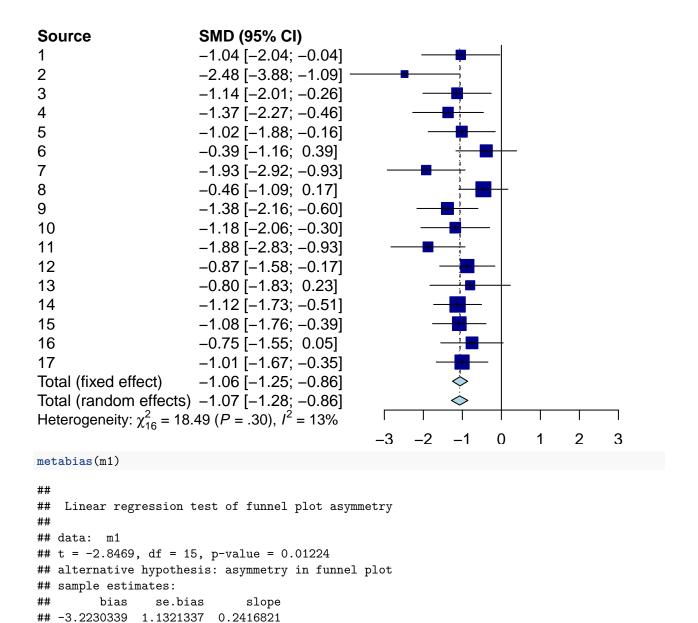
Appendix B

A contrast of analyses done using the R packages meta and metafor.

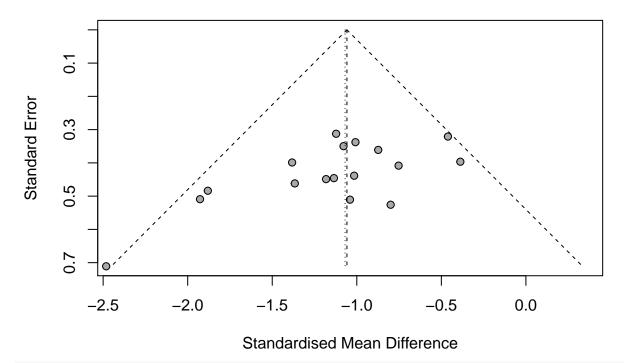
Contrasted meta and metafor using the classic Cochrane bronchoconstriction dataset used in many texts to demonstrate meta-analysis. Here is a link to these data as a tidy csv files on figshare.

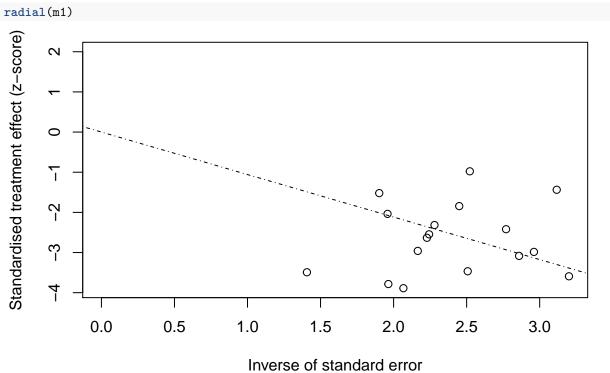
Meta

```
#load primary libraries
library(tidyverse) #tidy functions to read and format data
library(meta) #meta package current version effective March 2020
#Classic bronchoconstriction data from Cochrane
data <- read_csv(url("https://ndownloader.figshare.com/files/14460386"))
#continuous data
m1 <- metacont(Ne, Me, Se, Nc, Mc, Sc, data = data, sm = "SMD")
summary(m1)
## Number of studies combined: k = 17
##
                                            95%-CI
                            SMD
                                                         z p-value
## Fixed effect model
                        -1.0583 [-1.2537; -0.8630] -10.62 < 0.0001
## Random effects model -1.0694 [-1.2813; -0.8575] -9.89 < 0.0001
##
## Quantifying heterogeneity:
  tau^2 = 0.0265 [0.0000; 0.3559]; tau = 0.1629 [0.0000; 0.5966];
   I^2 = 13.5\% [0.0\%; 50.2\%]; H = 1.08 [1.00; 1.42]
##
## Test of heterogeneity:
##
        Q d.f. p-value
##
  18.49
            16 0.2959
##
## Details on meta-analytical method:
## - Inverse variance method
## - DerSimonian-Laird estimator for tau^2
## - Jackson method for confidence interval of tau^2 and tau
## - Hedges' g (bias corrected standardised mean difference)
forest(m1, layout = "JAMA")
```



funnel(m1)

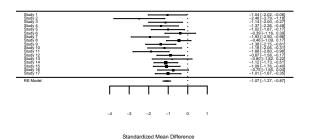




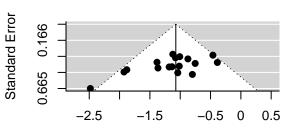
Metafor

```
#load primary libraries
library(tidyverse) #tidy functions to read and format data
library(metafor) #metafor package current version effective March 2020
#Classic bronchoconstriction data from Cochrane
data <- read_csv(url("https://ndownloader.figshare.com/files/14460386"))</pre>
#calculate effect sizes
data <- escalc(measure = "SMD", m1i=Me,m2i=Mc,sd1i=Se,sd2i=Sc,n1i=Ne,n2i=Nc, data=data,var.names=c("SMD"
#fit model
\#m2 \leftarrow rma(yi=SMD, vi=SMD\_var, mods = \sim study.ID, data = data)
m2 <- rma.uni(yi=SMD, vi=SMD_var, data = data, method = "REML") #restricted maximum-likelihood estimate
summary(m2)
##
## Random-Effects Model (k = 17; tau^2 estimator: REML)
##
    logLik deviance
                            AIC
                                      BIC
                                                AICc
## -10.5948
              21.1896
                        25.1896
                                  26.7348
                                             26.1127
##
## tau^2 (estimated amount of total heterogeneity): 0.0142 (SE = 0.0613)
## tau (square root of estimated tau^2 value):
                                                     0.1193
## I^2 (total heterogeneity / total variability):
                                                     7.88%
## H^2 (total variability / sampling variability): 1.09
##
## Test for Heterogeneity:
## Q(df = 16) = 19.4639, p-val = 0.2453
##
## Model Results:
##
                                 pval
## estimate
                         zval
                                         ci.lb
                                                   ci.ub
                 se
## -1.0727 0.1032 -10.3919 <.0001 -1.2750 -0.8703 ***
##
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#Viz
plot(m2)
```

Forest Plot

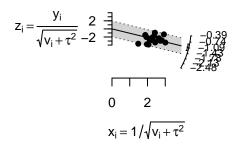


Funnel Plot

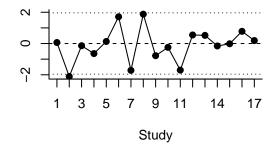


Standardized Mean Difference

Radial Plot



Standardized Residuals



Compiled contrasts

```
#compile random model outputs for contrast with metafor
estimate <- as_data_frame(m1$TE.random)</pre>
se <- as_data_frame(m1$seTE.random)</pre>
zval <- as_data_frame(m1$zval.random)</pre>
pval <- as_data_frame(m1$pval.random)</pre>
ci.lb <- as_data_frame(m1$lower.random)</pre>
ci.ub <- as_data_frame(m1$upper.random)</pre>
m1_tidy <- bind_cols(estimate, se, zval, pval, ci.lb, ci.ub) %>%
  rename(estimate = value, se = value1, zval = value2, pval = value3, ci.lb = value4, ci.ub = value5)
#compile output into table for contrast with meta
m2_tidy <- coef(summary(m2))</pre>
\#m2\_tidy
#compile key outputs
contrast_tidy <- bind_rows(m1_tidy, m2_tidy) %>%
  mutate(source = c("meta", "metafor")) %>%
  select(source, everything())
knitr::kable(contrast_tidy)
```

source	estimate	se	zval	pval	ci.lb	ci.ub
meta metafor	2.000000	$\begin{array}{c} 0.1081185 \\ 0.1032201 \end{array}$	-9.890843 -10.391944			-0.8574745 -0.8703497