

Reanalysis ManyLabs 4

Julia Haaf

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```
library(BayesFactor)
library(MCMCpack)
library(knitr)
library(kableExtra)
library(metafor)
library(papaja)
require(ggplot2)

ggplot2::theme_set(theme_apo(base_size = 10))

bayesBF <- function(dat, rScale = c(1, .4, .24), M = 30000, Mprior = 200000)
{
  N <- nrow(dat)
  J <- length(unique(dat$source))
  loc <- unique(dat$source)
  cond <- 2 - as.numeric(dat$ms_condition)
  alpha <- 1:J
  beta <- (J + 2):(2 * J + 1)
  mu <- J + 1
  X <- matrix(nrow = N, ncol = 2 * J + 1, 0)

  for(i in 1:N){
    locit <- which(loc == dat$source[i])
    X[i, locit] <- 1
    X[i, J + 1] <- cond[i]
    X[i, J + 1 + locit] <- cond[i]
  }

  gMap <- rep(0:2, c(J, 1, J))
  samples <- nWayAOV(dat$pro_minus_anti, X
    , gMap, rscale = rScale
    , posterior = T, iterations = M)
  bfFull <- nWayAOV(dat$pro_minus_anti, X
    , gMap, rscale = rScale
    , posterior = F, iterations = M)$bf
  bfNull <- nWayAOV(dat$pro_minus_anti, X[, 1:J]
    , gMap[1:J], rscale = rScale[1]
    , posterior = F, iterations = M)$bf
  bfOne <- nWayAOV(dat$pro_minus_anti, X[, 1:(J + 1)]
    , gMap = rep(0:1, c(J, 1)), rscale = rScale[1:2]
    , posterior = F, iterations = M)$bf
  samplesOne <- nWayAOV(dat$pro_minus_anti, X[, 1:(J + 1)]
    , gMap = rep(0:1, c(J, 1)), rscale = rScale[1:2]
    , posterior = T, iterations = M)

  #Positive Effects (random)
  effect <- samples[500:M, beta + 1] + samples[500:M, mu + 1]
  post.pos <- mean(apply(effect > 0, 1, mean) == 1)
```

```

gm <- rinvgamma(Mprior, .5, .5 * rScale[3]^2)
m.1 <- rnorm(Mprior, 0, sqrt(gm))
g <- rinvgamma(Mprior, .5, .5*rScale[2]^2)
a1 <- 1:Mprior
for (m in 1:Mprior) a1[m] = mean(rnorm(J, m.1[m], sqrt(g[m]))) > 0)
prior.pos <- mean(a1 == 1)

#Positive Effect (common)
effectOne <- samplesOne[500:M, mu + 1]
post.pos.One <- mean(effectOne > 0)
bfpostUpdate <- post.pos.One / .5

bf <- c(exp(bfFull - bfNull)
        , exp(bfOne - bfNull) * bfpostUpdate
        , exp(bfFull - bfNull) * post.pos/prior.pos)
out <- c(bf, post.pos, prior.pos)
names(out) <- c("F0", "10", "P0", "post.pos", "prior.pos")
return(list("bfs" = out, "effects" = effect, "N" = nrow(dat)))
}

simple.fig <- function(dat){
  meansbycondloc <- with(dat
    , tapply(pro_minus_anti
      , list(source, ms_condition)
      , mean, na.rm = TRUE))
  effects <- meansbycondloc[, 1] - meansbycondloc[, 2]
  plot(sort(effects)
    , pch = 19, ylab = "Effect", xlab = "Source")
  abline(h = 0)
}

```

Reanalysis with Exclusion Criterion .1.1

This is the original main analysis that is the basis for the key claims of the Many Labs 4 project.

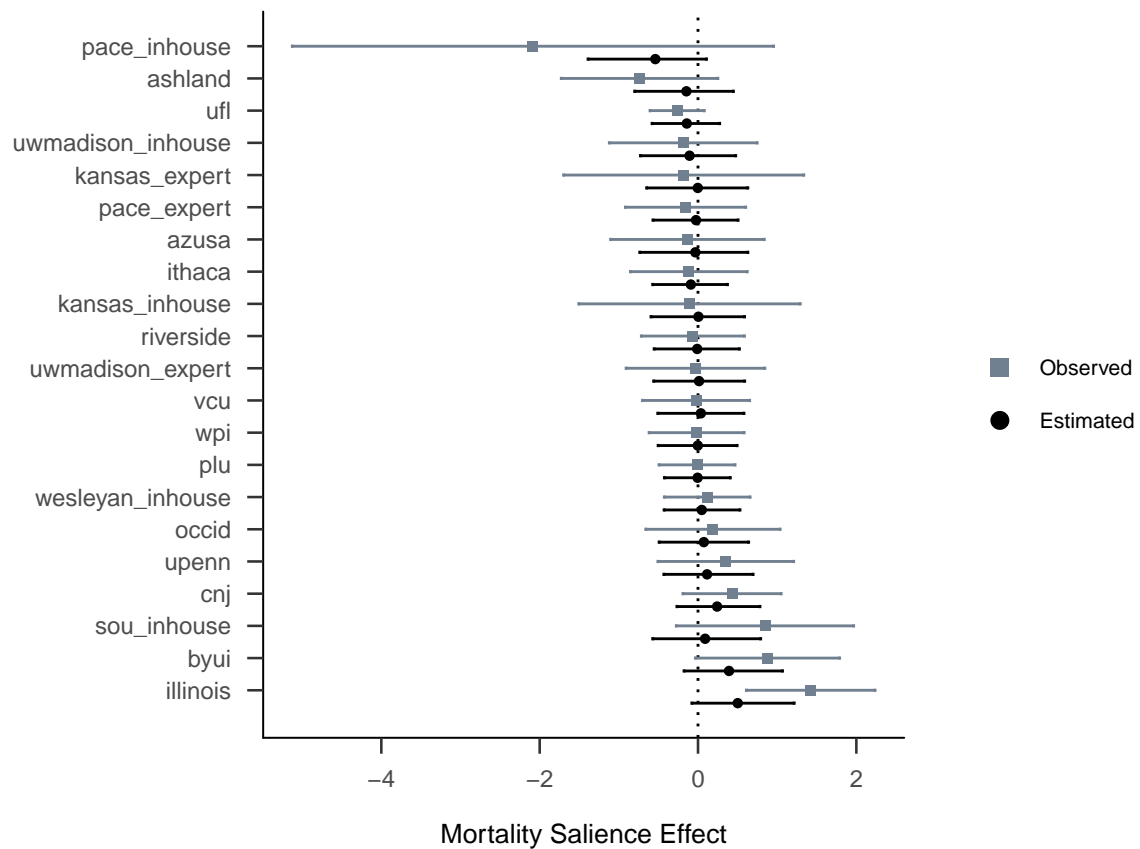
```

dat.111 <- read.csv2("data/reanalysis_111.csv", header = T)
dat.211 <- read.csv2("data/reanalysis_211.csv", header = T)
dat.311 <- read.csv2("data/reanalysis_311.csv", header = T)

rean.111 <- bayesBF(dat = dat.111)
rean.111$bfs

##           F0           10           P0    post.pos    prior.pos
## 2.862329e-02 9.560658e-02 5.989185e-05 1.694858e-04 8.100000e-02
resFig(rean.111$effects, dat = dat.111)

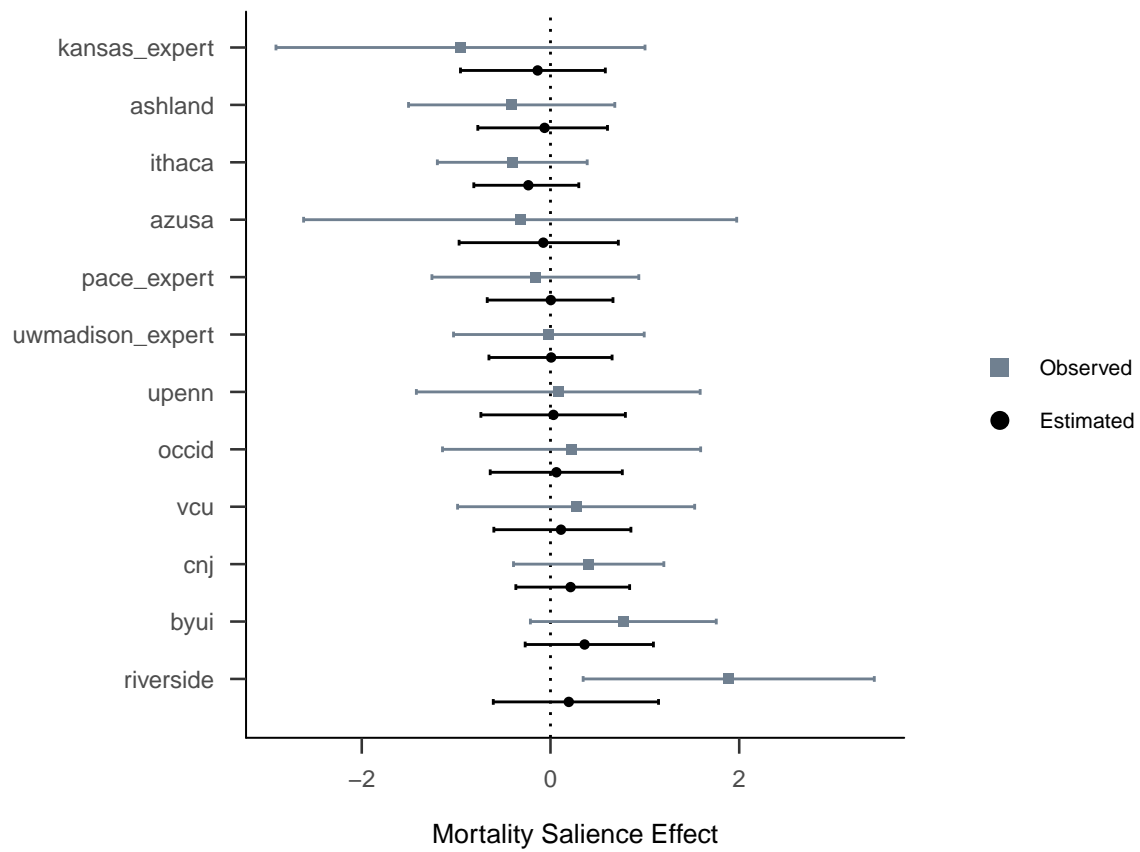
```



```
rean.211 <- bayesBF(dat = dat.211)
rean.211$bfs

##          F0          10          P0    post.pos    prior.pos
## 0.051124216 0.178002055 0.008001081 0.015016440 0.095950000

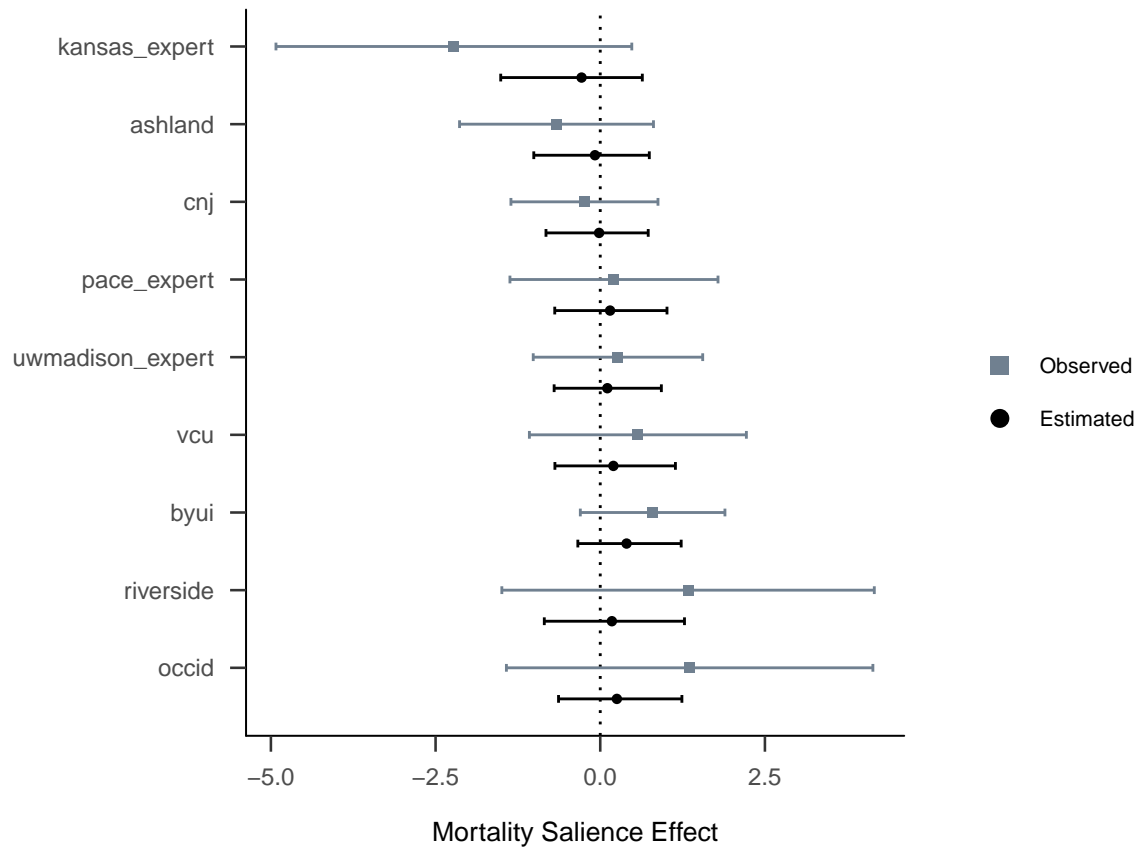
resFig(rean.211$effects, dat = dat.211)
```



```
rean.311 <- bayesBF(dat = dat.311)
rean.311$bfs

##          F0          10          P0  post.pos  prior.pos
## 0.10987357 0.36120277 0.07667120 0.07487882 0.10730500

resFig(rean.311$effects, dat = dat.311)
```



Reanalysis with Exclusion Criterion .3.2

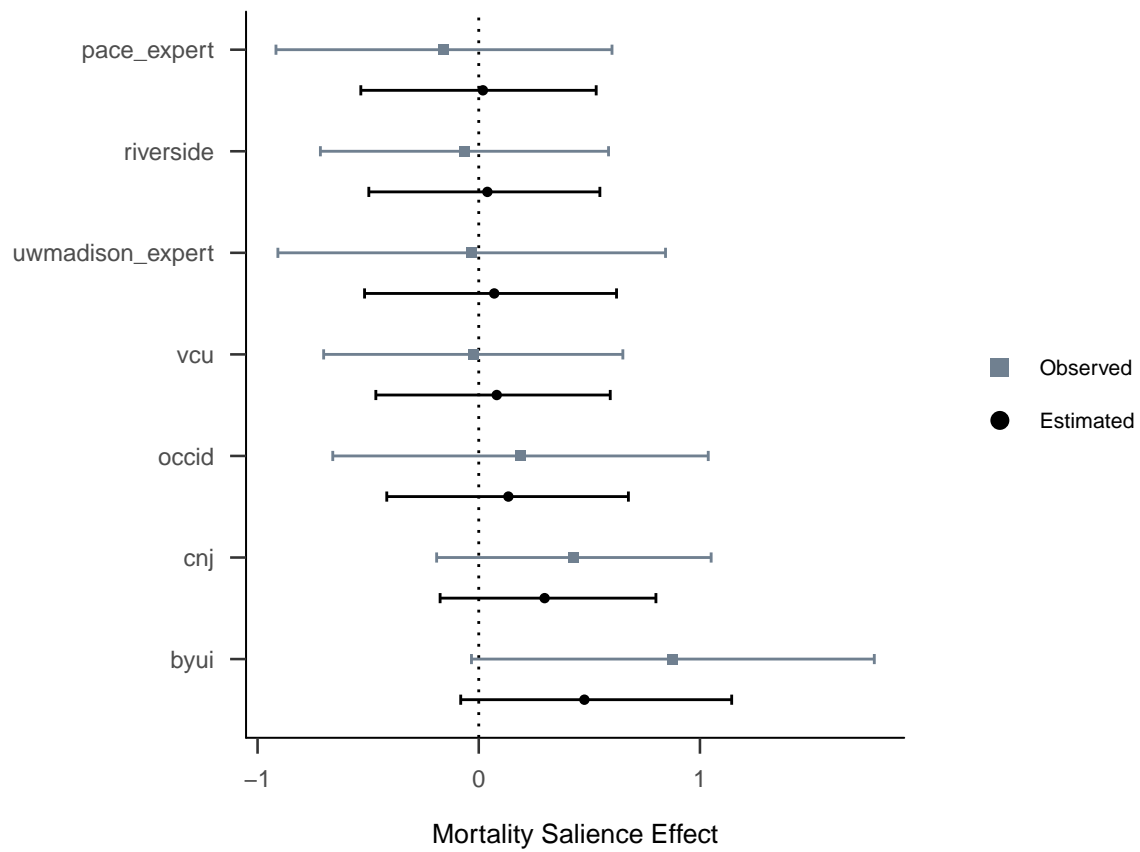
(1,3,2), (2,3,2), and (3,3,2)

```
dat.132 <- read.csv2("data/reanalysis_132.csv", header = T)
dat.232 <- read.csv2("data/reanalysis_232.csv", header = T)
dat.332 <- read.csv2("data/reanalysis_332.csv", header = T)
```

```
rean.132 <- bayesBF(dat = dat.132)
rean.132$bfs
```

```
##          F0          10          P0 post.pos prior.pos
## 0.07335040 0.48437815 0.08537658 0.14291041 0.12278000
```

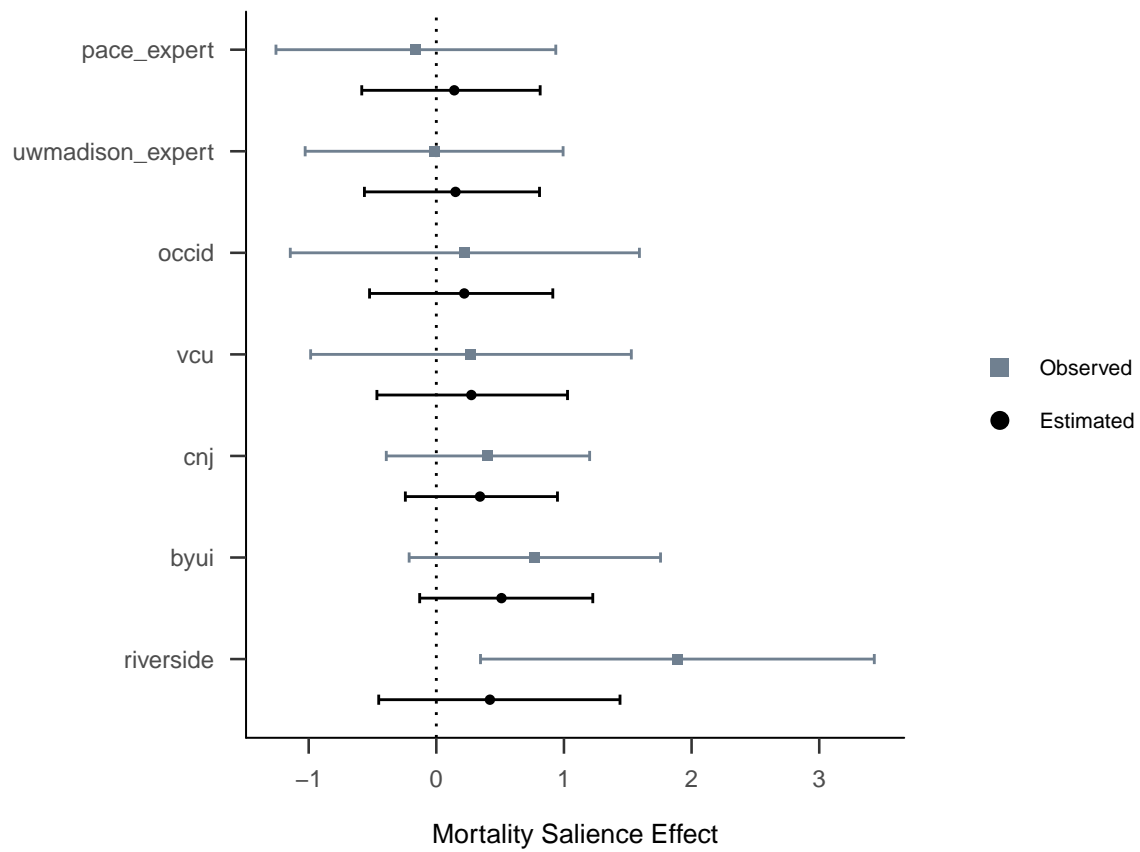
```
resFig(rean.132$effects, dat = dat.132)
```



```
rean.232 <- bayesBF(dat = dat.232)
rean.232$bfs
```

```
##          F0          10          P0 post.pos prior.pos
## 0.1501145 1.0302587 0.3725873 0.3018881 0.1216300
```

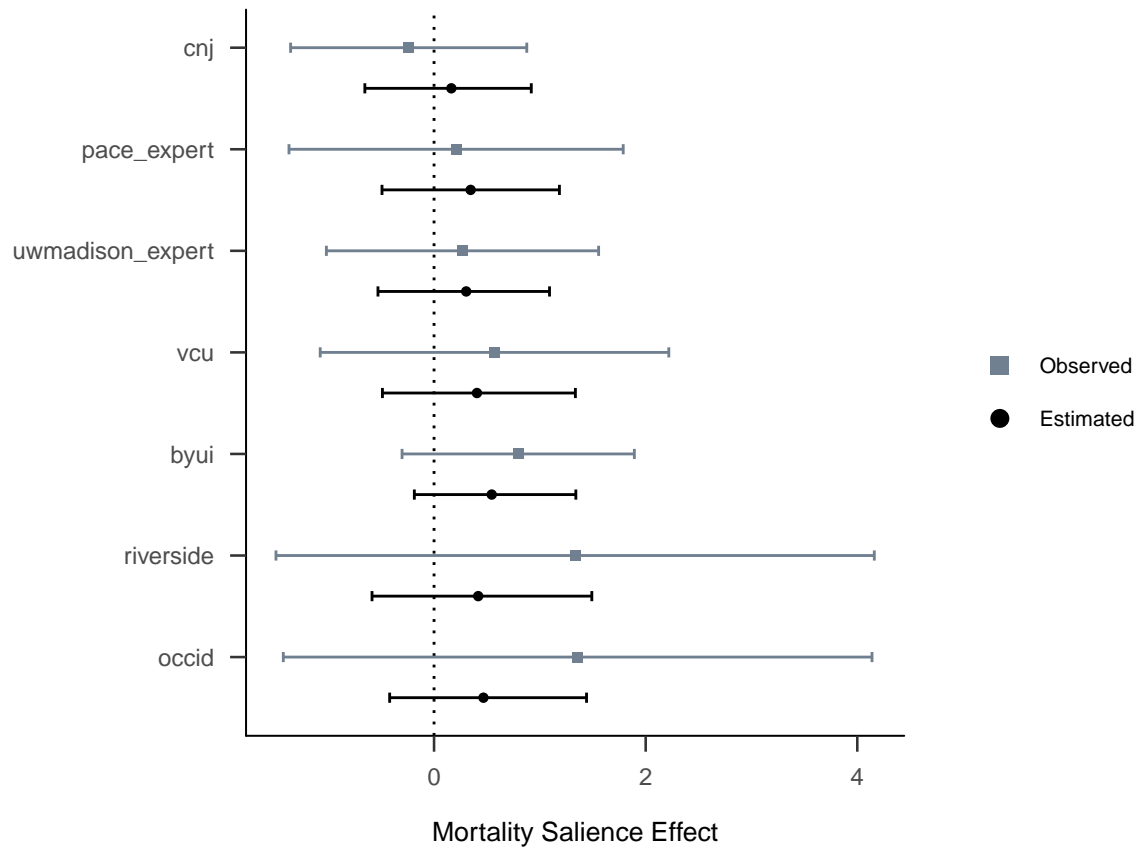
```
resFig(rean.232$effects, dat = dat.232)
```



```
rean.332 <- bayesBF(dat = dat.332)
rean.332$bfs
```

```
##          F0          10          P0 post.pos prior.pos
## 0.2063963 1.2245972 0.6351083 0.3767330 0.1224300
```

```
resFig(rean.332$effects, dat = dat.332)
```



Summary

```
BFs <- rbind(rean.111$bfs, rean.211$bfs, rean.311$bfs, rean.132$bfs, rean.232$bfs, rean.332$bfs)
BFs <- round(1/ BFs[, 1:3], 2)
Ns <- c(rean.111$N, rean.211$N, rean.311$N, rean.132$N, rean.232$N, rean.332$N)
BFs <- cbind(Ns, BFs)
rownames(BFs) <- paste("Exclusion Criterion", c(111, 211, 311, 132, 232, 332))
colnames(BFs) <- c("Sample Size", "$BF_{0f}$", "$BF_{01}$", "$BF_{0+}$")

apa_table(BFs, escape = FALSE, caption = "Bayes factors for key analyses.", note = "All Bayes factors a

#
# kable(BFs, escape = FALSE, format = "latex") %>%
# kable_styling(latex_options = "striped", font_size = 12)
```


Table 1: Bayes factors for key analyses.

	Sample Size	BF_{0f}	BF_{01}	BF_{0+}
Exclusion Criterion 111	2,211.00	34.94	10.46	16,696.76
Exclusion Criterion 211	637.00	19.56	5.62	124.98
Exclusion Criterion 311	277.00	9.10	2.77	13.04
Exclusion Criterion 132	700.00	13.63	2.06	11.71
Exclusion Criterion 232	386.00	6.66	0.97	2.68
Exclusion Criterion 332	229.00	4.85	0.82	1.57

Note. All Bayes factors are reported in favor of the null model.