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

Giulia Bertoldo

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Pooled effect size 8

```
# 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()
```

```
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
```

```
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)
```

```
library(readxl)
```

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

Data cleaning

```
# 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 ...
```

```
# 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...
```

```
# 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"
```

```
# 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"
```

```
# 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"
```

```
# 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 == '.')

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

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

```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)
```

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

```
## [1] "N" "Y"
```

Meta-analysis 1: Random-effects model (REM)

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

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

# REM of the transformed correlations
meta1 <- rma (yi = yi,
                  vi = vi,
                  measure = 'ZCOR',
                  data = df3)
meta1
```

```
##
## Random-Effects Model (k = 273; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0187 (SE = 0.0023)
## tau (square root of estimated tau^2 value):      0.1369
## I^2 (total heterogeneity / total variability):   95.68%
## H^2 (total variability / sampling variability):  23.13
##
## Test for Heterogeneity:
## Q(df = 272) = 8958.2395, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval   ci.lb   ci.ub
##   0.1071  0.0103  10.4110  <.0001  0.0869  0.1272  ***
##
## ---
## 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. **Question: Is the estimate a Pearson correlation or Fisher's z**?

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

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

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

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

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

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

```
# 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
```

- When transforming, the values that I obtain do make sense. The transformed values align with the values from the outuput of meta, which I know that they are already back-transformed. So, I guess I need to use the transformed values:
- 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)
```

```
##
##         estimate   ci.lb   ci.ub
## tau^2     0.0187  0.0164  0.0284
## tau       0.1369  0.1279  0.1685
## I^2(%)   95.6770 95.0769 97.1034
## H^2      23.1320 20.3122 34.5233
```

- 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?**