Multilevel Meta-Analysis (Pearson r) Tutorial

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Introduction

The following script is designed to perform a multilevel meta-analysis using the `metafor`, `lmerTest` and `psych` packages in R. Specifically, this tutorial utilises Pearson's r and Fisher's Z as the effect size measures, to demonstrate how to convert between the two measures.

The analysis is based on data from Lua et al. (2023) and focuses on the overall relationship between the need for cognition and well-being. The original paper can be found here: https://doi.org/10.1007/s11031-023-10047-w.

The script includes steps for data preparation, effect size calculation, overall effect size computation, forest plot generation, tests for publication bias, and moderation analysis.

The script is structured to be run in RStudio, and it includes comments to guide users through each step of the process.

Setting Up

This section sets up the working environment, installs necessary packages, loads the required libraries, and reads in the data.

If the `metafor`, `lmerTest` and `psych` and packages are not already installed, use the `install.packages()` function to install it.

Explanation of the Code

- The `setwd()` function sets the working directory to the location of the script, ensuring that all file paths are relative to the script's location.
- The `library()` function loads the `metafor`, `lmerTest` and `psych` packages.
- The `options()` function is used to adjust the display settings, specifically to disable scientific notation and set the number of digits displayed.
- The `read.csv()` function reads in the data from a CSV file named "NFCWB.csv", which contains the data drawn from Lua et al.(2023).

```
### Set Up --------------

# R version 4.5.0

# Set working directory to that of script's current location
setwd(dirname(rstudioapi::getActiveDocumentContext()$path))

# Load packages
library(metafor)  # version 4.8-0
```

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

```
## Loading required package: metadat

## Loading required package: numDeriv

##
## Loading the 'metafor' package (version 4.8-0). For an
## introduction to the package please type: help(metafor)
```

```
library(lmerTest) # version 3.1-3
```

```
## Loading required package: lme4

##
## Attaching package: 'lmerTest'

## The following object is masked from 'package:lme4':
##
##     lmer

## The following object is masked from 'package:stats':
##
##     step
```

```
library(psych)    # version 2.5.3

# Display settings (to disable scientific notation)
options(scipen = 9999, digits = 4)

# Read in data drawn from Lua et al. (2023)
mlmmeta_raw = read.csv("NFCWB.csv")
```

Prepare Data

This section prepares the data for analysis by computing effect sizes for each study and organizing the data frame.

For more information on the `escalc()` function, refer to ?escalc in R.

Explanation of the Code

- The `corr_nfcwb` variable has to be reversed for studies with negative well-being, ensuring that the correlation reflects that the lower the correlation, the lower the well-being. The `ifelse()` function is used to reverse the correlation for studies with negative well-being.
- The `measure` argument specifies the type of effect size to be calculated, in this case, "ZCOR" (Fisher's Z). ZCOR is used to calculate the effect size from the raw correlation coefficients instead of Pearson's r as Fisher's Z normalises the distribution of the effect sizes. Thus, Fisher's Z would be less affected by the sampling distribution skew.
- The ri variable `corr_nfcwb` is the column containing the raw correlation coefficients.
- The ni variable `sample_size` is the column containing the sample sizes for each study.
- Afterwards, the `escalc()` function computes the effect sizes (yi) and their corresponding sampling variances (vi) for each study.
- The publication type is categorised into "Published" and "Unpublished" based on the type of publication (e.g., journal article, conference paper, thesis/dissertation).

- The `mlmmeta` data frame is then sorted by the type of publication (published vs unpublished) to facilitate clearer visualization in the forest plot. Do note that the comma before the closing square bracket is required, as it indicates that we are keeping the columns while reordering the rows.

```
### Prepare Data --------------

# Clean data file (reverse correlation for negative well-being)
mlmmeta_raw$corr_nfcwb = with(mlmmeta_raw,
ifelse(wellbeing_category == "Negative well-being", -corr_nfcwb, corr_nfcwb))

# Compute effect sizes for each study
mlmmeta = escalc(
  # Type of effect size measure
  measure = "ZCOR",

  # Column for raw correlation coefficients
  ri = corr_nfcwb,

  # Column for sample sizes
  ni = sample_size,

  # Specify data.frame that the information will be extracted from
  data = mlmmeta_raw
  )

# Categorise publication type into "published" and "unpublished"
# Published: Journal articles
# Unpublished: Conference, Panel Data, Thesis/dissertation, Unpublished data
mlmmeta$publication_type = ifelse(
  mlmmeta$publication_type == "Journal article",
  "Published",
  "Unpublished")

# Order the data frame based on publication type and effect sizes (yi)
mlmmeta = mlmmeta[order(mlmmeta$publication_type, mlmmeta$yi), ]
```

Computing the Overall Effect Size

This section estimates the overall effect size using the `rma.mv()` function from the `metafor` package.

Explanation of the Multilevel Meta-Analysis Code

- The `rma.mv()` function is used to compute the overall effect size, accounting for the nested structure of the data.
- The `random` argument specifies the random effects structure, where `~ 1 | sample_id/meta_id`, indicates that random effects are nested within the sample and meta ID.
- The `yi` and `vi` arguments specify the effect size estimates and their corresponding sampling variances, respectively.
- The `data` argument specifies the data frame containing the effect size estimates and variances.
- The `summary()` function is used to display the results of the meta-analysis, including the overall effect size estimate and its confidence interval.

- The `fisherz2r()` function is used to convert the effect size estimates from Fisher's Z to Pearson's r.

```
### Compute Overall Effect Size --------------

# Effect size estimates
mlmmetaresults = rma.mv(
  # Effect size estimates
  yi = yi,
  # Sampling variances
  V = vi,
  # Include random effects for grouping variable (i.e., sample)
  random = ~ 1 | sample_id/meta_id,
  # Specify where to get the data from
  data = mlmmeta
)

# summary function used to provide detailed results of the meta-analysis
summary(mlmmetaresults)
```

```
##
## Multivariate Meta-Analysis Model (k = 108; method: REML)
##
##   logLik  Deviance       AIC       BIC      AICc
##  40.9843  -81.9687  -75.9687  -67.9502  -75.7357
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed             factor
## sigma^2.1  0.0076  0.0873     52     no          sample_id
## sigma^2.2  0.0156  0.1250    108     no  sample_id/meta_id
##
## Test for Heterogeneity:
## Q(df = 107) = 1573.7169, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval   ci.lb   ci.ub
##   0.1977  0.0200  9.8908  <.0001  0.1585  0.2369  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Convert from Fisher's Z to Pearson's r
mlmmetaresults$b |> fisherz2r()
```

```
##           [,1]
## intrcpt 0.1952
```

Forest Plot

This section generates a forest plot to visually represent the effect sizes and confidence intervals for each study included in the meta-analysis.

The forest plot is created using the `forest()` function from the `metafor` package.

The plot includes the following features:

- Arrangement of studies by effect sizes
- Sample size information for need for cognition and well-being group
- Custom headers for the plot
- Custom labels for the studies

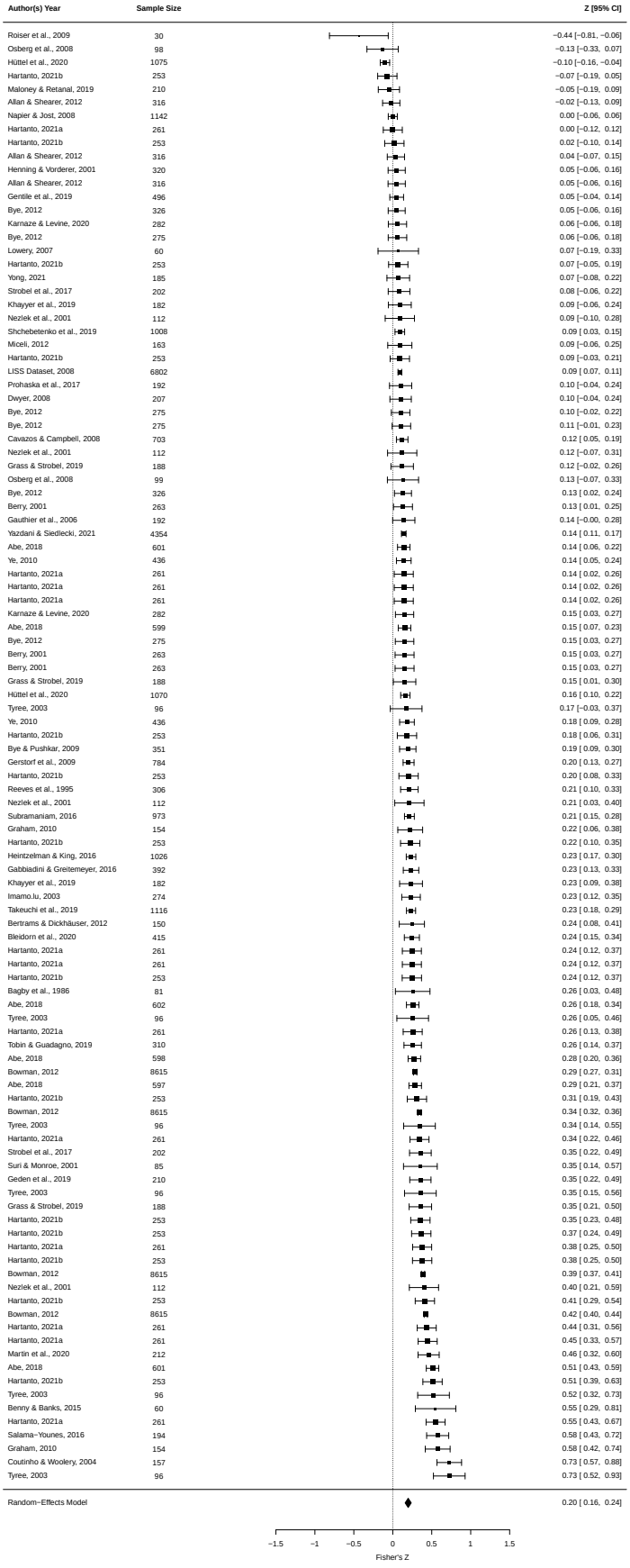
Saving the forest plot as a PDF file allows for easy sharing and presentation, and allows adjustment to the plot's dimensions.

Explanation of the Code

- The `cairo_pdf()` function starts the graphics device driver to create PDF files, and the `file` argument specifies the name of the file. Specifically, the `cairo_pdf` function is used for font compatibility and in this case, it is for the author's names.
- The `width` and `height` arguments adjust the dimensions of the PDF file.
- The `forest()` function is used to create the forest plot, and the `tradmetaresults` object contains the results of the meta-analysis.
- The `order` argument specifies the arrangement of studies, with "obs" indicating that the studies should be arranged by effect sizes. To organise by column, replace "obs" with the specific column in the data frame.
- The `ylim` argument sets the y-axis limits for the plot.
- The `ilab` argument is used to add extra columns of information to the forest plot beyond just the effect sizes. Here, we are adding sample size data for cognition and well-being group into the forest plot.
- The `ilab.xpos` argument specifies where the sample size columns appear horizontally on the plot. The negative values position the columns on the left side of the plot, just after the study names.
- The `slab` argument is used to label each effect size with its respective study.
- The `paste()` function creates the label by combining the author and year columns. The `sep` argument specifies the separator between author and the year label, which is set to "," in this case. Hence, the label will be in the format "Author(s), Year" (e.g., "Smith et al., Study 1").
- The `xlim` argument sets the x-axis limits for the plot.
- The `alim` argument sets the confidence interval limits, and the `steps` argument determines the number of intervals in the x-axis.
- The `efac` argument controls the size of the diamond shapes that represent the effect sizes in the plot.
- The `header` argument is set to FALSE to allow for manual specification of headers.
- The `xlab` argument specifies the confidence interval label for the funnel plot, in this case, "Fisher's Z"
- The `text()` function is used to manually include text within the plot, such as the "Author(s) Year" header and specific sample size column headers.
- The `x` and `y` arguments in the `text()` function adjust the position of the headers, with the `x` argument specifying the horizontal arrangement of the columns and the `y` argument specifying the vertical arrangement of the columns.
- The `font` argument adjusts the font size.
- The `dev.off()` function is used to close the graphics device and finalize the plot as a saved file.

```
### Forest Plot --------------

# Start creating the forest plot itself
```

```r
# Specify dataset
forest(
  mlmmetaresults,

  # Arrangement of studies
  order = "obs",

  # Add y-axis limits
  ylim = c(-3, 111),

  # Add sample size information for need for cognition and well-being group
  ilab = sample_size,
  ilab.xpos = -3,

  # Label studies on the forest plot
  slab = paste(author, year, sep = ", "),

  # Add x-axis limits
  xlim = c(-5, 3),

  # Add confidence interval limits
  # Adjust intervals based on the number of steps
  alim = c(-1.5, 1.5),
  steps = 7,

  # Change size of effect size polygons
  efac = 0.3,

  # Show (TRUE) or hide (FALSE) default headers
  # Hide when we want to manually specify our own headers
  header = FALSE,

  # Add label for confidence interval, in this case, "Fisher's Z"
  xlab = "Fisher's Z"
)

# For the following lines of code,
# Use text function to manually include text within the plot

# Add "Author(s) Year" header
text(x = -4.6, y = 110, "Author(s) Year", font = 2)

# Add "Sample Size" header
text(x = -3, y = 110, "Sample Size", font = 2)

# Add "r [95% CI]" header
text(x = 2.7, y = 110, "Z [95% CI]", font = 2)
```


Author(s) Year
Sample Size
Z [95% CI]
Roiser et al., 2009 30 −0.44 [−0.81, −0.06]
Osberg et al., 2008 98 −0.13 [−0.33, 0.07]
Hüttel et al., 2020 1075 −0.10 [−0.16, −0.04]
Hartanto, 2021b 253 −0.07 [−0.19, 0.05]
Maloney & Retanal, 2019 210 −0.05 [−0.19, 0.09]
Allan & Shearer, 2012 316 −0.02 [−0.13, 0.09]
Napier & Jost, 2008 1142 0.00 [−0.06, 0.06]
Hartanto, 2021a 261 0.00 [−0.12, 0.12]
Hartanto, 2021b 253 0.02 [−0.10, 0.14]
Allan & Shearer, 2012 316 0.04 [−0.07, 0.15]
Henning & Vorderer, 2001 320 0.05 [−0.06, 0.16]
Allan & Shearer, 2012 316 0.05 [−0.06, 0.16]
Gentile et al., 2019 496 0.05 [−0.04, 0.14]
Bye, 2012 326 0.05 [−0.06, 0.16]
Karnaze & Levine, 2020 282 0.06 [−0.06, 0.18]
Bye, 2012 275 0.06 [−0.06, 0.18]
Lowery, 2007 60 0.07 [−0.19, 0.33]
Hartanto, 2021b 253 0.07 [−0.05, 0.19]
Yong, 2021 185 0.07 [−0.08, 0.22]
Strobel et al., 2017 202 0.08 [−0.06, 0.22]
Khayyer et al., 2019 182 0.09 [−0.06, 0.24]
Nezlek et al., 2001 112 0.09 [−0.10, 0.28]
Shchebetenko et al., 2019 1008 0.09 [0.03, 0.15]
Miceli, 2012 163 0.09 [−0.06, 0.25]
Hartanto, 2021b 253 0.09 [−0.03, 0.21]
LISS Dataset, 2008 6802 0.09 [0.07, 0.11]
Prohaska et al., 2017 192 0.10 [−0.04, 0.24]
Dwyer, 2008 207 0.10 [−0.04, 0.24]
Bye, 2012 275 0.10 [−0.02, 0.22]
Bye, 2012 275 0.11 [−0.01, 0.23]
Cavazos & Campbell, 2008 703 0.12 [0.05, 0.19]
Nezlek et al., 2001 112 0.12 [−0.07, 0.31]
Grass & Strobel, 2019 188 0.12 [−0.02, 0.26]
Osberg et al., 2008 99 0.13 [−0.07, 0.33]
Bye, 2012 326 0.13 [0.02, 0.24]
Berry, 2001 263 0.13 [0.01, 0.25]
Gauthier et al., 2006 192 0.14 [−0.00, 0.28]
Yazdani & Siedlecki, 2021 4354 0.14 [0.11, 0.17]
Abe, 2018 601 0.14 [0.06, 0.22]
Ye, 2010 436 0.14 [0.05, 0.24]
Hartanto, 2021a 261 0.14 [0.02, 0.26]
Hartanto, 2021a 261 0.14 [0.02, 0.26]
Hartanto, 2021a 261 0.14 [0.02, 0.26]
Karnaze & Levine, 2020 282 0.15 [0.03, 0.27]
Abe, 2018 599 0.15 [0.07, 0.23]
Bye, 2012 275 0.15 [0.03, 0.27]
Berry, 2001 263 0.15 [0.03, 0.27]
Berry, 2001 263 0.15 [0.03, 0.27]
Grass & Strobel, 2019 188 0.15 [0.01, 0.30]
Hüttel et al., 2020 1070 0.16 [0.10, 0.22]
Tyree, 2003 96 0.17 [−0.03, 0.37]
Ye, 2010 436 0.18 [0.09, 0.28]
Hartanto, 2021b 253 0.18 [0.06, 0.31]
Bye & Pushkar, 2009 351 0.19 [0.09, 0.30]
Gerstorf et al., 2009 784 0.20 [0.13, 0.27]
Hartanto, 2021b 253 0.20 [0.08, 0.33]
Reeves et al., 1995 306 0.21 [0.10, 0.33]
Nezlek et al., 2001 112 0.21 [0.03, 0.40]
Subramaniam, 2016 973 0.21 [0.15, 0.28]
Graham, 2010 154 0.22 [0.06, 0.38]
Hartanto, 2021b 253 0.22 [0.10, 0.35]
Heintzelman & King, 2016 1026 0.23 [0.17, 0.30]
Gabbiadini & Greitemeyer, 2016 392 0.23 [0.13, 0.33]
Khayyer et al., 2019 182 0.23 [0.09, 0.38]
Imamo.lu, 2003 274 0.23 [0.12, 0.35]
Takeuchi et al., 2019 1116 0.23 [0.18, 0.29]
Bertrams & Dickhäuser, 2012 150 0.24 [0.08, 0.41]
Bleidorn et al., 2020 415 0.24 [0.15, 0.34]
Hartanto, 2021a 261 0.24 [0.12, 0.37]
Hartanto, 2021a 261 0.24 [0.12, 0.37]
Hartanto, 2021b 253 0.24 [0.12, 0.37]
Bagby et al., 1986 81 0.26 [0.03, 0.48]
Abe, 2018 602 0.26 [0.18, 0.34]
Tyree, 2003 96 0.26 [0.05, 0.46]
Hartanto, 2021a 261 0.26 [0.13, 0.38]
Tobin & Guadagno, 2019 310 0.26 [0.14, 0.37]
Abe, 2018 598 0.28 [0.20, 0.36]
Bowman, 2012 8615 0.29 [0.27, 0.31]
Abe, 2018 597 0.29 [0.21, 0.37]
Hartanto, 2021b 253 0.31 [0.19, 0.43]
Bowman, 2012 8615 0.34 [0.32, 0.36]
Tyree, 2003 96 0.34 [0.14, 0.55]
Hartanto, 2021a 261 0.34 [0.22, 0.46]
Strobel et al., 2017 202 0.35 [0.22, 0.49]
Suri & Monroe, 2001 85 0.35 [0.14, 0.57]
Geden et al., 2019 210 0.35 [0.22, 0.49]
Tyree, 2003 96 0.35 [0.15, 0.56]
Grass & Strobel, 2019 188 0.35 [0.21, 0.50]
Hartanto, 2021b 253 0.35 [0.23, 0.48]
Hartanto, 2021b 253 0.37 [0.24, 0.49]
Hartanto, 2021a 261 0.38 [0.25, 0.50]
Hartanto, 2021b 253 0.38 [0.25, 0.50]
Bowman, 2012 8615 0.39 [0.37, 0.41]
Nezlek et al., 2001 112 0.40 [0.21, 0.59]
Hartanto, 2021b 253 0.41 [0.29, 0.54]
Bowman, 2012 8615 0.42 [0.40, 0.44]
Hartanto, 2021a 261 0.44 [0.31, 0.56]
Hartanto, 2021a 261 0.45 [0.33, 0.57]
Martin et al., 2020 212 0.46 [0.32, 0.60]
Abe, 2018 601 0.51 [0.43, 0.59]
Hartanto, 2021b 253 0.51 [0.39, 0.63]
Tyree, 2003 96 0.52 [0.32, 0.73]
Benny & Banks, 2015 60 0.55 [0.29, 0.81]
Hartanto, 2021a 261 0.55 [0.43, 0.67]
Salama−Younes, 2016 194 0.58 [0.43, 0.72]
Graham, 2010 154 0.58 [0.42, 0.74]
Coutinho & Woolery, 2004 157 0.73 [0.57, 0.88]
Tyree, 2003 96 0.73 [0.52, 0.93]
Random−Effects Model 0.20 [0.16, 0.24]
−1.5
−1
−0.5
0
0.5
1
1.5
Fisher's Z

Optional: Saving the Forest Plot as a Separate File

Explanation of the Code

- To save the forest plot as a PDF file, the plotting code can be enclosed within `pdf()` and `dev.off()` functions:
- The `pdf()` function starts the graphics device driver to create PDF files, and the `file` argument specifies the name of the file.
- The `width` and `height` arguments adjust the dimensions of the PDF file.
- Following the `pdf()` function, the same code used to create the forest plot of moderators is repeated to generate the plot within the PDF file. The graphical output will be directed to the specified PDF file instead of the RStudio plotting window.
- The `dev.off()` function is used to close the graphics device and finalise the plot as a saved file.

```
### Forest Plot --------------

# Save the forest plot as a PDF file
# Name the pdf file of the forest plot
cairo_pdf(file = "NFCWBforestplot.pdf", width = 14, height = 35)

# Same forest plot code as above
forest(
  mlmmetaresults,
  order = "obs",
  ylim = c(-3, 111),
  ilab = sample_size,
  ilab.xpos = -3,
  slab = paste(author, year, sep = ", "),
  xlim = c(-5, 3),
  alim = c(-1.5, 1.5),
  steps = 7,
  efac = 0.3,
  header = FALSE,
  xlab = "Fisher's Z"
)

text(x = -4.6, y = 110, "Author(s) Year", font = 2)

text(x = -3, y = 110, "Sample Size", font = 2)

text(x = 2.7, y = 110, "Z [95% CI]", font = 2)

# Close the forest plot and finalise it as a saved file
dev.off()
```

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

Tests for Publication Bias

This section performs tests for publication bias, including a funnel plot and Egger's test.

For multilevel meta-analysis, we do not recommend conducting a rank correlation test as it is prone to Type 1 error.

Researchers may refer to this article by Fernández-Castilla et al. (2019) on a detailed discussion of the limitations of rank correlation tests in multilevel meta-analysis, as well as an overview on other publication bias tests: https://doi.org/10.1080/00220973.2019.1582470:

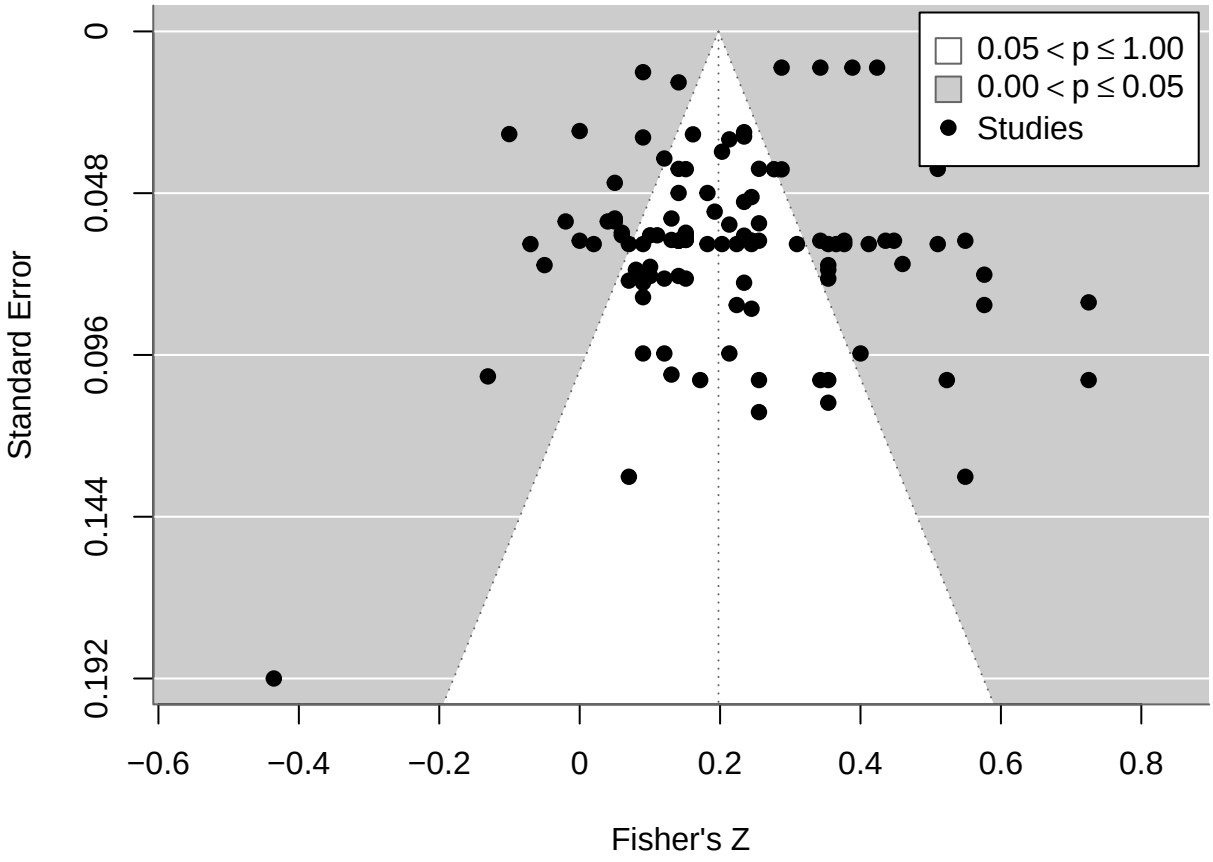
Funnel Plot

The funnel plot visually represents the distribution of effect sizes and their standard errors, allowing for the identification of potential publication bias. Saving the funnel plot as a PDF file allows for easy sharing and presentation, and allows adjustment to the plot's dimensions.

Explanation of the Code

- The `pdf()` function starts the graphics device driver to create PDF files, and the `file` argument specifies the name of the file.
- The `width` and `height` arguments adjust the dimensions of the PDF file.
- The `par()` function is used to adjust the margins of the funnel plot, with the `mar` argument specifying the bottom, left, top, and right margins.
- The `funnel()` function is used to create the funnel plot, and the `tradmetaresults` object contains the results of the meta-analysis.
- The `legend` argument specifies whether to include a legend in the plot. TRUE indicates that a legend should be included, FALSE indicates that it should not.
- The `xlab` argument specifies the confidence interval label for the funnel plot, in this case, "Fisher's Z".
- The `dev.off()` function is used to close the graphics device and finalize the plot as a saved file.

```
### Tests for Publication Bias --------------

# Funnel Plot #

# Adjust margins of the funnel plot
# Set the bottom, left, top, and right margins
par(mar = c(4, 4, 0.3, 1))
# Create the funnel plot
funnel(mlmmetaresults, legend = TRUE, xlab = "Fisher's Z")
```



Optional: Saving the Funnel Plot as a Separate File

Explanation of the Code

- To save the funnel plot as a PDF file, the plotting code can be enclosed within `pdf()` and `dev.off()` functions:
- The `pdf()` function starts the graphics device driver to create PDF files, and the `file` function specifies the name of the file.
- The `width` and `height` arguments adjust the dimensions of the PDF file.
- Following the `pdf()` function, the same code used to create the funnel plot is repeated to generate the plot within the PDF file. The graphical output will be directed to the specified PDF file instead of the RStudio plotting window.
- The `dev.off()` function is used to close the graphics device and finalize the plot as a saved file.

```
### Tests for Publication Bias --------------

# Funnel Plot #

# Save the funnel plot as a PDF file
# Name the pdf file of the funnel plot
# Adjust the width and height of the pdf file
pdf(file = "NFCWBfunnelplot.pdf", width = 8, height = 5)
# Same funnel plot code as above
par(mar = c(4, 4, 0.3, 1))
```

```r
funnel(mlmmetaresults, legend = TRUE, xlab = "Fisher's Z")
# Close the funnel plot and finalise it as a saved file
dev.off()
```

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

Egger's Test

The Egger's test is a statistical test that quantifies the degree of asymmetry in the funnel plot, providing a more formal assessment of publication bias.

Explanation of the Code

- The `lmer()` function is used to fit a linear mixed-effects model, where the effect size weighted by the standard error is predicted by the intercept and the inverse of the corrected standard error. metafor::rma.mv does not have a weights argument, and metafor::regtest does not support rma.mv objects. For three (or more) level meta-analysis, use `lmerTest::lmer` instead.
- The `I(yi / vi)` expression indicates that the effect size (yi) is divided by the standard error (vi), which is used to weight the effect sizes in the model.
- The `I(1 / vi)` expression indicates that the inverse of the standard error is included in the model as a predictor.
- The `1 | sample_id` expression indicates that random intercepts are included for each lab, accounting for the nested structure of the data.
- The `data` argument specifies the dataset to be used for the analysis.
- The `summary()` function provides the results of the Egger's test, including the slope estimate and its significance.

```r
### Tests for Publication Bias --------------

# Eggers' Test #
lmer(
  # g weighted by SE is predicted by intercept and inverse SE
  # with random intercept by sample
  I(yi / vi) ~ 1 + I(1 / vi) + (1 | sample_id),
  data = mlmmeta
) |>
  # Estimate of interest is the intercept
  summary(correlation = TRUE)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: I(yi/vi) ~ 1 + I(1/vi) + (1 | sample_id)
##    Data: mlmmeta
##
## REML criterion at convergence: 1427
##
## Scaled residuals:
```

```
##    Min     1Q Median     3Q    Max
## -4.537 -0.103  0.022  0.110  5.077
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  sample_id (Intercept) 42221    205
##  Residual              14832    122
## Number of obs: 108, groups:  sample_id, 52
##
## Fixed effects:
##             Estimate Std. Error       df t value            Pr(>|t|)
## (Intercept) -41.0231    35.3050  50.5712   -1.16               0.25
## I(1/vi)       0.2564     0.0202  45.8603   12.67 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##         (Intr)
## I(1/vi) -0.420
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
```

Moderation Analysis

This section performs moderation analysis to explore the influence of categorical moderators on the effect sizes.

Explanation of the Code

- The `rma.mv()` function is used to compute the multilevel meta-analysis with moderators.
- The `yi` and `vi` arguments specify the effect size estimates and their corresponding sampling variances, respectively.
- The `random` argument specifies the random effects structure, where `~ 1 | sample_id/meta_id` indicates that random intercepts are included for both the lab and individual studies, accounting for the nested structure of the data.
- The `subset` argument is used to specify the subset of data for each moderator analysis.
- The `data` argument specifies the data frame containing the effect size estimates and variances.

Note that if convergence issues arise, the `control` function can be used to address it. Researchers may also refer more to the `metafor` package documentation for more information on how to address convergence issues.

```r
### Moderation Analysis --------------

# Categorical Variable (i.e., publication type)
rma.mv(
  yi = yi,
  V = vi,
  random = ~ 1 | sample_id/meta_id,
  # Specify categorical moderator (i.e., Published articles)
  subset = (publication_type == "Published"),
  data = mlmmeta,
  # To address convergence issues (if it exists)
```

```
  control = list(rel.tol=1e-8)
)
```

```
##
## Multivariate Meta-Analysis Model (k = 54; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed             factor
## sigma^2.1  0.0158  0.1257     37     no          sample_id
## sigma^2.2  0.0103  0.1016     54     no  sample_id/meta_id
##
## Test for Heterogeneity:
## Q(df = 53) = 1058.6768, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval   ci.lb   ci.ub
##   0.1915  0.0275  6.9686  <.0001  0.1376  0.2453  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
rma.mv(
  yi = yi,
  V = vi,
  random = ~ 1 | sample_id/meta_id,
  # Specify categorical moderator (i.e., Unpublished articles)
  subset = (publication_type == "Unpublished"),
  data = mlmmeta,
  # To address convergence issues (if it exists)
  control = list(rel.tol=1e-8)
)
```

```
##
## Multivariate Meta-Analysis Model (k = 54; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed             factor
## sigma^2.1  0.0040  0.0633     15     no          sample_id
## sigma^2.2  0.0170  0.1304     54     no  sample_id/meta_id
##
## Test for Heterogeneity:
## Q(df = 53) = 351.3640, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval   ci.lb   ci.ub
##   0.2126  0.0289  7.3678  <.0001  0.1561  0.2692  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Forest Plot of Moderators

This section generates a forest plot that includes moderators to visually represent the effect sizes and confidence intervals for each study included in the meta-analysis.

The plot is saved as a PDF file for easy sharing and presentation.

The forest plot includes the following features:

- Arrangement of studies by effect sizes and types of moderators
- Sample size information for need for cognition and well-being group
- Custom headers for the plot
- Custom labels for the studies
- Summary effect sizes for each moderator

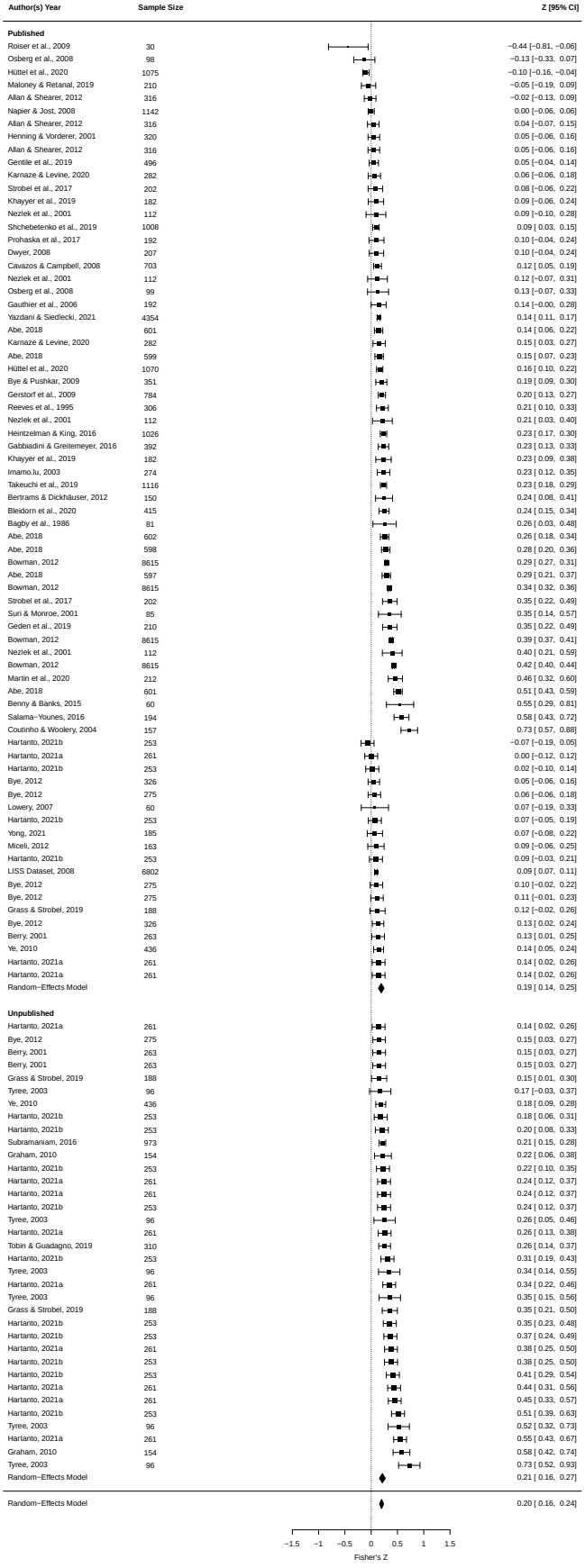
Explanation of the Code

- The `cairo_pdf()` function starts the graphics device driver to create PDF files, and the `file` argument specifies the name of the file. Specifically, the `cairo_pdf` function is used for font compatibility and in this case, it is for the author's names.
- The `width` and `height` arguments adjust the dimensions of the PDF file.
- The `forest()` function is used to create the forest plot, and the `mlmmetaresults` object contains the results of the meta-analysis.
- The `rows` argument specifies the arrangement of studies by publication type, and in ascending order of effect sizes per publication type.
- The `ylim` argument sets the y-axis limits for the plot.
- The `ilab` argument is used to add extra columns of information to the forest plot beyond just the effect sizes. Here, we are adding sample size data for cognition and well-being group into the forest plot.
- The `ilab.xpos` argument specifies where the sample size columns appear horizontally on the plot. The negative values position the columns on the left side of the plot, just after the study names.
- The `slab` argument is used to label each effect size with its respective study.
- The `paste()` function creates the label by combining the author and year columns. The `sep` argument specifies the separator between author and the year label, which is set to "," in this case. Hence, the label will be in the format "Author(s), Year" (e.g., "Smith et al., Study 1").
- The `xlim` argument sets the x-axis limits for the plot.
- The `alim` argument sets the confidence interval limits, and the `steps` argument determines the number of intervals in the x-axis.
- The `efac` argument controls the size of the diamond shapes that represent the effect sizes in the plot.
- The `header` argument is set to FALSE to allow for manual specification of headers.
- The `xlab` argument specifies the label for the confidence interval, in this case, "Hedge's g".
- The `text()` function is used to manually include text within the plot, such as the "Author(s) Year" header and specific sample size column headers.
- The `x` and `y` arguments in the `text()` function adjust the position of the headers, with the `x` argument specifying the horizontal arrangement of the columns and the `y` argument specifying the vertical arrangement of the columns.
- The `font` argument adjusts the font size.

- The `pos` argument specifies the position of the text relative to the specified coordinates
- The `rma.mv()` function is used to perform moderation analysis for each publication type, with the `subset` argument specifying the subset of data for each category.
- The `rest.j`, `res.t`, and `res.c` variables store the results of the moderation analysis for journal articles, thesis/dissertations, and conference papers, respectively.
- The `subset` argument is used to specify the subset of data for categorical moderators, allowing for separate analyses for each category.
- The `addpoly()` function is used to add summary effect sizes for each of the moderators, with the `row` argument specifying the position of the summary in the plot.
- The `dev.off()` function is used to close the graphics device and finalize the plot as a saved file.

```
### Forest Plot of Moderators --------------

# Start creating the forest plot itself
# Specify dataset
forest(
  mlmmetaresults,
  # Manually arrange effect sizes by publication type
  # - Unpublished: Rows 108 to 51
  # - Published: Rows 50 to 48
  # The arrangement must consider spacing and must end at row 2
  rows = c(112:40, 36:2),

  # Add y-axis limits
  ylim = c(-3, 116),

  # Add sample size information for need for cognition and well-being group
  # Values indicate the x-axis position of the sample size columns
  ilab = sample_size,
  ilab.xpos = -4.2,

  # Label studies on the forest plot
  slab = paste(author, year, sep = ", "),

  # Add x-axis limits
  xlim = c(-7, 4),

  # Add confidence interval limits
  # Adjust intervals based on the number of steps
  alim = c(-1.5, 1.5),
  steps = 7,

  # Change size of effect size polygons
  efac = 0.3,

  # Remove headers (if any), for manual input
  header = FALSE,

  # Add label for confidence interval, in this case, "Fisher's Z"
  xlab = "Fisher's Z"
)
```

```r
# For the following lines of code,
# Use text function to manually include text within the plot

# Add text labels for moderator (type of publication)
# Labels for different publication types (Moderator Analysis)
# - "Unpublished" (Unpublished data, Panel Data, Thesis/Dissertations) at y = 37
# - "Published" (Journal Articles, Conference) at y = 113
text(
  x = -7,
  y = c(37, 113),
  pos = 4,
  c("Unpublished", "Published"),
  font = 2
)

# Moderation analysis
res.p = rma.mv(
  yi,
  vi,
  random = ~ 1 | sample_id/meta_id,
  subset = (publication_type == "Published"),
  data = mlmmeta,
  # To address convergence issues (if it exists)
  control = list(rel.tol=1e-8)
)
res.u = rma.mv(
  yi,
  vi,
  random = ~ 1 | sample_id/meta_id,
  subset = (publication_type == "Unpublished"),
  data = mlmmeta,
  # To address convergence issues (if it exists)
  control = list(rel.tol=1e-8)
)

# Add summary effect sizes for each of the moderators
addpoly(res.u, row = 1) # summary effect for "Unpublished" group
addpoly(res.p, row = 39) # summary effect for "Published" group

# Add"Author(s) Year" header
text(x = -6.4, y = 115, "Author(s) Year", font = 2)

# Add "Sample Size" header
text(x = -4.0, y = 115, "Sample Size", font = 2)

# Add "r [95% CI]" header
text(x = 3.6, y = 115, "Z [95% CI]", font = 2)
```


Author(s) Year
Sample Size
Z [95% CI]
Published
Roiser et al., 2009 30 −0.44 [−0.81, −0.06]
Osberg et al., 2008 98 −0.13 [−0.33, 0.07]
Hüttel et al., 2020 1075 −0.10 [−0.16, −0.04]
Maloney & Retanal, 2019 210 −0.05 [−0.19, 0.09]
Allan & Shearer, 2012 316 −0.02 [−0.13, 0.09]
Napier & Jost, 2008 1142 0.00 [−0.06, 0.06]
Allan & Shearer, 2012 316 0.04 [−0.07, 0.15]
Henning & Vorderer, 2001 320 0.05 [−0.06, 0.16]
Allan & Shearer, 2012 316 0.05 [−0.06, 0.16]
Gentile et al., 2019 496 0.05 [−0.04, 0.14]
Karnaze & Levine, 2020 282 0.06 [−0.06, 0.18]
Strobel et al., 2017 202 0.08 [−0.06, 0.22]
Khayyer et al., 2019 182 0.09 [−0.06, 0.24]
Nezlek et al., 2001 112 0.09 [−0.10, 0.28]
Shchebetenko et al., 2019 1008 0.09 [0.03, 0.15]
Prohaska et al., 2017 192 0.10 [−0.04, 0.24]
Dwyer, 2008 207 0.10 [−0.04, 0.24]
Cavazos & Campbell, 2008 703 0.12 [0.05, 0.19]
Nezlek et al., 2001 112 0.12 [−0.07, 0.31]
Osberg et al., 2008 99 0.13 [−0.07, 0.33]
Gauthier et al., 2006 192 0.14 [−0.00, 0.28]
Yazdani & Siedlecki, 2021 4354 0.14 [0.11, 0.17]
Abe, 2018 601 0.14 [0.06, 0.22]
Karnaze & Levine, 2020 282 0.15 [0.03, 0.27]
Abe, 2018 599 0.15 [0.07, 0.23]
Hüttel et al., 2020 1070 0.16 [0.10, 0.22]
Bye & Pushkar, 2009 351 0.19 [0.09, 0.30]
Gerstorf et al., 2009 784 0.20 [0.13, 0.27]
Reeves et al., 1995 306 0.21 [0.10, 0.33]
Nezlek et al., 2001 112 0.21 [0.03, 0.40]
Heintzelman & King, 2016 1026 0.23 [0.17, 0.30]
Gabbiadini & Greitemeyer, 2016 392 0.23 [0.13, 0.33]
Khayyer et al., 2019 182 0.23 [0.09, 0.38]
Imamo.lu, 2003 274 0.23 [0.12, 0.35]
Takeuchi et al., 2019 1116 0.23 [0.18, 0.29]
Bertrams & Dickhäuser, 2012 150 0.24 [0.08, 0.41]
Bleidorn et al., 2020 415 0.24 [0.15, 0.34]
Bagby et al., 1986 81 0.26 [0.03, 0.48]
Abe, 2018 602 0.26 [0.18, 0.34]
Abe, 2018 598 0.28 [0.20, 0.36]
Bowman, 2012 8615 0.29 [0.27, 0.31]
Abe, 2018 597 0.29 [0.21, 0.37]
Bowman, 2012 8615 0.34 [0.32, 0.36]
Strobel et al., 2017 202 0.35 [0.22, 0.49]
Suri & Monroe, 2001 85 0.35 [0.14, 0.57]
Geden et al., 2019 210 0.35 [0.22, 0.49]
Bowman, 2012 8615 0.39 [0.37, 0.41]
Nezlek et al., 2001 112 0.40 [0.21, 0.59]
Bowman, 2012 8615 0.42 [0.40, 0.44]
Martin et al., 2020 212 0.46 [0.32, 0.60]
Abe, 2018 601 0.51 [0.43, 0.59]
Benny & Banks, 2015 60 0.55 [0.29, 0.81]
Salama−Younes, 2016 194 0.58 [0.43, 0.72]
Coutinho & Woolery, 2004 157 0.73 [0.57, 0.88]
Hartanto, 2021b 253 −0.07 [−0.19, 0.05]
Hartanto, 2021a 261 0.00 [−0.12, 0.12]
Hartanto, 2021b 253 0.02 [−0.10, 0.14]
Bye, 2012 326 0.05 [−0.06, 0.16]
Bye, 2012 275 0.06 [−0.06, 0.18]
Lowery, 2007 60 0.07 [−0.19, 0.33]
Hartanto, 2021b 253 0.07 [−0.05, 0.19]
Yong, 2021 185 0.07 [−0.08, 0.22]
Miceli, 2012 163 0.09 [−0.06, 0.25]
Hartanto, 2021b 253 0.09 [−0.03, 0.21]
LISS Dataset, 2008 6802 0.09 [0.07, 0.11]
Bye, 2012 275 0.10 [−0.02, 0.22]
Bye, 2012 275 0.11 [−0.01, 0.23]
Grass & Strobel, 2019 188 0.12 [−0.02, 0.26]
Bye, 2012 326 0.13 [0.02, 0.24]
Berry, 2001 263 0.13 [0.01, 0.25]
Ye, 2010 436 0.14 [0.05, 0.24]
Hartanto, 2021a 261 0.14 [0.02, 0.26]
Hartanto, 2021a 261 0.14 [0.02, 0.26]
Random−Effects Model 0.19 [0.14, 0.25]
Unpublished
Hartanto, 2021a 261 0.14 [0.02, 0.26]
Bye, 2012 275 0.15 [0.03, 0.27]
Berry, 2001 263 0.15 [0.03, 0.27]
Berry, 2001 263 0.15 [0.03, 0.27]
Grass & Strobel, 2019 188 0.15 [0.01, 0.30]
Tyree, 2003 96 0.17 [−0.03, 0.37]
Ye, 2010 436 0.18 [0.09, 0.28]
Hartanto, 2021b 253 0.18 [0.06, 0.31]
Hartanto, 2021b 253 0.20 [0.08, 0.33]
Subramaniam, 2016 973 0.21 [0.15, 0.28]
Graham, 2010 154 0.22 [0.06, 0.38]
Hartanto, 2021b 253 0.22 [0.10, 0.35]
Hartanto, 2021a 261 0.24 [0.12, 0.37]
Hartanto, 2021a 261 0.24 [0.12, 0.37]
Hartanto, 2021b 253 0.24 [0.12, 0.37]
Tyree, 2003 96 0.26 [0.05, 0.46]
Hartanto, 2021a 261 0.26 [0.13, 0.38]
Tobin & Guadagno, 2019 310 0.26 [0.14, 0.37]
Hartanto, 2021b 253 0.31 [0.19, 0.43]
Tyree, 2003 96 0.34 [0.14, 0.55]
Hartanto, 2021a 261 0.34 [0.22, 0.46]
Tyree, 2003 96 0.35 [0.15, 0.56]
Grass & Strobel, 2019 188 0.35 [0.21, 0.50]
Hartanto, 2021b 253 0.35 [0.23, 0.48]
Hartanto, 2021b 253 0.37 [0.24, 0.49]
Hartanto, 2021a 261 0.38 [0.25, 0.50]
Hartanto, 2021b 253 0.38 [0.25, 0.50]
Hartanto, 2021b 253 0.41 [0.29, 0.54]
Hartanto, 2021a 261 0.44 [0.31, 0.56]
Hartanto, 2021a 261 0.45 [0.33, 0.57]
Hartanto, 2021b 253 0.51 [0.39, 0.63]
Tyree, 2003 96 0.52 [0.32, 0.73]
Hartanto, 2021a 261 0.55 [0.43, 0.67]
Graham, 2010 154 0.58 [0.42, 0.74]
Tyree, 2003 96 0.73 [0.52, 0.93]
Random−Effects Model 0.21 [0.16, 0.27]
Random−Effects Model 0.20 [0.16, 0.24]
−1.5
−1
−0.5
0
0.5
1
1.5
Fisher's Z

Optional: Saving the Forest Plot of Moderators as a Separate File

Explanation of the Code

- To save the forest plot of moderators as a PDF file, the plotting code can be enclosed within `pdf()` and `dev.off()` functions:
- The `pdf()` function starts the graphics device driver to create PDF files, and the `file` argument specifies the name of the file.
- The `width` and `height` arguments adjust the dimensions of the PDF file.
- Following the `pdf()` function, the same code used to create the forest plot of moderators is repeated to generate the plot within the PDF file. The graphical output will be directed to the specified PDF file instead of the RStudio plotting window.
- The `dev.off()` function is used to close the graphics device and finalise the plot as a saved file.

```
### Forest Plot of Moderators --------------

# Save the forest plot as a PDF file
# Name the pdf file of the forest plot
# cairo_pdf function used for font compatibility
# Adjust the width and height of the pdf file
cairo_pdf(file = "NFCWBforestplotwithmod.pdf", width = 13, height = 35)

# Same forest plot code as above
forest(
  mlmmetaresults,
  rows = c(112:40, 36:2),
  ylim = c(-3, 116),
  ilab = sample_size,
  ilab.xpos = -4.2,
  slab = paste(author, year, sep = ", "),
  xlim = c(-7, 4),
  alim = c(-1.5, 1.5),
  steps = 7,
  efac = 0.3,
  header = FALSE,
  xlab = "Fisher's Z"
)

text(
  x = -7,
  y = c(37, 113),
  pos = 4,
  c("Unpublished", "Published"),
  font = 2
)

res.p = rma.mv(
  yi,
  vi,
  random = ~ 1 | sample_id/meta_id,
  subset = (publication_type == "Published"),
  data = mlmmeta,
  control = list(rel.tol=1e-8)
```

```
)
res.u = rma.mv(
  yi,
  vi,
  random = ~ 1 | sample_id/meta_id,
  subset = (publication_type == "Unpublished"),
  data = mlmmeta,
  control = list(rel.tol=1e-8)
)

addpoly(res.u, row = 1)
addpoly(res.p, row = 39)

text(x = -6.4, y = 115, "Author(s) Year", font = 2)

text(x = -4.0, y = 115, "Sample Size", font = 2)

text(x = 3.6, y = 115, "Z [95% CI]", font = 2)

# Close the forest plot and finalise it as a saved file
dev.off()
```

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

END OF CODE