

Bayesian Model Averaging Meta Analysis

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

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

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

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

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

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)
}

# BFr 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]])
    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(" ")

return(plot)
}

```

Original Analysis

```

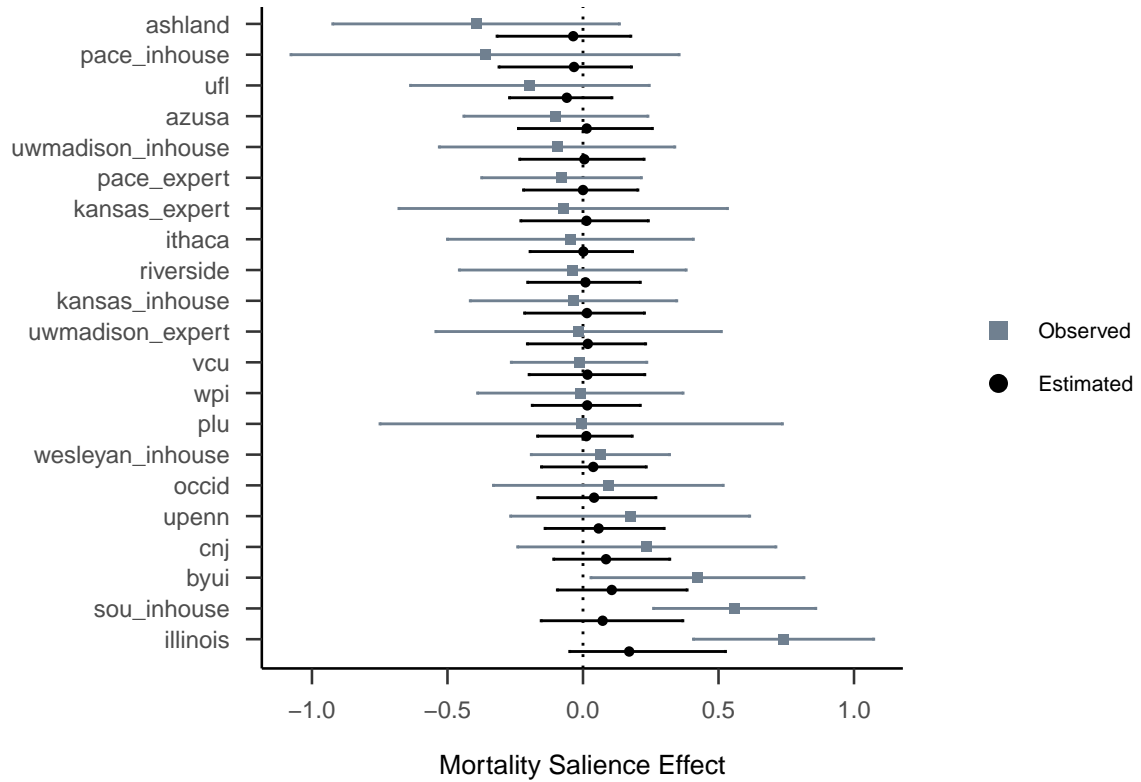
m.111 <- read.csv2("data/metaset_111.csv", header = T)
m.211 <- read.csv2("data/metaset_211.csv", header = T)
m.311 <- read.csv2("data/metaset_311.csv", header = T)

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)

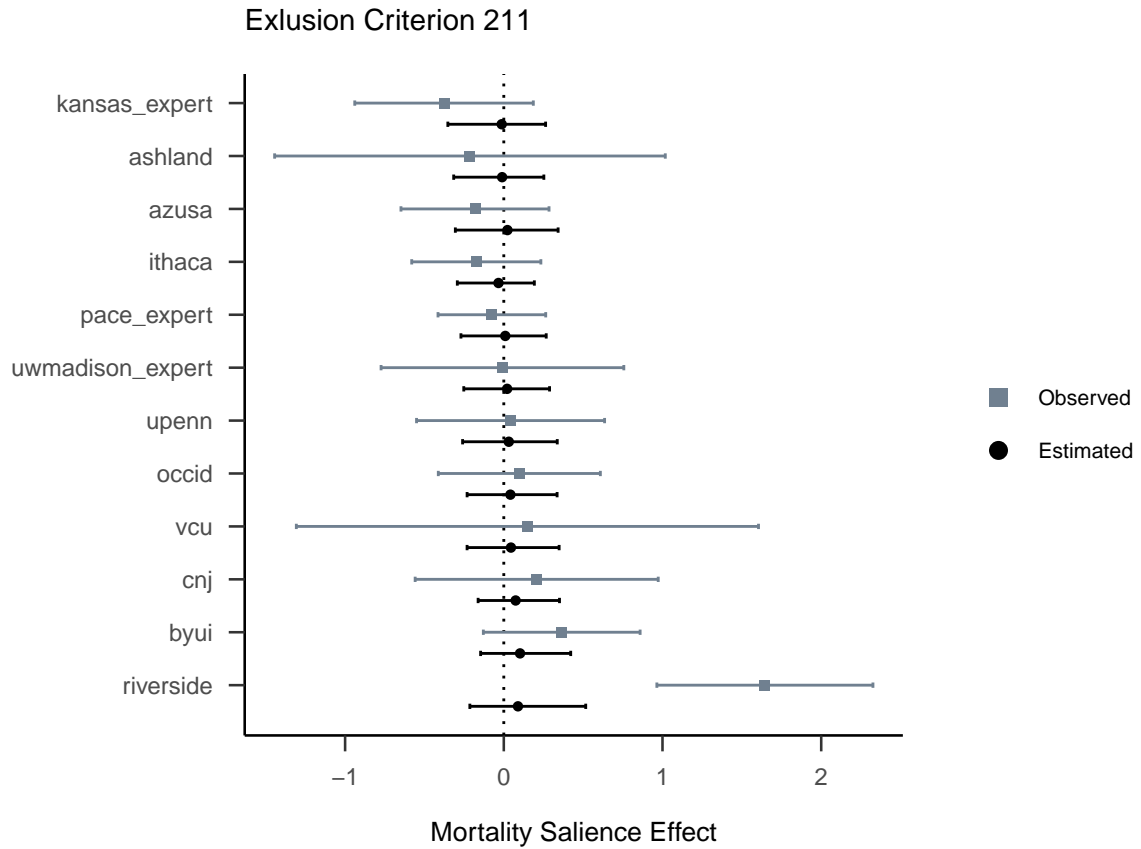
remaForest(m.111, rema.111$est$default) + ggtitle("Exclusion Criterion 111")

```

Exclusion Criterion 111



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

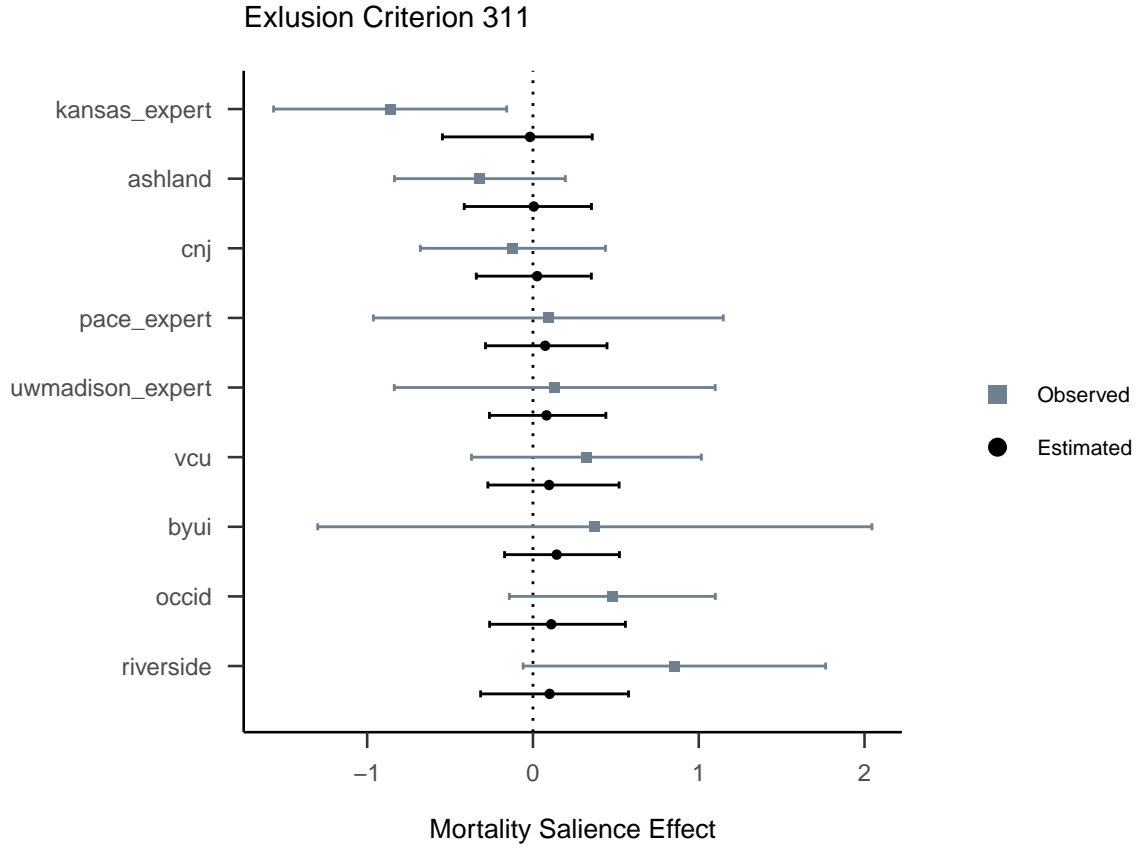


```
remaForest(m.311, rema.311$est$default) + ggtitle("Exclusion Criterion 311")
```

Table 1: Bayes factors for key analyses.

	Effect Size BF			Heterogeneity BF		
	Default	Oosterwijk	Vohs	Default	Oosterwijk	Vohs
Exclusion Criterion 111	17.40	37.66	14.57	0.44	0.43	0.44
Exclusion Criterion 211	10.10	15.14	6.63	0.41	0.42	0.42
Exclusion Criterion 311	6.01	3.94	2.45	0.56	0.57	0.57

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



```
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))

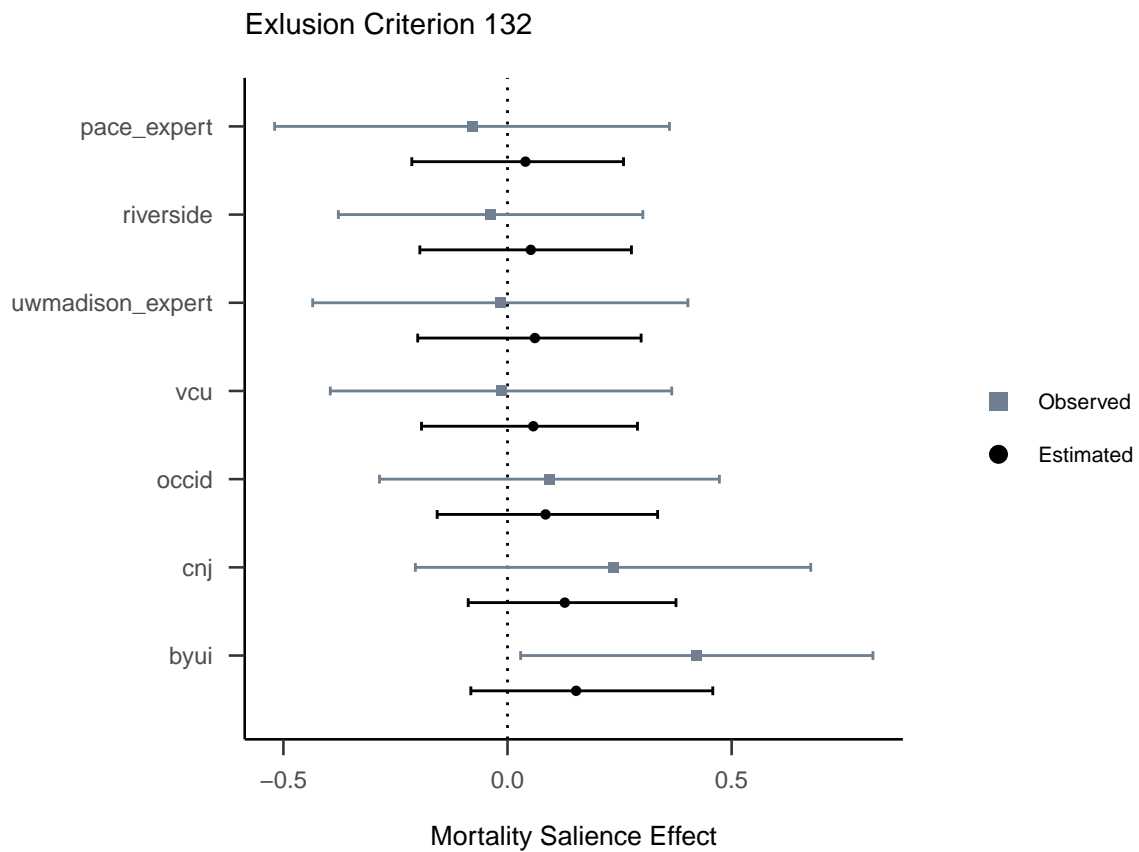
apa_table(BFs.og, escape = FALSE, caption = "Bayes factors for key analyses.",
          note = "All Bayes factors are reported in favor of the null model.",
          col_spanners = colhead)
```

Analysis for the Main Claim of the Comment

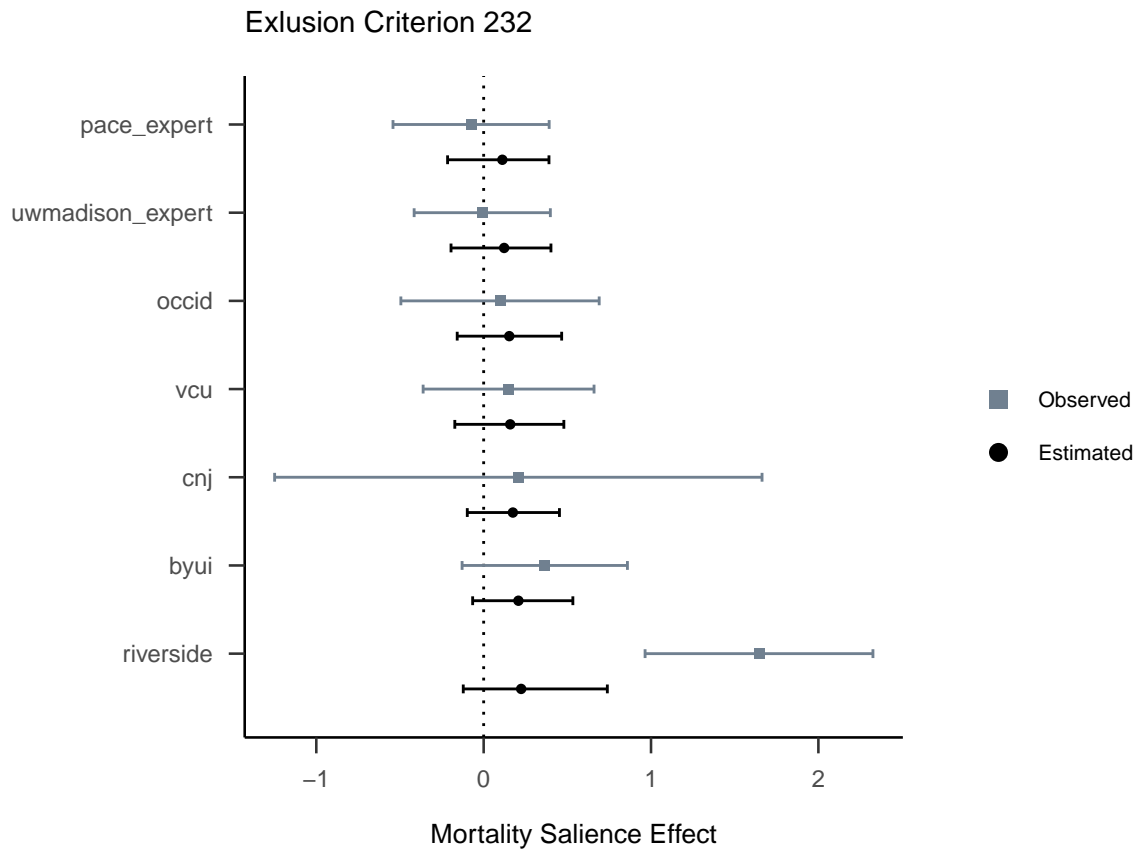
```
m.132 <- read.csv2("data/metaset_132.csv", header = T)
m.232 <- read.csv2("data/metaset_232.csv", header = T)
m.332 <- read.csv2("data/metaset_332.csv", header = T)

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("Exlusion Criterion 132")
```



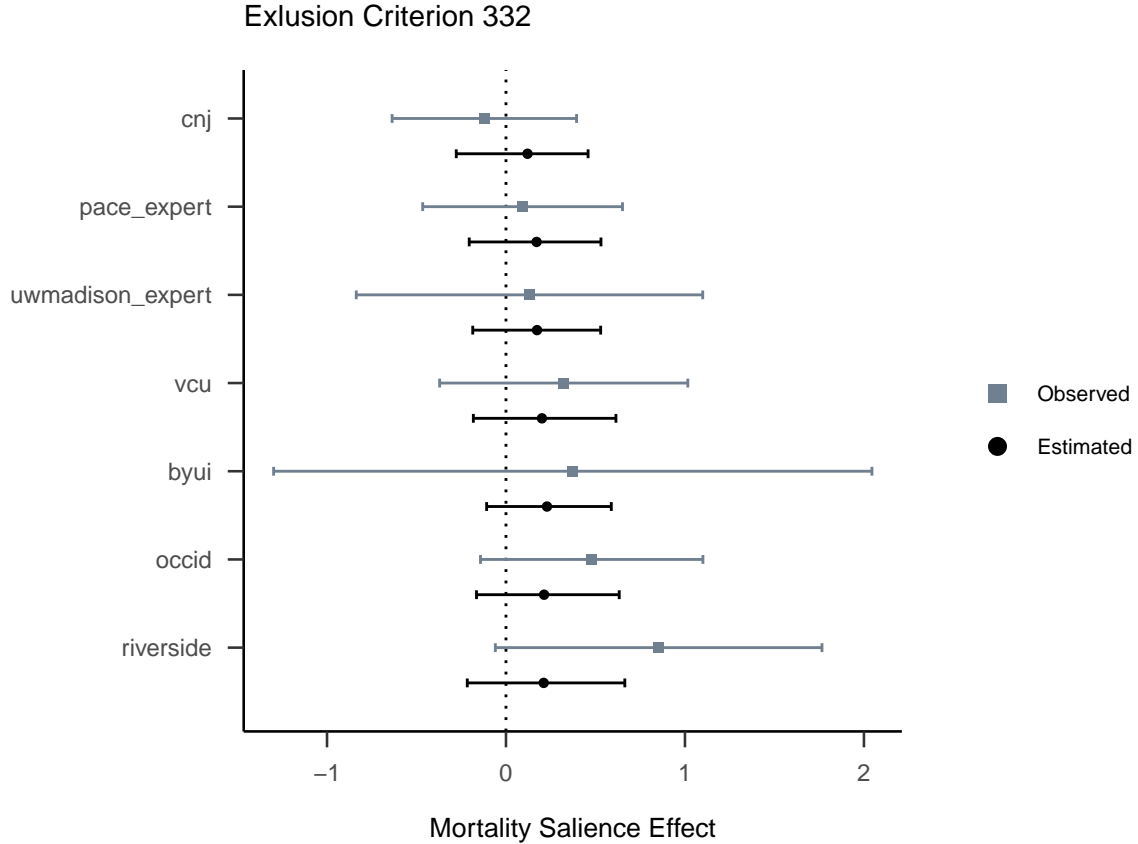
```
remaForest(m.232, rema.232$est$default) + ggtitle("Exlusion Criterion 232")
```



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


Table 2: Bayes factors for comment analyses.

	Effect Size BF			Heterogeneity BF		
	Default	Oosterwijk	Vohs	Default	Oosterwijk	Vohs
Exclusion Criterion 132	6.50	5.78	2.73	0.40	0.40	0.40
Exclusion Criterion 232	2.65	0.92	0.67	0.49	0.50	0.48
Exclusion Criterion 332	2.63	0.74	0.63	0.54	0.54	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 = "Bayes factors for comment analyses.",
          col_spanners = colhead)
```

All Other Variants

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

Table 3: Bayes factors for all other analyses.

	Default	Oosterwijk	VoHS
Exclusion Criterion 112	10.34	15.16	6.38
Exclusion Criterion 212	6.00	4.21	2.30
Exclusion Criterion 312	6.01	3.94	2.45
Exclusion Criterion 121	15.34	30.19	11.62
Exclusion Criterion 221	6.92	5.78	2.95
Exclusion Criterion 321	2.63	0.74	0.63
Exclusion Criterion 122	6.50	5.78	2.73
Exclusion Criterion 222	2.65	0.92	0.67
Exclusion Criterion 322	2.63	0.74	0.63
Exclusion Criterion 131	10.46	15.88	6.21
Exclusion Criterion 231	6.92	5.78	2.95
Exclusion Criterion 331	2.63	0.74	0.63

```

                                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 = "Bayes factors for all other analyses.")

```