

# Analyzing an experiment on involuntary attention using **brms**

Antonio Schettino

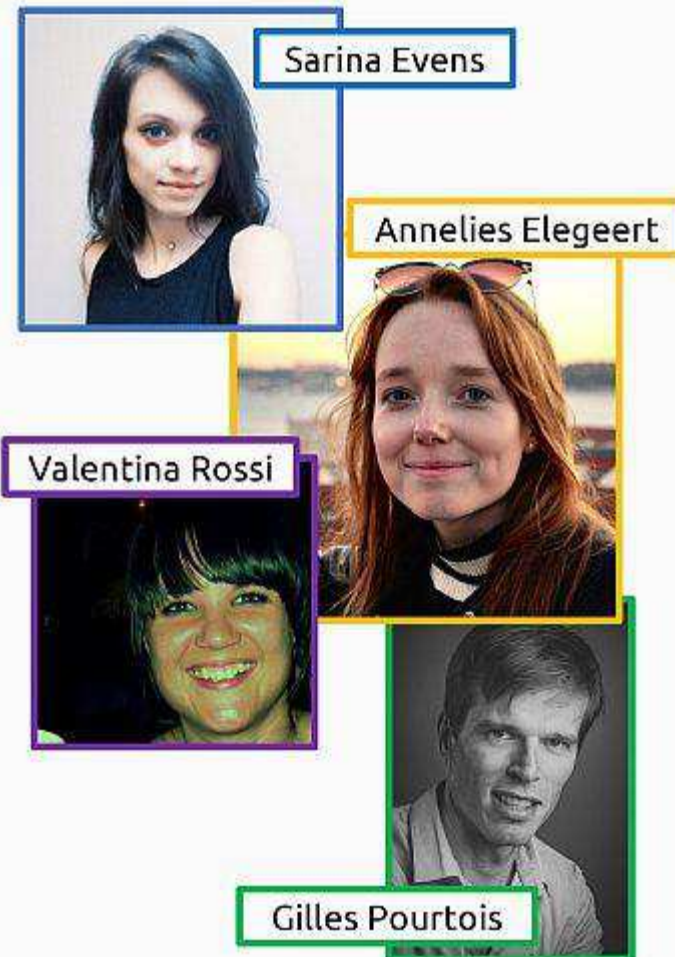
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# OUTLINE

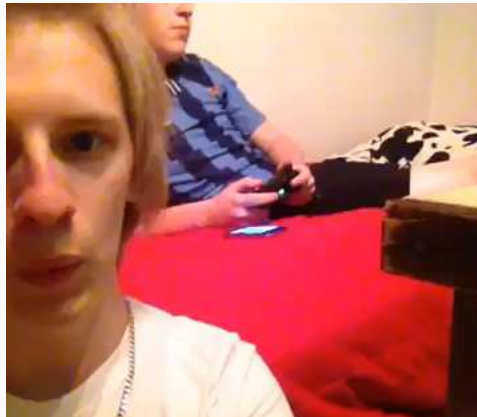
- background
- experimental paradigm
- data and results
- conclusions

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# Involuntary attention



source: <https://www.youtube.com/watch?v=0M2L9XNYfLs>

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- The guy in the background was attracted to the phone...
- ... despite *knowing* that his friend was making the notification sounds
- His attention was **automatically** attracted to ~~uninformative~~ **counterproductive** sounds (distraction from current task: watching TV)



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- Involuntary attentional orienting can be dangerous in some real-life situations
- Car driver distracted by flashing mobile phone, worker operating heavy machinery distracted by blinking lights, ...
- How to study this phenomenon in the lab?

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- Flash two stimuli on screen
- Task: which stimulus appeared **first**?
- Difficulty depends on the time between the onset of the stimuli (**SOA**)

# Temporal Order Judgment (TOJ)





# Counterproductive T0J

- An **exogenous cue** is used to attract attention towards one placeholder

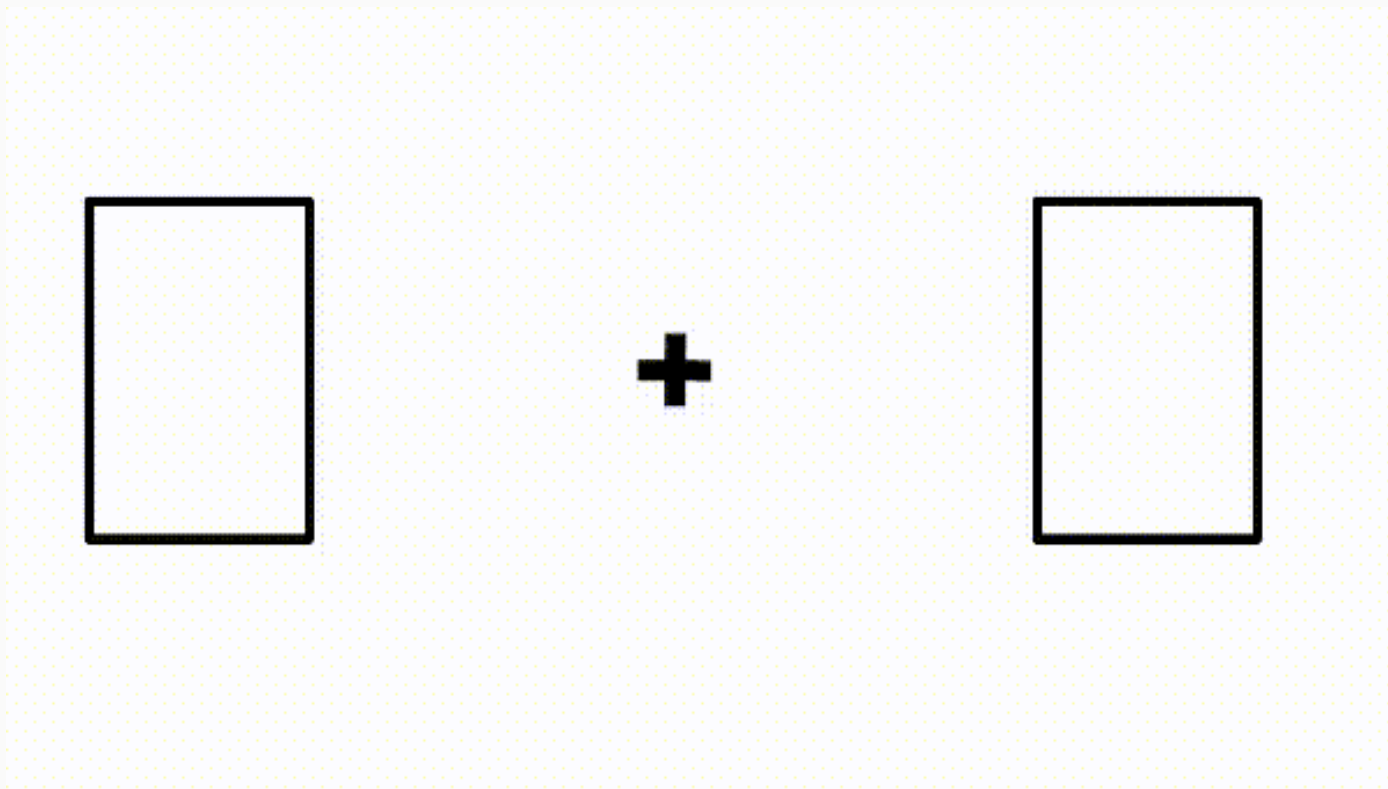
# Counterproductive T0J

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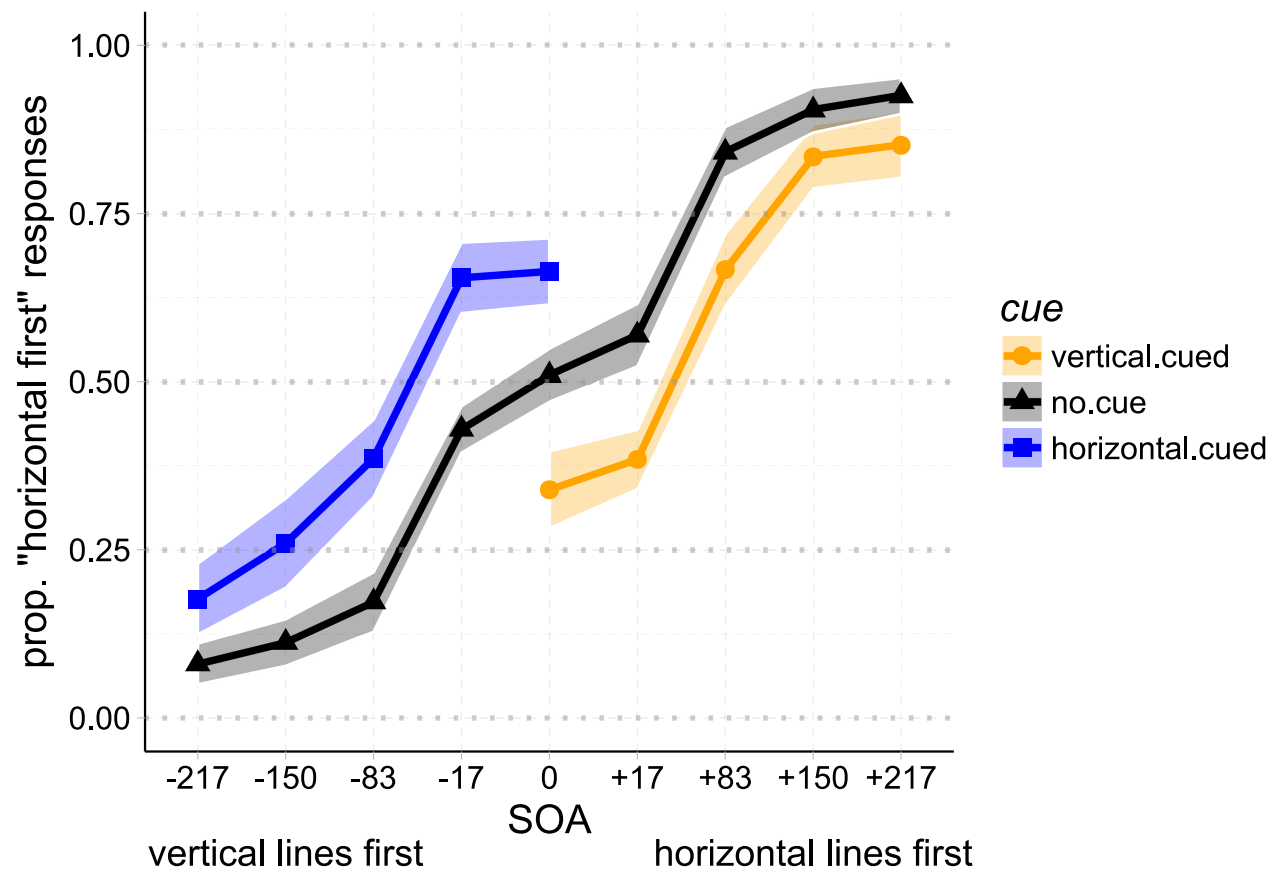
# Counterproductive T0J

- An **exogenous cue** is used to attract attention towards one placeholder
- The stimulus on the attended location is perceived as **first** even when appearing second
- What if the cue is **always wrong**, i.e., appearing on the location of the *second* stimulus?

# Counterproductive T0J



# TOJ - Data



# Bayesian multilevel modeling

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- model comparison:
  1. full model (**SOA** + **cue** + **SOA** x **cue**)
  2. main effects (**SOA** + **cue**)
  3. main effect of **SOA**
  4. main effect of **cue**
  5. **null** model (intercept only)

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- on the winning model:
  - diagnostics & posterior predictive checks
  - hypothesis testing

# Bayesian multilevel modeling with **brms**

```
##### full model (SOA * cue) #####  
model.full <- brm(num.horiz1st | trials(tot.trials) ~ SOA * cue +  
  (SOA * cue || participant),  
  data = data.T0J,  
  family = binomial("logit"),  
  prior = priors.full,  
  sample_prior = TRUE,  
  inits = "random",  
  control = list(adapt_delta = .9),  
  chains = 4,  
  iter = 2000,  
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# Bayesian multilevel modeling with **brms**

```
##### main effect of SOA #####
```

```
model.SOA <- brm(num.horiz1st | trials(tot.trials) ~ SOA +  
  (SOA || participant),  
  data = data.T0J,  
  family = binomial("logit"),  
  prior = priors.SOA,  
  sample_prior = TRUE,  
  inits = "random",  
  control = list(adapt_delta = .9),  
  chains = 4,  
  iter = 2000,  
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  thin = 1,  
  algorithm = "sampling",  
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```

# Model comparison with **brms**

(*leave-one-out* cross-validation)

```
model.comparison <- LOO( # list with all models
  model.full, model.mains, model.SOA, model.cue, model.null,
  reloo = TRUE, # exact CV for problematic observations
  compare = FALSE) # do not compare models with each other
```

```
## models L00.IC
## 1 mains 2727.31
## 2 full 2844.49
## 3 SOA 3628.22
## 4 cue 7998.10
## 5 null 8275.49
```

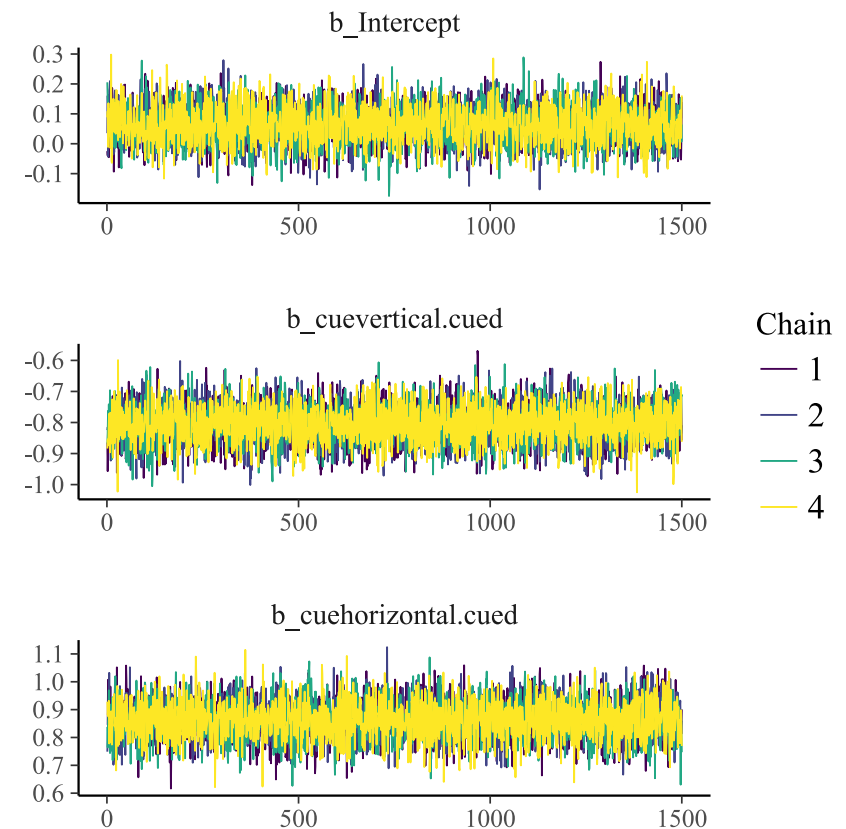
# brms output

(**main effects** model, only **constant** effects)

```
## [1] "Population-Level Effects: "  
## [2] "                Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat"  
## [3] "Intercept          0.06      0.06   -0.06    0.19      4716 1.00"  
## [4] "SOAM217             -2.64     0.13   -2.89   -2.38      4256 1.00"  
## [5] "SOAM150             -2.23     0.13   -2.50   -1.97      3727 1.00"  
## [6] "SOAM83              -1.53     0.10   -1.73   -1.34      4928 1.00"  
## [7] "SOAM17              -0.35     0.06   -0.47   -0.22      6000 1.00"  
## [8] "SOAP17              0.21     0.06    0.09    0.33      6000 1.00"  
## [9] "SOAP83              1.60     0.11    1.39    1.81      4528 1.00"  
## [10] "SOAP150             2.42     0.16    2.11    2.72      3422 1.00"  
## [11] "SOAP217             2.73     0.16    2.41    3.06      3851 1.00"  
## [12] "cuevertical.cued    -0.80     0.06   -0.93   -0.68      6000 1.00"  
## [13] "cuehorizontal.cued  0.86     0.07    0.73    1.00      5145 1.00"
```

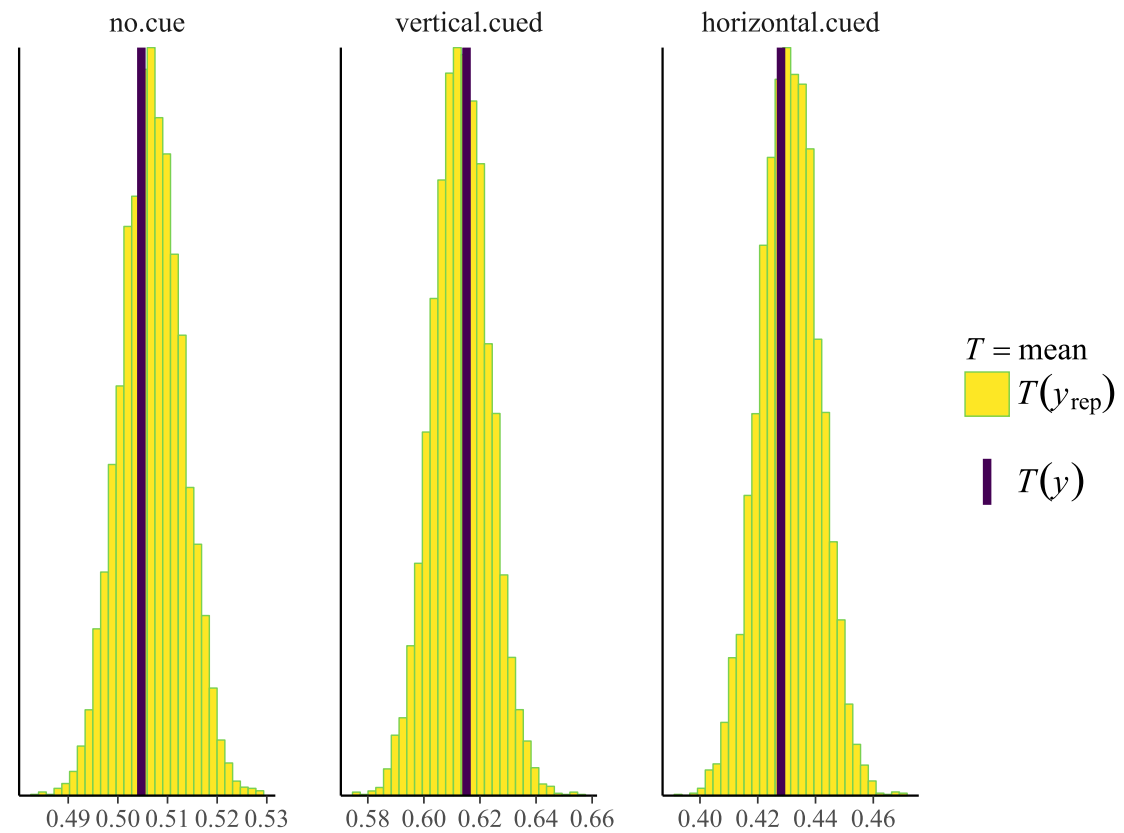
# MCMC chains

```
library(bayesplot)
mcmc_trace(as.array(model.mains),
  pars = c("b_Intercept",
    "b_cuevertical.cued",
    "b_cuehorizontal.cued"),
  facet_args = list(ncol=1))
```

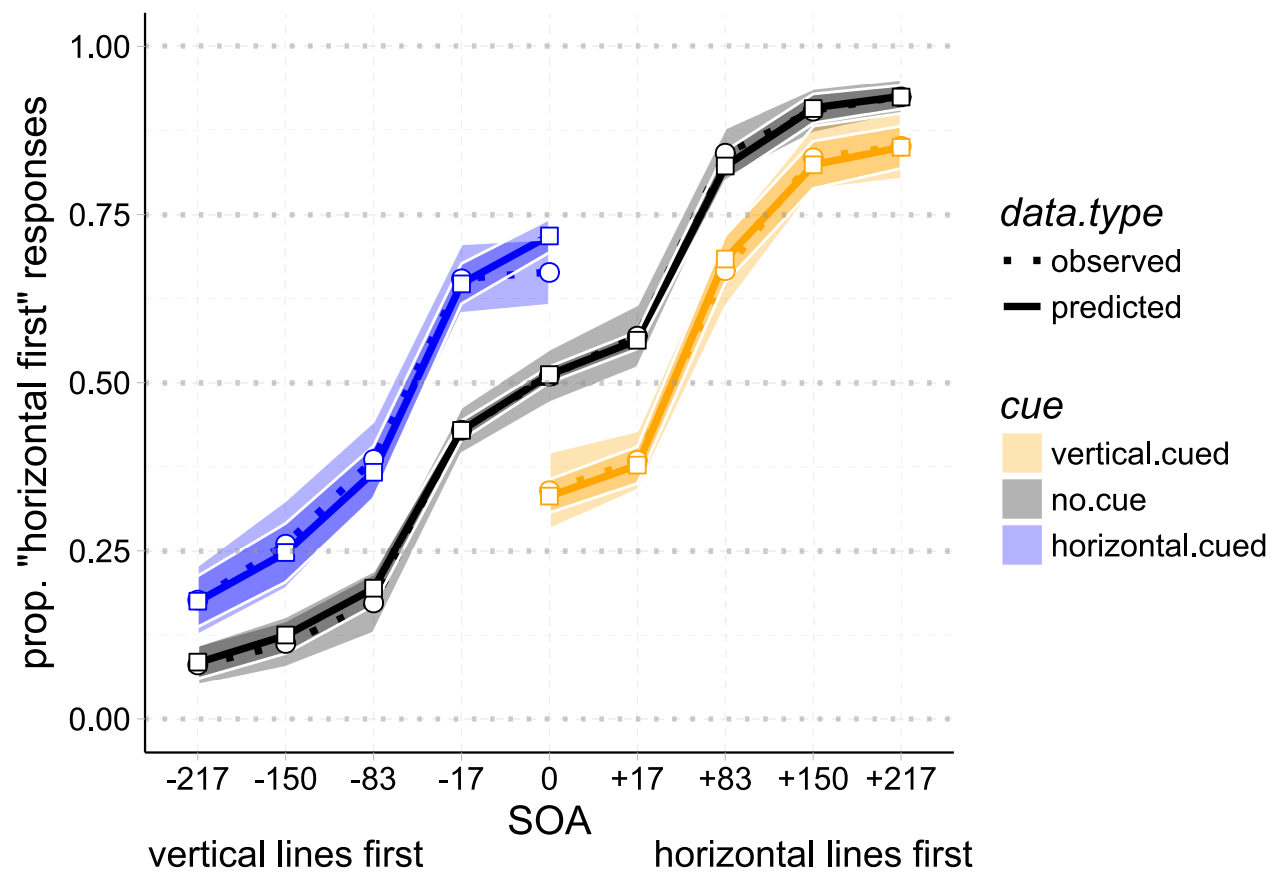


# Posterior Predictive Checks

```
pp_check(model.mains,  
nsamples = NULL,  
type = "stat_grouped",  
group = "cue")
```



# Observed vs. predicted data

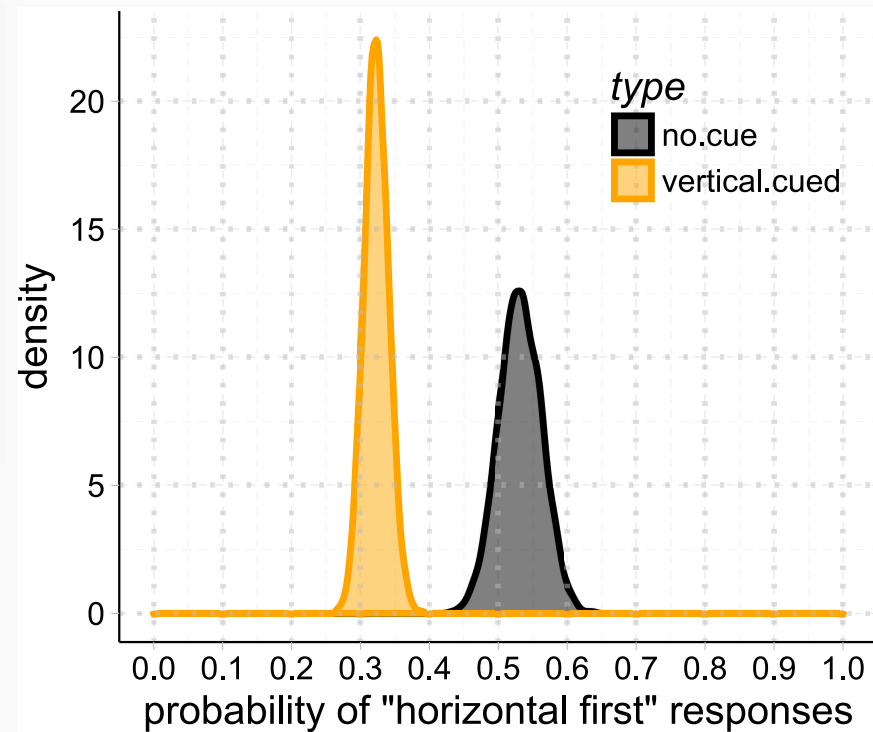




# Hypothesis testing

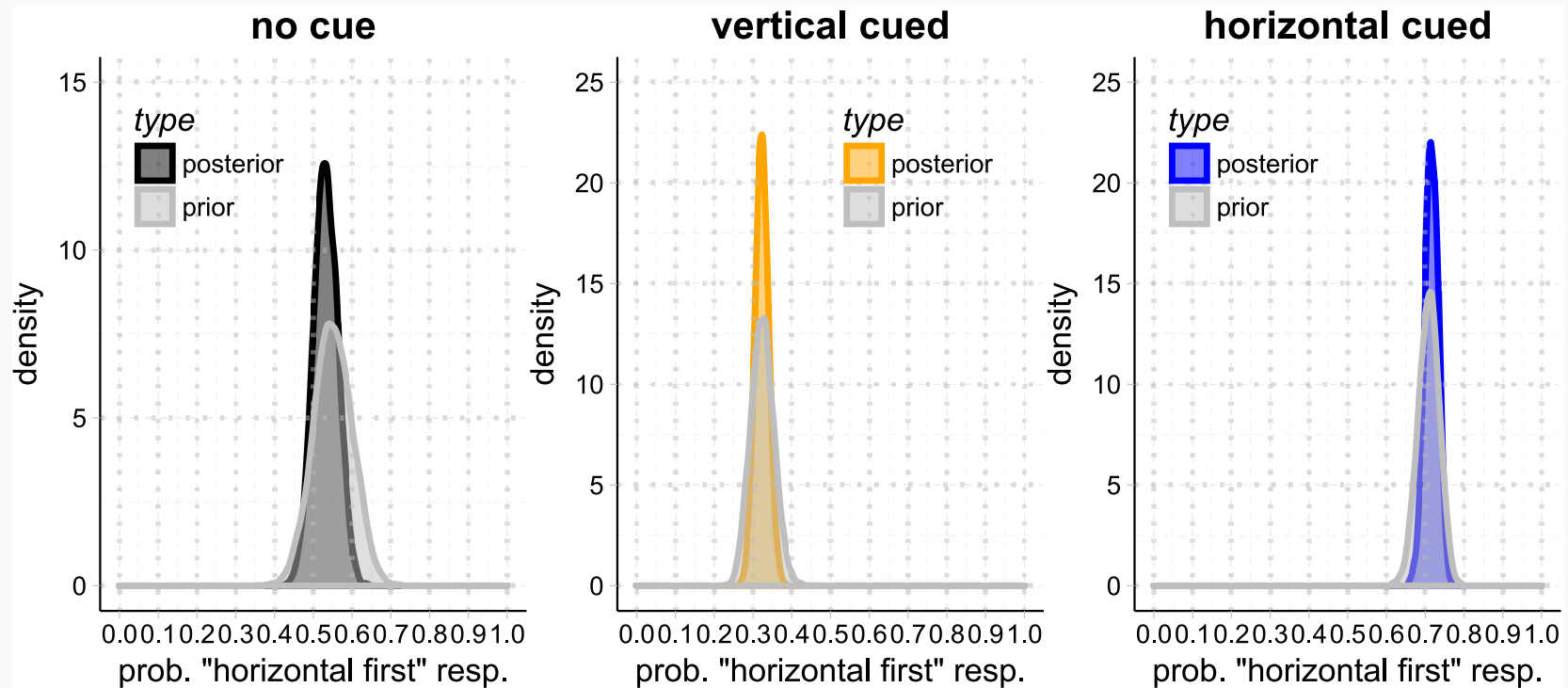
(**no cue** vs. **vertical cued** conditions)

```
# posterior probability  
# under the hypothesis  
# (no.cue=vertical.cued)  
# against its alternative  
# (no.cue!=vertical.cued)  
hypothesis(model.mains,  
"Intercept = Intercept + cuevertical.cued")
```



# Hypothesis testing

(**pilot** vs. **current** experiment)



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  - comparison of the posterior distributions of no cue and vertical cued conditions

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  - comparison of prior and posterior distributions of cue conditions
- ... and much more! Thanks for `brms`, @paulbuerkner!

# Thanks for your attention!

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Slides available here:

<https://asch3tti.netlify.com/post/bayesatlund2018/>