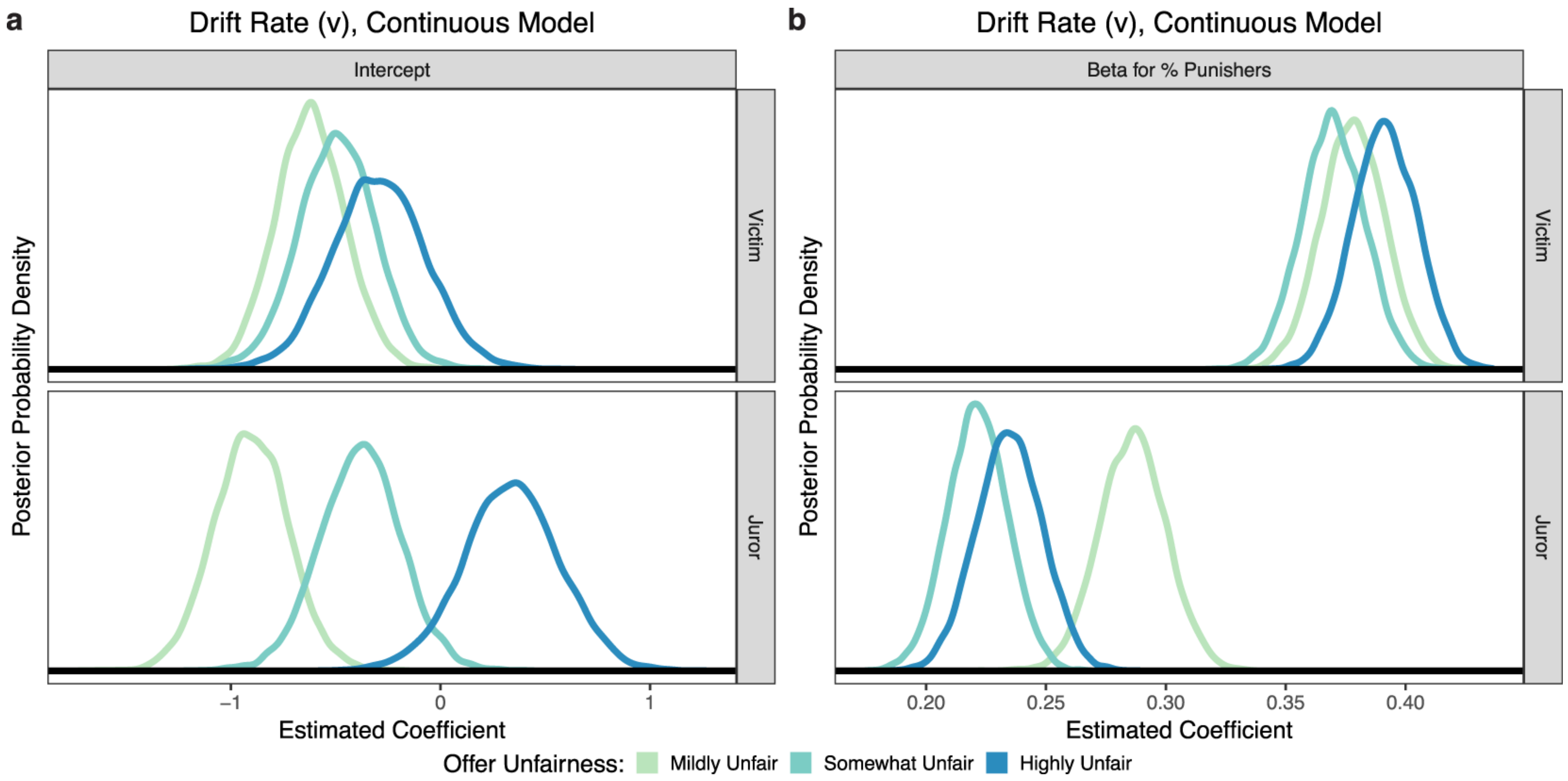
Analyze data



Analysis Overview

1. Fit models
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4. **Posterior predictive check (PPC)**
5. Parameter recovery

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Posterior predictive check (PPC)

- Did my model make predictions that actually describe my data?
- High-level overview:
  - Perform many simulations
  - In each of these simulations, randomly sample parameter values from your estimated parameter posteriors
  - Each simulation returns a predicted choice and reaction time for every trial that each subject completed
  - In other words, a single simulation returns a dataset that precisely mirrors the structure of your empirical dataset
  - Analyze RT density and percentages of choices

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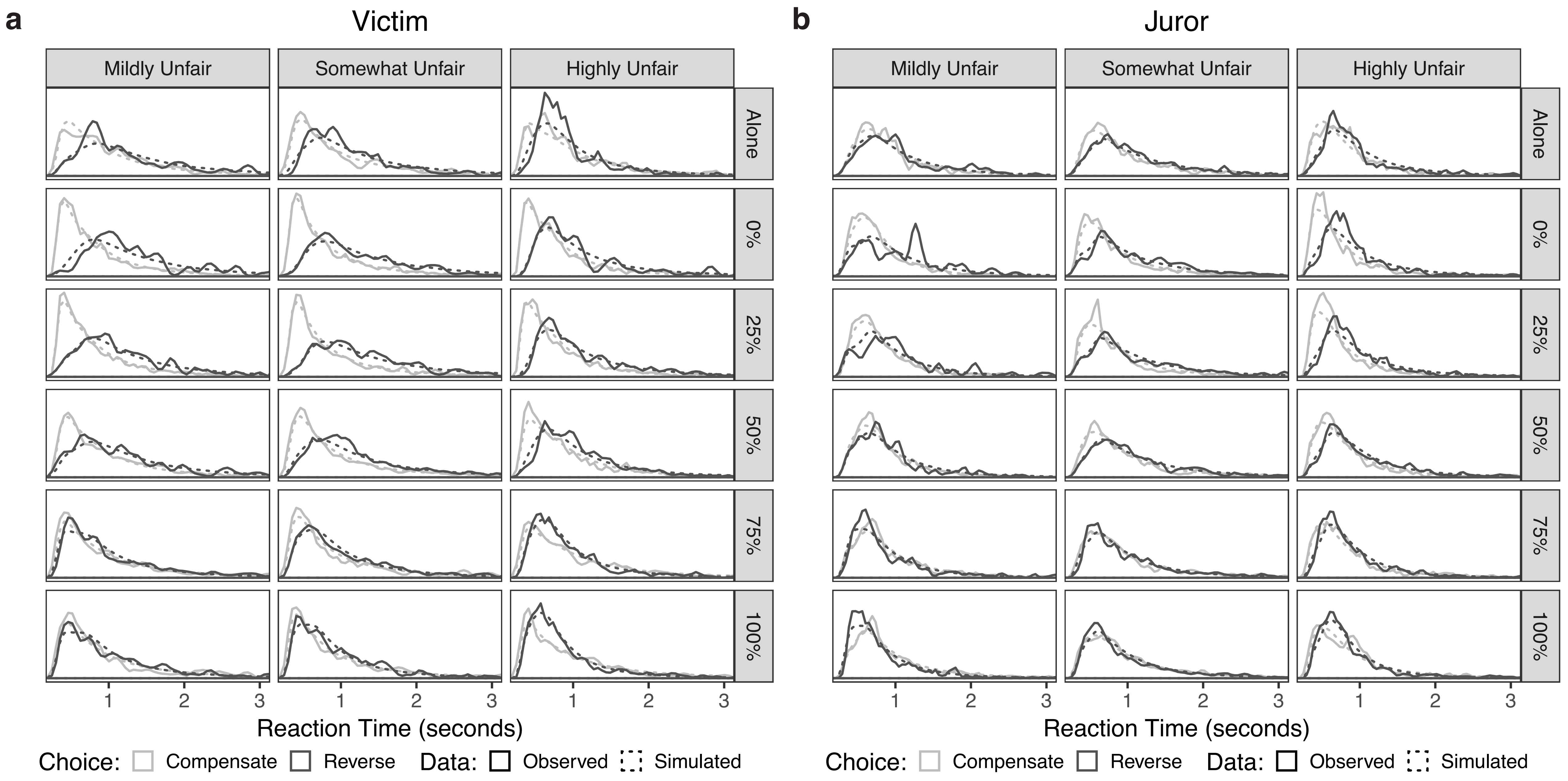
Posterior predictive check (PPC)



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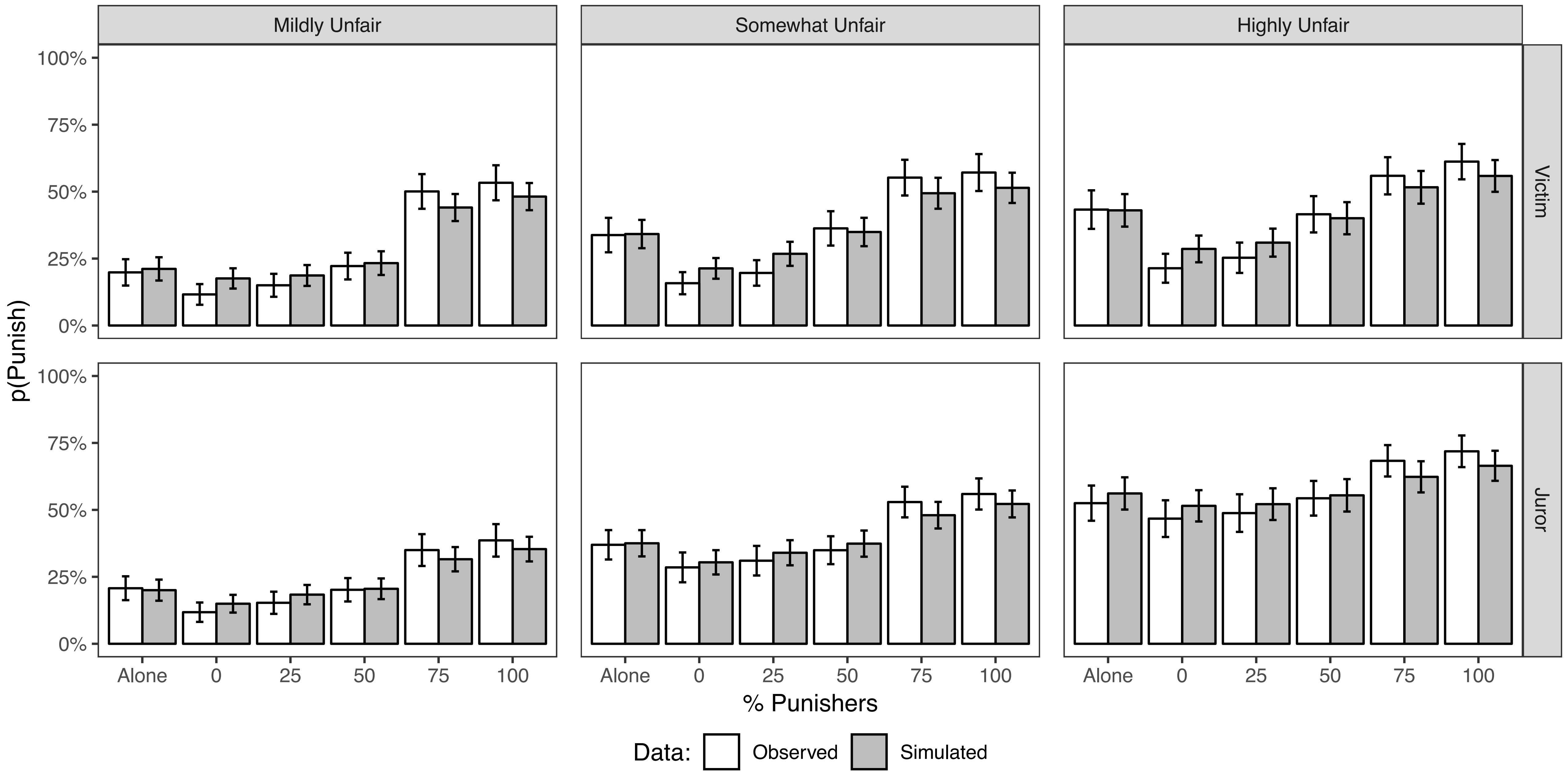
Posterior predictive check (PPC)



Analysis Overview

1. Fit models
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5. **Parameter recovery**

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Parameter recovery

- How reliable is the estimation process for the specific parameters I got out of my model?
- High-level overview:
  - Simulate new data using estimated mean parameter estimates
  - Feed this simulated data to the same regression model you used to estimate your parameters
  - If HDDM is consistently capable of estimating these parameters (i.e., recovering them), you should see a close match between the parameter estimates from your empirical and simulated data

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Should you run it locally or on the cluster?

- Yes!
- On your machine (or on the cloud via Google Colab):
  - Rigorously test for bugs using a Jupyter notebook
  - Don't run long chains
- On the computing cluster:
  - Utilize the awesome power of our cluster
  - Don't waste communal computing time/resources by doing small-scale bug testing if you can help it

Cluster computing tips

Efficient use of memory

- After running a job, type: `myjobinfo -j JobNumberHere`
- If you don't know the job number, `myjobinfo` shows you the most recent jobs you've run

- This shows you some important information:
  - `ReqMem`: how much memory did I request?
  - `MaxRSS`: max residence set size, i.e. the most memory that was in use at any one time
  - `AveRSS`: average RSS, or the average memory used

- If `MaxRSS` and/or `AveRSS` is much lower than `ReqMem`, scale it down because it's otherwise a waste of computing resources.

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Cluster computing tips

Efficient use of cores

- If your code isn't threaded (doesn't make use of multiple cores), don't request more cores. It ties up computing resources, and it won't make your job run any faster.
- How do you know whether your code is threaded? Try running the same job with (say) 2 vs 8 cores and see if it speeds up. If not, your code isn't threaded.

General tips

- Before batching a big job (e.g., fitting model parameters to all of your subjects), try testing your code on a small subset (e.g., a single subject). Runtime usually scales in a linear manner.
- Same goes for MCMC chains.
- Test, test, test before running bigger jobs.

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Want to see all of the data/scripts for our analysis, and how everything fits together in a larger project?

Visit our Open Science Framework page here:
https://osf.io/8ka47/

Read the paper here:
https://www.nature.com/articles/s41598-019-48050-2

Special thanks to my project collaborators: