

Supplementary Information for

“Thinking more or thinking differently? Using drift-diffusion modeling to illuminate why accuracy prompts decrease misinformation sharing”

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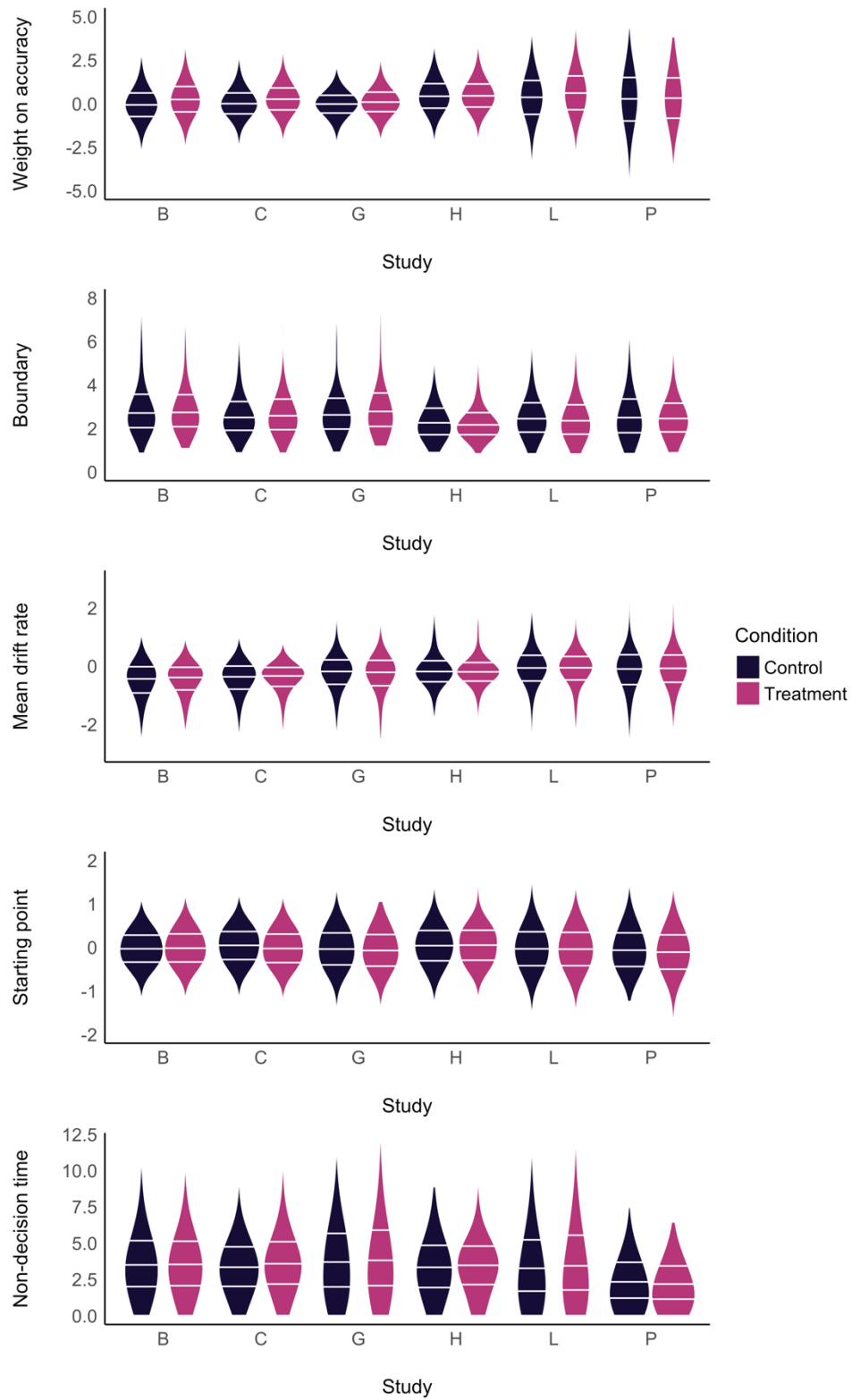


Figure S1. Diffusion-model parameters as a function of study and condition. Violin plots show the distribution of parameter values. White horizontal lines show the 25%, 50%, and 75% quantiles.

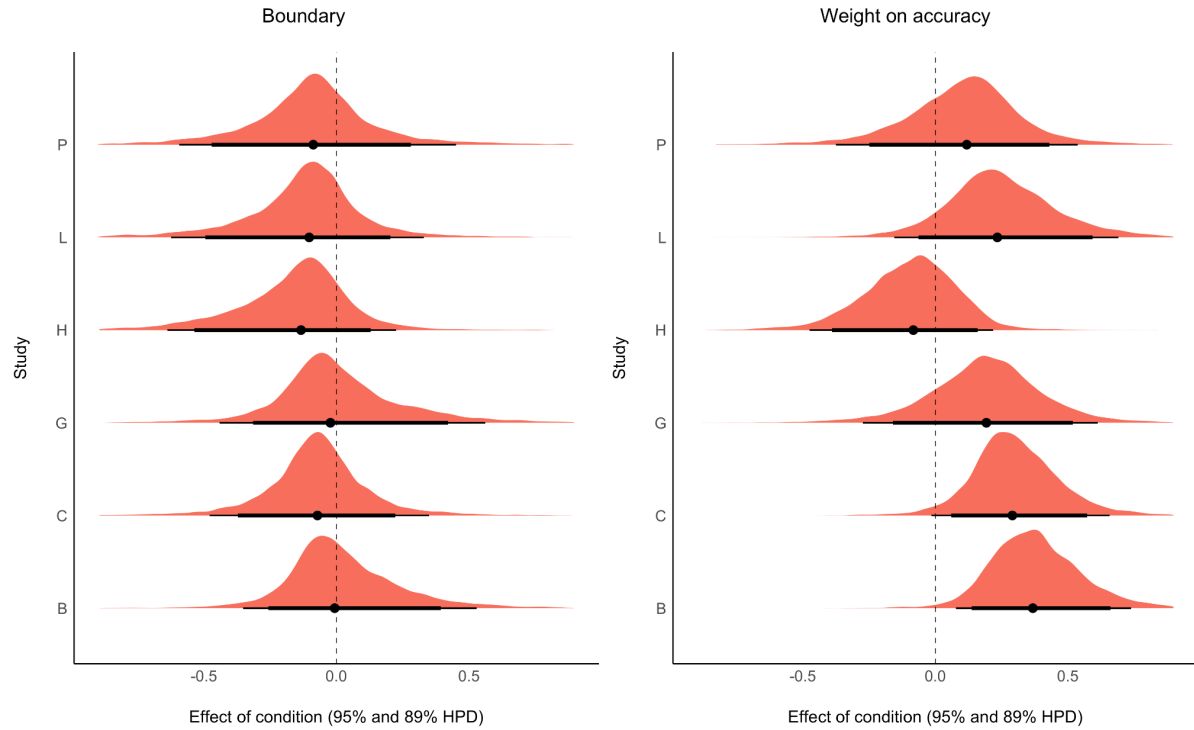


Figure S2. Bayesian posterior distributions for the effect of condition on boundary (left) and weight-on-accuracy (right) parameters for each study. Positive estimates indicate larger parameter values in the treatment (vs. control) condition. Error bars are 95% and 89% highest posterior-density (HPD) intervals.

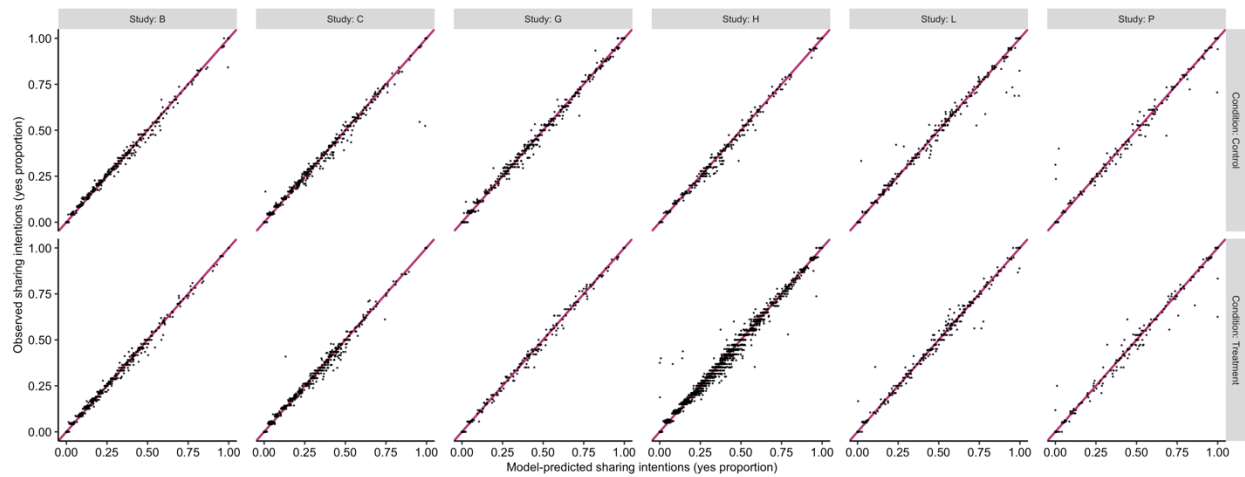


Figure S3. Empirical and model-predicted sharing intentions across the five studies and two conditions. Each dot is one participant. Diagonal line represents a perfect match between empirical and model-predicted values. Pearson's $r_s > 0.98$.

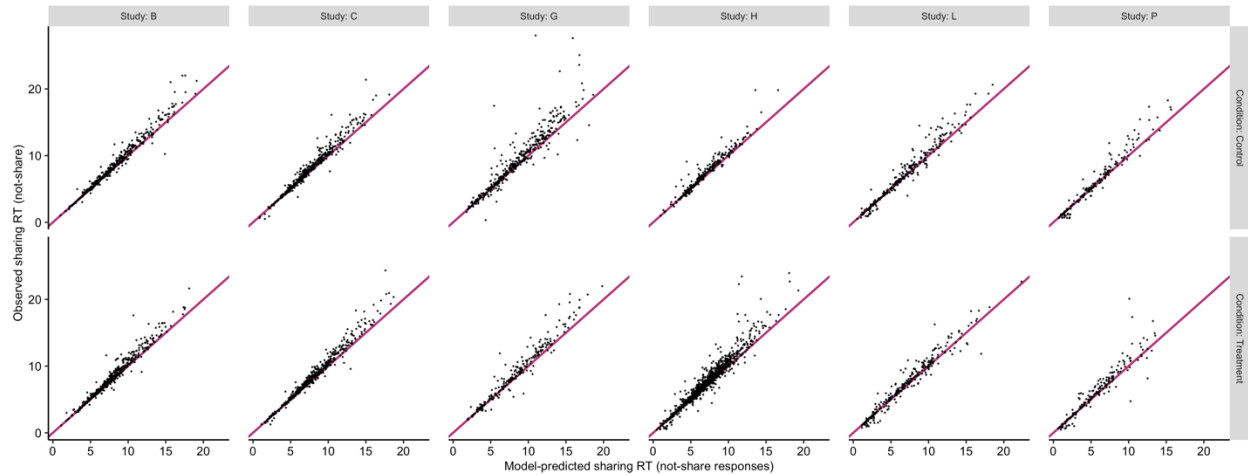


Figure S4. Empirical and model-predicted response times for “not-share” (lower bound) responses across the five studies and two conditions. Each dot is one participant. Diagonal line represents a perfect match between empirical and model-predicted values. Pearson’s $r_s > 0.95$.

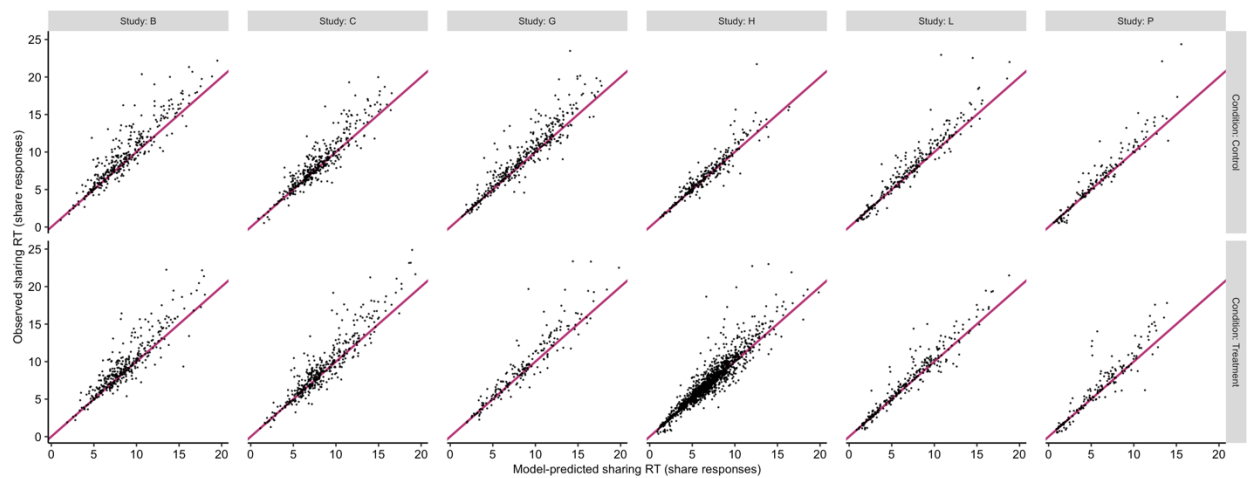


Figure S5. Empirical and model-predicted response times for “share” (upper bound) responses across the five studies and two conditions. Each dot is one participant. Diagonal line represents a perfect match between empirical and model-predicted values. Pearson’s $r_s > 0.90$.

Complete-pooling hierarchical Bayesian drift-diffusion models

The parameter estimates reported in the main text may be relatively noisy because the diffusion models were fitted separately to each participant (i.e., no-pooling approach) and there were relatively few trials per participant. Although noise (arising from the small number of trials) could lead to inaccurate or biased estimates, the two conditions within each study had the same number of trials, so the amount of noise between conditions (within each study) should be similar.

To verify that noise had not led to inaccurate or biased estimates, we used the complete-pooling approach¹ to estimate the diffusion parameters for each study and condition. The results from this approach are consistent with what we reported in the main text. In these analyses, we ignored individual differences across participants and fitted hierarchical Bayesian diffusion models (Wiecki, Sofer, & Frank, 2013), assuming all the data within each study and condition had come from a single participant (i.e., 12 “participants,” two from each study).

To estimate the overall effect of condition across the six studies, we fitted a Bayesian mixed-effects model to the diffusion-model parameter estimates (Bürkner, 2017) [brms syntax: *brm(parameter | mi(parameter_sd) ~ condition + (1 + condition | study)*, where *parameter* is the mean of the posterior distribution for a parameter, *parameter_sd* is the standard deviation of the corresponding parameter’s posterior distribution]. As shown in Figure S6, we replicated the results in the main text. We found a null effect of condition on the boundary parameter ($b = 0.04$ [-0.35, 0.39]), but a positive effect on the weight-on-accuracy parameter ($b = 0.14$ [0.00, 0.30]). The condition effect for each study is shown in Figure S7. Thus, the two contrasting modeling approaches (i.e., no pooling and complete pooling) led to similar conclusions, highlighting the robustness of our findings.

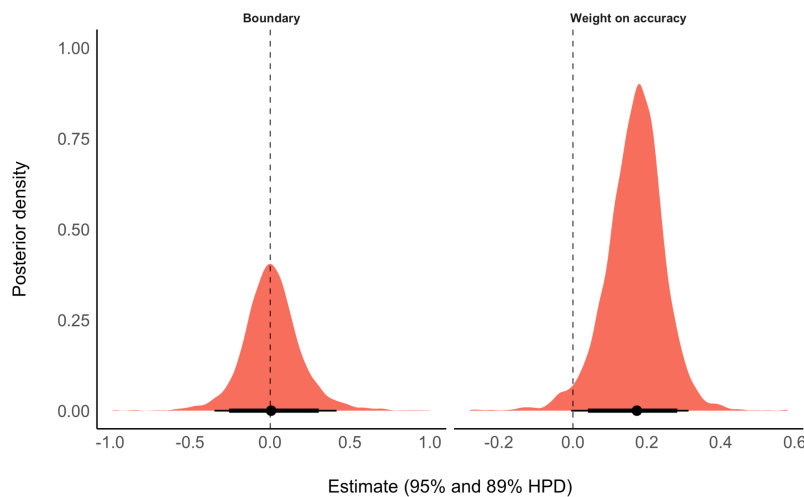


Figure S6. Bayesian posterior distributions for the overall effect of condition on boundary (left) and weight-on-accuracy (right) parameters. Bayesian mixed-effects models (Bürkner, 2017) were fitted to the diffusion parameter estimates (obtained from hierarchical Bayesian diffusion models; Wiecki, Sofer, & Frank, 2013) to estimate the overall effect of condition on parameter

¹ We thank Henrik Singmann for extensive discussions and for suggesting this analysis.

estimates across the six studies. Error bars are 95% and 89% highest posterior-density (HPD) intervals.

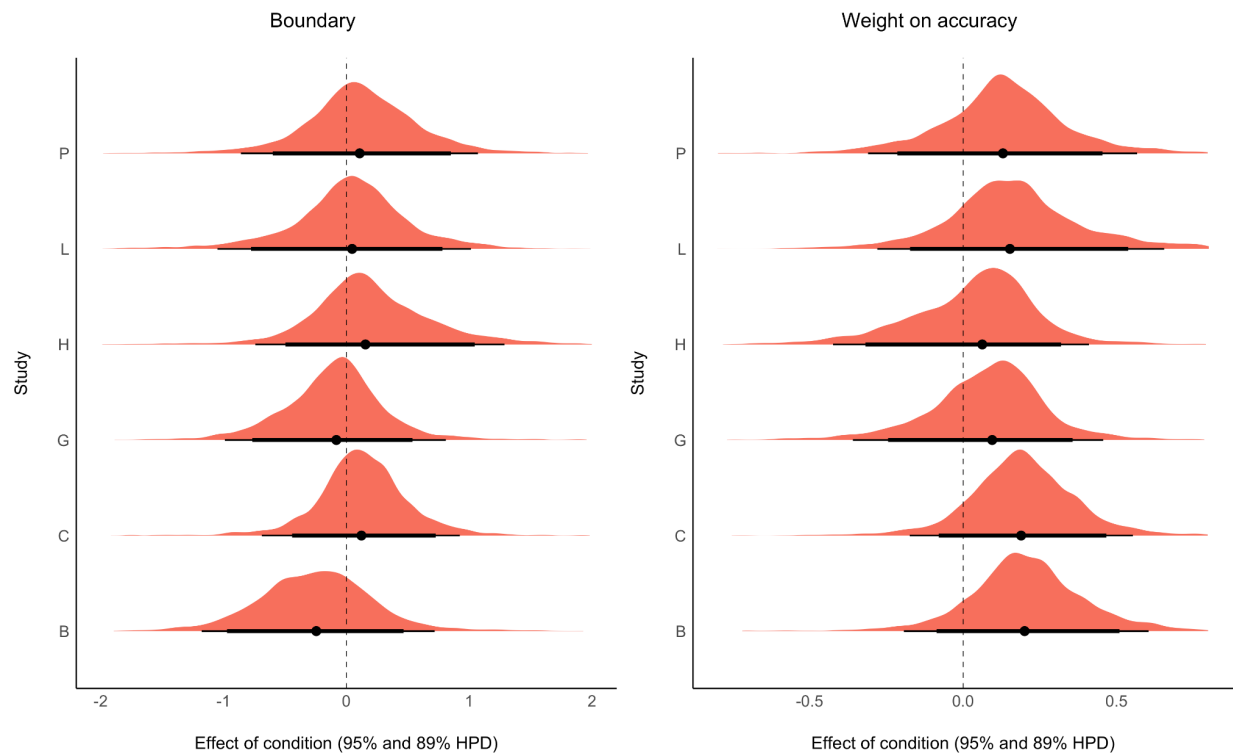


Figure S7. Bayesian posterior distributions for the effect of condition on boundary (left) and weight-on-accuracy (right) parameters for each study. Diffusion-model parameters were estimated using complete pooling (results in the main text used no pooling). Positive estimates indicate larger parameter values in the treatment (vs. control) condition. Error bars are 95% and 89% highest posterior-density (HPD) intervals.

References

- Bürkner, P. C. (2017). brms: An R package for Bayesian multilevel models using Stan. *Journal of Statistical Software*, 80(1), 1-28. doi:10.18637/jss.v080.i01
- Wiecki, T. V., Sofer, I., & Frank, M. J. (2013). HDDM: Hierarchical Bayesian estimation of the Drift-Diffusion Model in Python. *Frontiers in Neuroinformatics*, 7, 14. doi:10.3389/fninf.2013.00014