

Reanalysis

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```
library(ggpubr)

## Loading required package: ggplot2
## Loading required package: magrittr
library(metaBMA)

## Loading required package: Rcpp
library(ggplot2)
library(knitr)
library(kableExtra)
library(papaja)
library(lemon)

ggplot2::theme_set(theme_apa(base_size = 12))
```

This document combines all analyses to draw plots.

Running Analyses

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

ggplot2::theme_set(theme_apa(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", "I0", "P0", "post.pos", "prior.pos")

effsize <- samples[500:M, mu + 1]/sqrt(samples[500:M, 2 * J + 3])
effsizeCI <- quantile(effsize, probs = c(.025, .975))

return(list("bfs" = out, "effects" = effect, "N" = nrow(dat), "ES" = mean(effsize), "CI" = effsizeCI))
}

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
## 0.0286022429 0.0963455239 0.0000954560 0.0002711772 0.0812550000

```

```
rean.111$ES
```

```
## [1] 0.009109488
```

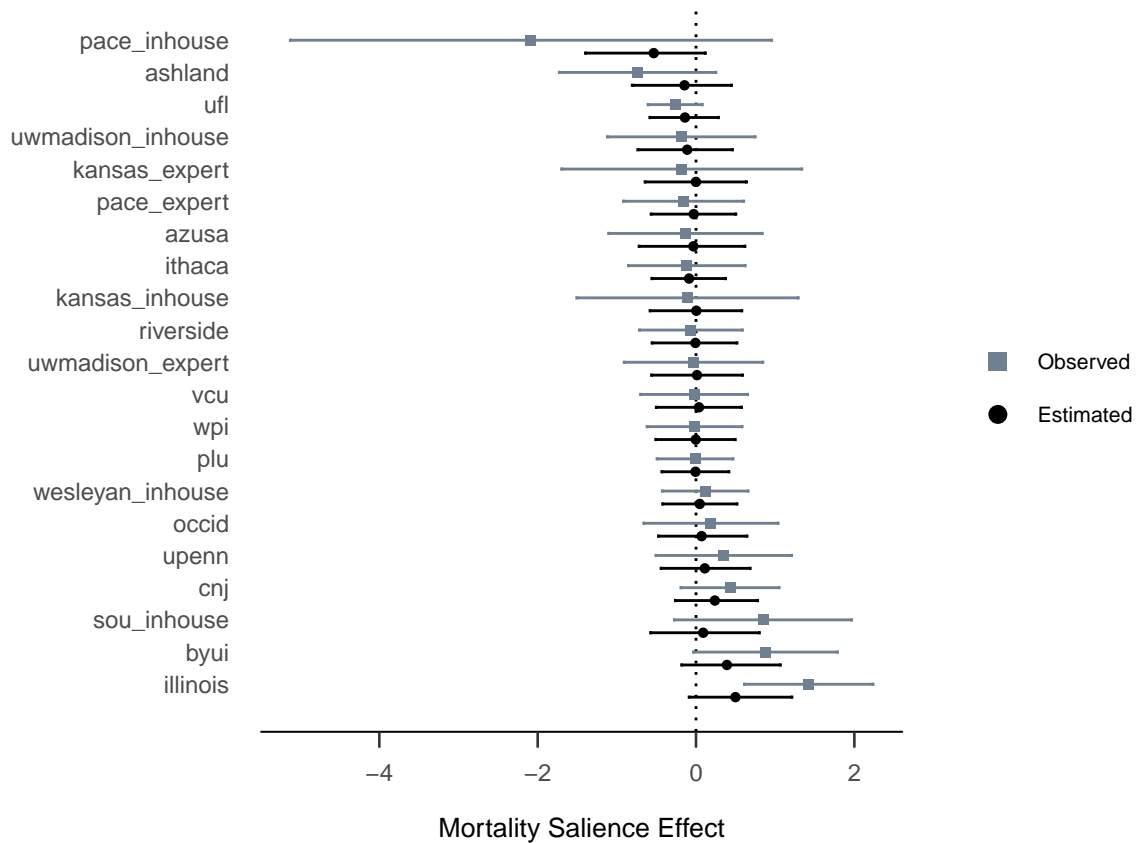
```
rean.111$CI
```

```

##      2.5%      97.5%
## -0.106000  0.123864

```

```
resFig(rean.111$effects, dat = dat.111)
```



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

```
##          F0          10          P0    post.pos    prior.pos
## 0.051258343 0.175450591 0.008369224 0.015796075 0.096745000
```

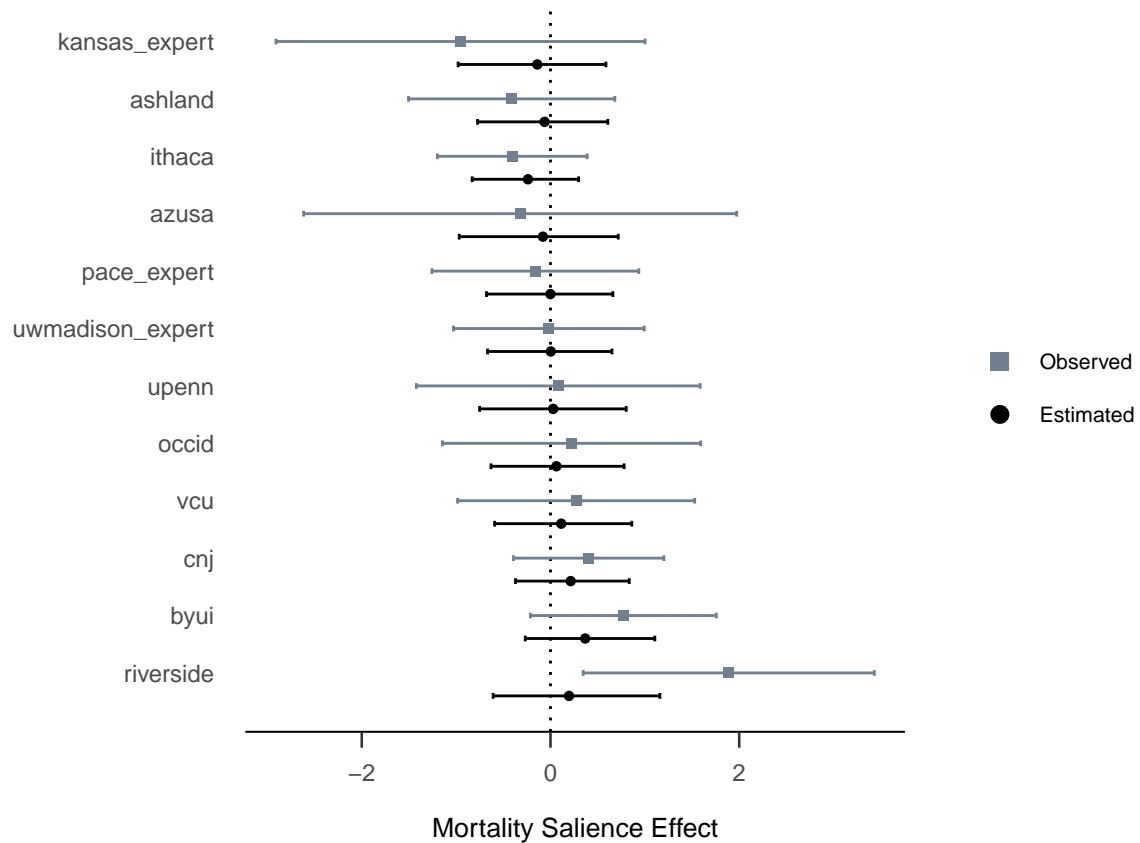
```
rean.211$ES
```

```
## [1] 0.01760426
```

```
rean.211$CI
```

```
##          2.5%          97.5%
## -0.1745616  0.2110923
```

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



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

##          F0          10          P0 post.pos prior.pos
## 0.10914313 0.35830152 0.07673534 0.07606522 0.10819000

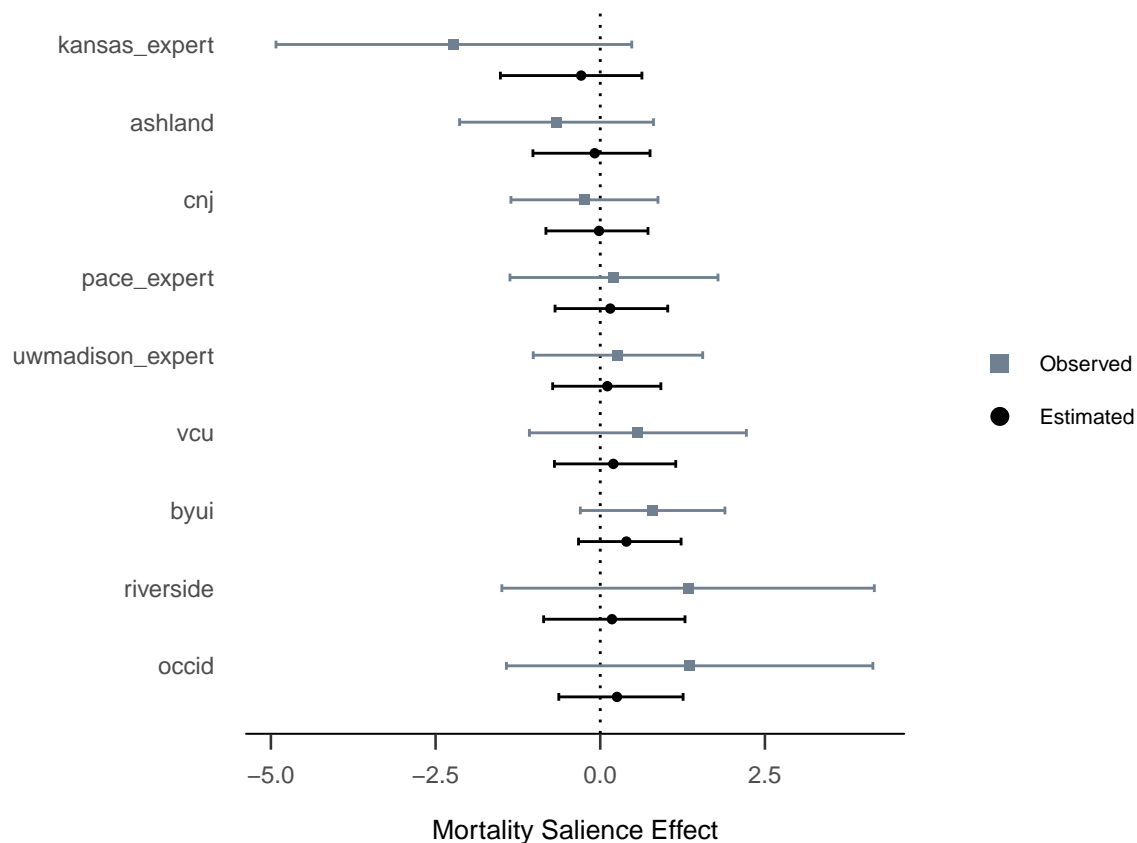
rean.311$ES

## [1] 0.04562541

rean.311$CI

##          2.5%          97.5%
## -0.2247833  0.3176610

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
## 0.07280708 0.48246173 0.08146795 0.13857157 0.12384000
```

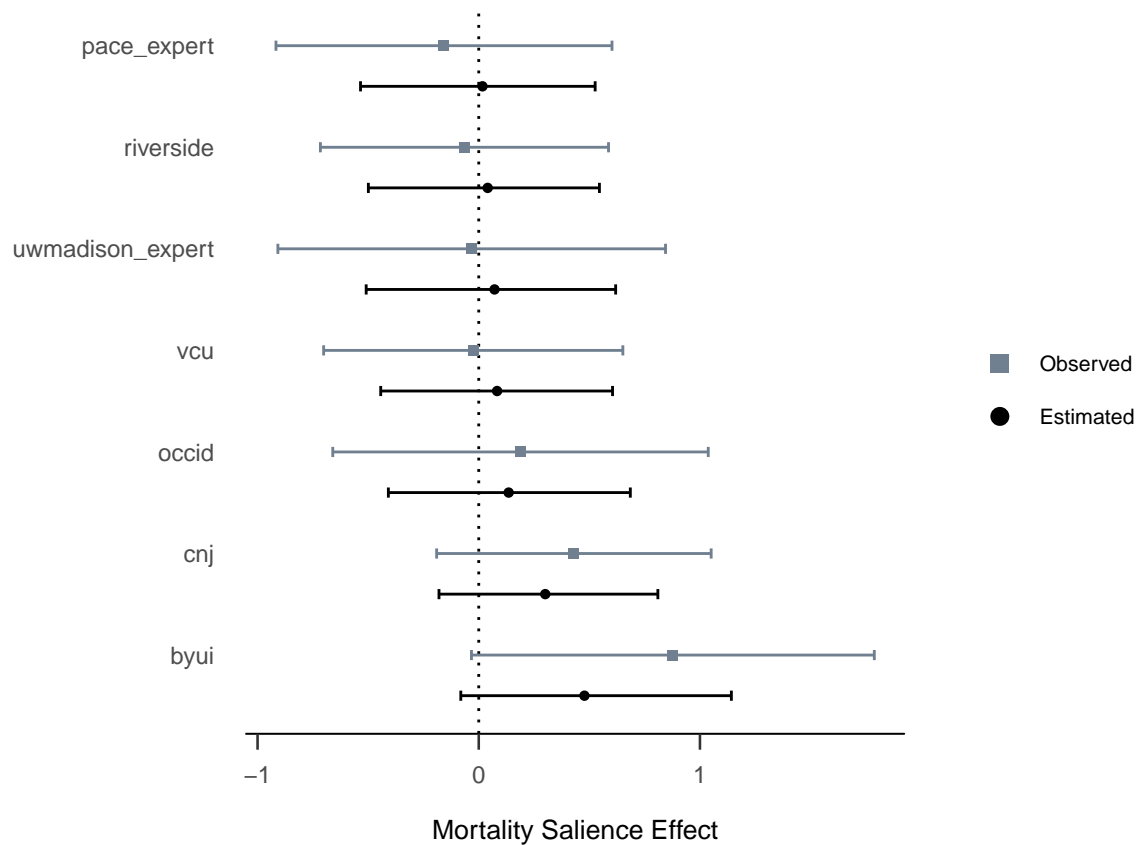
```
rean.132$ES
```

```
## [1] 0.08099185
```

```
rean.132$CI
```

```
##          2.5%          97.5%
## -0.1207725  0.2793634
```

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



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

```
##          F0          10          P0 post.pos prior.pos
## 0.1488152 1.0281878 0.3702084 0.3082268 0.1239000
```

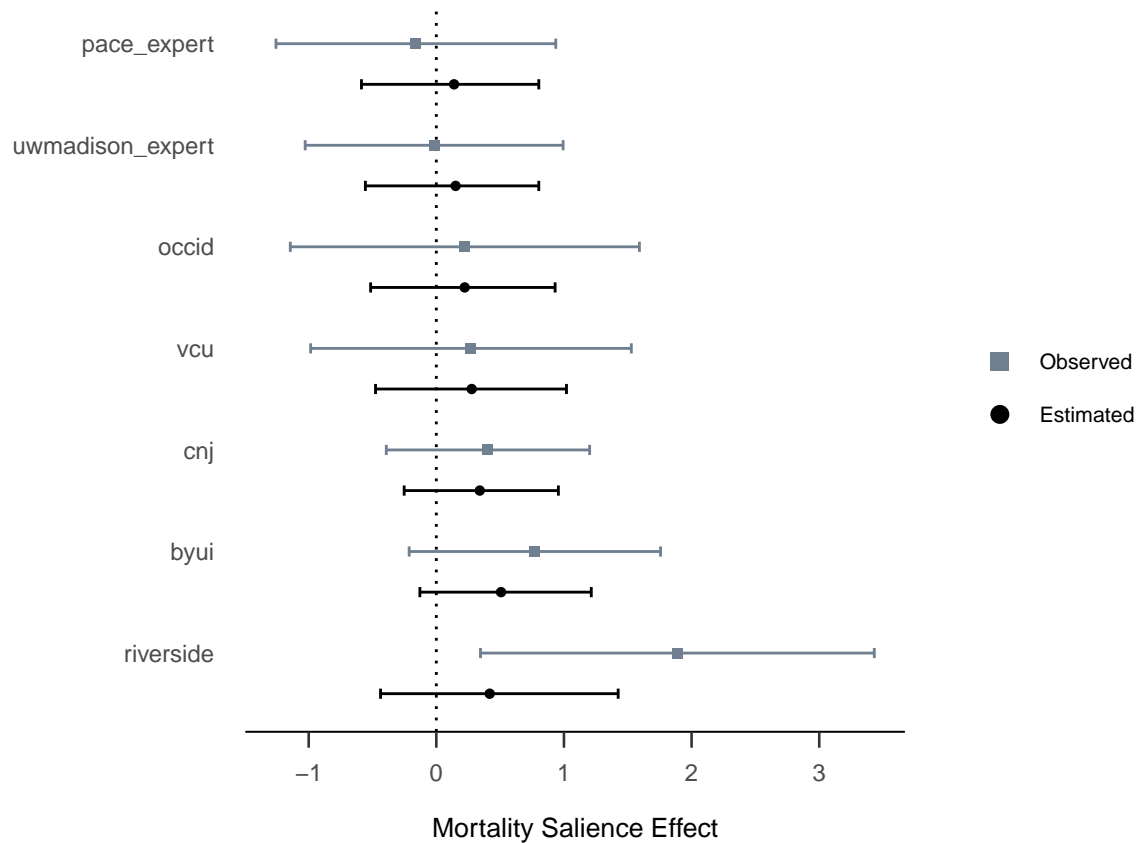
```
rean.232$ES
```

```
## [1] 0.1386719
```

```
rean.232$CI
```

```
##          2.5%          97.5%
## -0.1108561 0.3882399
```

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



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

```
##          F0          10          P0 post.pos prior.pos
## 0.2037756 1.1838467 0.6414410 0.3848005 0.1222450
```

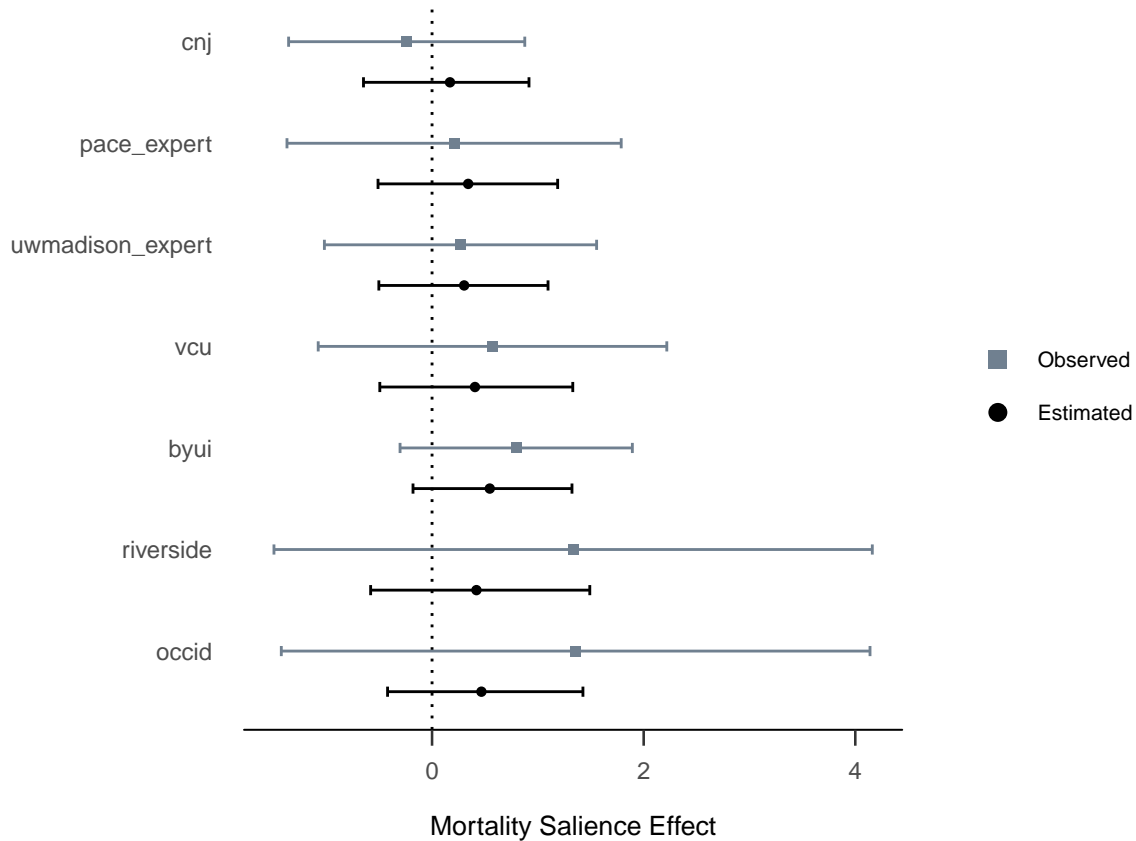
```
rean.332$ES
```

```
## [1] 0.1746868
```

```
rean.332$CI
```

```
##          2.5%          97.5%
## -0.1211669  0.4783894
```

```
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)

library(metaBMA)
library(ggplot2)
library(knitr)
library(kableExtra)
library(papaja)
library(lemon)

ggplot2::theme_set(theme_apa(base_size = 12))

default.prior <- prior(family = "t",
  param = c(0, 0.707, 1)
  , lower = 0
```

Table 1: Bayes factors for key analyses.

	Sample Size	BF_{0f}	BF_{01}	BF_{0+}
Exclusion Criterion 111	2,211.00	34.96	10.38	10,476.03
Exclusion Criterion 211	637.00	19.51	5.70	119.49
Exclusion Criterion 311	277.00	9.16	2.79	13.03
Exclusion Criterion 132	700.00	13.73	2.07	12.27
Exclusion Criterion 232	386.00	6.72	0.97	2.70
Exclusion Criterion 332	229.00	4.91	0.84	1.56

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

```

    )

oosterwijk.prior <- prior(family = "t",
                        param = c(0.35, 0.102, 3)
                        , lower = 0
                        )

vohs.prior      <- prior(family = "norm",
                        param = c(0.3, 0.15)
                        , lower = 0
                        )

priors <- list(default = default.prior,
              oosterwijk = oosterwijk.prior,
              vohs = vohs.prior
              )

# lower truncate priors at zero?

.bmaCalculateBFHeterogeneity <- function(prior_models, posterior_models){
# Returns the heterogeneity Bayes factor

  postOdds <- (posterior_models["random_H0"] + posterior_models["random_H1"]) /
              (posterior_models["fixed_H0"] + posterior_models["fixed_H1"])
  priorOdds <- (prior_models[3] + prior_models[4]) / (prior_models[1] + prior_models[2])
  BFheterogeneity <- postOdds/priorOdds
  return(BFheterogeneity)
}

# BFrf or BFfr?

.runRema <- function(y, SE, priors, extrainfo = FALSE){
# Returns a list containing:
# BFmu: dataframe with 1 row/3columns (BF per prior)

```

```

# BFtau: dataframe with 1 row/3columns (BF per prior)
# est: list containing 3 dataframes per prior
#       with effect size and 95% credible interval estimates

BFmu <- BFtau <- data.frame(default = 0,
                             oosterwijk = 0,
                             vohs = 0
                             )

empty.dataframe <- data.frame(est.es = numeric(),
                              est.lower = numeric(),
                              est.upper = numeric()
                              )

est <- list(default = empty.dataframe,
            oosterwijk = empty.dataframe,
            vohs = empty.dataframe
            )

for(i in 1:length(priors)){
  rema <- meta_bma(y, SE, d = priors[[i]], control = list(adapt_delta = 0.995))
  BFmu[, i] <- 1/rema$inclusion$incl.BF # BF in favour of the null model
  if(extrainfo){
    BFtau[i] <- .bmaCalculateBFHeterogeneity(rema$prior_models, rema$posterior_models)
    est.es <- rstan::summary(rema$meta$random$stanfit_dstudy)$summary[3:(length(y) + 2), "mean"]
    est.lower <- rstan::summary(rema$meta$random$stanfit_dstudy)$summary[3:(length(y) + 2), "2.5%"]
    est.upper <- rstan::summary(rema$meta$random$stanfit_dstudy)$summary[3:(length(y) + 2), "97.5%"]
    est[[i]] <- rbind(est[[i]], cbind(est.es, est.lower, est.upper))
  }
}
if(!extrainfo){
  return(BFmu)
} else {
  remaResult <- list(BFmu = BFmu,
                    BFtau = BFtau,
                    est = est
                    )
  return(remaResult)
}
}

remaForest <- function(obs.data, est.data){
# Returns a forest plot with observed and estimated effects

I <- nrow(obs.data)
ord <- order(obs.data$yi)
es <- obs.data$yi[ord]
est.es <- est.data[ord, "est.es"]
est.lower <- est.data[ord, "est.lower"]
est.upper <- est.data[ord, "est.upper"]
studyLabels <- obs.data[ord, "source"]

lower <- es - qnorm(1.95/2) * obs.data$sei
upper <- es + qnorm(1.95/2) * obs.data$sei

```

```

y.obs <- I:1
y.est <- rev(seq(.6, I - .4, 1))

dfBoth <- data.frame(es = c(es, est.es),
                     y = c(y.obs, y.est),
                     studyLabels = c(studyLabels, studyLabels),
                     lower = c(lower, est.lower), upper = c(upper, est.upper),
                     g = rep(c("Observed", "Estimated"), each = I)
                     )

plot <- ggplot(dfBoth, aes(x = es, y = y)) +
  geom_vline(xintercept = 0, linetype = "dotted") +
  geom_point(aes(shape = as.factor(dfBoth$g), colour = as.factor(dfBoth$g))) +
  geom_errorbarh(aes(xmin = dfBoth$lower, xmax = dfBoth$upper, colour = as.factor(dfBoth$g)),
                 height = .1, show.legend = FALSE) +
  scale_y_continuous(breaks = I:1, labels = as.character(studyLabels),
                     expand = c(0, 0.5)) +
  scale_color_manual("", values = c("black", "slategrey"),
                     labels = c(gettext("Estimated"), gettext("Observed"))) +
  scale_shape_manual("", values = c(16, 15)) +
  guides(shape = guide_legend(reverse=TRUE, override.aes = list(size=3)),
         colour = guide_legend(reverse=TRUE)) +
  xlab("Mortality Salience Effect") +
  ylab(" ") +
  theme(axis.line.y = element_blank(),
        axis.ticks.y = element_blank())

return(plot)
}

```

Original Analysis

```

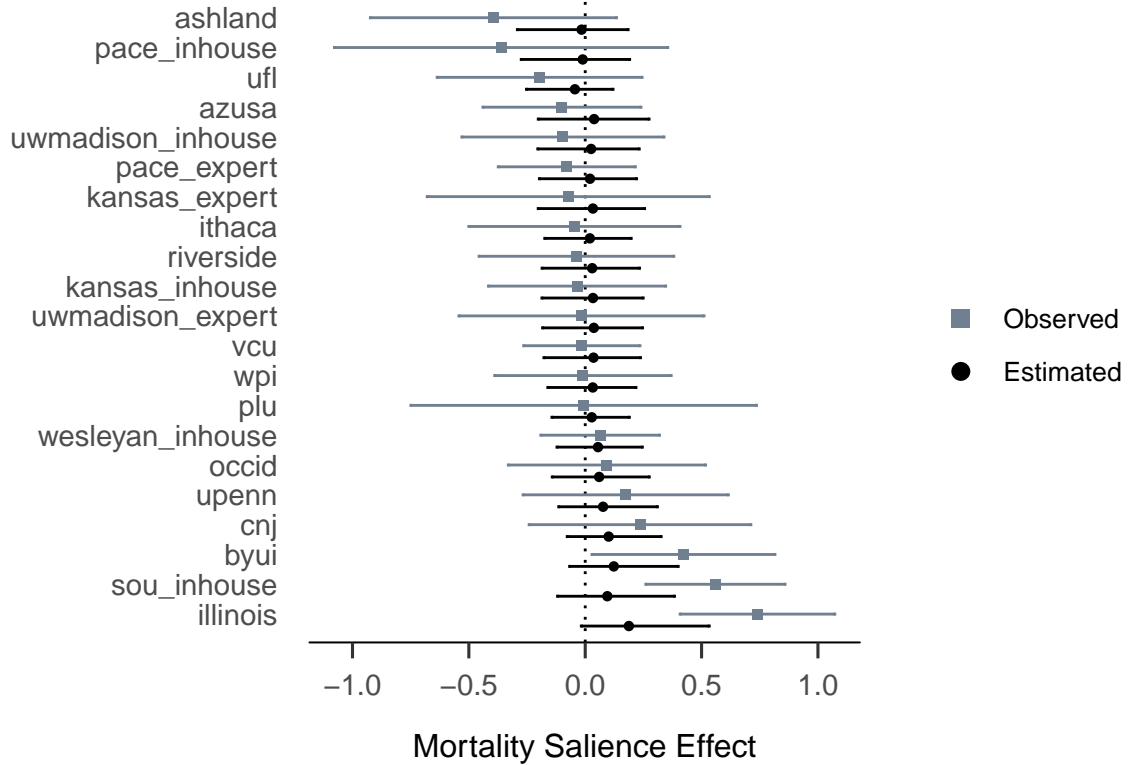
m.111 <- read.csv2("data/metaset_111.csv", header = T)
m.211 <- read.csv2("data/metaset_211.csv", header = T)
m.311 <- read.csv2("data/metaset_311.csv", header = T)

rema.111 <- .runRema(m.111$yi, m.111$sei, priors, TRUE)
rema.211 <- .runRema(m.211$yi, m.211$sei, priors, TRUE)
rema.311 <- .runRema(m.311$yi, m.311$sei, priors, TRUE)

remaForest(m.111, rema.111$est$default) + ggtitle("Exclusion Criterion 111")

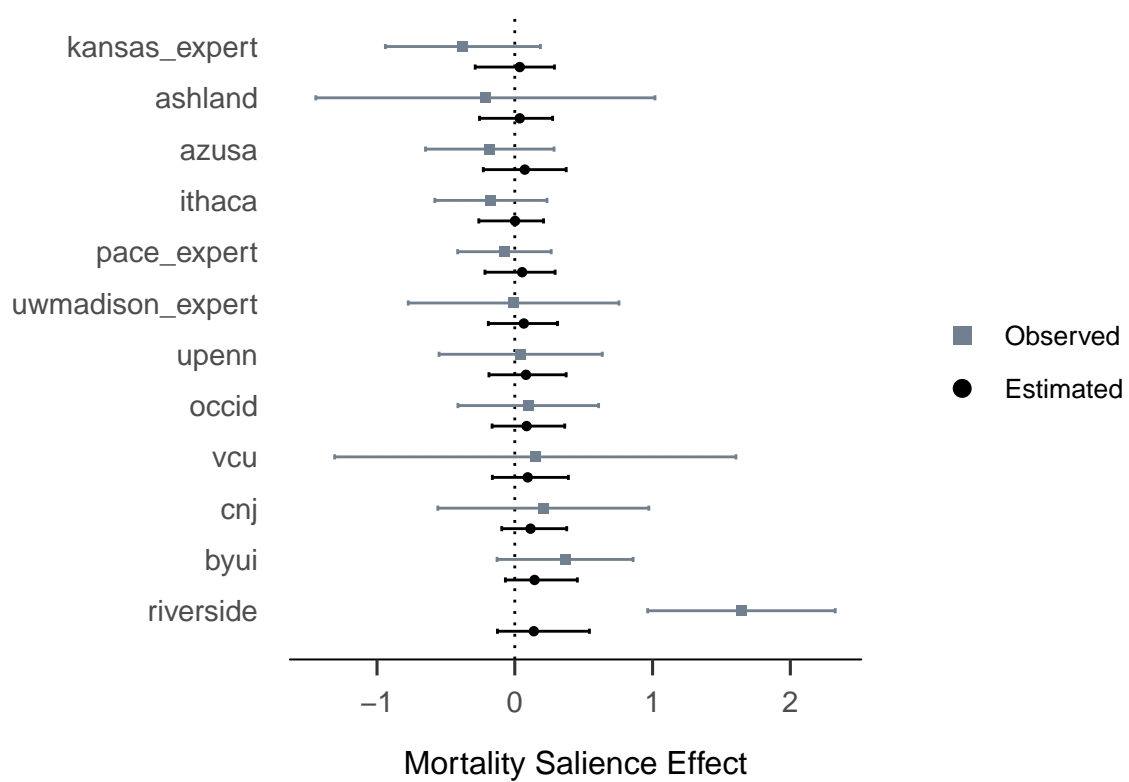
```

Exclusion Criterion 111



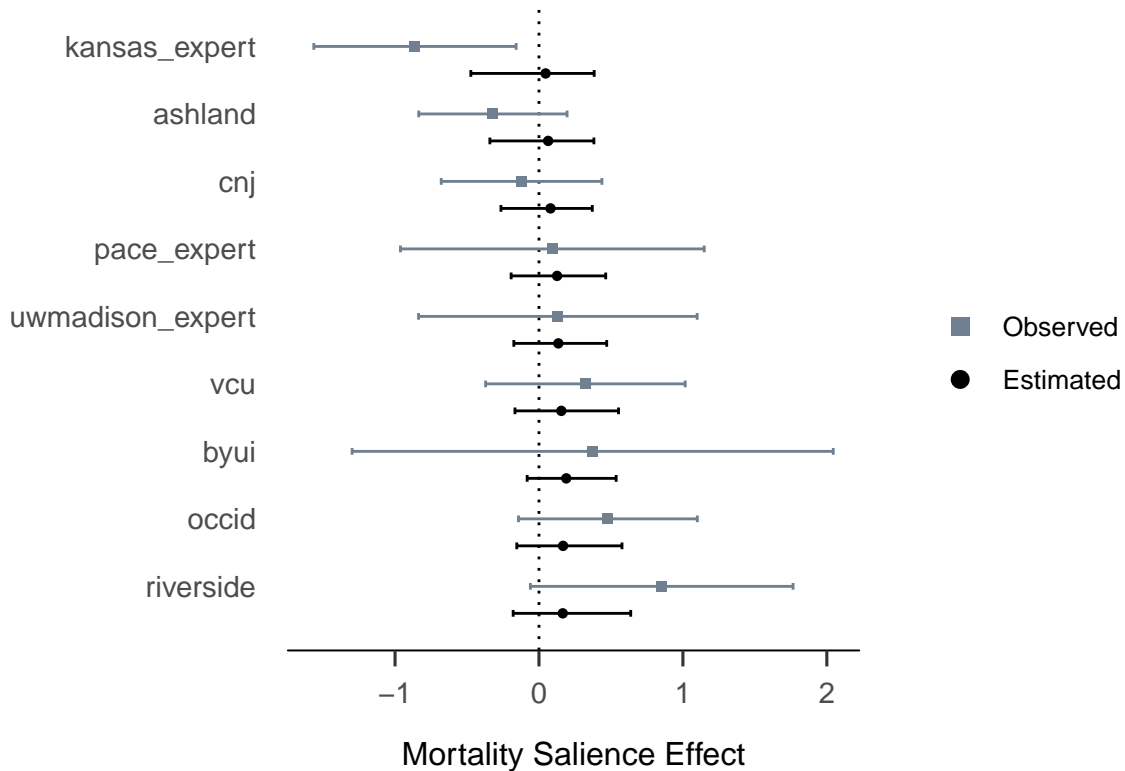
```
remaForest(m.211, rema.211$est$default) + ggtitle("Exclusion Criterion 211")
```

Exclusion Criterion 211



```
remaForest(m.311, rema.311$est$default) + ggtitle("Exclusion Criterion 311")
```

Exclusion Criterion 311



```
BFs.og <- cbind(rbind(rema.111$BFmu, rema.211$BFmu, rema.311$BFmu),
                rbind(rema.111$BFtau, rema.211$BFtau, rema.311$BFtau))
BFs.og <- round(BFs.og, 2)
rownames(BFs.og) <- paste("Exclusion Criterion", c(111, 211, 311))
subhead <- rep(c("Default", "Oosterwijk", "Vohs"), 2)
colnames(BFs.og) <- subhead
colhead <- list("Effect Size BF" = c(2, 4),
                "Heterogeneity BF" = c(5, 7))

apa_table(BFs.og, escape = FALSE, caption = "Model-averaged Bayes factors for key analyses.",
          note = "All Bayes factors are reported in favor of the null model.",
          col_spanners = colhead)
```

```
##
##
## \begin{table}[tbp]
## \begin{center}
## \begin{threeparttable}
## \caption{\label{tab:unnamed-chunk-14}Model-averaged Bayes factors for key analyses.}
## \begin{tabular}{lllllll}
## \toprule
## & \multicolumn{3}{c}{Effect Size BF} & \multicolumn{3}{c}{Heterogeneity BF} \\
## \cmidrule{r}{2-4} \cmidrule{r}{5-7}
## & \multicolumn{1}{c}{Default} & \multicolumn{1}{c}{Oosterwijk} & \multicolumn{1}{c}{Vohs} & \multicolumn{1}{c}{Default} & \multicolumn{1}{c}{Oosterwijk} & \multicolumn{1}{c}{Vohs} \\
## \midrule
## Exclusion Criterion 111 & 12.60 & 44.69 & 16.64 & 0.44 & 0.43 & 0.44 \\
## Exclusion Criterion 211 & 7.95 & 16.84 & 7.20 & 0.41 & 0.42 & 0.42
```

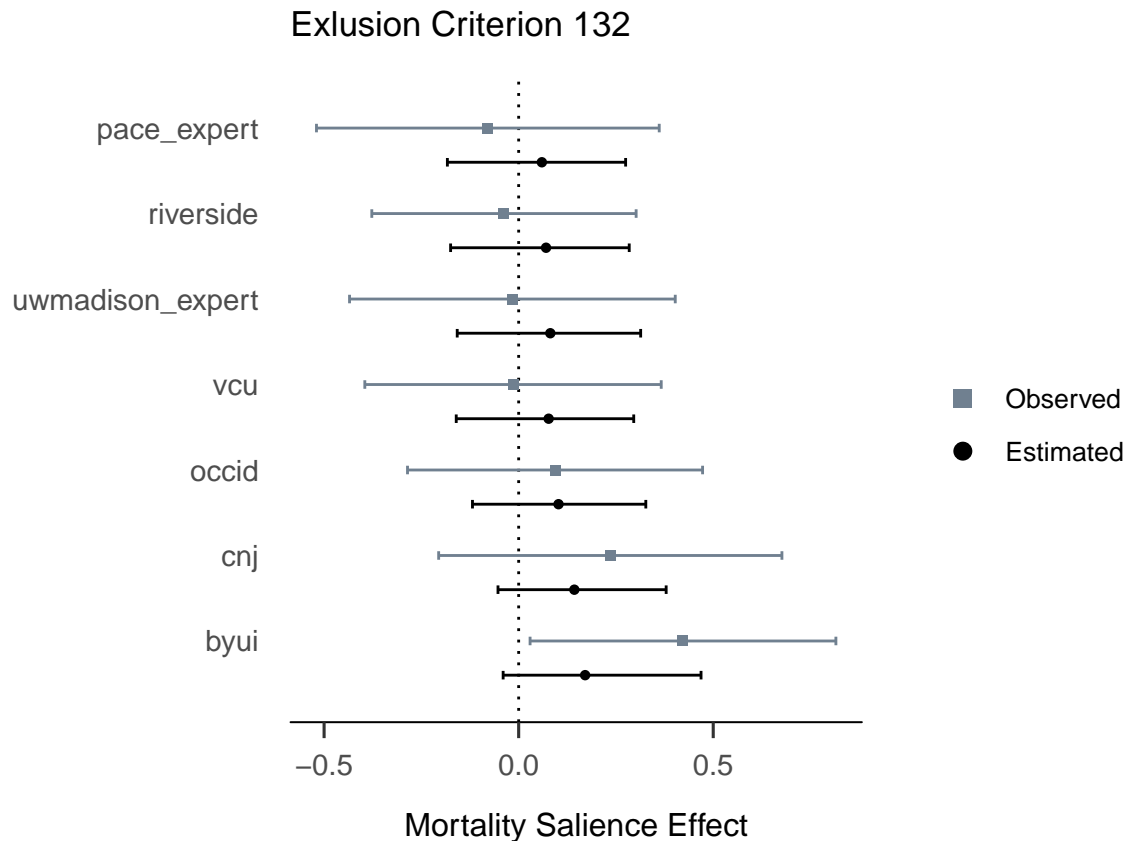
```
## Exclusion Criterion 311 & 4.18 & 4.01 & 2.49 & 0.56 & 0.57 & 0.57\\
## \bottomrule
## \addlinespace
## \end{tabular}
## \begin{tablenotes}[para]
## \normalsize{\textit{Note.} All Bayes factors are reported in favor of the null model.}
## \end{tablenotes}
## \end{threeparttable}
## \end{center}
## \end{table}
```

Analysis for the Main Claim of the Comment

```
m.132 <- read.csv2("data/metaset_132.csv", header = T)
m.232 <- read.csv2("data/metaset_232.csv", header = T)
m.332 <- read.csv2("data/metaset_332.csv", header = T)

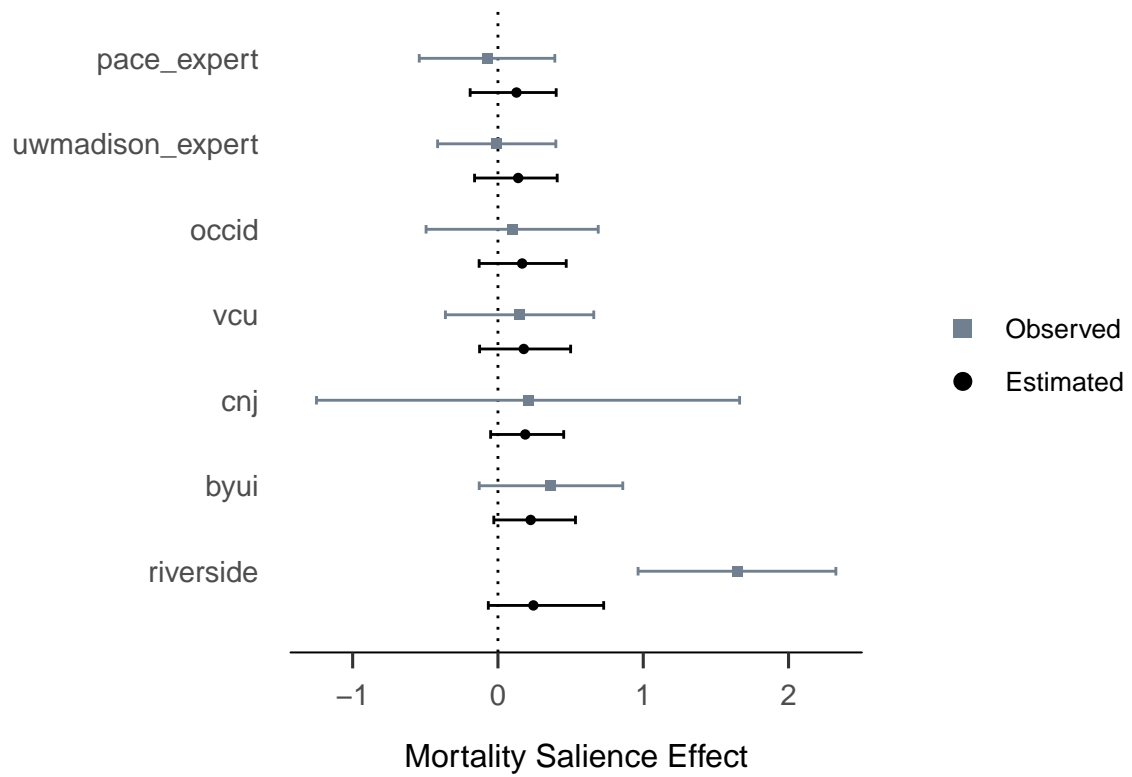
rema.132 <- .runRema(m.132$yi, m.132$sei, priors, TRUE)
rema.232 <- .runRema(m.232$yi, m.232$sei, priors, TRUE)
rema.332 <- .runRema(m.332$yi, m.332$sei, priors, TRUE)

remaForest(m.132, rema.132$est$default) + ggtitle("Exclusion Criterion 132")
```



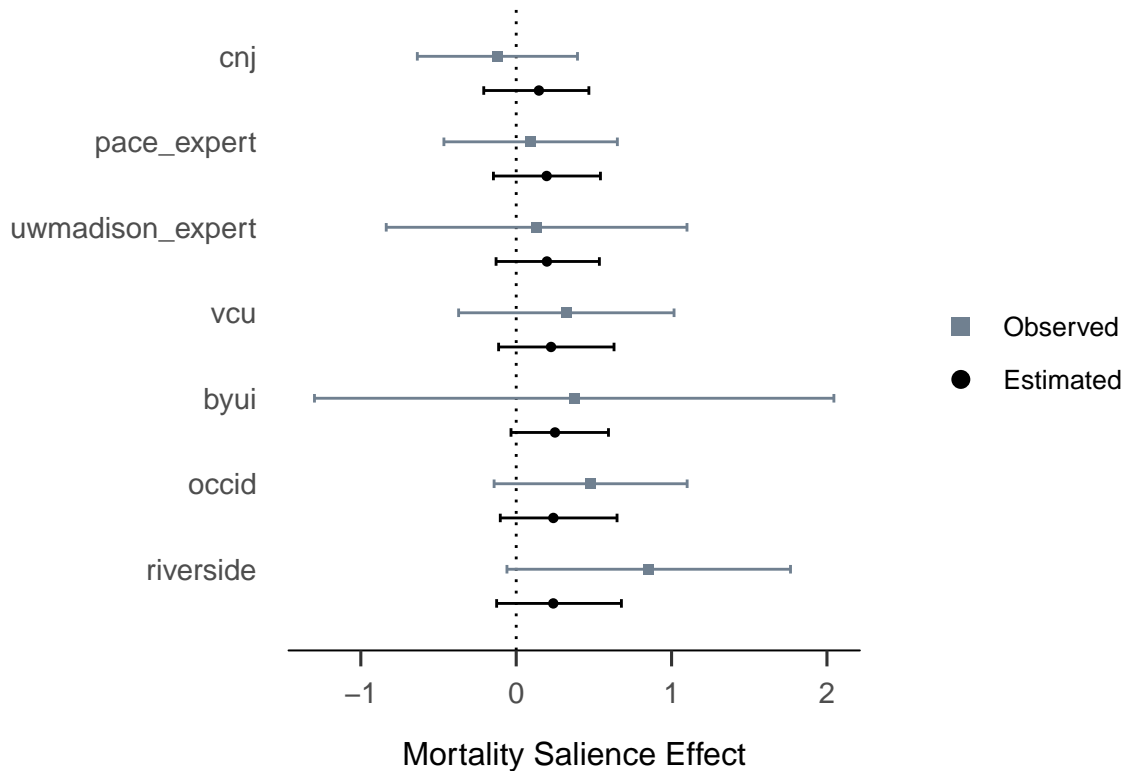
```
remaForest(m.232, rema.232$est$default) + ggtitle("Exclusion Criterion 232")
```


Exlusion Criterion 232



```
remaForest(m.332, rema.332$est$default) + ggtitle("Exlusion Criterion 332")
```

Exclusion Criterion 332



```
BFs.cmnt <- cbind(rbind(rema.132$BFmu, rema.232$BFmu, rema.332$BFmu),
                  rbind(rema.132$BFtau, rema.232$BFtau, rema.332$BFtau))
BFs.cmnt <- round(BFs.cmnt, 2)
rownames(BFs.cmnt) <- paste("Exclusion Criterion", c(132, 232, 332))
colnames(BFs.cmnt) <- subhead

apa_table(BFs.cmnt, escape = FALSE, caption = "Model-averaged Bayes factors for comment analyses.",
          col_spanners = colhead)
```

```
##
##
## \begin{table}[tbp]
## \begin{center}
## \begin{threeparttable}
## \caption{\label{tab:unnamed-chunk-16}Model-averaged Bayes factors for comment analyses.}
## \begin{tabular}{lllllll}
## \toprule
## & \multicolumn{3}{c}{Effect Size BF} & \multicolumn{3}{c}{Heterogeneity BF} \\
## \cmidrule(r){2-4} \cmidrule(r){5-7}
## & \multicolumn{1}{c}{Default} & \multicolumn{1}{c}{Oosterwijk} & \multicolumn{1}{c}{Vohs} & \multicolumn{1}{c}{Default} & \multicolumn{1}{c}{Oosterwijk} & \multicolumn{1}{c}{Vohs} \\
## \midrule
## Exclusion Criterion 132 & 3.82 & 5.84 & 2.75 & 0.39 & 0.40 & 0.40 \\
## Exclusion Criterion 232 & 1.42 & 0.90 & 0.66 & 0.48 & 0.50 & 0.47 \\
## Exclusion Criterion 332 & 1.45 & 0.73 & 0.62 & 0.53 & 0.53 & 0.52 \\
## \bottomrule
## \end{tabular}
## \end{threeparttable}
## \end{table}
```

```
## \end{center}
## \end{table}
```

All Other Variants

```
sets <- c(112, 212, 312, 121, 221, 321, 122, 222, 322, 131, 231, 331)
rema.other <- data.frame(metaset = character(),
                        default = numeric(),
                        oosterwijk = numeric(),
                        vohs = numeric()
                      )

for(i in sets){
  path.m <- paste0("data/metaset_", i, ".csv")
  m <- read.csv2(path.m, header = T)
  rema <- .runRema(m$yi, m$sei, priors, FALSE)
  rema.other <- rbind(rema.other, cbind(rema))
}
```

```
rema.other <- round(rema.other, 2)
rownames(rema.other) <- paste("Exclusion Criterion", sets)
colnames(rema.other) <- c("Default", "Oosterwijk", "Vohs")
```

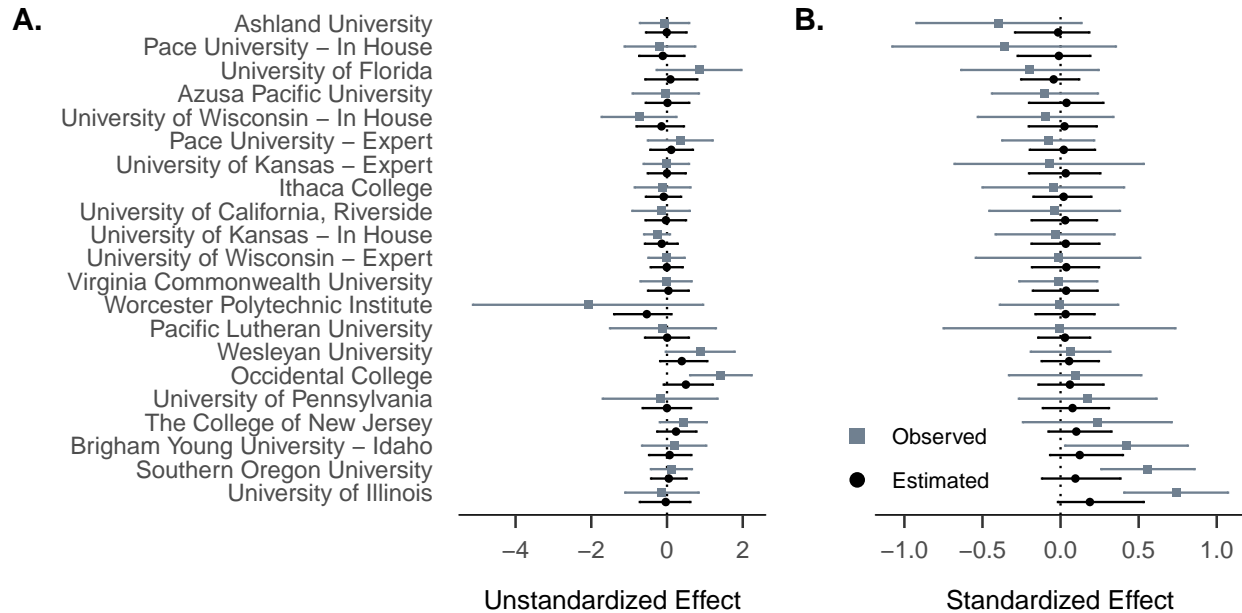
```
apa_table(rema.other, escape = FALSE, caption = "Model-averaged Bayes factors for all other analyses.")
```

```
##
##
## \begin{table}[tbp]
## \begin{center}
## \begin{threeparttable}
## \caption{\label{tab:unnamed-chunk-18}Model-averaged Bayes factors for all other analyses.}
## \begin{tabular}{llll}
## \toprule
## & \multicolumn{1}{c}{Default} & \multicolumn{1}{c}{Oosterwijk} & \multicolumn{1}{c}{Vohs} \\
## \midrule
## Exclusion Criterion 112 & 7.32 & 16.49 & 6.80 \\
## Exclusion Criterion 212 & 3.66 & 4.24 & 2.32 \\
## Exclusion Criterion 312 & 4.18 & 4.01 & 2.49 \\
## Exclusion Criterion 121 & 10.34 & 34.12 & 12.76 \\
## Exclusion Criterion 221 & 4.32 & 5.88 & 2.99 \\
## Exclusion Criterion 321 & 1.45 & 0.73 & 0.62 \\
## Exclusion Criterion 122 & 3.82 & 5.84 & 2.75 \\
## Exclusion Criterion 222 & 1.42 & 0.90 & 0.66 \\
## Exclusion Criterion 322 & 1.45 & 0.73 & 0.62 \\
## Exclusion Criterion 131 & 6.17 & 16.58 & 6.40 \\
## Exclusion Criterion 231 & 4.32 & 5.88 & 2.99 \\
## Exclusion Criterion 331 & 1.45 & 0.73 & 0.62 \\
## \bottomrule
## \end{tabular}
## \end{threeparttable}
## \end{center}
## \end{table}
```

Plots Original Analysis

```
m.111$labelpretty <- c("Ashland University", "Azusa Pacific University", "Brigham Young University - Idaho")
```

```
forest.all(obs.data = dat.111, es.data = m.111, est.averaging = rema.111$est$default, est.multilevel = 1)
```



Combining Evidence from multiverse analysis

```
sets <- c(111, 211, 311, 132, 232, 332, 112, 212, 312, 121, 221, 321, 122, 222, 322, 131, 231, 331)
ssize <- data.frame("metaset" = character(),
                    "N" = numeric(),
                    "N.study" = numeric()
                    )
```

```
for(i in sets){
  path.m <- paste0("data/reanalysis_", i, ".csv")
  m <- read.csv2(path.m, header = T)
  N <- nrow(m)
  path.m <- paste0("data/metaset_", i, ".csv")
  m <- read.csv2(path.m, header = T)
  N.study <- nrow(m)
  ssize <- rbind(ssize, c(i, N, N.study))
}
```

```
rema.all <- rbind(BFs.og[, 1:3],
                  BFs.cmnt[, 1:3],
                  rema.other
                  )
```

```
rema.all <- 1/rema.all
rema.all <- cbind(rema.all, "N" = ssize[, 2], "N.study" = ssize[, 3])
rema.all <- cbind(rema.all, "Crit" = rownames(rema.all))
result <- tidyr::gather(rema.all, prior, bf, Default=Vohs, factor_key = TRUE)
result$Nscaled <- result$N.study/2
```

```
result <- result[!duplicated(result$bf),]
```

```

xrange <- c(0, 2500)
yrange <- c(1/50, 50) # log scale

# Plot with n participants included on the x-axis, BF01 on the y-axis, colors for
# participant exclusion sets and bubble sizes for number of studies included
ggplot(aes(x = N, y = bf, size = Nscaled, color = as.factor(prior)), data = result) +
  geom_jitter(alpha = 0.6, width = 15) +
  scale_y_continuous(trans='log', limits = yrange, breaks = c(1/50, 1/5, 1, 5, 50)) +
  scale_size_identity() +
  scale_colour_brewer(palette = 'Dark2') +
  labs(x = 'Sample Size', y = expression(BF["10"]), color = "Priors") +
  xlim(xrange) +
  geom_hline(yintercept = 1) +
  theme_apo() +
  theme_classic(base_size = 19) +
  theme(axis.line=element_line()) +
  guides(color = guide_legend(override.aes = list(size = 4))) +
  coord_capped_cart(gap = 0.1, bottom = 'none', left = 'none') + #caps the axes so they don't touch
  theme(axis.title.x = element_text(vjust=-0.5),
        axis.text.x = element_text(vjust=-0.5),
        axis.text.y = element_text(hjust=.8),
        axis.ticks.length = unit(0.25, 'cm'))
  )

```

