

Appendix

1. R code that generates inconsistency visualization for binary outcomes

Input: Studies should be in rows. Four columns are needed for the number of events (r1 and r2) and sample sizes (n1 and n2) for the intervention and control group, respectively.

```
library(meta); library(ggplot2)

thresholds <- c(-Inf, -0.2, -0.1, -0.01, 0.01, 0.1, 0.2, Inf)
labels <- c("Large\nReduction", "Medium\nReduction", "Small\nReduction",
           "Trivial", "Small\nIncrease", "Medium\nIncrease", "Large\nIncrease")

meta_object <- metabin(event.e = r1, n.e = n1, event.c = r2, n.c = n2,
                      studlab=Study, data = dat, sm = "RR")
BR <- sum(summary(meta_object)$event.c) / sum(summary(meta_object)$n.c)
pooled.RD <- (exp(summary(meta_object)$TE.random) - 1) * BR
pooled.reg <- labels[findInterval(pooled.RD, thresholds)]
RDs <- ((exp(summary(meta_object)$TE)) - 1) * BR
RDs_regions <- labels[findInterval(RDs, thresholds)]
RDs_regions <- factor(RDs_regions, levels = labels)
wts <- summary(meta_object)$w.random
total_wt <- sum(wts)
region_total_wt <- tapply(wts, RDs_regions, sum)
region_total_wt[is.na(region_total_wt)] <- 0
region_percent_wts <- region_total_wt / total_wt

df_plot <- data.frame(labels = factor(labels, levels = labels),
                     region_percent_wts = region_percent_wts,
                     pooled_reg = pooled.reg)
ggplot(df_plot, aes(x = labels, y = region_percent_wts)) +
  geom_bar(stat = "identity", fill = ifelse(df_plot$labels == df_plot$pooled_reg, "green", "red")) +
  geom_text(aes(label = paste0(round(region_percent_wts * 100, 1), "%")),
           vjust = -0.5, size = 3) +
  labs(x = NULL, y = NULL) +
  ggtitle("Percentage of MA Weights Per Effect Size Range") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = "white"),
        plot.title = element_text(hjust = 0.5)) +
  theme(plot.margin = margin(1, 1, 1, 4, "lines"))
```

```
forest(meta_object, common = F)
```

2. R code that generates inconsistency visualization for continuous outcomes

Input: Studies should be in rows. Six columns are needed for sample sizes (n1 and n2), means (m1 and m2) and standard deviations (sd1 and sd2) for the intervention and control group, respectively.

```
library(meta); library(ggplot2)

thresholds <- c(-Inf, -0.8, -0.5, -0.2, 0.2, 0.5, 0.8, Inf)
labels <- c("Large\nReduction", "Medium\nReduction", "Small\nReduction",
           "Trivial", "Small\nIncrease", "Medium\nIncrease", "Large\nIncrease")

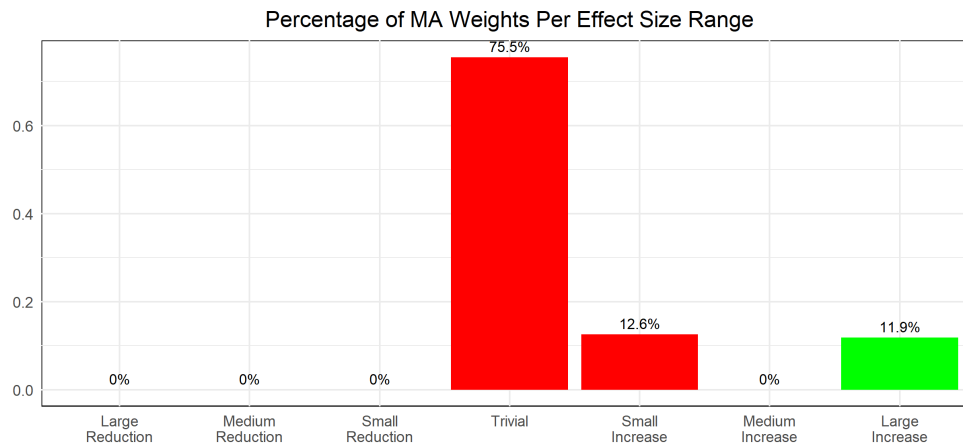
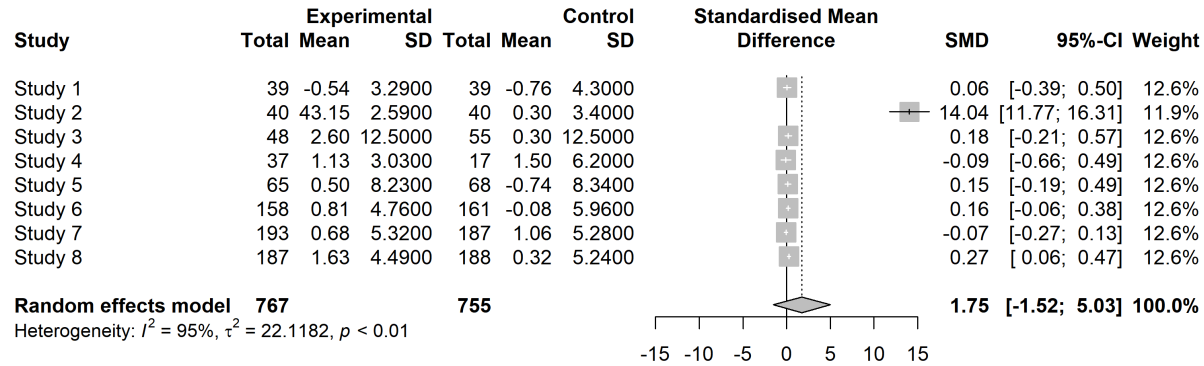
meta_object <- metacont(n.e = n1, mean.e = m1, sd.e=sd1, n.c=n2,mean.c=m2, sd.c=sd2,
                      studlab=Study, data = dat, sm = "SMD")
pooled.smd <- summary(meta_object)$TE.random
pooled.reg <- labels[findInterval(pooled.smd, thresholds)]
SMDs <- summary(meta_object)$TE
SMDs_regions <- labels[findInterval(SMDs, thresholds)]
SMDs_regions <- factor(SMDs_regions, levels = labels)
wts <- summary(meta_object)$w.random
total_wt <- sum(wts)
region_total_wt <- tapply(wts, SMDs_regions, sum)
region_total_wt[is.na(region_total_wt)] <- 0
region_percent_wts <- region_total_wt / total_wt

df_plot <- data.frame(labels = factor(labels, levels = labels),
                     region_percent_wts = region_percent_wts,
                     pooled_reg = pooled.reg)

ggplot(df_plot, aes(x = labels, y = region_percent_wts)) +
  geom_bar(stat = "identity", fill = ifelse(df_plot$labels == df_plot$pooled_reg, "green", "red")) +
  geom_text(aes(label = paste0(round(region_percent_wts * 100, 1), "%")),
           vjust = -0.5, size = 3) +
  labs(x = NULL, y = NULL) +
  ggtitle("Percentage of MA Weights Per Effect Size Range") +
  theme_minimal() +
  theme(
    panel.background = element_rect(fill = "white"),
```

```
plot.title = element_text(hjust = 0.5)) +  
theme(plot.margin = margin(1, 1, 1, 4, "lines"))  
  
png("fig3_panelA.png", width=12*ppi, height=4*ppi, res=ppi)  
forest(meta_object, common = F)
```

Supplemental Figure 1. Meta-analysis of trials of health coaching for chronic illness



Bottom Panel B demonstrates a bar graph showing the distribution of meta-analysis weights per effect size range. The green bar represents the inference associated with the target of certainty (the pooled estimate).