Meta-analysis based on Sisks et al. (2018) - V.2

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Contents

Packages and Data

```r
# Load packages
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.0.4     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(meta)
```

```
## Warning: package 'meta' was built under R version 4.0.5
```

```
## Loading 'meta' package (version 5.2-0).
## Type 'help(meta)' for a brief overview.
## Readers of 'Meta-Analysis with R (Use R!)' should install
## older version of 'meta' package: https://tinyurl.com/dt4y5drs
```

```r
library(metafor)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack

##
## Loading the 'metafor' package (version 3.0-2). For an
## introduction to the package please type: help(metafor)
```

```r
library(readxl)
library(gridExtra) # for arranging qqplots
```

```
##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##     combine
```

```r
library(multcomp) # for multiple comparisons
```

```
## Loading required package: mvtnorm

## Loading required package: survival

## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##     geyser
```

```r
# Import data
df1 <- read_excel('data/mindset.xlsx', sheet = 'Meta-analysis 1')
```

```r
# FUNCTION TO CALCULATE I^2 FOR EACH LEVEL IN A 3-LEVEL MODEL

# Formulae 4.29 Chen 2015 + Paper
# Higgins and Thompson (2002) preferred to define the typical within-study
# sampling variance ... using the Q statistic:


# Inputs:
# v: variance (e.g. df$vi)
# k: number of studies (e.g. length(df$vi))
# rma_obj: meta-analysis object (e.g. multilevel1)

multilevel_i2 <- function(v, k, rma_obj)
```

```r
{
  k <- length(v)
  list.inverse.variances <- 1 /(v)
  sum.inverse.variances <- sum(list.inverse.variances)
  numerator <- (k - 1) * sum.inverse.variances

  squared.sum.inverse.variances <- (sum.inverse.variances)^2

  list.inverse.variances.square <- 1 / (v^2)
  sum.inverse.variances.square <- sum(list.inverse.variances.square)
  denominator <- squared.sum.inverse.variances - sum.inverse.variances.square

  estimated.sampling.variance <- numerator / denominator

  I2_1 <- (estimated.sampling.variance) / (rma_obj$sigma2[1] + rma_obj$sigma2[2] + estimated.sampling.va

  I2_2 <- (rma_obj$sigma2[1]) / (rma_obj$sigma2[1] + rma_obj$sigma2[2] + estimated.sampling.variance)

  I2_3 <- (rma_obj$sigma2[2]) / (rma_obj$sigma2[1] + rma_obj$sigma2[2] + estimated.sampling.variance)

  I2_1 <- round((amountvariancelevel1 <- I2_1 * 100),2)
  I2_2 <- round((amountvariancelevel2 <- I2_2 * 100),2)
  I2_3 <- round((amountvariancelevel3 <- I2_3 * 100),2)

  col1 <- rbind(I2_1, I2_2, I2_3)
  col2 <- rbind('Level 1', 'Level 2', 'Level 3')
  I2_partition <- data.frame(col1, col2)
  names(I2_partition) <- c('I2', 'Level')
  print(I2_partition)

  # Barplot
  ggplot(I2_partition, aes(x="", y=I2, fill=Level))+
    geom_bar(width = 1, stat = "identity") +
    theme_light()

}
```

Data cleaning

```r
# Glimpse data
glimpse(df1)
```

```
## Rows: 273
## Columns: 35
## $ `Document #`                          <dbl> 1, 2, 2, 2, 3, 3, 3, 3, 4, 5, 6...
## $ `Study #`                             <dbl> 1, 2, 2, 2, 3, 3, 3, 3, 4, 5, 6...
## $ `Sample #`                            <dbl> 1, 2, 3, 4, 5, 163, 164, 165, 6...
## $ `Sample Country`                      <chr> "Indonesia", "USA", "USA", "USA...
## $ `ES #`                                <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, ...
## $ Reference                            <chr> "Adatitomo (2015)", "Bagley (20...
## $ N                                    <dbl> 123, 400, 1019, 710, 250, 272, ...
## $ `Adjusted N`                          <dbl> 123.000000, 400.000000, 1019.00...
## $ `Student Description`                 <chr> "second semester university stu...
## $ `School Level`                        <chr> "post-secondary", "post-seconda...
## $ `Development Stage`                   <chr> "Adults", "Adults", "Adults", "...
## $ `Risk status`                         <chr> "low", "moderate", "moderate", ...
## $ SES                                  <chr> "not reported", "not reported",...
## $ `MS Measure`                          <chr> "Mindset about intelligence", "...
## $ `MS Measure Description`              <chr> "6 items, 3 growth and 3 fixed ...
## $ `Mindset Type`                        <chr> "Intelligence", "Personal attri...
## $ `Achievement Measure Description`     <chr> "Statistics final exam grade", ...
## $ `Academic Achievement Measure Type`  <chr> "Course exam", "Course grade", ...
## $ `Lab-based`                           <chr> "no", "no", "no", "no", "no", "...
## $ Published                            <chr> "yes", "no", "no", "no", "no", ...
## $ `ES type`                             <chr> "continuous", "continuous", "co...
## $ Calculation                          <chr> "Pearson's r", "sqrt of bivaria...
## $ Variance                             <dbl> 0.0079425749, 0.0024188215, 0.0...
## $ `Adjusted Variance`                   <dbl> 0.0079425749, 0.0024188215, 0.0...
## $ `Significant?`                        <chr> "N", "Y", "Y", "Y", "Y", "Y", "...
## $ r                                    <dbl> -0.12500000, 0.13266499, 0.1972...
## $ `Growth M`                            <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ `Growth SD`                           <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ `Other M`                             <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ `Other SD`                            <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ `Cohen's d`                           <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ rpb                                  <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ rb                                   <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ `Calculated r`                        <dbl> NA, NA, NA, NA, NA, NA, NA, NA,...
## $ Notes                                <chr> "the authors of the study also ...
```

```r
# Rename columns
df2 <- rename(df1,
          document_id = 'Document #',
          study_id = 'Study #',
          sample_id = 'Sample #',
          sample_country = 'Sample Country',
          es_id = 'ES #',
          reference = 'Reference',
          n = N,
          adjusted_n = 'Adjusted N',
          student_description = 'Student Description',
```

```
          school_level = 'School Level',
          development_stage = 'Development Stage',
          risk_status = 'Risk status',
          ses = SES,
          ms_measure = 'MS Measure',
          ms_measure_description = 'MS Measure Description',
          mindset_type = 'Mindset Type',
          achievement_measure_description = 'Achievement Measure Description',
          academic_achievement_measure_type = 'Academic Achievement Measure Type',
          lab_based = 'Lab-based',
          published = 'Published',
          es_type = 'ES type',
          calculation = 'Calculation',
          variance = 'Variance',
          adjusted_variance = 'Adjusted Variance',
          is_significant = 'Significant?',
          growth_m = 'Growth M',
          growth_sd = 'Growth SD',
          other_m = 'Other M',
          other_sd = 'Other SD',
          cohen_d = "Cohen's d",
          calculated_r = 'Calculated r',
          notes = Notes)


# Check that variable types is correct
glimpse(df2)
```

```
## Rows: 273
## Columns: 35
## $ document_id                         <dbl> 1, 2, 2, 2, 3, 3, 3, 3, 4, 5, 6, ...
## $ study_id                            <dbl> 1, 2, 2, 2, 3, 3, 3, 3, 4, 5, 6, ...
## $ sample_id                           <dbl> 1, 2, 3, 4, 5, 163, 164, 165, 6, ...
## $ sample_country                      <chr> "Indonesia", "USA", "USA", "USA",...
## $ es_id                               <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11...
## $ reference                           <chr> "Adatitomo (2015)", "Bagley (2016...
## $ n                                   <dbl> 123, 400, 1019, 710, 250, 272, 27...
## $ adjusted_n                          <dbl> 123.000000, 400.000000, 1019.0000...
## $ student_description                 <chr> "second semester university stude...
## $ school_level                        <chr> "post-secondary", "post-secondary...
## $ development_stage                   <chr> "Adults", "Adults", "Adults", "Ad...
## $ risk_status                         <chr> "low", "moderate", "moderate", "m...
## $ ses                                 <chr> "not reported", "not reported", "...
## $ ms_measure                          <chr> "Mindset about intelligence", "Dw...
## $ ms_measure_description              <chr> "6 items, 3 growth and 3 fixed fr...
## $ mindset_type                        <chr> "Intelligence", "Personal attribu...
## $ achievement_measure_description     <chr> "Statistics final exam grade", "D...
## $ academic_achievement_measure_type   <chr> "Course exam", "Course grade", "C...
## $ lab_based                           <chr> "no", "no", "no", "no", "no", "no...
## $ published                           <chr> "yes", "no", "no", "no", "no", "n...
## $ es_type                             <chr> "continuous", "continuous", "cont...
## $ calculation                         <chr> "Pearson's r", "sqrt of bivariate...
## $ variance                            <dbl> 0.0079425749, 0.0024188215, 0.000...
## $ adjusted_variance                   <dbl> 0.0079425749, 0.0024188215, 0.000...
```

```
## $ is_significant                 <chr> "N", "Y", "Y", "Y", "Y", "Y", "Y"...
## $ r                              <dbl> -0.12500000, 0.13266499, 0.197230...
## $ growth_m                       <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ growth_sd                      <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ other_m                        <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ other_sd                       <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ cohen_d                        <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ rpb                            <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ rb                             <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ calculated_r                   <dbl> NA, NA, NA, NA, NA, NA, NA, NA, N...
## $ notes                          <chr> "the authors of the study also me...
```

```r
# Change school_level from character to factor
df2$school_level <- as.factor(df2$school_level)
levels(df2$school_level)
```

```
##  [1] "elementary, middle and high"
##  [2] "graduate"
##  [3] "middle"
##  [4] "middle and secondary"
##  [5] "middle and secondary (mostly secondary)"
##  [6] "post-secondary"
##  [7] "primary"
##  [8] "primary and middle"
##  [9] "secondary"
## [10] "vocational courses"
```

```r
# Change development_stage from character to factor
df2$development_stage <- as.factor(df2$development_stage)
levels(df2$development_stage)
```

```
## [1] "Adolescents" "Adults"      "Children"    "Wide range"  "Wide Range"
```

```r
# Convert all "Wide range" level to "Wide Range"
df2$development_stage <- recode_factor(df2$development_stage,
                                       'Wide range' = 'Wide Range')
levels(df2$development_stage)
```

```
## [1] "Wide Range"  "Adolescents" "Adults"      "Children"
```

```r
# Change risk_status from character to factor
df2$risk_status <- as.factor(df2$risk_status)
levels(df2$risk_status)
```

```
## [1] "."        "high"     "low"      "moderate"
```

```
## Note: The category '.' applies to 4 rows
## These are studies from which it was not possible to determine the risk status
## df2 %>%
##   filter(risk_status == '.')
```

```r
# Change ses from character to factor
df2$ses <- as.factor(df2$ses)
levels(df2$ses)
```

```
## [1] "low SES"      "not low"      "not reported"
```

6

```r
# Change mindset_type from character to factor
df2$mindset_type <- as.factor(df2$mindset_type)
levels(df2$mindset_type)
```

```
##  [1] "Ability"
##  [2] "Ability and Intelligence"
##  [3] "Ability and Performance"
##  [4] "Ability to learn"
##  [5] "Art Ability"
##  [6] "Biology Ability"
##  [7] "English Ability"
##  [8] "Intelligence"
##  [9] "Intelligence and Reading Ability"
## [10] "Intelligence and Talent"
## [11] "Intelligence, Math Ability, and Effort"
## [12] "Math ability"
## [13] "Math Ability"
## [14] "Math intelligence"
## [15] "Math Intelligence"
## [16] "Performance and Intelligence"
## [17] "Personal attributes"
## [18] "Personality"
## [19] "Physics Intelligence"
## [20] "Reading Ability"
## [21] "School Ability"
## [22] "Science ability"
## [23] "Science Ability"
## [24] "Talent for School"
## [25] "Verbal Intelligence"
```

```r
# Change academic_achievement_measure_type from character to factor
df2$academic_achievement_measure_type <- as.factor(df2$academic_achievement_measure_type)
levels(df2$academic_achievement_measure_type)
```

```
## [1] "Course exam"       "Course grade"       "GPA"
## [4] "Standardized test"
```

```r
# Change lab_based from character to factor
df2$lab_based <- as.factor(df2$lab_based)
levels(df2$lab_based)
```

```
## [1] "no"  "yes"
```

```r
# Change published from character to factor
df2$published <- as.factor(df2$published)
levels(df2$published)
```

```
## [1] "no"  "yes"
```

```r
# Change es_type from character to factor
df2$es_type <- as.factor(df2$es_type)
levels(df2$es_type)
```

```
## [1] "categorical" "continuous"
```

```r
# Change is_significant from character to factor
df2$is_significant <- as.factor(df2$is_significant)
```

```
levels(df2$is_significant)
```

```
## [1] "N" "Y"
```
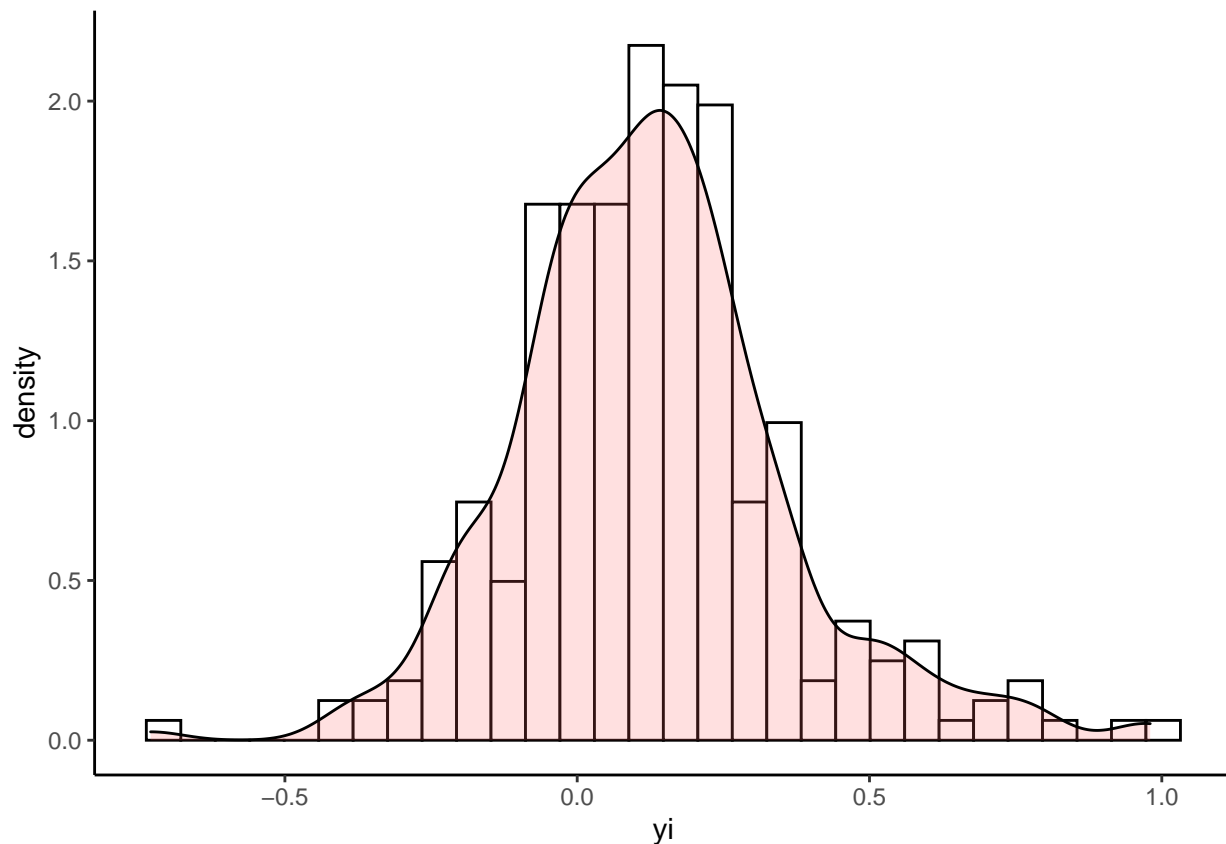
```
# Create dataframe for metafor:
# Calculate r-to-z transformed correlations and corresponding sampling variances
df3 <- escalc(measure="ZCOR", ri=r, ni=n, data=df2)
```

```
# Explore graphically Fisher's Z
ggplot(df3, aes(x=yi)) +
  geom_histogram(aes(y=..density..), colour = 'black', fill = "white") +
  geom_density(alpha=.2, fill="#FF6666") +
  theme_classic()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
# Fisher's Z
qqplot_z <- ggplot(df3, aes(sample=yi)) +
  stat_qq() +
  stat_qq_line() +
  theme_classic()
```

```
# Original r
qqplot_r <- ggplot(df3, aes(sample=r))+
  stat_qq() +
  stat_qq_line() +
  theme_classic()
```

```
grid.arrange(qqplot_r, qqplot_z, ncol=2)
```
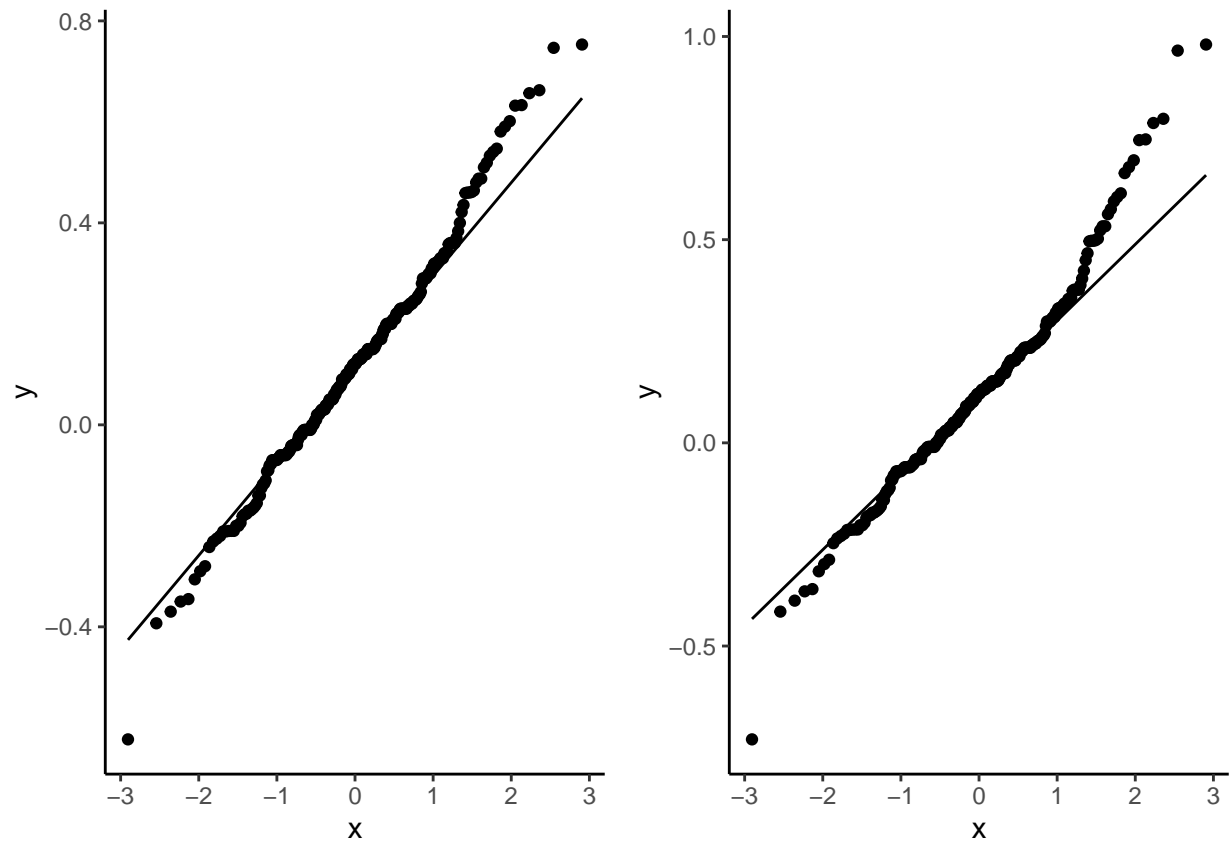
Meta-analysis 1: Random-effects model (REM)

Other notes: REML to estimate tau, no hakn correction.

```r
# REM of the transformed correlations
meta1 <- rma (yi = yi,
              vi = vi,
              measure = 'ZCOR',
              data = df3,
              slab = es_id)
summary(meta1, digits = 3)
```

```
##
## Random-Effects Model (k = 273; tau^2 estimator: REML)
##
##   logLik  deviance       AIC       BIC      AICc
##   60.314  -120.628  -116.628  -109.416  -116.583
##
## tau^2 (estimated amount of total heterogeneity): 0.019 (SE = 0.002)
## tau (square root of estimated tau^2 value):      0.137
## I^2 (total heterogeneity / total variability):   95.68%
## H^2 (total variability / sampling variability):  23.13
##
## Test for Heterogeneity:
## Q(df = 272) = 8958.240, p-val < .001
##
## Model Results:
##
## estimate     se    zval   pval  ci.lb  ci.ub
##    0.107  0.010  10.411  <.001  0.087  0.127  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pooled effect size

- Number of studies = 273

- estimate = 0.1071, with 95% CI [0.0869, 0.1272], z = 10.4110 and p-value <.0001. However, this Fisher's z, so, we need to transform it back to Pearson r for interpretation

```r
# Transform from z to r and see if the values you obtain make sense:
transf.ztor(0.1071)
```

```
## [1] 0.1066924
```

```r
transf.ztor(0.0869)
```

```
## [1] 0.08668191
```

```r
transf.ztor(0.1272)
```

```
## [1] 0.1265184
```

```r
# From examples: https://wviechtb.github.io/metadat/reference/dat.molloy2014.html
# Documentation: predict.rma
## returns the estimated (average) outcome in the hypothetical population of studies from which the set
predict(meta1, digits=3, transf=transf.ztor)
```

```
## 
##   pred ci.lb ci.ub  pi.lb pi.ub
##  0.107 0.087 0.127 -0.161 0.359
```

- estimate = 0.107, with 95% CI [0.087, 0.127]

- The prediction interval ranges is $r = [-0.161, 0.359]$. This means that it is possible that some future studies will find a negative correlation between mindset and academic achievement based on the present evidence. But the interval spans also over to a substantial positive effect.

Analysis of between-studies heterogeneity

- Cochrane's Q: If there was no heterogeneity this statistics should be distributed as a χ^2 distribution with 272 degrees of freedom. In our meta-analysis $Q = 8958.24$ with p < .0001. We reject the null hypothesis of homogeneity. There is evidence for heterogeneity.

```
# Obtain confidence interval for tau^2, I^2, H
# Interval for tau^2 is obtained iteratively either via the Q-profile method or via the generalized Q-s
# The square root of the inter- val bounds is also returned for easier interpretation.
# Confidence intervals for I2 and H2 are also provided (Higgins & Thompson, 2002). Since I2 and H2 are
confint.rma.uni(meta1, digits = 3)
```

```
##
##          estimate  ci.lb   ci.ub
## tau^2       0.019  0.016   0.028
## tau         0.137  0.128   0.169
## I^2(%)     95.677 95.077  97.103
## H^2        23.132 20.312  34.523
```

- $I^2 = 95.68$ (95%CI:95.08 - 97.10%), meaning that about 96% of the variability in effect sizes is due between-study heterogeneity. This can be considered substantial heterogeneity (according to Thomppson's rule of thumb).

- H^2 is 23.13. Values greater than 1 indicate heterogeneity.

- τ^2, the between-study variance, is 0.0187 with 95% confidence interval [0.016, 0.0284], which does not include zero. Indicates heterogeneity. The confidence interval for τ^2 was calculated based on the Q-profile method or the generalized Q-statistic method.

- τ, is the 'standard deviation of the true effect size and [...] it tells us something about the range of the true effect sizes. The true effect sizes have an estimated standard deviation of $SD = 0.1369$ expressed on the scale of (**Question: Pearson correlation or Fisher's Z?**)

Forest plot

```
pdf(file='forestplot_metafor.pdf', width = 8, height = 30)
forest(meta1,
       header = TRUE,
       transf = transf.ztor,
       showweights = TRUE,
       order = 'obs',
       efac = 0.2)

### add text with Q-value, dfs, p-value, and I^2 statistic
# https://www.metafor-project.org/doku.php/plots:forest_plot
text(-4.6, -3, pos=4, cex=0.75, bquote(paste("RE Model (Q = ",
     .(formatC(meta1$QE, digits=2, format="f")), ", df = ", .(meta1$k - meta1$p),
     ", p = ", .(formatC(meta1$QEp, digits=2, format="f")), "; ", I^2, " = ",
     .(formatC(meta1$I2, digits=1, format="f")), "%)")))
dev.off()
```

```
## pdf
##   2
```

Notes:

- Many of the more precise studies (smaller confidence interval), have an average correlation between -0.03 and 0.24

Caterpillar plot

```r
# Source code:
# http://www.metafor-project.org/doku.php/plots:caterpillar_plot
### create plot
forest(df3$yi, df3$vi,
       xlim=c(-2.5,3.5),         ### adjust horizontal plot region limits
       order="obs",              ### order by size of yi
       slab=NA, annotate=FALSE,  ### remove study labels and annotations
       efac=0,                   ### remove vertical bars at end of CIs
       pch=19,                   ### changing point symbol to filled circle
       col="gray40",             ### change color of points/CIs
       psize=2,                  ### increase point size
       cex.lab=1, cex.axis=1,    ### increase size of x-axis title/labels
       lty=c("solid","blank"),   ### remove horizontal line at top of plot
       transf = transf.ztor)

### draw points one more time to make them easier to see
points(sort(df3$yi), length(df3$vi):1, pch=19, cex=0.5)

### add summary polygon at bottom and text
addpoly(meta1, mlab="", cex=1, col = 'red')
text(-2, -2, "RE Model", pos=4, offset=0, cex=1)
```
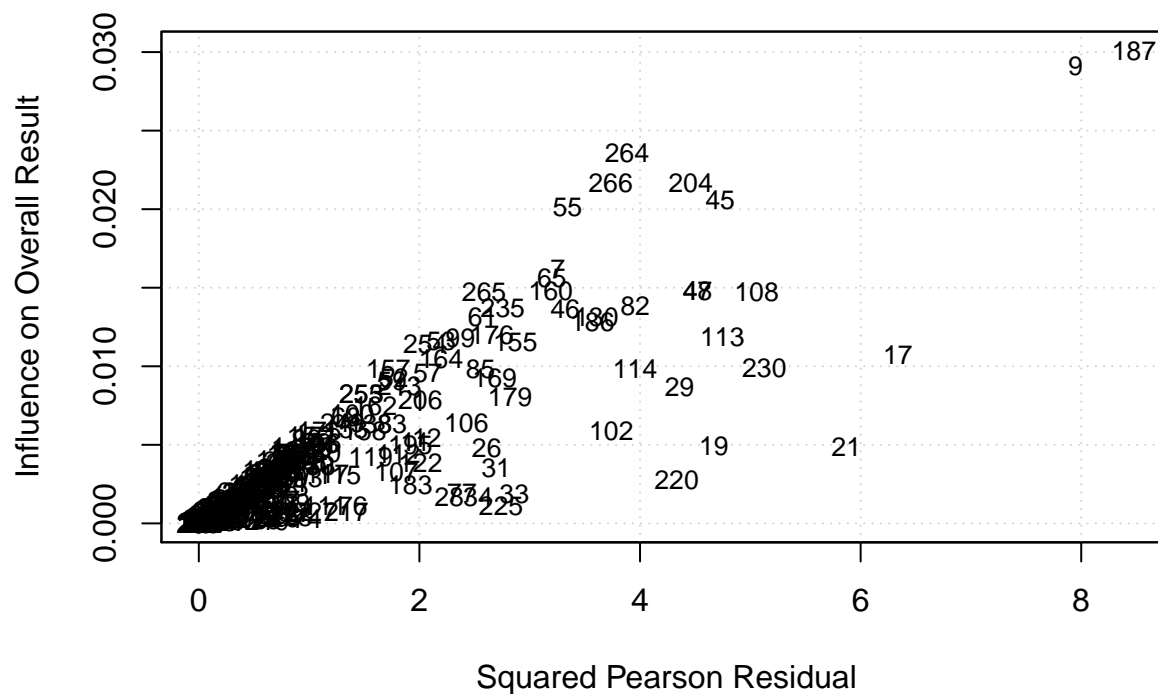

RE Model   0.11 [0.09, 0.13]

−1   −0.5   0   0.5   1

Correlation Coefficient
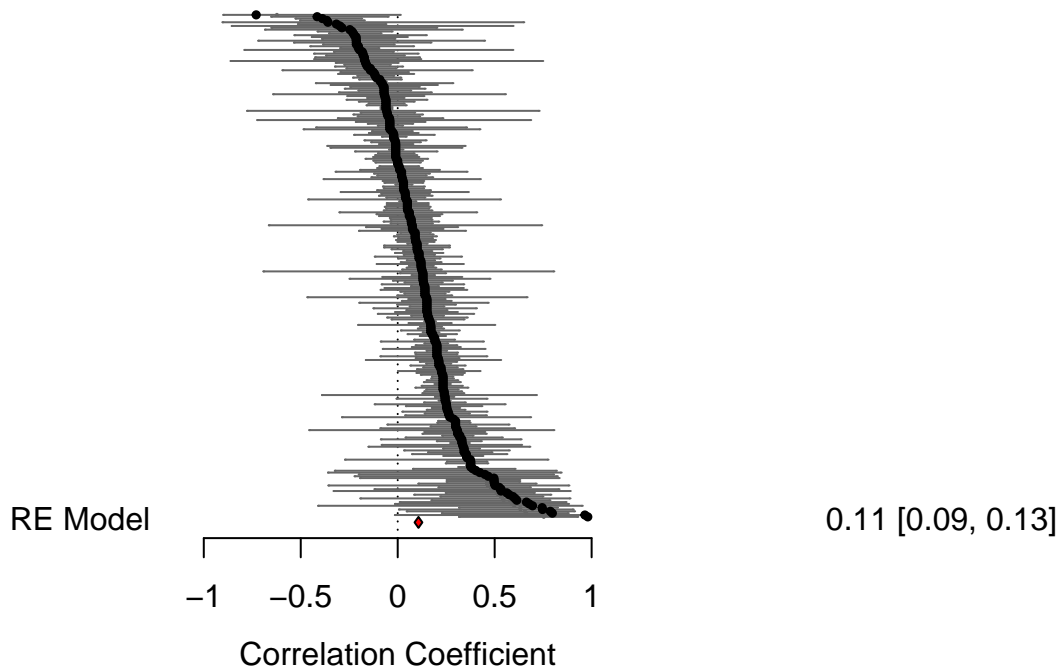
Outliers and Influential cases

```
inf <- influence(meta1)
pdf(file='infleunce.pdf')
plot(inf)
dev.off()
```

```
## pdf
##   2
```

```
### create Baujat plot
baujat(meta1, symbol="slab")
```



```
# Look at es_id = 9 and 187
df3 %>% filter(es_id == 9)
```

```
##   document_id study_id sample_id sample_country es_id     reference   n
## 1           4        4         6            USA     9 Bergen (1991) 110
##   adjusted_n student_description   school_level development_stage risk_status
## 1        110      undergraduates post-secondary            Adults         low
##          ses          ms_measure     ms_measure_description mindset_type
## 1 not reported Theory of Intelligence 8 items on a 7-point scale Intelligence
##   achievement_measure_description academic_achievement_measure_type lab_based
## 1                      ACT scores                Standardized test        no
##   published    es_type calculation    variance adjusted_variance is_significant
## 1        no continuous Pearson's r 0.007064278       0.007064278              Y
##      r growth_m growth_sd other_m other_sd cohen_d rpb rb calculated_r
## 1 -0.35       NA        NA      NA       NA      NA  NA NA           NA
##
## 1 the authors of the study used a measure where greater incremental theory was associated with lower
##       yi     vi
## 1 -0.3654 0.0093
```

Subgroup analysis

Sisks et al. (2018) found as **significant** moderators:

- Student factors:
    - Developmental stage of the student: children, adolescents, adults
- Developmental stage as a moderator of mind-set on GPA

Sisks et al. (2018) found as **non- significant** moderators:

- Student factors:
    - Academic risk status: low-risk, moderately at risk, highly at-risk students
    - Socioeconomic status
- Academic achievement measure: Course exam, Course grade, GPA, Standardized test

Developmental stage

```r
# Prepare dataset
levels(df3$development_stage)
```

```
## [1] "Wide Range"  "Adolescents" "Adults"      "Children"
```

```r
# Subset to exclude "Wide Range"
df3_develop <- filter(df3,
                      (development_stage == "Adolescents") |
                        (development_stage == "Adults") |
                        (development_stage == "Children"))
# Adjust labels
df3_develop$development_stage <- droplevels(df3_develop$development_stage)
levels(df3_develop$development_stage)
```

```
## [1] "Adolescents" "Adults"      "Children"
```

```r
# Inspect visually the relationship between Fisher's z and the categories
# x = developmental_stage y = Fisher's z
ggplot(data=df3_develop, mapping = aes(x=development_stage, y = yi)) +
  geom_dotplot(binaxis='y',
               stackdir='center',
               stackratio=1.5,
               dotsize=0.5,
               fill="#3399ff") +
  stat_summary(fun.y=mean, geom="point", shape=18,
               size=3, color="#ff5050")+
  theme_classic()
```

```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```
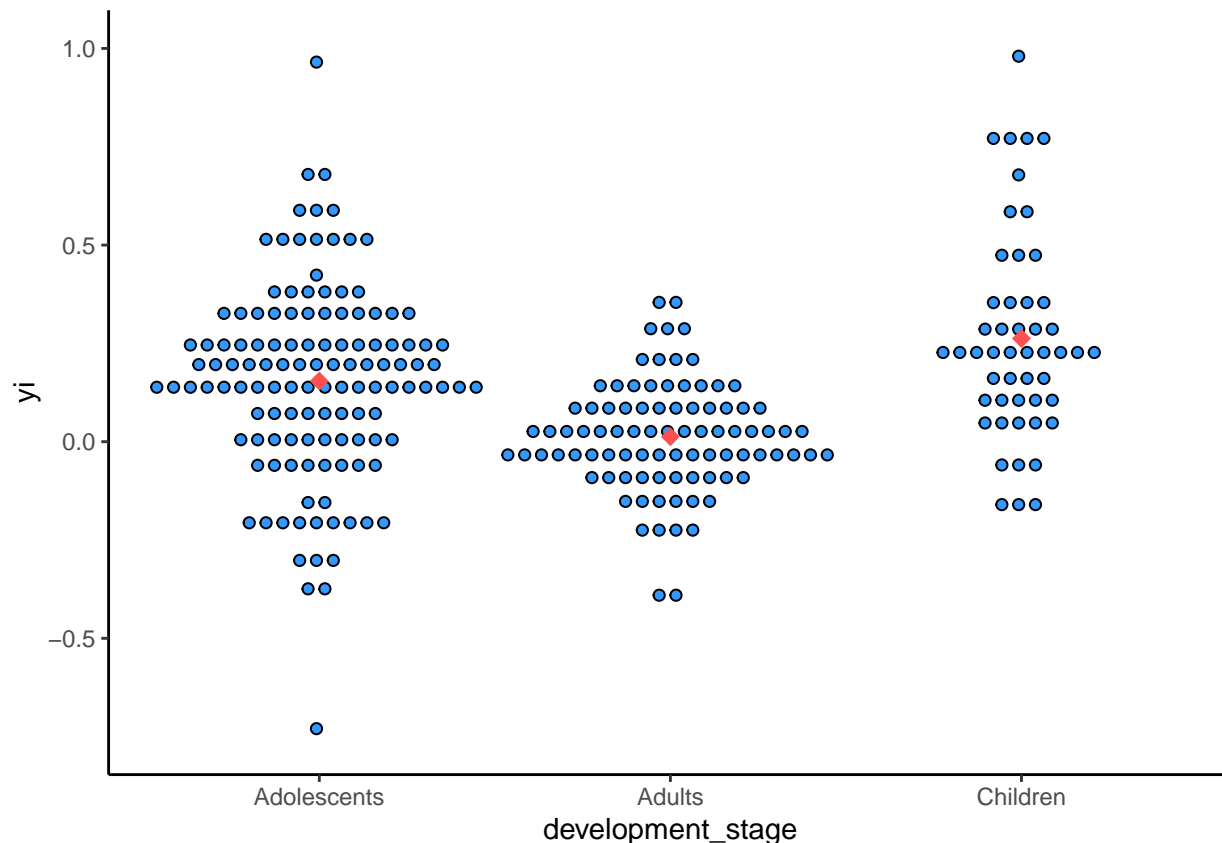
We see overlap in the outcome between the three categories, though it may be that children and adolescents show a higher effect than adults.

The range of values is larger for adolescents and children compared to adults. Probably this would call for estimating different tau^2 for each group

Next, I a weighted ANOVA. There are two options:

- common τ^2:

- different τ^2

```r
# Fit meta-analysis:
# COMMON TAU^2:
## Same between-study variance within each subgroup (Adolescents, Adults, Children)
meta1_develop1 <- rma (yi = yi,
                       vi = vi,
                       measure = 'ZCOR',
                       data = df3_develop,
                       mods = ~ development_stage-1)
summary(meta1_develop1, digits = 3)
```

```
##
## Mixed-Effects Model (k = 265; tau^2 estimator: REML)
##
##   logLik  deviance       AIC       BIC      AICc
##   78.298  -156.597  -148.597  -134.323  -148.441
##
## tau^2 (estimated amount of residual heterogeneity):     0.014 (SE = 0.002)
## tau (square root of estimated tau^2 value):             0.119
```

```
## I^2 (residual heterogeneity / unaccounted variability): 94.13%
## H^2 (unaccounted variability / sampling variability):   17.03
##
## Test for Residual Heterogeneity:
## QE(df = 262) = 5395.403, p-val < .001
##
## Test of Moderators (coefficients 1:3):
## QM(df = 3) = 184.782, p-val < .001
##
## Model Results:
##
##                                estimate    se    zval   pval   ci.lb  ci.ub
## development_stageAdolescents      0.151  0.014  10.649  <.001   0.123  0.179
## development_stageAdults           0.021  0.015   1.370  0.171  -0.009  0.050
## development_stageChildren         0.201  0.024   8.337  <.001   0.154  0.248
##
## development_stageAdolescents  ***
## development_stageAdults
## development_stageChildren      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Transform the estimates of the differences from z to r
transf.ztor(meta1_develop1$b)
```

```
##                                 [,1]
## development_stageAdolescents 0.14963377
## development_stageAdults      0.02051523
## development_stageChildren    0.19851106
```

```
# Multiple comparisons
# https://wviechtb.github.io/metafor/reference/rma.uni.html
multcomp_develop1 <- glht(meta1_develop1,
                   linfct=contrMat(c("Adolescents"=1,"Adults"=1,"Children"=1),
                                 type="Tukey"),test=adjusted("bonferroni"))

summary(multcomp_develop1)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: rma(yi = yi, vi = vi, mods = ~development_stage - 1, measure = "ZCOR",
##     data = df3_develop)
##
## Linear Hypotheses:
##                            Estimate Std. Error z value Pr(>|z|)
## Adults - Adolescents == 0   -0.13025    0.02061  -6.321    <1e-04 ***
## Children - Adolescents == 0  0.05042    0.02798   1.802     0.166
## Children - Adults == 0       0.18066    0.02840   6.362    <1e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
# Note that the estimate of the differences in the output are Fisher z

# Fit meta-analysis:
# DIFFERENT TAU^2 PER SUBGROUP:
## Different between-study variance within each subgroup (Adolescents, Adults, Children)
# https://wviechtb.github.io/metafor/reference/rma.uni.html

# We have to fit 3 models: ado, adu, chi
meta1_develop2_ado <- rma (yi = yi,
                           vi = vi,
                           measure = 'ZCOR',
                           data = df3_develop,
                           mods = ~ development_stage-1,
                           subset = (development_stage=="Adolescents"))
```

Warning: Redundant predictors dropped from the model.

```
summary(meta1_develop2_ado, digits = 3)
```

```
##
## Random-Effects Model (k = 126; tau^2 estimator: REML)
##
##   logLik  deviance       AIC       BIC      AICc
##   20.075   -40.150   -36.150   -30.493   -36.051
##
## tau^2 (estimated amount of total heterogeneity): 0.019 (SE = 0.004)
## tau (square root of estimated tau^2 value):      0.139
## I^2 (total heterogeneity / total variability):   97.43%
## H^2 (total variability / sampling variability):  38.85
##
## Test for Heterogeneity:
## Q(df = 125) = 4868.986, p-val < .001
##
## Model Results:
##
## estimate      se    zval    pval  ci.lb  ci.ub
##     0.150   0.016   9.467   <.001  0.119  0.181   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta1_develop2_adu <- rma (yi = yi,
                           vi = vi,
                           measure = 'ZCOR',
                           data = df3_develop,
                           mods = ~ development_stage-1,
                           subset = (development_stage=="Adults"))
```

Warning: Redundant predictors dropped from the model.

```
summary(meta1_develop2_adu,  digits = 3)
```

```
##
## Random-Effects Model (k = 89; tau^2 estimator: REML)
##
##   logLik  deviance       AIC       BIC      AICc
```

```
##     52.299   -104.599   -100.599    -95.644   -100.457
##
## tau^2 (estimated amount of total heterogeneity): 0.011 (SE = 0.002)
## tau (square root of estimated tau^2 value):      0.104
## I^2 (total heterogeneity / total variability):   81.25%
## H^2 (total variability / sampling variability):  5.33
##
## Test for Heterogeneity:
## Q(df = 88) = 394.676, p-val < .001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##     0.021   0.014   1.564   0.118   -0.005   0.048
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
meta1_develop2_chi <- rma (yi = yi,
                           vi = vi,
                           measure = 'ZCOR',
                           data = df3_develop,
                           mods = ~ development_stage-1,
                           subset = (development_stage=="Children"))
```

```
## Warning: Redundant predictors dropped from the model.
```

```r
summary(meta1_develop2_chi, digits =3)
```

```
##
## Random-Effects Model (k = 50; tau^2 estimator: REML)
##
##    logLik  deviance       AIC        BIC       AICc
##     8.434   -16.869   -12.869     -9.085    -12.608
##
## tau^2 (estimated amount of total heterogeneity): 0.008 (SE = 0.003)
## tau (square root of estimated tau^2 value):      0.090
## I^2 (total heterogeneity / total variability):   68.25%
## H^2 (total variability / sampling variability):  3.15
##
## Test for Heterogeneity:
## Q(df = 49) = 131.742, p-val < .001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##     0.198   0.020   9.862   <.001   0.159   0.237   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Compare tau^2
tau2_comp <- data.frame(rbind(meta1_develop1$tau2,
                        meta1_develop2_ado$tau2,
                        meta1_develop2_adu$tau2,
                        meta1_develop2_chi$tau2))
```

```r
names(tau2_comp) <- 'tau^2'
rownames(tau2_comp) <- c('Common', 'Adolescents', 'Adults', 'Children')
round(tau2_comp, 3)
```

```
##             tau^2
## Common      0.014
## Adolescents 0.019
## Adults      0.011
## Children    0.008
```

```r
# Compare I^2
i2_comp <- data.frame(rbind(meta1_develop1$I2,
                            meta1_develop2_ado$I2,
                            meta1_develop2_adu$I2,
                            meta1_develop2_chi$I2))
names(i2_comp) <- 'I^2'
rownames(i2_comp) <- c('Common', 'Adolescents', 'Adults', 'Children')
round(i2_comp,2)
```

```
##               I^2
## Common      94.13
## Adolescents 97.43
## Adults      81.25
## Children    68.25
```

Multilevel meta-analysis

```
meta1_multi1 <- rma.mv(yi = yi,
                       V = vi,
                       random = list(~1 | study_id/es_id),
                       data = df3,
                       slab = es_id)

# QUESTION: I don't have to specify  measure = 'ZCOR'?

summary(meta1_multi1, digits =3)

##
## Multivariate Meta-Analysis Model (k = 273; method: REML)
##
##    logLik  Deviance       AIC       BIC      AICc
##    83.431  -166.861  -160.861  -150.044  -160.772
##
## Variance Components:
##
##             estim   sqrt  nlvls  fixed          factor
## sigma^2.1   0.015  0.124    129     no         study_id
## sigma^2.2   0.004  0.064    273     no  study_id/es_id
##
## Test for Heterogeneity:
## Q(df = 272) = 8958.240, p-val < .001
##
## Model Results:
##
## estimate      se   zval   pval  ci.lb  ci.ub
##    0.091   0.013  6.842  <.001  0.065  0.117  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Variance components:
    - The between-study variance is sigma^2.1 = 0.0153 (equivalent to tau^2 in REM)- At this level we have 129 studies.
    - The within-study variance is sigma^2.2 = 0.0041. At this level we have 273 effect sizes.
- Estimate: 0.0906. However, this is a Fisher's z, so we have to transform the effect back to a normal correlation:

```
round(transf.ztor(meta1_multi1$b), 3)

##         [,1]
## intrcpt 0.09
```
```
round(transf.ztor(meta1_multi1$ci.lb), 3)

## [1] 0.065
```
```
round(transf.ztor(meta1_multi1$ci.ub), 3)

## [1] 0.116
```

- The correlation is approximately 0.09 with 95%CI [0.065,0.116]

- The test for heterogeneity rejects the null hypothesis of homogeneity, "however this is not informative.

Instead, we should look at the amount of heterogeneity caputred by each level in our model." "We are interested in within-study variance (level 2) as well as between-study variance (level 3) and not the variance between all effect sizes in the dataset".

Testing the within-study variance

```
# Two-level model without within-study variance

meta1_multi2 <- rma.mv(yi = yi,
                       V = vi,
                       random = list(~1 | study_id/es_id),
                       data = df3,
                       slab = es_id,
                       sigma2 = c(0, NA))

# Perform a likelihood-ratio test to determine the significance of
# the within-study variance
anova(meta1_multi1, meta1_multi2)
```

```
##
##          df       AIC       BIC      AICc  logLik     LRT    pval        QE
## Full      3 -160.8614 -150.0440 -160.7718 83.4307                 8958.2395
## Reduced   2 -116.6280 -109.4164 -116.5834 60.3140 46.2334 <.0001 8958.2395
```

- From the LRT we "found significant variability between effect-sizes within studies"

Testing the between-study variance

```
# Two-level model without between-study variance

meta1_multi3 <- rma.mv(yi = yi,
                       V = vi,
                       random = list(~1 | study_id/es_id),
                       data = df3,
                       slab = es_id,
                       sigma2 = c(NA, 0))

# Perform a likelihood-ratio test to determine the significance of
# the within-study variance
anova(meta1_multi1, meta1_multi3)
```

```
##
##          df       AIC       BIC      AICc  logLik     LRT    pval        QE
## Full      3 -160.8614 -150.0440 -160.7718 83.4307                 8958.2395
## Reduced   2  -77.8763  -70.6647  -77.8317 40.9382 84.9850 <.0001 8958.2395
```

- "Between-study variance is significant, since the fit of the full model is significantly better than the fit of the reduced model". "We found significant variability between studies"

- However, we would like to know how the total variance is splitted in the different levels. See next section

Distribution of variance over the three levels of the meta-analytic model

```
# I^2 at different levels
# See function description under 'Packages and data' at the top
multilevel_i2(v = df3$vi,
```

```
            k = length(df3$vi),
            rma_obj = meta1_multi1)
```

```
##          I2   Level
## I2_1   4.17 Level 1
## I2_2 75.43 Level 2
## I2_3 20.40 Level 3
```
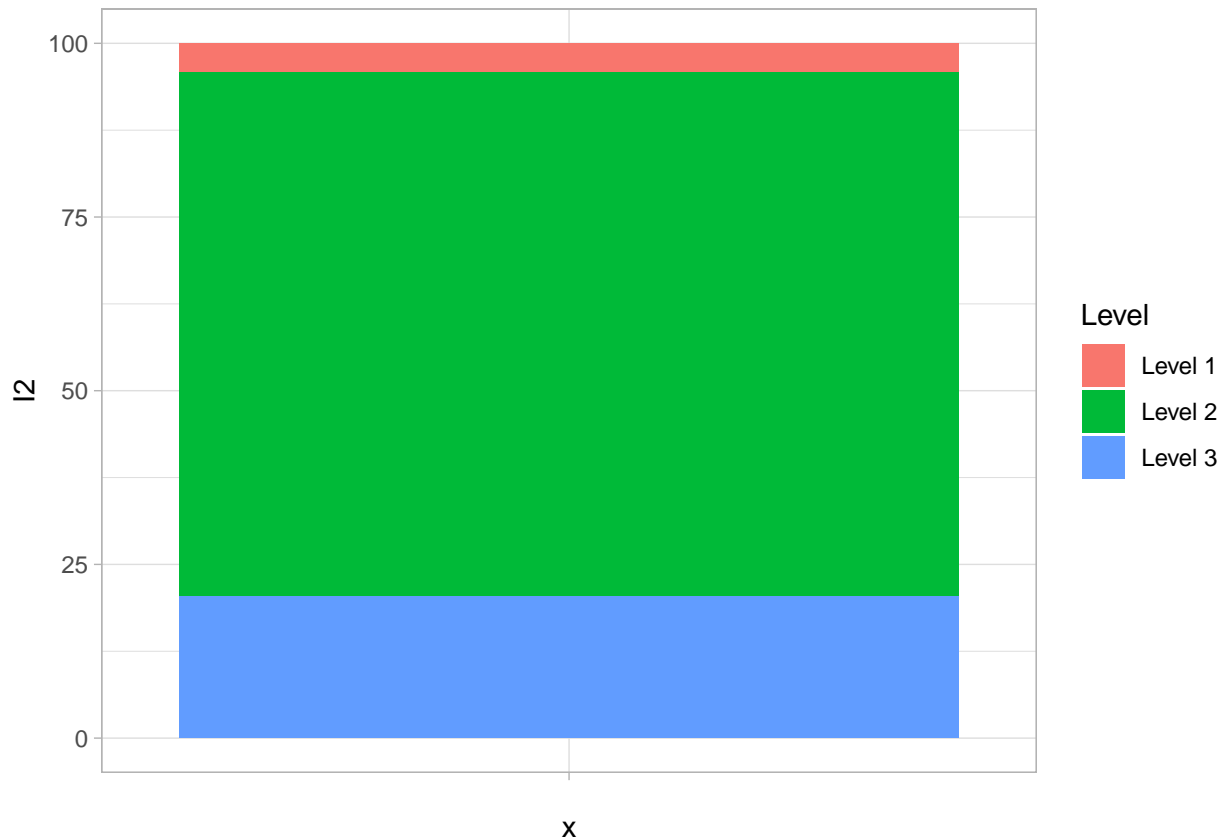

Chen, 2015 pg. 92: "I2 can be interpreted as the proportion of the total variation of the effect size that is due to the between-study heterogeneity"

- 4.17 % of the total variance can be attributed to within-study sampling variance (level-1)

- 75.43 % of the total variance can be attributed to within study variance (differences between effect sizes within studies)

- 20.4 % of the total variance can be attributed to differences between studies at level 3.

Conclusion: A lot of the variance is within-studies

Subgroup analysis

```r
# Fit 3-level model with developmental_stage as moderator

meta1_multi1_develop1 <- rma.mv(yi = yi,
                                V = vi,
                                random = list(~1 | study_id/es_id),
                                data = df3_develop,
                                slab = es_id,
```

```
                               mods = ~ development_stage -1)

# QUESTION: I don't have to specify  measure = 'ZCOR'?
summary(meta1_multi1_develop1, digits =3)
```

Developmental stage

```
##
## Multivariate Meta-Analysis Model (k = 265; method: REML)
##
##   logLik  Deviance       AIC       BIC       AICc
##   93.340  -186.680  -176.680  -158.839  -176.446
##
## Variance Components:
##
##           estim   sqrt  nlvls  fixed        factor
## sigma^2.1  0.011  0.103    123     no       study_id
## sigma^2.2  0.004  0.063    265     no  study_id/es_id
##
## Test for Residual Heterogeneity:
## QE(df = 262) = 5395.403, p-val < .001
##
## Test of Moderators (coefficients 1:3):
## QM(df = 3) = 100.545, p-val < .001
##
## Model Results:
##
##                               estimate      se   zval   pval   ci.lb  ci.ub
## development_stageAdolescents     0.146   0.017  8.444  <.001   0.112  0.180  ***
## development_stageAdults          0.006   0.018  0.316  0.752  -0.030  0.042
## development_stageChildren        0.195   0.035  5.627  <.001   0.127  0.262  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Multiple comparisons
multcomp_multi1_develop1 <- glht(meta1_multi1_develop1,
                    linfct=contrMat(c("Adolescents"=1,"Adults"=1,"Children"=1),
                          type="Tukey"),test=adjusted("bonferroni"))

summary(multcomp_multi1_develop1)
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: rma.mv(yi = yi, V = vi, mods = ~development_stage - 1, random = list(~1 |
##     study_id/es_id), data = df3_develop, slab = es_id)
##
## Linear Hypotheses:
##                           Estimate Std. Error z value Pr(>|z|)
## Adults - Adolescents == 0  -0.14067    0.02523  -5.575    <1e-04 ***
## Children - Adolescents == 0  0.04808    0.03825   1.257    0.413
```

```
## Children - Adults == 0        0.18875    0.03913   4.824    <1e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
# Note that the estimate of the differences in the output are Fisher z
```

- Test for residual heterogeneity is significant: there is significant unexplained variance left between all effect sizes in the data set after publication status has been added to the meta-analytic model

- Test of moderators: Omnibus test. We reject the null hypothesis of no moderation ? Developmental stage is a moderator

- Effects: Adolescents and children significantly different from zero, adults no.

```
multilevel_i2(df3_develop$vi,
              k = length(df3_develop$vi),
              rma_obj = meta1_multi1_develop1)
```

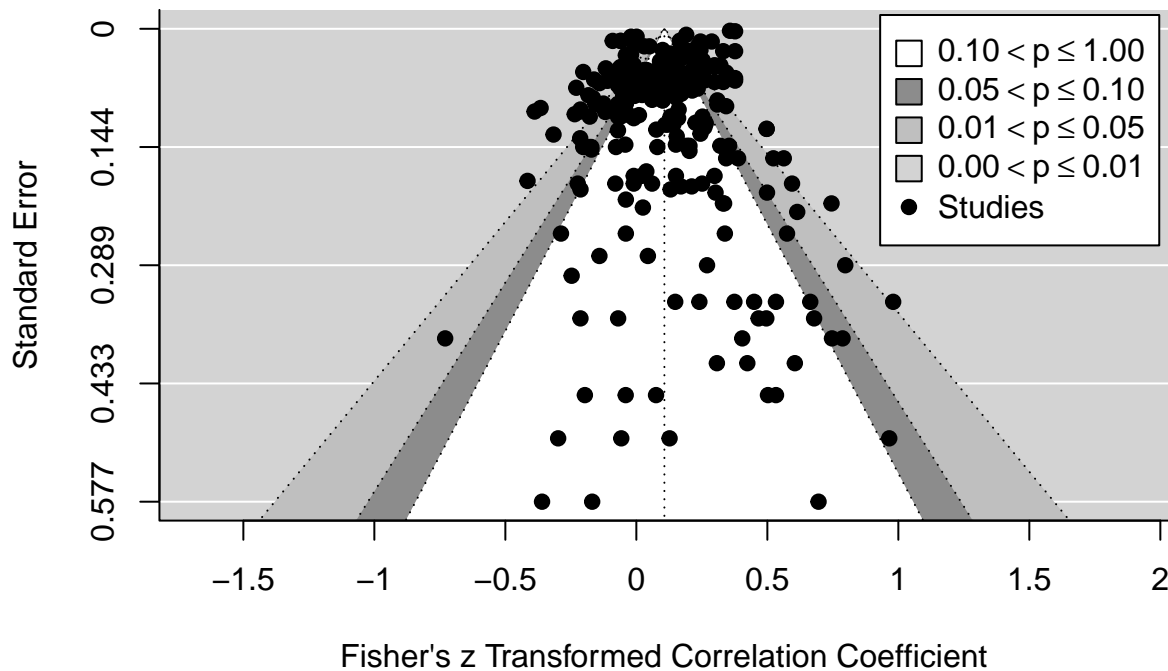**Examine the residual within-study and between-study variance**

```
##          I2   Level
## I2_1  5.47 Level 1
## I2_2 68.39 Level 2
## I2_3 26.14 Level 3
```
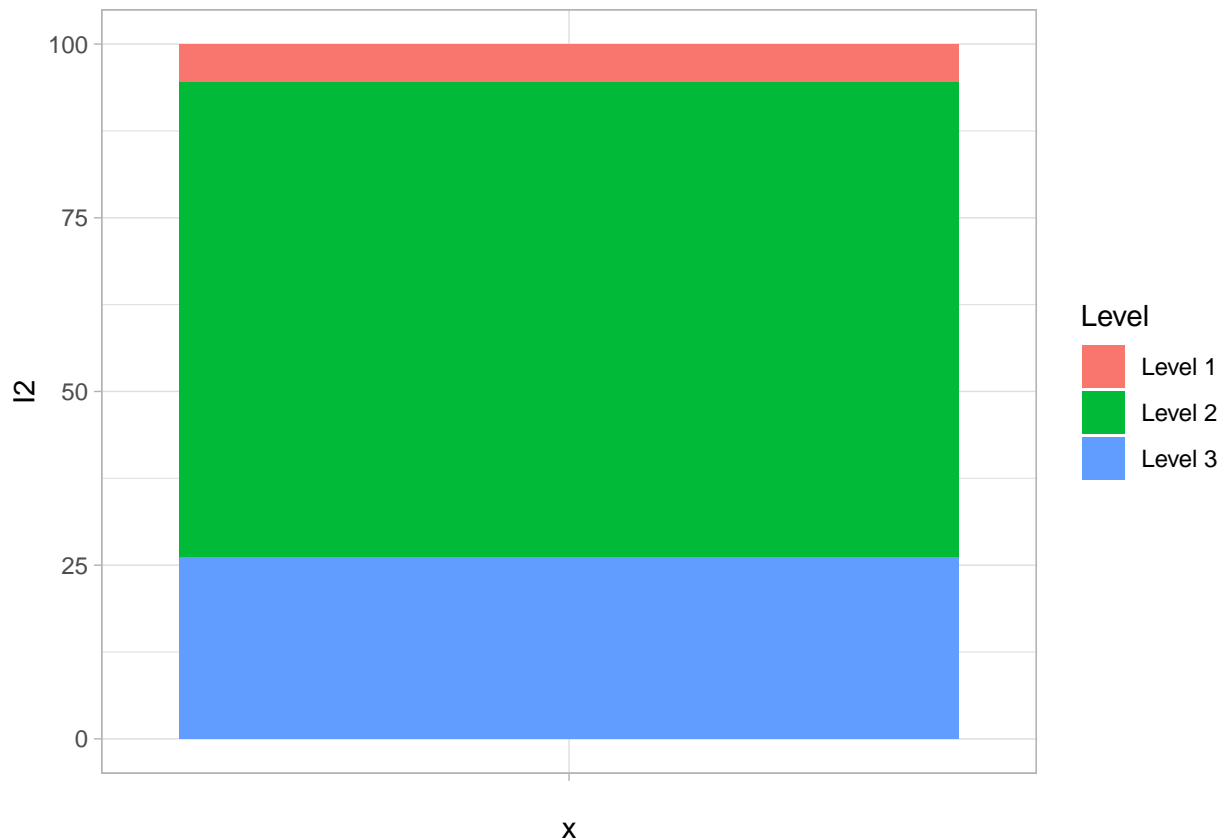
Publication bias

Funnel plot

```
# Reference: https://wviechtb.github.io/metafor/reference/funnel.html
funnel(meta1,
       level=c(90, 95, 99),
       shade=c("white", "gray55", "gray75"),
       legend=TRUE)
```


Egger's regression test

```
# Reference: https://wviechtb.github.io/metafor/reference/regtest.html
regtest(meta1, model = 'lm')
```

```
##
## Regression Test for Funnel Plot Asymmetry
##
## Model:     weighted regression with multiplicative dispersion
## Predictor: standard error
##
## Test for Funnel Plot Asymmetry: t = -9.1604, df = 271, p < .0001
## Limit Estimate (as sei -> 0):   b = 0.3149 (CI: 0.2975, 0.3323)
```

We cannot reject the null hypothesis that the intercept is equal to zero. Therefore we do not have evidence for funnel plot asymmetry. ("When there is no publication bias, the expected z score should be scattered around zero. No publication bias means means that the precision is not related to the effect size reported (beta1=0)).

```
# Manually do calculations
df3 %>%
  mutate(inv_se = 1/sqrt(vi)) %>%
  lm(yi ~ inv_se, data =.) %>%
  summary()
```

```
## 
## Call:
## lm(formula = yi ~ inv_se, data = .)
## 
## Residuals:
##       Min       1Q   Median       3Q      Max
## -0.85153 -0.14745 -0.00592  0.10915  0.85830
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1210423  0.0161335   7.503    9e-13 ***
## inv_se      0.0002918  0.0004118   0.709    0.479
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.2344 on 271 degrees of freedom
## Multiple R-squared:  0.001849,   Adjusted R-squared:  -0.001834
## F-statistic: 0.5021 on 1 and 271 DF,  p-value: 0.4792
```

```r
# Plot precision vs effect size
df3 %>%
  mutate(inv_se = 1/sqrt(vi)) %>%
  ggplot(mapping = aes(x = inv_se, y =yi)) +
  geom_point() +
  geom_abline() +
  theme_light()
```
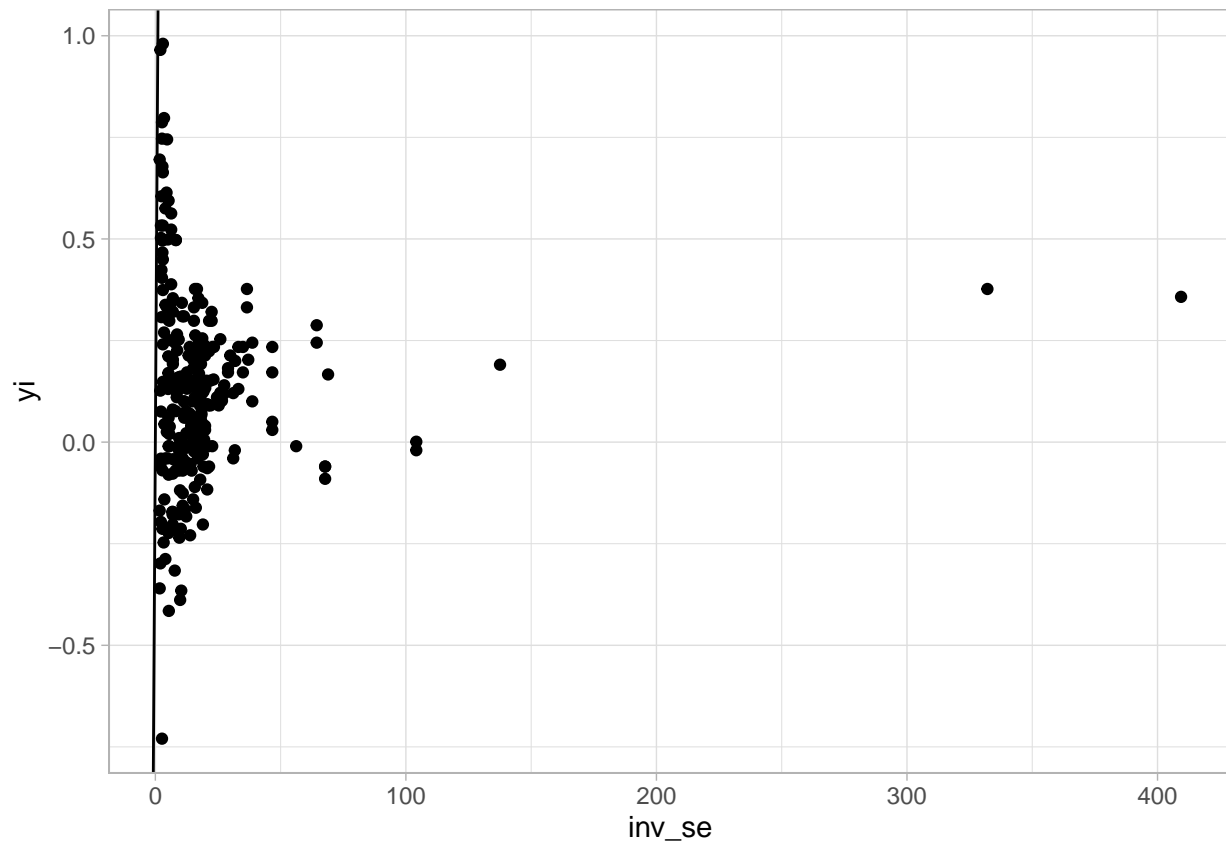
```
# Check with meta
library(meta)
meta_del <- metacor(cor = r,
                    n = n,
                    studlab = reference,
                    data= df2,
                    fixed = FALSE,
                    random = TRUE,
                    method.tau = 'REML',
                    hakn = FALSE,
                    title = "Mindset and Academic Achievement",
                    prediction = TRUE)
metabias(meta_del, method.bias = 'linreg')
```

```
## Review:     Mindset and Academic Achievement
##
## Linear regression test of funnel plot asymmetry
##
## Test result: t = -9.16, df = 271, p-value < 0.0001
##
## Sample estimates:
##      bias se.bias intercept se.intercept
##   -3.1671  0.3457    0.3149       0.0088
##
## Details:
## - multiplicative residual heterogeneity variance (tau^2 = 25.2407)
## - predictor: standard error
## - weight:    inverse variance
## - reference: Egger et al. (1997), BMJ
```

Trim and Fill method

```
# Reference:
meta1_tf <- trimfill(meta1)
summary(meta1_tf)
```

```
##
## Estimated number of missing studies on the left side: 10 (SE = 10.0506)
##
## Random-Effects Model (k = 283; tau^2 estimator: REML)
##
##   logLik  deviance      AIC       BIC      AICc
##  43.4255  -86.8511  -82.8511  -75.5673  -82.8081
##
## tau^2 (estimated amount of total heterogeneity): 0.0195 (SE = 0.0023)
## tau (square root of estimated tau^2 value):      0.1397
## I^2 (total heterogeneity / total variability):   95.69%
## H^2 (total variability / sampling variability):  23.23
##
## Test for Heterogeneity:
## Q(df = 282) = 9026.8722, p-val < .0001
##
## Model Results:
##
```

```
## estimate      se    zval    pval   ci.lb   ci.ub
##   0.1014  0.0104  9.7543  <.0001  0.0811  0.1218  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
funnel(meta1_tf, legend=TRUE, cex=1.2)
```
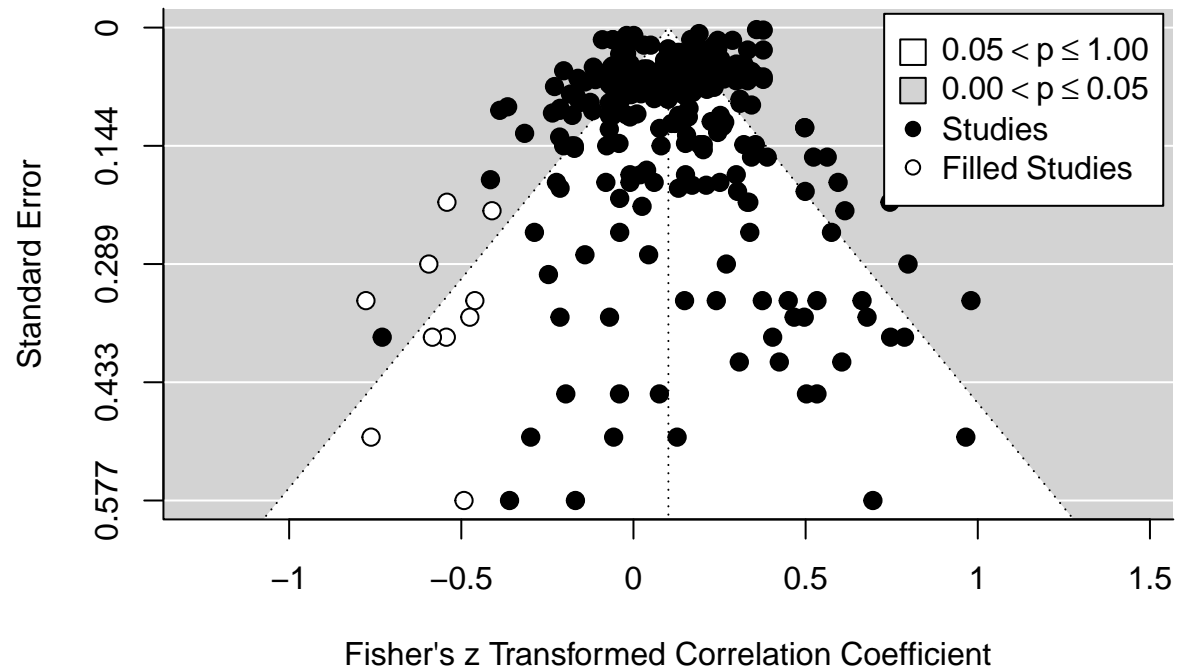
Selection models

```
meta1_3psm1 <- selmodel(meta1,
                        type = 'stepfun',
                        steps = 0.025)
summary(meta1_3psm1)
```

Three-parameter selection model

```
##
## Random-Effects Model (k = 273; tau^2 estimator: ML)
##
##     logLik    deviance        AIC         BIC        AICc
##    61.4796  -122.9593  -116.9593  -106.1309  -116.8701
##
## tau^2 (estimated amount of total heterogeneity): 0.0184 (SE = 0.0024)
## tau (square root of estimated tau^2 value):      0.1358
##
## Test for Heterogeneity:
## LRT(df = 1) = 7767.9817, p-val < .0001
##
## Model Results:
##
## estimate       se    zval     pval   ci.lb   ci.ub
##   0.0977   0.0157  6.2393   <.0001  0.0670  0.1283   ***
##
## Test for Selection Model Parameters:
## LRT(df = 1) = 0.6219, p-val = 0.4304
##
## Selection Model Results:
##
##                       k  estimate       se     zval    pval   ci.lb   ci.ub
## 0     < p <= 0.025  102    1.0000      ---      ---     ---     ---     ---
## 0.025 < p <= 1      171    0.8452   0.1800  -0.8599  0.3898  0.4923  1.1980
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta1_3psm2 <- selmodel(meta1,
                        type = 'stepfun',
                        steps = 0.05)
summary(meta1_3psm2)
```

```
##
## Random-Effects Model (k = 273; tau^2 estimator: ML)
##
##     logLik    deviance        AIC         BIC        AICc
##    61.2635  -122.5271  -116.5271  -105.6987  -116.4379
##
## tau^2 (estimated amount of total heterogeneity): 0.0186 (SE = 0.0024)
## tau (square root of estimated tau^2 value):      0.1364
##
## Test for Heterogeneity:
## LRT(df = 1) = 7772.5697, p-val < .0001
##
```

```
## Model Results:
##
## estimate      se    zval    pval   ci.lb   ci.ub
##   0.1018  0.0158  6.4316  <.0001  0.0708  0.1328   ***
##
## Test for Selection Model Parameters:
## LRT(df = 1) = 0.1897, p-val = 0.6632
##
## Selection Model Results:
##
##                      k   estimate      se     zval    pval   ci.lb   ci.ub
## 0    < p <= 0.05   114     1.0000     ---      ---     ---     ---     ---
## 0.05 < p <= 1      159     0.9141  0.1883  -0.4560  0.6484  0.5451  1.2831
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```