RD9, thresholds, P-values, 0.2s <= spikes <= 1s, AI

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## Read preprocessed RD9 data

rd\_00read\_data\_06RD2019-01-23.R: reads timestamps, counts stikes, QC;

rd\_03SC\_AI\_19\_RD9.R: fits Bayesian multilevel model for the asymmetry index AI = log2( (1+Contra)/(1+Ipsi) ) using neuronal spikes counts at [0.2; 1] sec after stimulation (slow responses).

load(file="../HarmonizedData Nabe RD 2019-01-23/EMG-RD2019-01-23-data.RData")  
load(file="AI\_Threshold\_RD9-2019-02-02.RData")  
  
myname <- "RD9 TBI-SO Stud AI\_Thr=log2(Contra\_Ipsi)" # TBI vs Sham, merging OperationSide  
#myname <- "RD9 LTBI-RTBI-SO Stud AI\_Thr=log2(Contra\_Ipsi)"   
#myname <- "RD9 LTBI-RTBI-LSO-RSO Stud AI\_Thr=log2(Contra\_Ipsi)"   
mymod <- fit[["AI.2.Thr"]] # AI.2.Thr , AI.3.Thr or AI.4.Thr  
  
d <- emgThrLat %>% # AI = log2 Contra/Ipsi  
 mutate( MSL = paste(Muscle, StimLocat, sep="."),  
 MSL = factor(MSL, sort(unique(MSL))),  
 Op3 = replace(paste0(OperationSide,Operation), Operation=="Sham", "Sham"),  
 Op3 = factor(Op3, c("Sham","LeftTBI","RightTBI"), c("SO","LTBI","RTBI")) ) %>%  
 droplevels(.)

The group sizes are (distinct rats only, same rats with different stimulation locations are counted as duplicates)

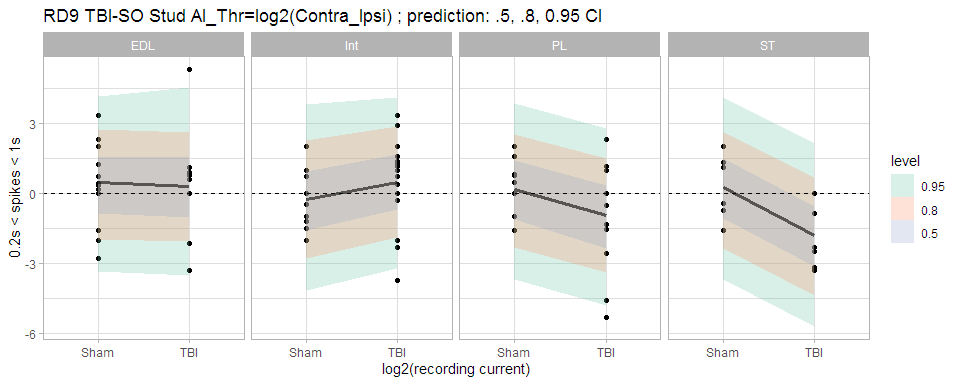
| Muscle | Sham | TBI |
| --- | --- | --- |
| EDL | 10 | 8 |
| Int | 9 | 17 |
| PL | 10 | 10 |
| ST | 7 | 7 |

## Model Overview

Model fit summary from brms:

## Family: student   
## Links: mu = identity; sigma = identity; nu = identity   
## Formula: AI\_Threshold ~ Operation \* Muscle + (1 || RatNo)   
## Data: tmp (Number of observations: 84)   
## Samples: 4 chains, each with iter = 40000; warmup = 20000; thin = 1;  
## total post-warmup samples = 80000  
##   
## Group-Level Effects:   
## ~RatNo (Number of levels: 29)   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sd(Intercept) 0.58 0.33 0.03 1.26 1.00 17761 28534  
##   
## Population-Level Effects:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS  
## Intercept 0.35 0.55 -0.72 1.43 1.00 43178  
## OperationTBI -0.08 0.84 -1.73 1.57 1.00 37841  
## MuscleInt -0.61 0.75 -2.09 0.88 1.00 49757  
## MusclePL -0.07 0.71 -1.46 1.33 1.00 53159  
## MuscleST -0.20 0.83 -1.84 1.44 1.00 53564  
## OperationTBI:MuscleInt 0.81 1.06 -1.27 2.90 1.00 40726  
## OperationTBI:MusclePL -1.20 1.10 -3.40 0.95 1.00 44440  
## OperationTBI:MuscleST -1.91 1.23 -4.33 0.49 1.00 45859  
## Tail\_ESS  
## Intercept 55772  
## OperationTBI 52010  
## MuscleInt 57527  
## MusclePL 56070  
## MuscleST 58770  
## OperationTBI:MuscleInt 52758  
## OperationTBI:MusclePL 56272  
## OperationTBI:MuscleST 57744  
##   
## Family Specific Parameters:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sigma 1.63 0.18 1.28 2.00 1.00 42793 40569  
## nu 21.30 13.59 4.73 55.66 1.00 78622 49497  
##   
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample   
## is a crude measure of effective sample size, and Rhat is the potential   
## scale reduction factor on split chains (at convergence, Rhat = 1).

Overlay of data points and model fit



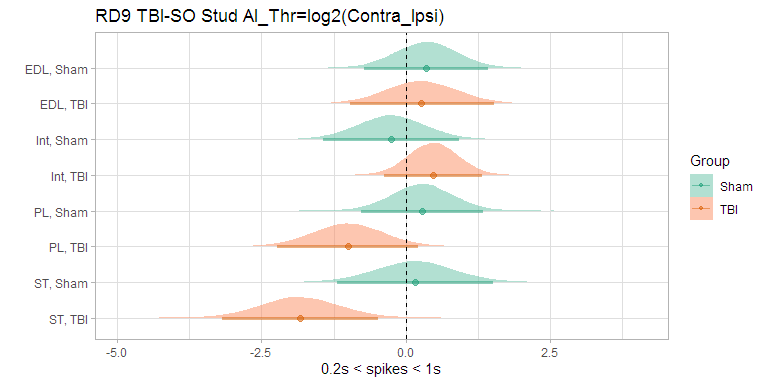
## Estimated model means

Estimated model means as a table:

emm <- emmeans(mymod, ~ Operation | Muscle)  
# emm <- emmeans(mymod, ~ Op3 | Muscle)  
# emm <- emmeans(mymod, ~ Operation\*OperationSide | Muscle)  
emm\_show(emm)

| Operation | Muscle | emmean | lower.HPD | upper.HPD | p.value |
| --- | --- | --- | --- | --- | --- |
| Sham | EDL | 0.357 | -0.702 | 1.447 | 7.68e-01 |
| TBI | EDL | 0.268 | -0.997 | 1.496 | 8.89e-01 |
| Sham | Int | -0.256 | -1.440 | 0.917 | 8.92e-01 |
| TBI | Int | 0.478 | -0.370 | 1.340 | 4.74e-01 |
| Sham | PL | 0.285 | -0.763 | 1.351 | 8.38e-01 |
| TBI | PL | -0.999 | -2.219 | 0.224 | 2.05e-01 |
| Sham | ST | 0.157 | -1.202 | 1.497 | 9.67e-01 |
| **TBI** | **ST** | **-1.840** | **-3.169** | **-0.477** | **1.52e-02** |

Estimated model means as a median +- 95% QI (QI = quantile interval):



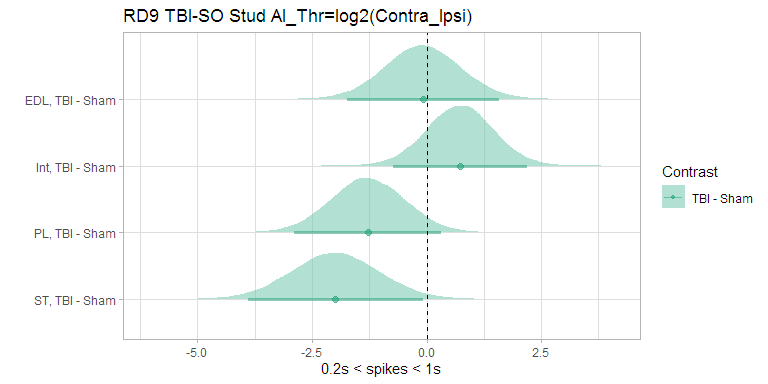
## Contrasts

Contrasts as a table:

emmc <- pairs(emm, simple="Operation", reverse=TRUE)  
# emmc <- pairs(emm, simple="Op3", reverse=TRUE)  
# emmc <- rbind( pairs(emm, simple="Operation", reverse=TRUE), pairs(emm, simple="OperationSide", reverse=TRUE))  
emm\_show(emmc)

| contrast | Muscle | estimate | lower.HPD | upper.HPD | p.value |
| --- | --- | --- | --- | --- | --- |
| TBI - Sham | EDL | -0.085 | -1.746 | 1.554 | 9.23e-01 |
| TBI - Sham | Int | 0.734 | -0.744 | 2.188 | 3.26e-01 |
| TBI - Sham | PL | -1.287 | -2.907 | 0.316 | 1.18e-01 |
| **TBI - Sham** | **ST** | **-1.992** | **-3.911** | **-0.106** | **4.01e-02** |

Contrasts TBI vs Sham as a median +- 95% QI (QI = quantile interval):



Contrasts Left operation vs Right operation as a median +- 95% QI (QI = quantile interval):

Contrasts of contrasts: “TBI vs Sham for Left-Right” is the same as “Left vs Right for TBI-Sham”

# emmc2c <- pairs(pairs(emm, simple="OperationSide", reverse=TRUE), simple="Operation", reverse=TRUE)  
# emm\_show(emmc2c)

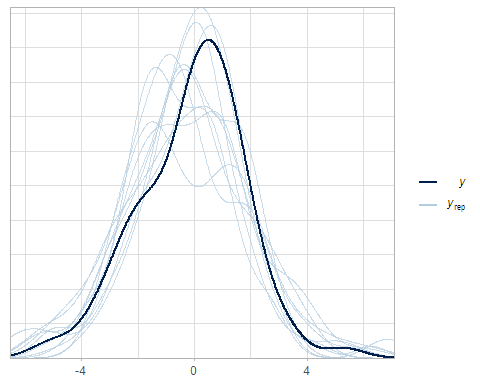
TBI vs Sham as a median +- 95% QI (QI = quantile interval) of Left operation - Right operation:

## MCMC conversion diagnostics

Posterior predictive check

print( plt5 <- pp\_check(mymod) )

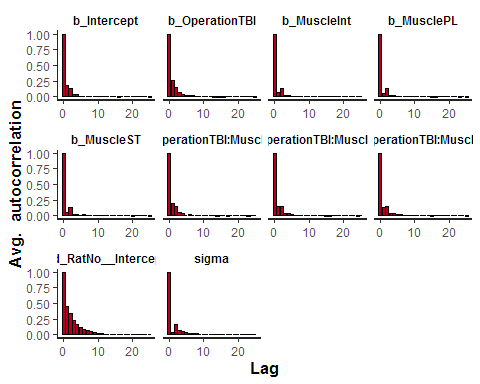
## Using 10 posterior samples for ppc type 'dens\_overlay' by default.



Autocorrelations

print( plt6 <- stan\_ac(mymod$fit) )

## 'pars' not specified. Showing first 10 parameters by default.



## Generate PowerPoint plots

Also export plots into the PowerPoint as editable objects instead of bitmaps