

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 = 14))
```

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" = effsizeC
})

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
## 2.871235e-02 9.665975e-02 9.592383e-05 2.711772e-04 8.117000e-02

```

```
rean.111$ES
```

```
## [1] 0.009033331
```

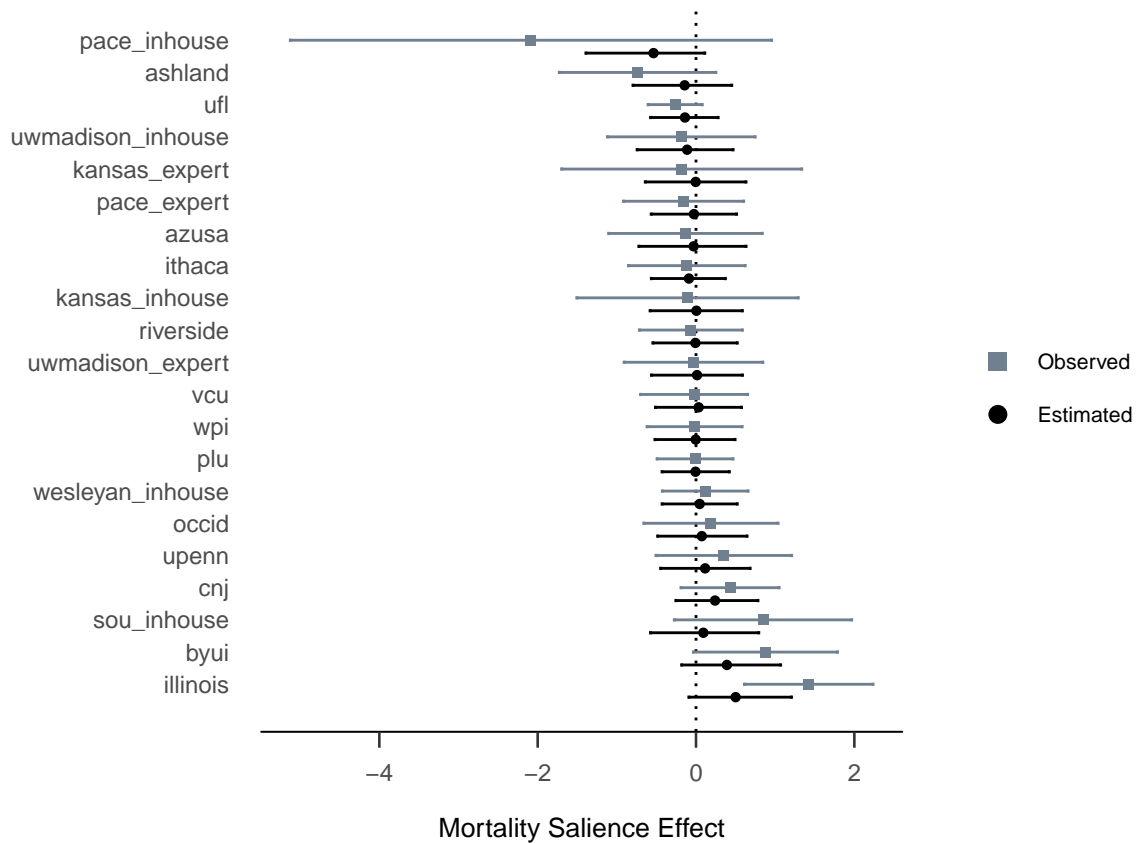
```
rean.111$CI
```

```

##          2.5%          97.5%
## -0.1071739  0.1222694

```

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



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

```
##          F0          10          P0    post.pos    prior.pos
## 0.051531827 0.177922280 0.008499185 0.015863869 0.096185000
```

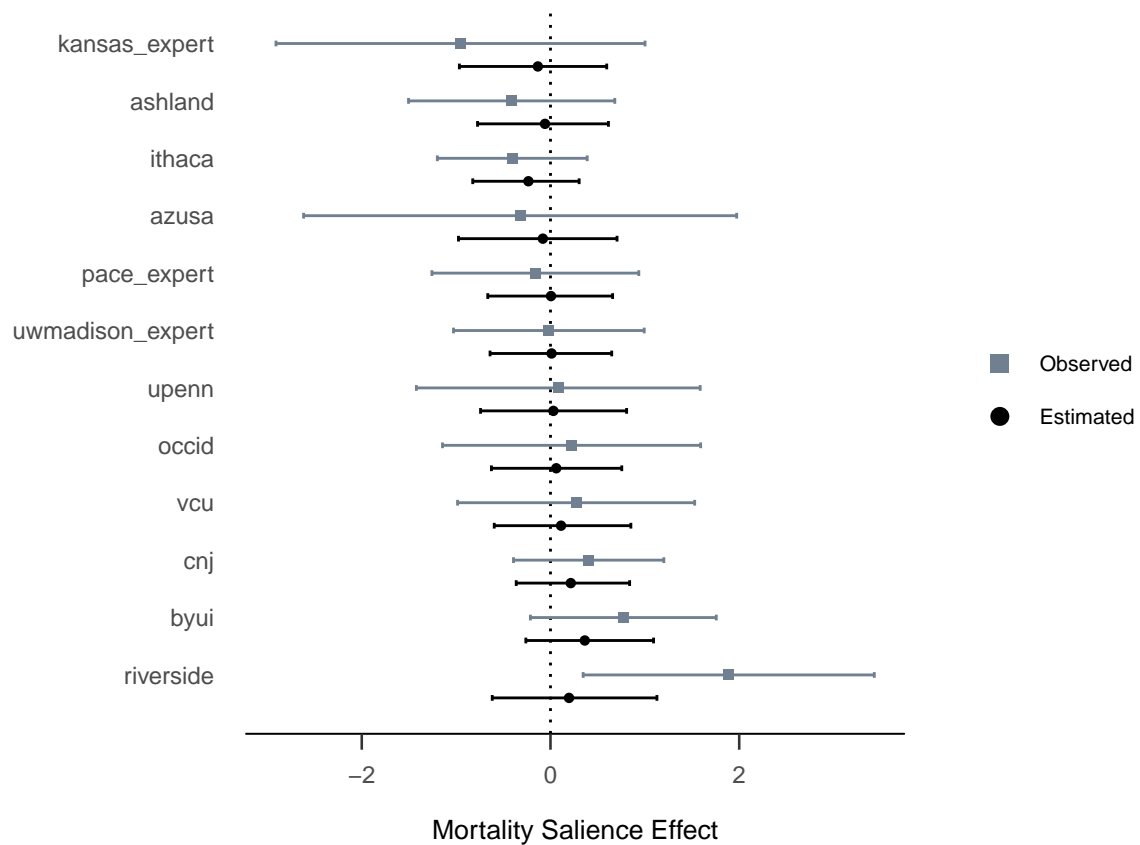
```
rean.211$ES
```

```
## [1] 0.01896612
```

```
rean.211$CI
```

```
##          2.5%          97.5%
## -0.1716215  0.2133810
```

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



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

##          F0          10          P0  post.pos  prior.pos
## 0.11074030 0.35693300 0.07413884 0.07189587 0.10739000

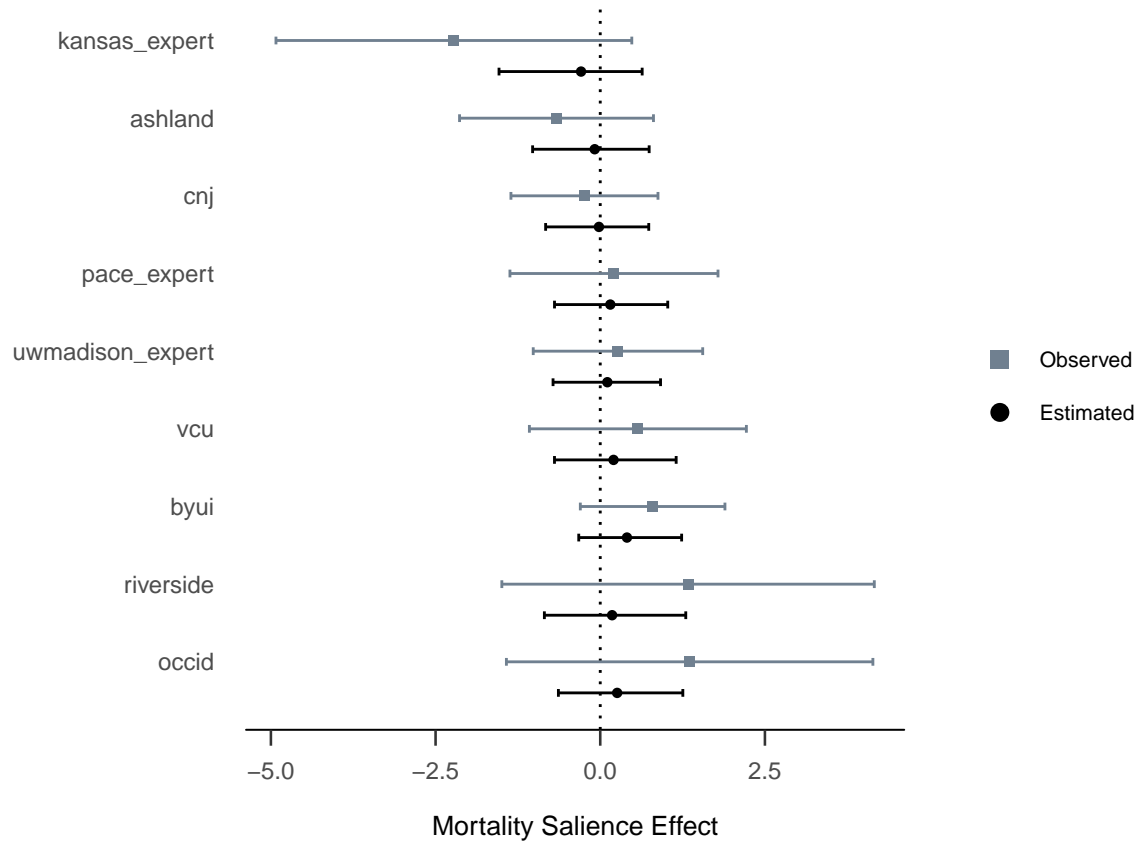
rean.311$ES

## [1] 0.04682775

rean.311$CI

##          2.5%          97.5%
## -0.2249348  0.3170858

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
## 0.07421107 0.48624378 0.08351309 0.13663944 0.12142000
```

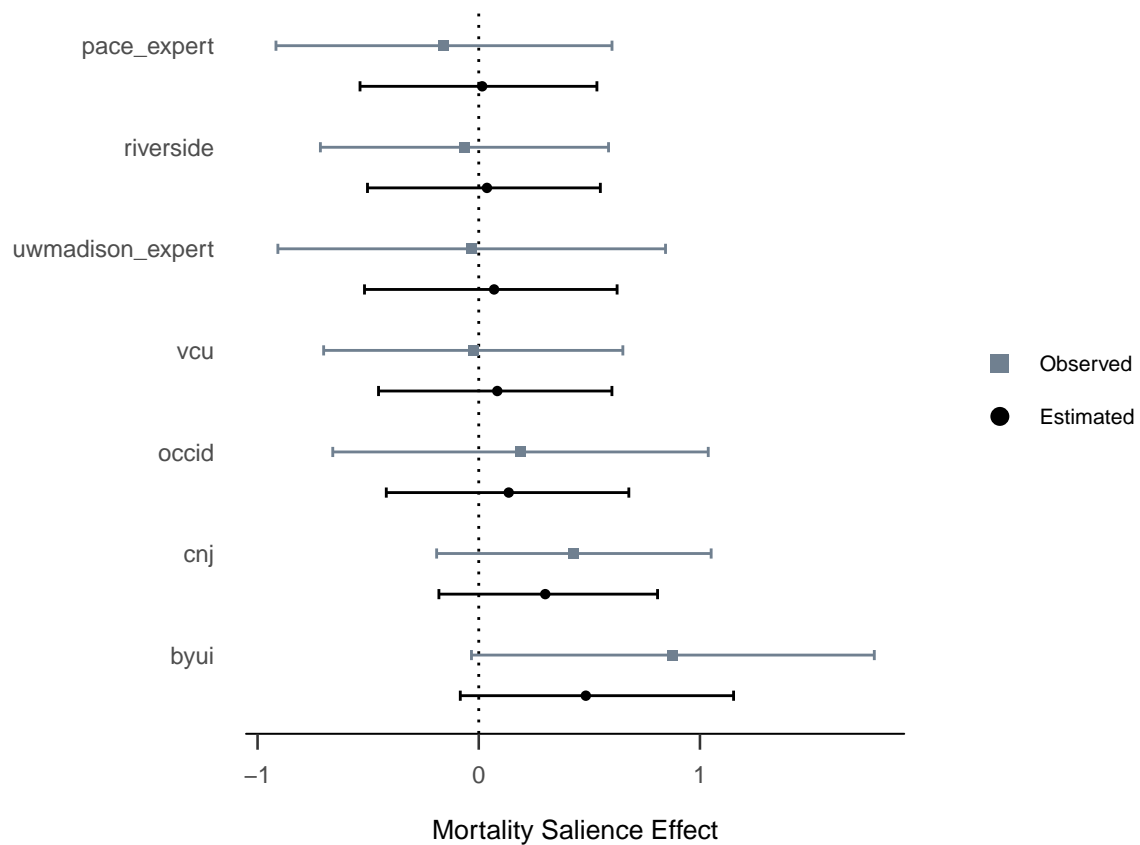
```
rean.132$ES
```

```
## [1] 0.08095625
```

```
rean.132$CI
```

```
##          2.5%          97.5%
## -0.1242964 0.2870481
```

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



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

```
##          F0          10          P0 post.pos prior.pos
## 0.1477902 1.0323751 0.3681414 0.3052439 0.1225400
```

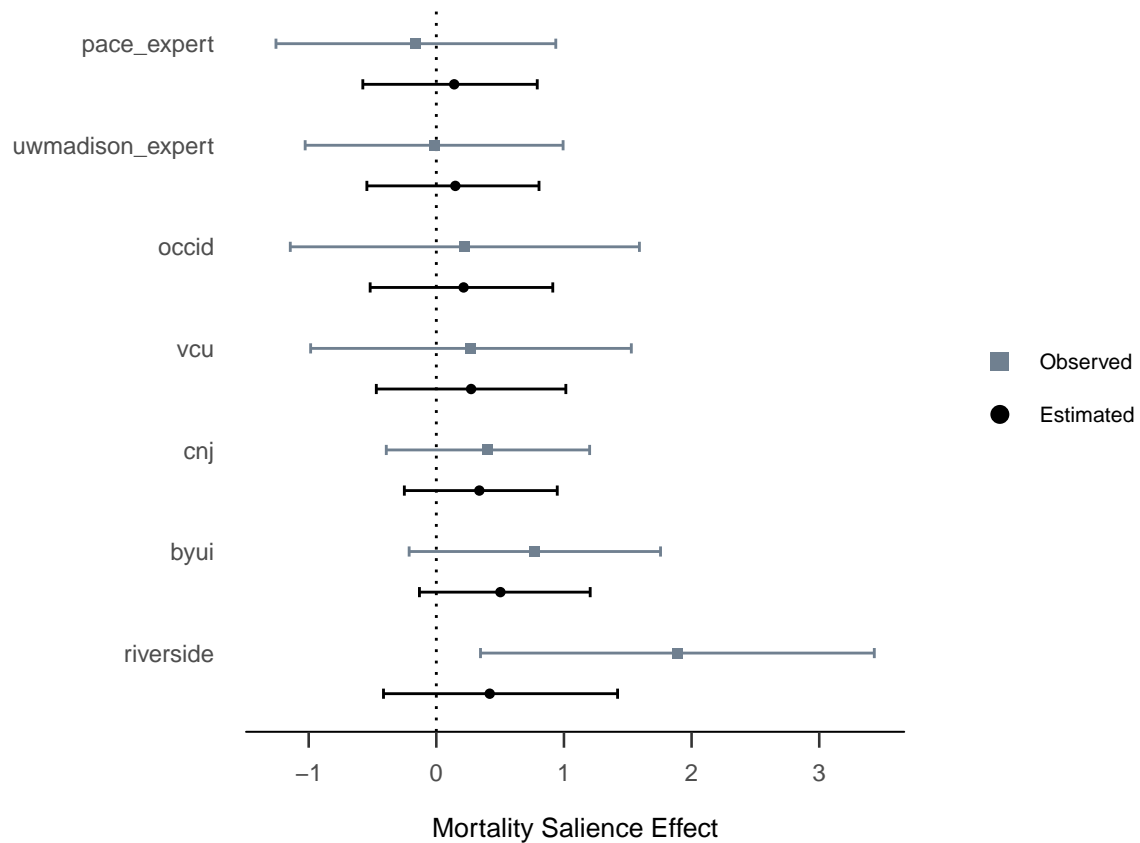
```
rean.232$ES
```

```
## [1] 0.1376586
```

```
rean.232$CI
```

```
##          2.5%          97.5%
## -0.1060859 0.3862968
```

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



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

```
##          F0          10          P0 post.pos prior.pos
## 0.2034751 1.2116533 0.6369582 0.3821904 0.1220900
```

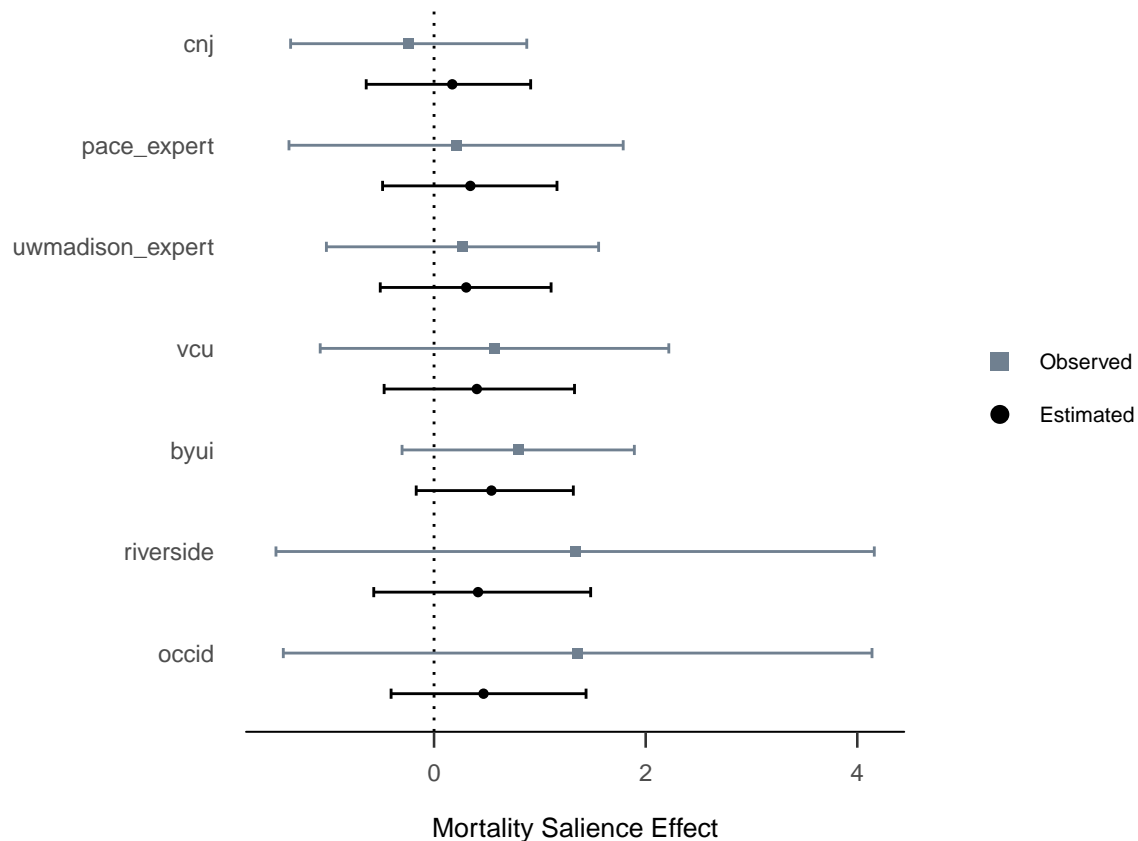
```
rean.332$ES
```

```
## [1] 0.1756868
```

```
rean.332$CI
```

```
##          2.5%          97.5%
## -0.1147384  0.4802415
```

```
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_apo(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	34.83	10.35	10,424.94
Exclusion Criterion 211	637.00	19.41	5.62	117.66
Exclusion Criterion 311	277.00	9.03	2.80	13.49
Exclusion Criterion 132	700.00	13.48	2.06	11.97
Exclusion Criterion 232	386.00	6.77	0.97	2.72
Exclusion Criterion 332	229.00	4.91	0.83	1.57

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
            )

m.est <- list(default = c(),
              oosterwijk = c(),
              vohs = c()
              )

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))
    m.est.es <- rstan::summary(rema$meta$random$stanfit_dstudy)$summary[1, "mean"]
    m.est.lower <- rstan::summary(rema$meta$random$stanfit_dstudy)$summary[1, "2.5%"]
    m.est.upper <- rstan::summary(rema$meta$random$stanfit_dstudy)$summary[1, "97.5%"]
    m.est[[i]] <- c(m.est.es, m.est.lower, m.est.upper)
  }
}
if(!extrainfo){
  return(BFmu)
} else {
  remaResult <- list(BFmu = BFmu,
                     BFtau = BFtau,
                     est = est,
                     m.est = m.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

```

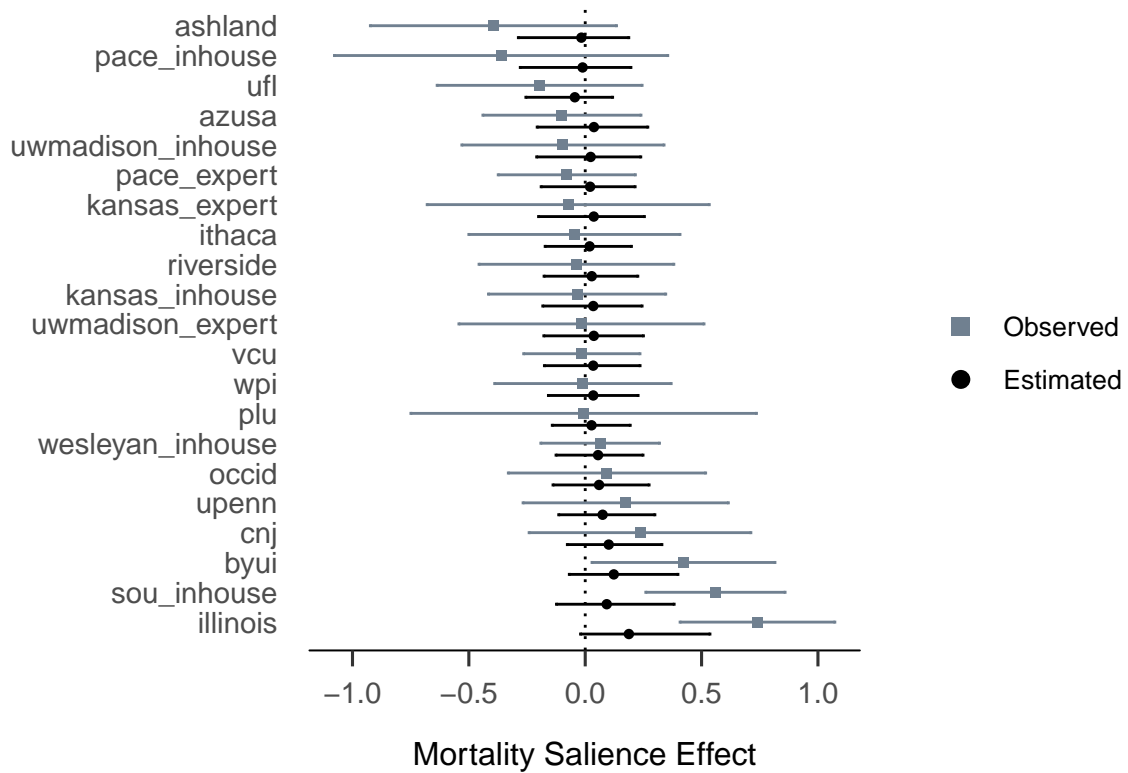
m.111 <- read.csv2("data/metaset_111.csv", header = T)
m.211 <- read.csv2("data/metaset_211.csv", header = T)
m.311 <- read.csv2("data/metaset_311.csv", header = T)

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")

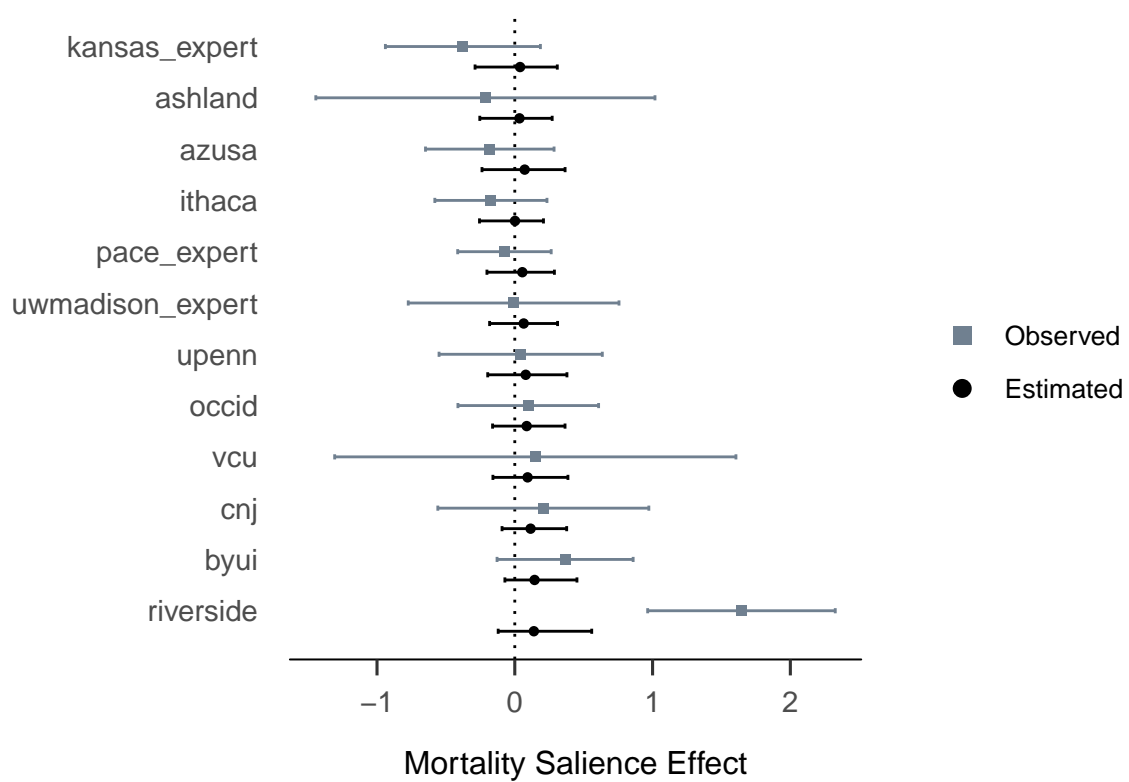
```

Exclusion Criterion 111



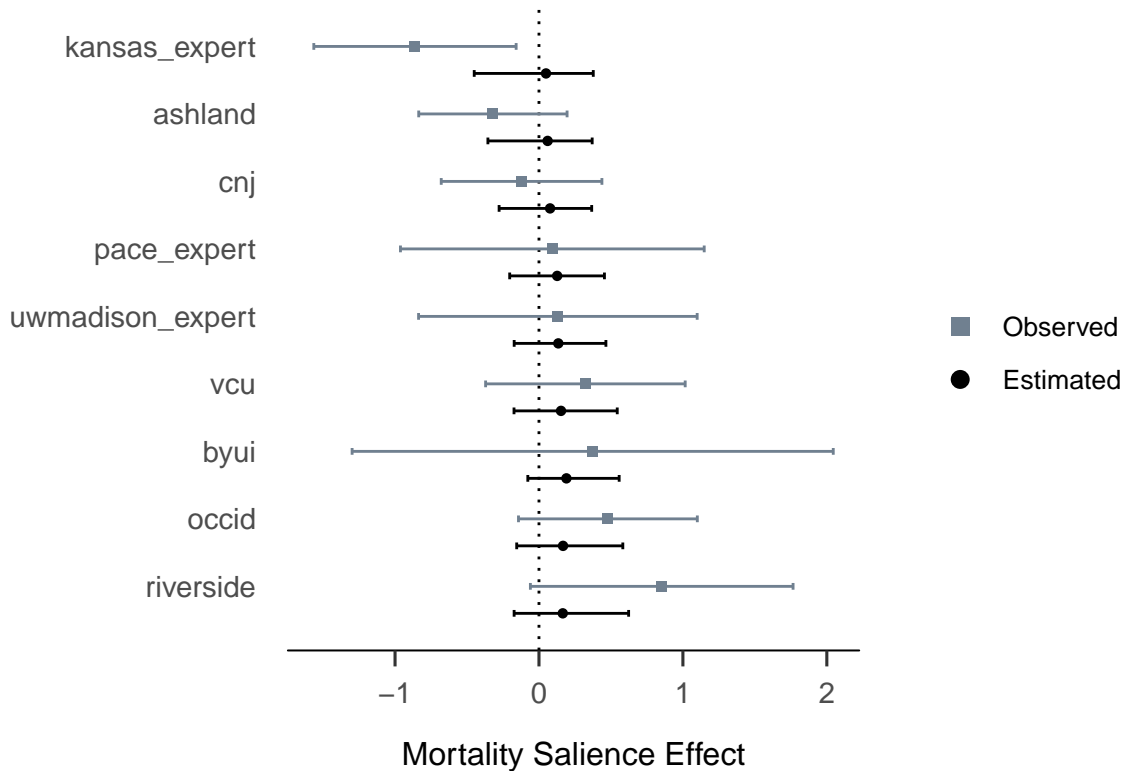
```
remaForest(m.211, rema.211$est$default) + ggtitle("Exclusion Criterion 211")
```

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)
```

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)

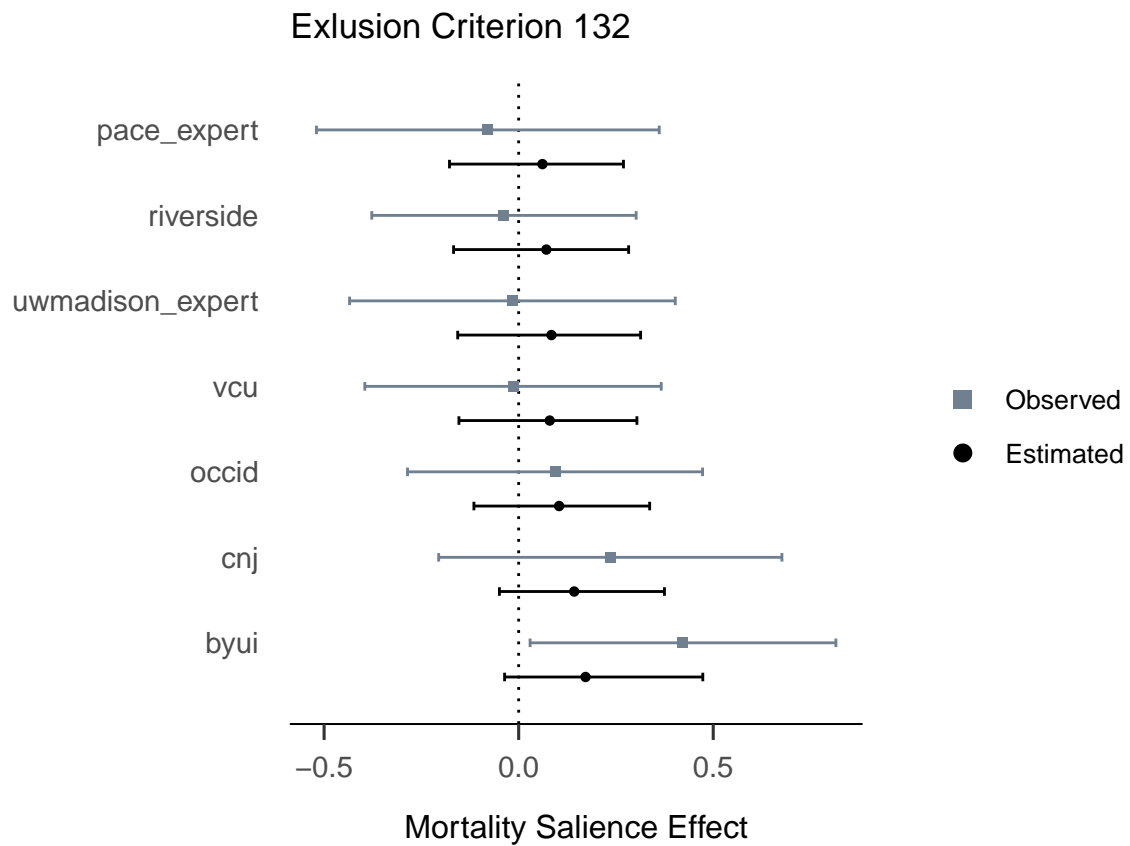
rema.132 <- .runRema(m.132$yi, m.132$sei, priors, TRUE)
rema.232 <- .runRema(m.232$yi, m.232$sei, priors, TRUE)
rema.332 <- .runRema(m.332$yi, m.332$sei, priors, TRUE)

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

Table 2: Model-averaged Bayes factors for key analyses.

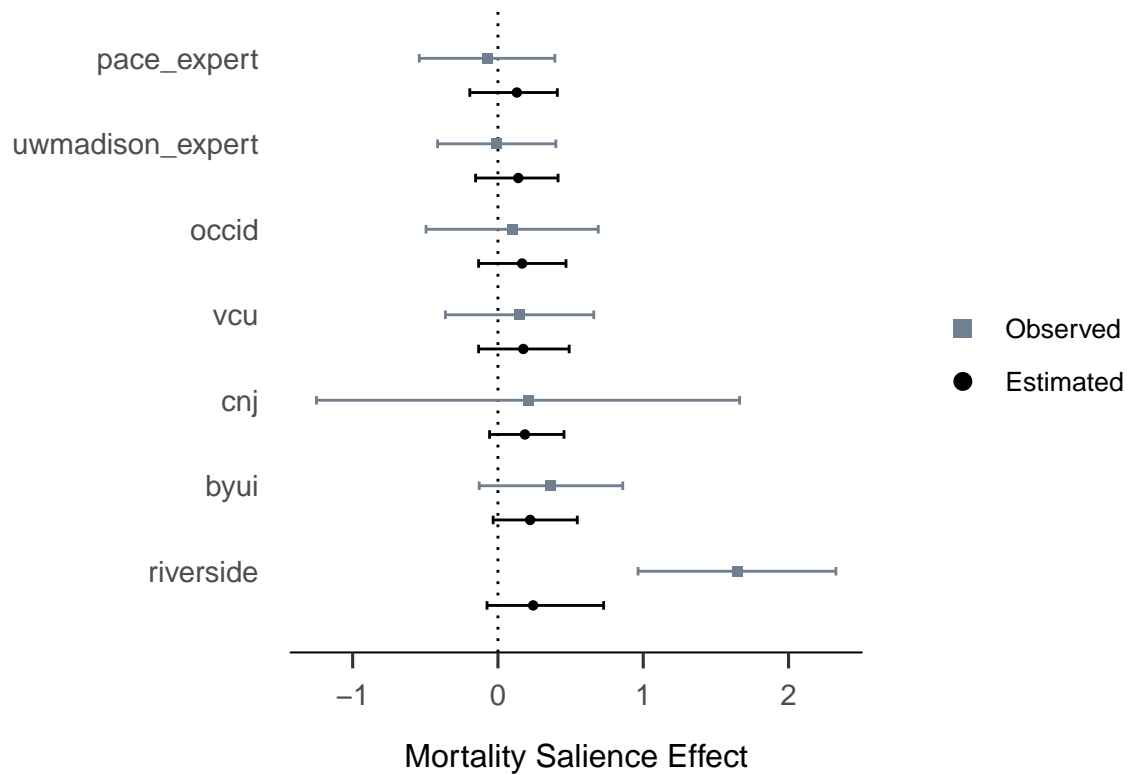
	Effect Size BF			Heterogeneity BF		
	Default	Oosterwijk	Vohs	Default	Oosterwijk	Vohs
Exclusion Criterion 111	12.60	44.69	16.64	0.44	0.43	0.44
Exclusion Criterion 211	7.95	16.84	7.20	0.41	0.42	0.42
Exclusion Criterion 311	4.18	4.01	2.49	0.56	0.57	0.57

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



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

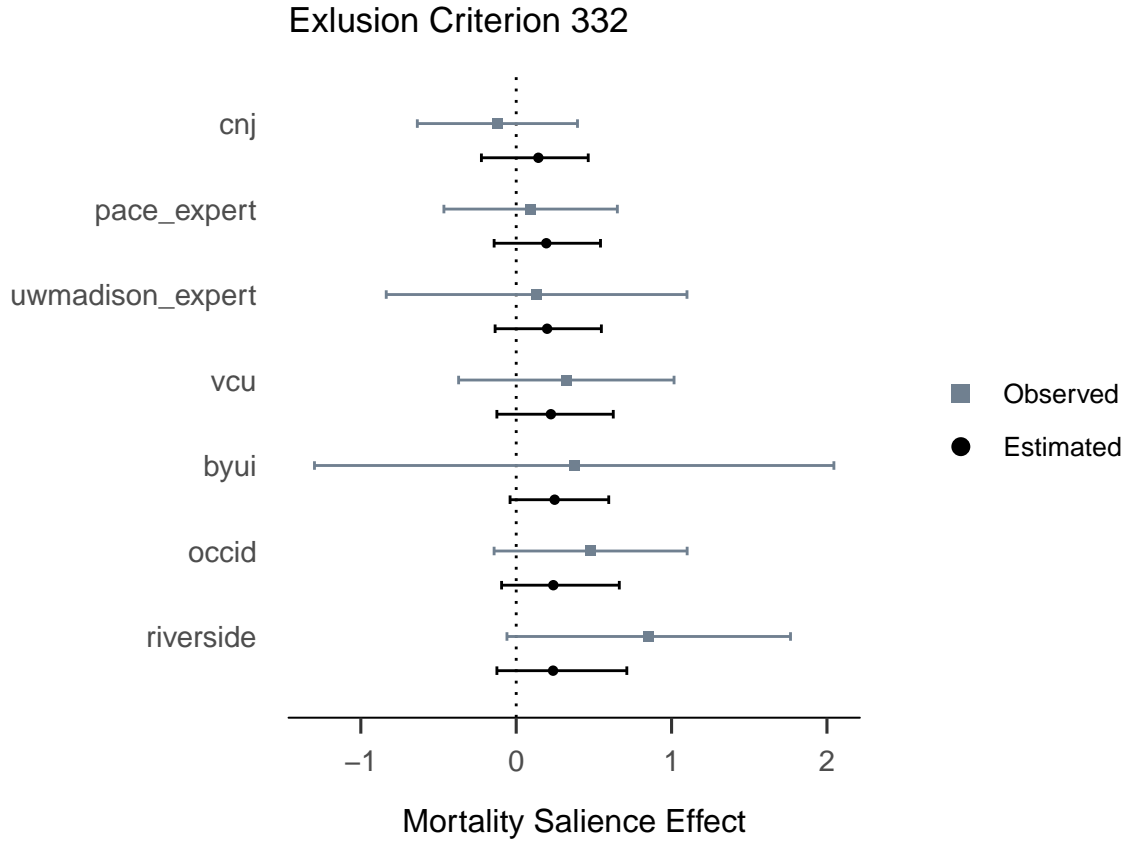

Exclusion Criterion 232



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

Table 3: Model-averaged Bayes factors for comment analyses.

	Effect Size BF			Heterogeneity BF		
	Default	Oosterwijk	Vohs	Default	Oosterwijk	Vohs
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



```
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.",
          colspanners = colhead)
```

All Other Variants

Table 4: Model-averaged Bayes factors for all other analyses.

	Default	Oosterwijk	Vohs
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

```

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.")
```

Plots Original Analysis

```
m.111$source
```

```
## [1] ashland          azusa             byui
```

```

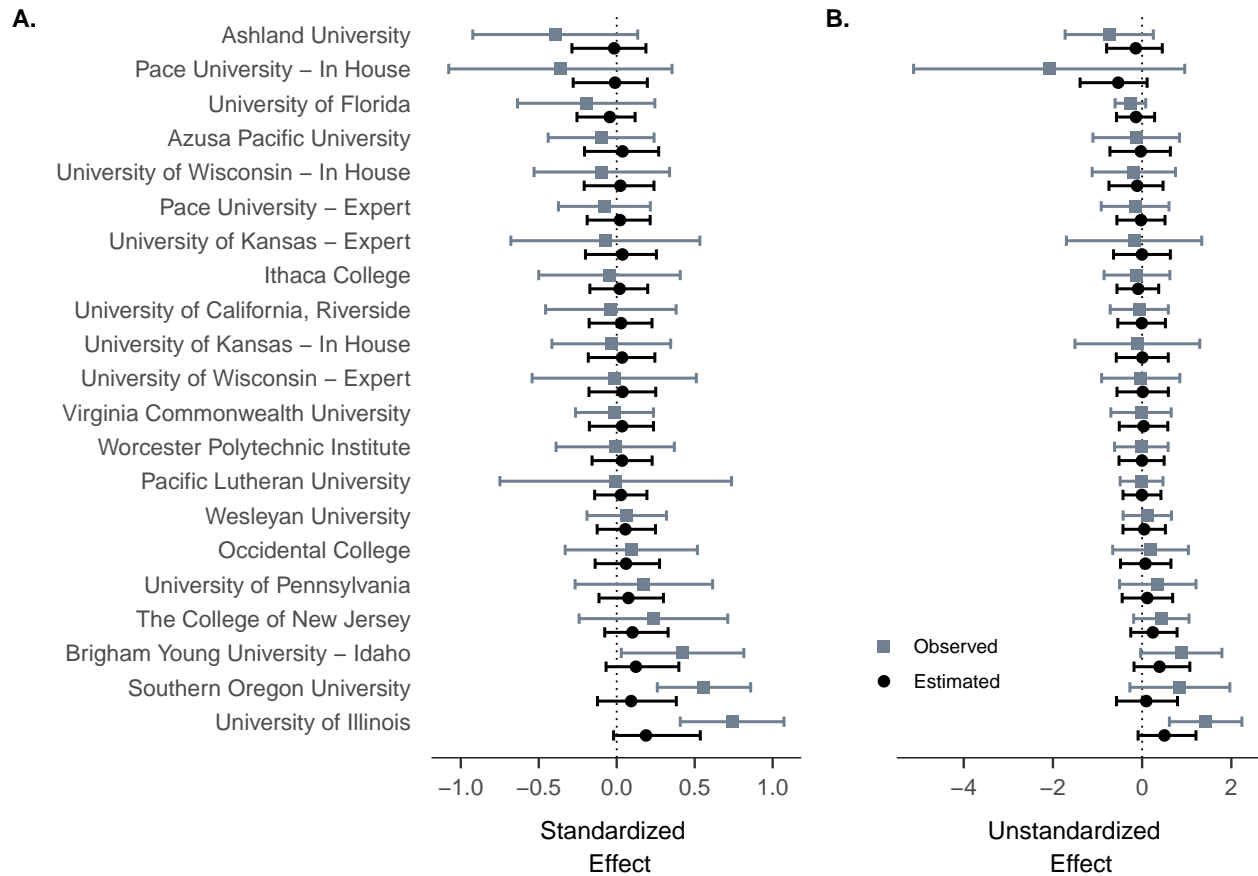
## [4] cnj                illinois            ithaca
## [7] kansas_expert        kansas_inhouse    occid
## [10] pace_expert          pace_inhouse       plu
## [13] riverside            sou_inhouse        ufl
## [16] upenn                uwmadison_expert   uwmadison_inhouse
## [19] vcu                  wesleyan_inhouse   wpi
## 21 Levels: ashland azusa byui cnj illinois ithaca ... wpi
m.111$labelpretty <- c("Ashland University", "Azusa Pacific University", "Brigham Young University - Idaho")
m.211$source

## [1] ashland            azusa              byui               cnj
## [5] ithaca             kansas_expert      occid              pace_expert
## [9] riverside          upenn              uwmadison_expert   vcu
## 12 Levels: ashland azusa byui cnj ithaca kansas_expert ... vcu
m.211$labelpretty <- c("Ashland University", "Azusa Pacific University", "Brigham Young University - Idaho")
m.311$source

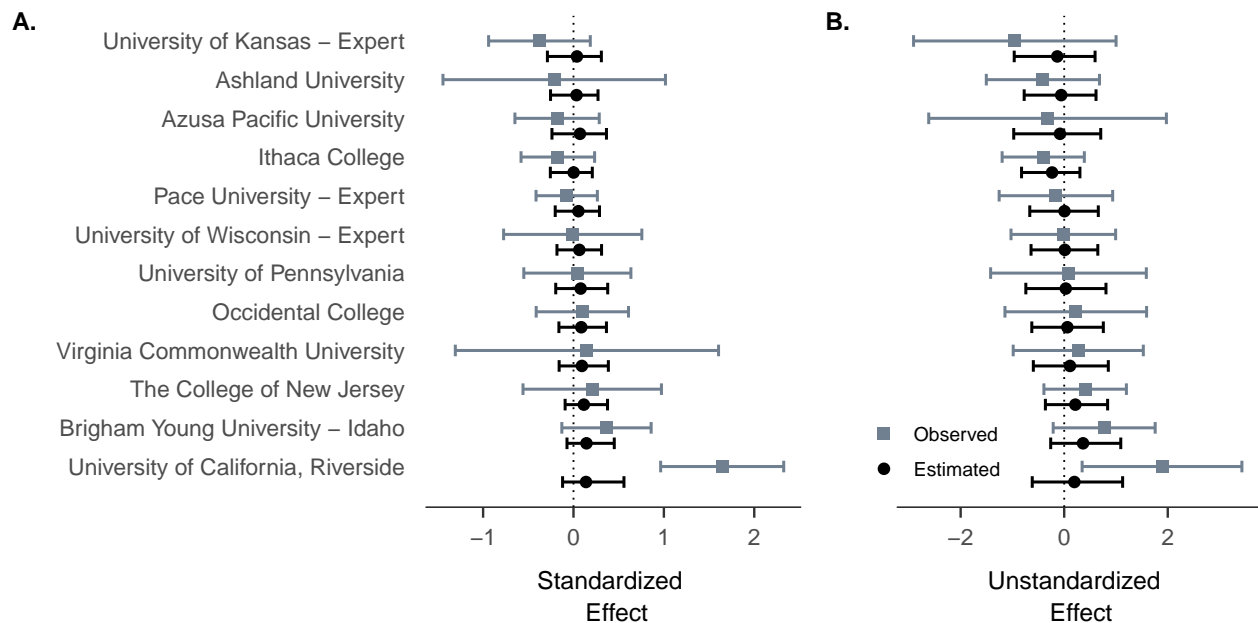
## [1] ashland            byui               cnj                kansas_expert
## [5] occid              pace_expert        riverside          uwmadison_expert
## [9] vcu
## 9 Levels: ashland byui cnj kansas_expert occid pace_expert ... vcu
m.311$labelpretty <- c("Ashland University", "Brigham Young University - Idaho", "The College of New Jersey")
m.332$source

## [1] byui              cnj                occid              pace_expert
## [5] riverside         uwmadison_expert   vcu
## Levels: byui cnj occid pace_expert riverside uwmadison_expert vcu
m.332$labelpretty <- c("Brigham Young University - Idaho", "The College of New Jersey", "Occidental College")
forest.all(obs.data = dat.111, es.data = m.111, est.averaging = rema.111$est$default, est.multilevel = 1)

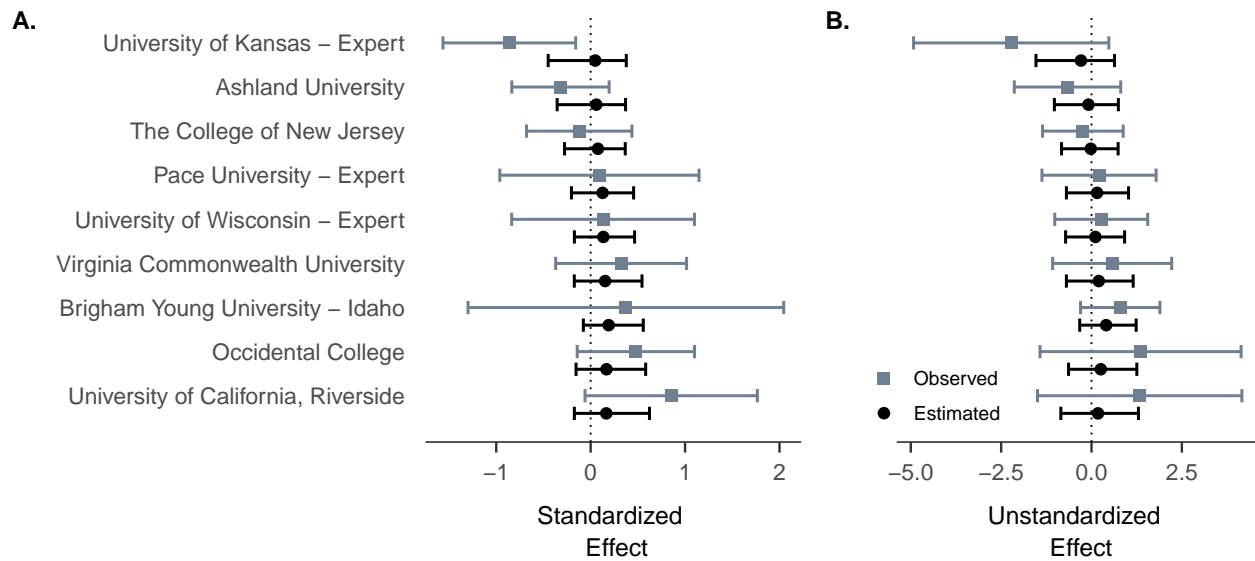
```



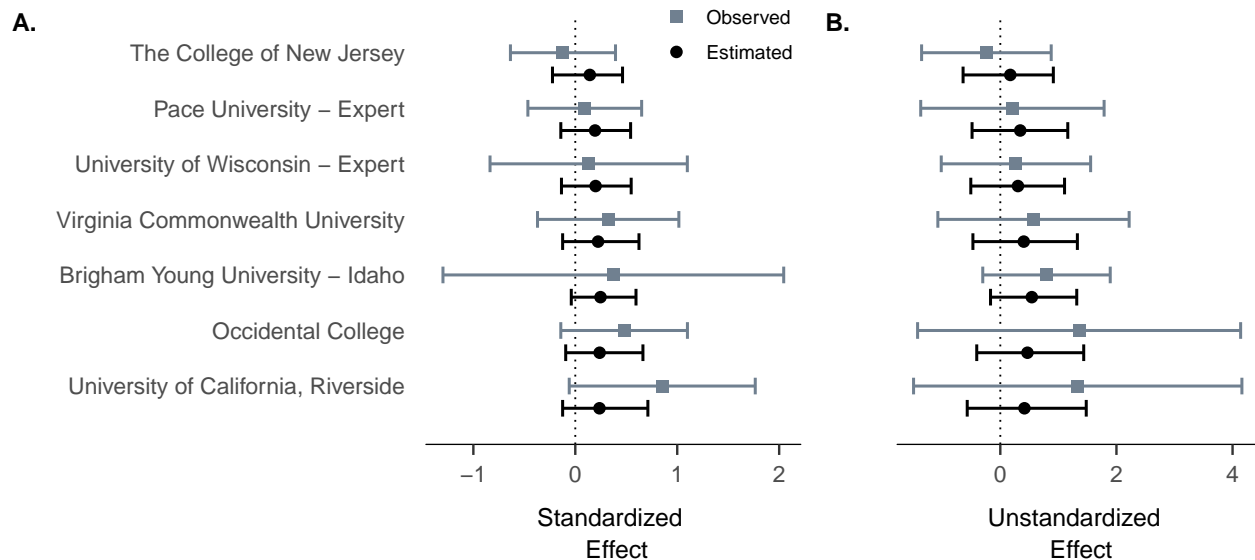
```
forest.all(obs.data = dat.211, es.data = m.211, est.averaging = rema.211$est$default, est.multilevel = 1)
```



```
forest.all(obs.data = dat.311, es.data = m.311, est.averaging = rema.311$est$default, est.multilevel = 1)
```



```
forest.all(obs.data = dat.332, es.data = m.332, est.averaging = rema.332$est$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))
}
```

```

}

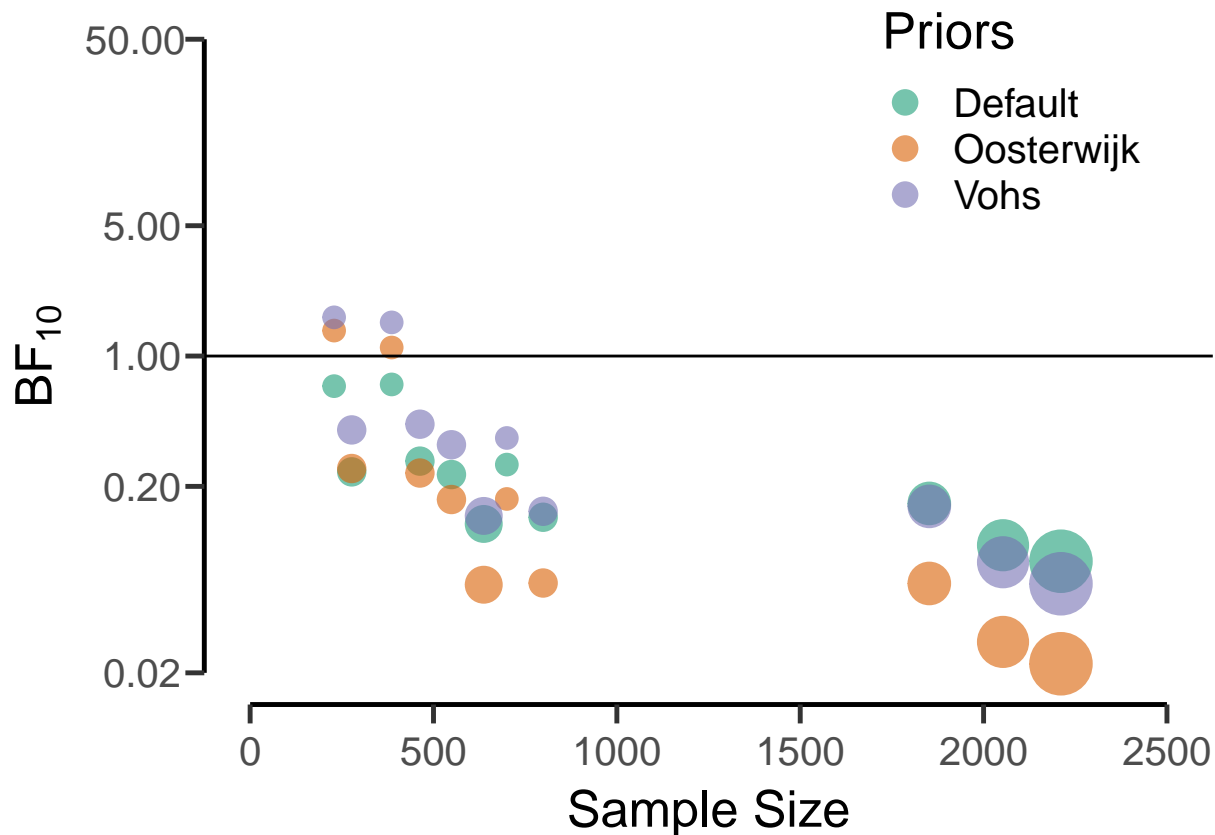
rema.all <- rbind(BFs.og[, 1:3]
                 , BFs.cmnt[, 1:3]
                 , rema.other
                 )
rema.all <- 1/rema.all
rema.all <- cbind(rema.all, "N" = ssize[, 2], "N.study" = ssize[, 3])
rema.all <- cbind(rema.all, "Crit" = rownames(rema.all))
result <- tidyr::gather(rema.all, prior, 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_point(alpha = 0.6) +
  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'),
        legend.position = c(0.8, .85)
        )

```



```
crits <- data.frame(matrix(unlist(strsplit(as.character(sets), split = c()))), ncol = 3, byrow = T))
colnames(crits) <- c("Participant-level", "N-based", "Protocol")
crits$`Participant-level` <- ifelse(crits$`Participant-level` == 1, "All"
                                , ifelse(crits$`Participant-level` == 2, "White & US-born", "US-Iden
crits$`N-based` <- ifelse(crits$`N-based` == 1, "All"
                        , ifelse(crits$`N-based` == 2, "N > 60", "N > 80"))
crits$Protocol <- ifelse(crits$Protocol == 1, "All", "AA")

tab.all <- cbind(crits, rema.all[, c("N", "N.study")])
tab.all <- tab.all[order(tab.all$`N-based`), ]
tab.all <- tab.all[c(1:12, 16:18, 13:15),]

apa_table(tab.all
          , note = "Bla"
          , caption = "Exclusion constellations and resulting sample sizes"
          , col.names = c("Participant-level", "N-based", "Protocol", "Sample Size", "Number of Studies")
          , row.names = F
          , digits = 0)
```

```
##
##
## \begin{table}[tbp]
## \begin{center}
## \begin{threeparttable}
## \caption{\label{tab:unnamed-chunk-4}Exclusion constellations and resulting sample sizes}
## \begin{tabular}{llllll}
## \toprule
```



```

## Participant-level & N-based & Protocol & Sample Size & Number of Studies\\
## \midrule
## All & All & All & 2,211 & 21\\
## White \& US-born & All & All & 637 & 12\\
## US-Identity > 7 & All & All & 277 & 9\\
## All & All & AA & 799 & 9\\
## White \& US-born & All & AA & 463 & 9\\
## US-Identity > 7 & All & AA & 277 & 9\\
## All & N > 60 & All & 2,053 & 17\\
## White \& US-born & N > 60 & All & 549 & 9\\
## US-Identity > 7 & N > 60 & All & 229 & 7\\
## All & N > 60 & AA & 700 & 7\\
## White \& US-born & N > 60 & AA & 386 & 7\\
## US-Identity > 7 & N > 60 & AA & 229 & 7\\
## All & N > 80 & All & 1,852 & 14\\
## White \& US-born & N > 80 & All & 549 & 9\\
## US-Identity > 7 & N > 80 & All & 229 & 7\\
## All & N > 80 & AA & 700 & 7\\
## White \& US-born & N > 80 & AA & 386 & 7\\
## US-Identity > 7 & N > 80 & AA & 229 & 7\\
## \bottomrule
## \addlinespace
## \end{tabular}
## \begin{tablenotes}[para]
## \normalsize{\textit{Note.} Bla}
## \end{tablenotes}
## \end{threeparttable}
## \end{center}
## \end{table}

```

Additional Info

Overall effect size estimates

```

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

priors.es <- list(default = default.prior.unconstrained
                  )

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

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

es.tab <- rbind(
  rema.111.es$m.est[[1]]
  , rema.211.es$m.est[[1]]
  , rema.311.es$m.est[[1]]
  , rema.132.es$m.est[[1]]
  , rema.232.es$m.est[[1]]
  , rema.332.es$m.est[[1]]
)

```

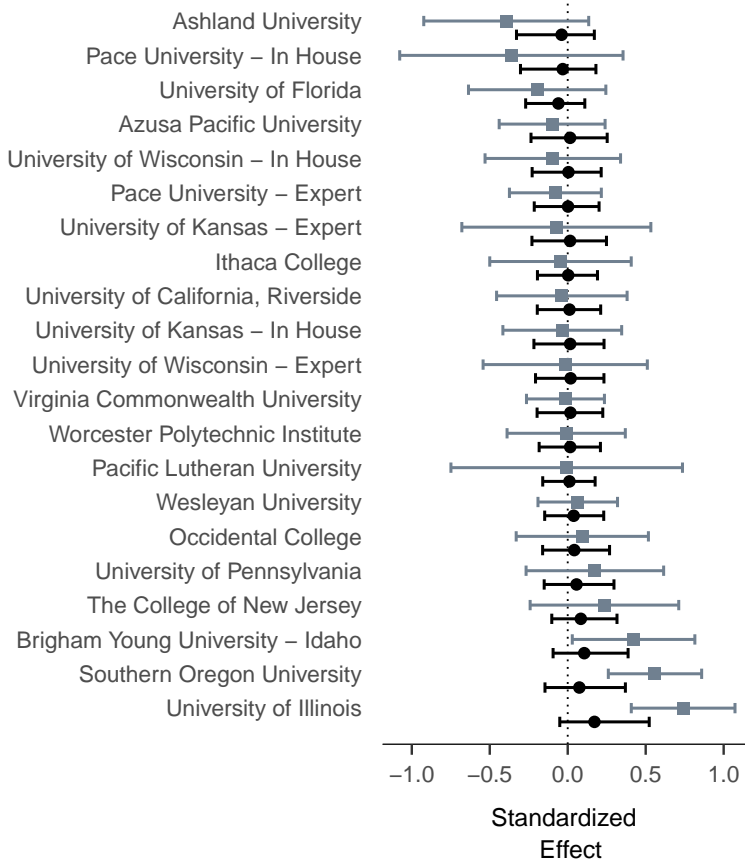
)

```
kable(round(es.tab, 2), col.names = c("ES", "2.5%", "95%"))
```

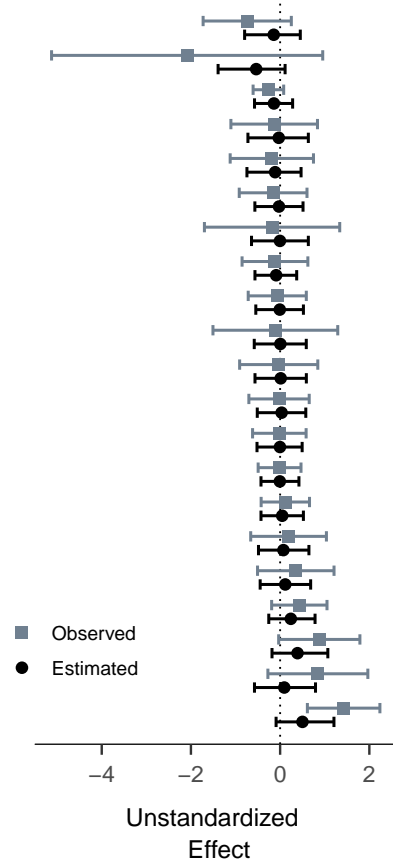
ES	2.5%	95%
0.03	-0.07	0.13
0.03	-0.14	0.21
0.07	-0.21	0.33
0.08	-0.09	0.25
0.16	-0.07	0.40
0.18	-0.10	0.47

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

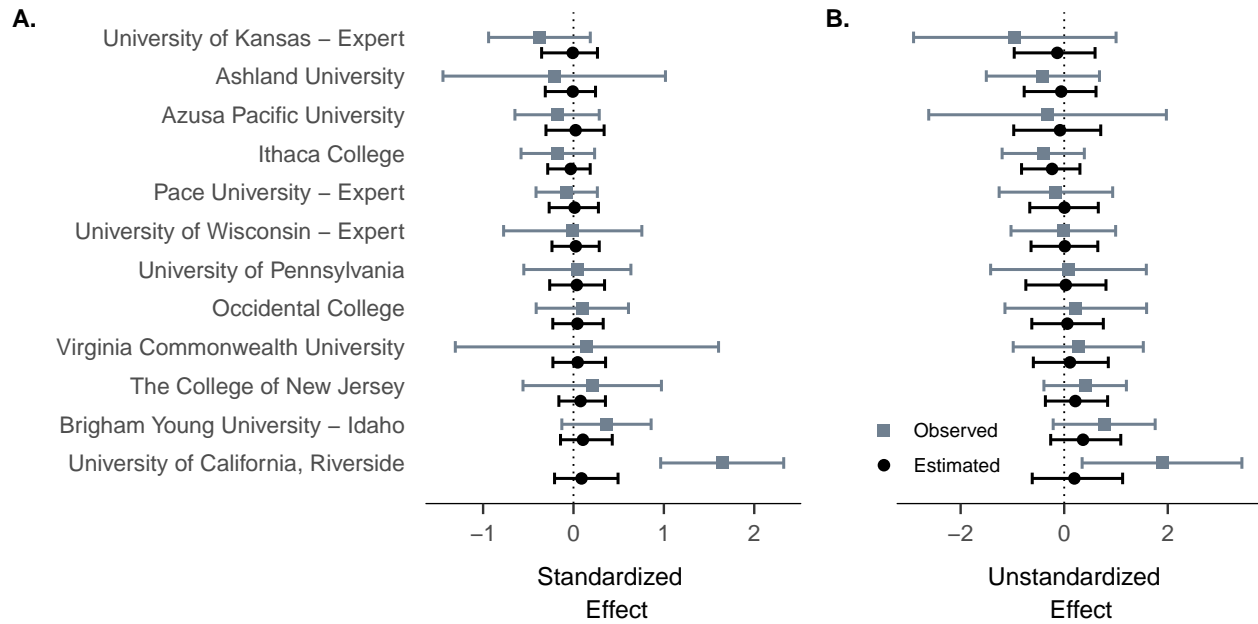
A.



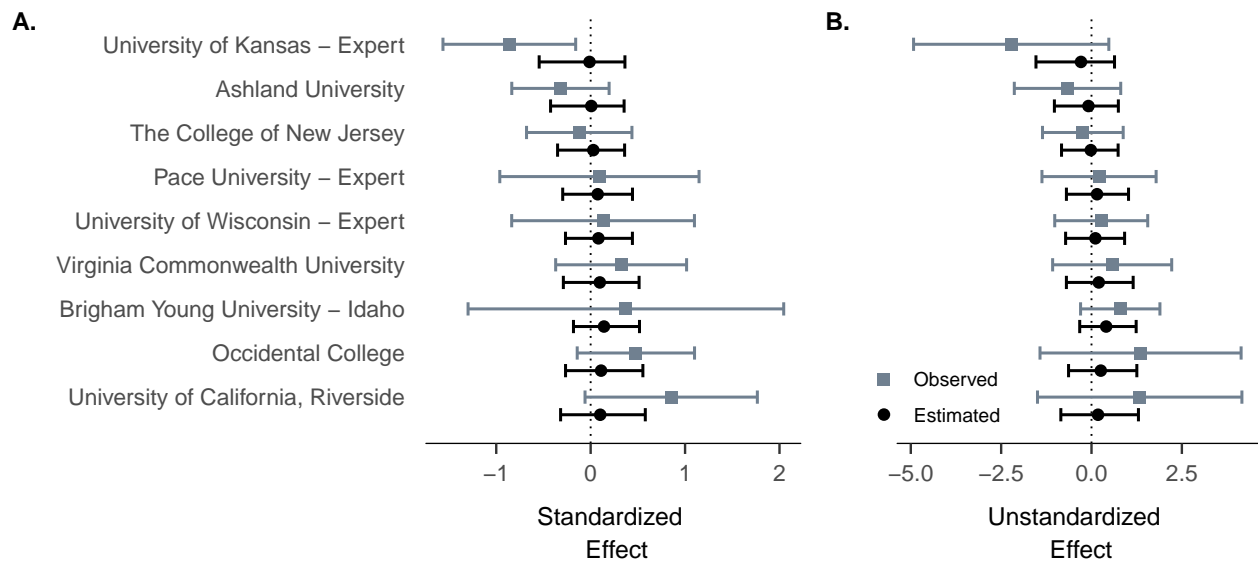
B.



```
forest.all(obs.data = dat.211, es.data = m.211, est.averaging = rema.211.es$est$default, est.multilevel
```

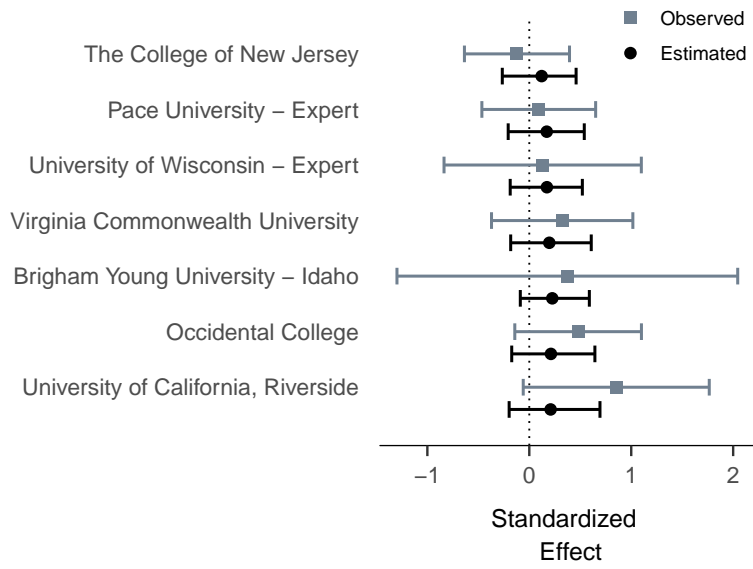


```
forest.all(obs.data = dat.311, es.data = m.311, est.averaging = rema.311.es$est$default, est.multilevel
```



```
forest.all(obs.data = dat.332, es.data = m.332, est.averaging = rema.332.es$est$default, est.multilevel
```

A.



B.

