Multilevel Meta-Analysis Tutorial

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Introduction

The following script is designed to perform a multilevel meta-analysis using the metafor and lmerTest packages in R.

The analysis is based on data from Hartanto et al. (2024) and focuses on the relationship between smartphone presence and cognitive functions. The original paper can be found here: https://doi.org/10.1037/tmb0000123.

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 and lmerTest packages are not already installed, use the install.packages() function to install them.

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 and lmerTest 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 "SPC.csv", which contains the data drawn from Hartanto et al. (2024).
- A new column named "ID" is created in the data frame to assign unique IDs to each row of data.

```
### 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':
##
##
# Display settings (to disable scientific notation)
options(scipen = 9999, digits = 4)
# Read in data drawn from Hartanto et al. 2024
multilevelmeta_raw = read.csv("SPC.csv")
# Create new column with unique IDs
multilevelmeta_raw$ID = 1:nrow(multilevelmeta_raw)
```

Prepare Data

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

The multimeta_raw data frame does not include pre-computed effect sizes for each study. However, the data frame does include the necessary information to compute effect sizes, such as sample sizes, means, and standard deviations for each group (presence of smartphones and absence of smartphones). The escalc() function from metafor package can use this information to compute the effect sizes directly.

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

- The measure argument specifies the type of effect size to be calculated, which in this case is "SMD" (Standardized Mean Difference). In the metafor package, specifying "SMD" computes Hedge's g by default.
- The n1i and n2i arguments specify the columns for the sample sizes of each group.
- The m1i and m2i arguments specify the columns for the means of each group.
- The sd1i and sd2i arguments specify the columns for the standard deviations of each group.
- Afterwards, the escalc() function computes the effect sizes (yi) and their corresponding sampling variances (vi) for each study.

- The multilevelmeta\$publication variable is converted to a factor with specified levels to ensure that the publication types (e.g., journal articles, thesis/dissertation, conference) are ordered correctly in the forest plot.
- The c() function combines the types of publication into a character vector.
- The multilevelmeta data frame is then sorted by the type of publication (e.g., journal articles, thesis/dissertation, conference) and corresponding effect sizes 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 -----
# Compute effect sizes for each study
multilevelmeta = escalc(
       # Type of effect size measure
       measure = "SMD",
       # Columns for sample size of each group
       n1i = n_p,
      n2i = n_a,
       # Columns for means of each group
       m1i = cog M p,
       m2i = cog_M_a,
       # Columns for standard deviation of each group
       sd1i = cog_SD_p,
       sd2i = cog_SD_a,
       # Specify data.frame that the information will be extracted from
       data = multilevelmeta_raw
)
# Convert publication type to a factor with specified levels
multilevelmeta$publication = factor(
      multilevelmeta$publication,
       levels = c("Journal article", "Thesis/dissertation", "Conference")
)
# Order the data frame based on publication type and effect sizes (yi)
multilevelmeta = multilevelmeta[order(multilevelmeta$publication, multilevelmeta$yi), ]
```

Computing the Overall Effect Size

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

Specifically, we demonstrate the difference in calculating the overall effect size using a traditional meta-analysis approach versus a multilevel meta-analysis approach.

The traditional meta-analysis approach is not recommended for multilevel data, as it does not account for the nested structure of the data (i.e., studies nested within labs).

The multilevel meta-analysis approach is more appropriate for this type of data, as it accounts for the hierarchical structure and allows for the inclusion of random effects.

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 | lab_id / ID indicates that random intercepts are included for both the lab and individual studies, accounting for the nested structure of the data.
- 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.

```
### Compute Overall Effect Size -----
# Using multilevel code
# The code below is the recommended approach for multilevel meta-analysis
mlmmetaresults = rma.mv(
       # Effect size estimates
      yi = yi,
       # Sampling variances
       V = vi,
       # Include random effects for grouping variable (i.e., lab)
       random = ~ 1 | lab_id / ID,
       # Specify where to get the data from
       data = multilevelmeta
)
# summary function used to provide detailed results of the meta-analysis
summary(mlmmetaresults)
##
## Multivariate Meta-Analysis Model (k = 136; method: REML)
##
                                      BIC
                                               AICc
##
     logLik Deviance
                            AIC
```

```
##
     3.5443
              -7.0885
                        -1.0885
                                   7.6273
                                            -0.9053
##
## Variance Components:
##
##
               estim
                        sqrt nlvls
                                     fixed
                                               factor
## sigma^2.1
             0.0305
                      0.1747
                                 22
                                               lab_id
                                        no
## sigma^2.2
             0.0000
                      0.0000
                                136
                                           lab_id/ID
                                        no
##
## Test for Heterogeneity:
## Q(df = 135) = 213.5023, p-val < .0001
##
## Model Results:
##
## estimate
                 se
                        zval
                                pval
                                        ci.lb
                                                ci.ub
   -0.0315 0.0498 -0.6335
                             0.5264
                                      -0.1291 0.0660
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
##
## Random-Effects Model (k = 136; tau^2 estimator: REML)
##
##
    logLik deviance
                            AIC
                                      BIC
                                               AICc
   -5.3141
              10.6282
                        14.6282
                                  20.4387
                                            14.7191
##
##
## tau^2 (estimated amount of total heterogeneity): 0.0106 (SE = 0.0049)
## tau (square root of estimated tau^2 value):
                                                    0.1027
## I^2 (total heterogeneity / total variability):
                                                    25.36%
## H^2 (total variability / sampling variability): 1.34
##
## Test for Heterogeneity:
## Q(df = 135) = 213.5023, p-val < .0001
## Model Results:
##
## estimate
                                        ci.lb
                se
                        zval
                                pval
   -0.0481 0.0181 -2.6651 0.0077
                                     -0.0835
##
                                              -0.0127 **
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

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 both presence of smartphones and absence of smartphones groups
- 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 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 forest() function is used to create the forest plot, and the mlmmetaresults 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 both the presence of smartphones and absence of smartphones groups.
- The cbind() function combines multiple columns side-by-side. In this case, the sample sizes of the groups (n_p and n_a) will appear side-by-side in 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_published" columns. The sep argument specifies the separator between the columns, which is set to "," in this case. Hence, the label will be in the format "Author(s), Year_Published" (e.g., "Smith, 2020").
- 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 forest plot, 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 dev.off() function is used to close the graphics device and finalize the plot as a saved file.

```
# -3 for presence of smartphones (n_p)
       # -2.55 for absence of smartphones (n_a)
       ilab = cbind(n_p, n_a),
       ilab.xpos = c(-3, -2.55),
       # Label studies on the forest plot
       slab = paste(author, year_published, sep = ", "),
       # Add x-axis limits
       xlim = c(-5, 3),
       # Add confidence interval limits
       # Adjust intervals based on the number of steps
       alim = c(-2, 2),
       steps = 9,
       # 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, "Hedge's g"
       xlab = "Hedge's g"
)
# 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 = 139, "Author(s) Year", font = 2)
# Add "Sample Size" header
text(x = -2.8, y = 139.6, "Sample Size", font = 2)
# Add specific sample size column headers, "Presence" and "Absence"
\# x = -3 for for presence of smartphones
# x = -2.55 for absence of smartphones
# y = 139  for  both
text(c(x = -3, x = -2.55), y = 139, c("Presence", "Absence"), font = 2)
# Add "g [95% CI]" header
text(x = 2.7, y = 139, "g [95\% CI]", font = 2)
```

Author(s) Year	Sample Size Presence Absence		g (95%
Itone, 2020	19 18	——	-0.95 [-1.64, -0
kowronek et al., 2023 hornton et al., 2014	21 21	H	-0.75 [-1.38, -0
hornton et al., 2014	27 27 23 24		-0.73 [-1.28, -0 -0.69 [-1.28, -0
hornton et al., 2014	27 27	' <u> </u>	-0.64 [-1.19, -0
ohannes et al., 2019	21 18	<u> </u>	-0.64 [-1.28, 0
yngs, 2017	28 25	├	-0.62 [-1.18, -0
/ard et al., 2017	40 51	├	-0.59 [-1.01, -0
hornton et al., 2014	23 24		-0.58 (-1.16, 0 -0.57 (-1.13, -0
ailey, 2018 anil & Yong, 2020	27 24 61 58		-0.57 [-1.13, -0 -0.44 [-0.80, -0
uiz Pardo, 2022	75 85		-0.42 [-0.73, -0
tahl, 2018	51 47		-0.41 [-0.81, -0
lard et al., 2017	40 93	├	-0.40 [-0.78, -0
uiz Pardo, 2022	75 162	⊢-	-0.33 [-0.60, -0
rantino, 2019	22 25	H	-0.32 (-0.89, 0
uiz Pardo, 2022 u et al., 2022	75 85 50 50	, — — — — — — — — — — — — — — — — — — —	-0.30 (-0.62, 0 -0.29 (-0.68, 0
anale et al. 2019	41 39		-0.28 (-0.72, 0
ard et al., 2017	167 175	·	-0.28 [-0.49, -0
uiz Pardo, 2022	75 162	⊢-	-0.26 (-0.54, 0
ard et al., 2017	167 178	⊢• →	-0.26 [-0.47, -0
ard et al., 2017	167 353	⊢= →	-0.26 [-0.44, -0
essmeier & Büttner, 2022	58 45		-0.26 (-0.65, 0 -0.24 (-0.65, 0
ahl, 2018 guila, 2019	46 48 41 16	, -	-0.24 (-0.66, 0
uiz Pardo. 2022	75 85		-0.24 (-0.55, 0
rantino, 2019	22 50		-0.24 (-0.74, 0
siz Pardo, 2022	75 77	⊢-	-0.24 [-0.56, 0
siz Pardo, 2022	85 90	 +	-0.23 [-0.53, 0
nale et al., 2019	41 39		-0.23 [-0.66, 0
ard et al., 2017 ard et al., 2017	48 45 167 178		-0.22 [-0.63, 0 -0.22 [-0.43, -0
iz Pardo & Minda, 2022	58 64		-0.20 (-0.56, 0
ard et al., 2017	40 42	<u> </u>	-0.20 (-0.63, 0
siz Pardo, 2022	75 77	·	-0.20 (-0.52, 0
ard et al., 2017	48 94		-0.18 (-0.53, 0
uiz Pardo, 2022	75 162	 	-0.17 (-0.45, 0
ard et al., 2017 uiz Pardo & Minda, 2022	167 353 58 64	<u> </u>	-0.17 [-0.35, 0 -0.16 [-0.52, 0
siz Pardo & Minda, 2022 rantino, 2019	58 64 22 25		-0.16 (-0.52, 0 -0.16 (-0.74, 0
iz Pardo, 2022	22 25 85 90	' <u> </u>	-0.16 (-0.46, 0
siz Pardo, 2022	85 90	⊢- ∔	-0.16 (-0.45, 0
uiz Pardo & Minda, 2022	70 67	⊢ •	-0.15 (-0.49, 0
ard et al., 2017	48 49		-0.15 (-0.55, 0
uiz Pardo, 2022 uiz Pardo, 2022	75 85 75 85		-0.14 (-0.45, 0 -0.14 (-0.45, 0
siz Pardo, 2022 ard et al., 2017	75 85 40 93		-0.14 (-0.45, 0 -0.14 (-0.51, 0
siz Pardo & Minda, 2022	58 129	` ⊢₌ —'	-0.13 (-0.44, 0
ard et al., 2017	40 51	⊢	-0.13 (-0.55, 0
uiz Pardo, 2022	75 162	⊢- ++	-0.13 (-0.40, 0
uiz Pardo, 2022	75 77		-0.11 [-0.43, 0
uiz Pardo, 2022 normion et al., 2014	75 85 23 24	, H	-0.11 [-0.42, 0
ard et al., 2014	23 24 40 42		-0.10 (-0.68, 0 -0.10 (-0.53, 0
siz Pardo & Minda, 2022	58 129	' <u></u> '	-0.10 (-0.41, 0
siz Pardo, 2022	75 77	<u> </u>	-0.09 (-0.41, 0
siz Pardo & Minda, 2022	70 126	⊢- ∔	-0.08 (-0.38, 0
iornton et al., 2014	27 27	 	-0.08 (-0.62, 0
ard et al., 2017	167 175	. ⊢• ⊢•	-0.08 [-0.29, 0
uiz Pardo & Minda, 2022 uiz Pardo, 2022	70 67		-0.08 [-0.42, 0 -0.08 [-0.37, 0
uiz Pardo, 2022 uiz Pardo & Minda, 2022	85 90 58 65		-0.08 (-0.37, 0
uiz Pardo, 2022	75 85		-0.07 (-0.38, 0
uiz Pardo, 2022	75 162	` 	-0.06 (-0.33, 0
uiz Pardo, 2022	75 162	⊢ • →	-0.05 (-0.32, 0
uiz Pardo, 2022	85 90	⊢+	-0.04 [-0.34, 0
pessmeier & Büttner, 2022 artmann et al., 2020	58 45		-0.04 (-0.43, 0
uiz Pardo & Minda, 2022	151 151 58 65	_ ,	-0.04 (-0.26, 0 -0.03 (-0.38, 0
iz Pardo, 2022	75 77		-0.02 (-0.34, 0
uiz Pardo, 2022	75 162	` ⊢- +-i`	-0.02 (-0.30, 0
uiz Pardo & Minda, 2022	70 59	⊢	-0.02 (-0.37, 0
hannes et al., 2018	50 51		-0.00 (-0.39, 0
nares & Sellier, 2021 uiz Pardo, 2022	73 73 85 90		0.00 [-0.32, 0
iz Pardo, 2022	85 90 75 77		0.02 [-0.30, 0
uiz Pardo & Minda, 2022	70 126	—	0.03 (-0.27, 0
uiz Pardo, 2022	75 85	⊢	0.04 [-0.27, 0
uiz Pardo, 2022	85 90	 	0.05 (-0.25, 0
guila, 2019 o & Kawahara, 2017	41 16	, 	0.05 (-0.53, 0
a Kawahara, 2017 uiz Pardo. 2022	20 20 85 90		0.06 (-0.56, 0 0.06 (-0.24, 0
anale et al. 2019	85 90 41 39		0.06 (-0.37, 0
anaie et al., 2019 uiz Pardo, 2022	41 39 85 90		0.06 (-0.37, 0
iz Pardo, 2022	75 77	\vdash	0.08 (-0.24, 0
iornton et al., 2014	27 27	 	0.08 (-0.45, 0
uiz Pardo, 2022	85 90	⊢-	0.09 (-0.21, 0
julla, 2019 uiz Pardo. 2022	41 16	 	0.09 (-0.49, 0
uiz Pardo, 2022 uiz Pardo, 2022	75 77 85 90		0.10 (-0.22, 0
ard et al., 2017	85 90 48 45		0.10 (-0.20, 0
essmeier & Büttner, 2022	58 45	—	0.10 (-0.29, 0
uiz Pardo, 2022	75 85	· 	0.10 (-0.21, 0
siz Pardo, 2022	75 77	 - 	0.10 (-0.21, 0
uiz Pardo, 2022	75 85	□ -	0.11 (-0.20, 0
siz Pardo, 2022 siz Pardo, 2022	75 162 75 162		0.11 (-0.16, 0 0.11 (-0.16, 0
siz Pardo, 2022	75 162 85 90	<u>↓</u>	0.12 (-0.18, 0
uiz Pardo, 2022	75 77	i → - · i	0.12 (-0.20, 0
uiz Pardo, 2022	75 162	⊢-	0.13 (-0.15, 0
ard et al., 2017	48 49	. • 	0.13 (-0.27, 0
ard et al., 2017	48 94	 • 	0.13 [-0.22, 0
uiz Pardo, 2022 uiz Pardo, 2022	75 162 75 162		0.14 (-0.14, 0 0.14 (-0.14, 0
siz Pardo & Minda, 2022	75 162 70 59		0.14 (-0.21, 0
uiz Pardo, 2022	75 85	—	0.14 [-0.17, 0
uiz Pardo, 2022	75 77	⊢- -i	0.16 (-0.16, 0
hannes et al., 2019	21 18	 	0.16 (-0.47, 0
llowe et al., 2015	36 29	 	0.16 (-0.33, 0
iz Pardo, 2022 essmejer & Blittner 2022	75 85 58 45	, - .	0.17 (-0.14, 0
essmeier & Büttner, 2022	58 45 40 39		0.19 (-0.20, 0
ila et al., 2020	40 39 22 22	<u> </u>	0.19 (-0.40, 0
siz Pardo, 2022	75 77	·	0.19 (-0.13, 0
artmann et al., 2020	151 151	⊢	0.19 (-0.03, 0
ngs, 2017	28 25		0.20 (-0.34, 0
nale et al., 2019	40 39		0.21 (-0.23, 0
essmeier & Büttner, 2022 nier, 2020	58 45 38 36	<u></u>	0.21 [-0.18, 0
njer, 2020 hannes et al., 2018	38 36 53 51		0.22 [-0.24, 0
ornton et al., 2014	53 51 23 24		0.25 (-0.14, 0
rantino, 2019	22 25	———	0.29 (-0.29, 0
Werd, 2020	30 30	⊢	0.31 (-0.20, 0
inale et al., 2019	40 39	· +	0.38 (-0.07, 0
	22 25	! .	0.38 (-0.20, 0
rantino, 2019	20 20 22 50	<u> </u>	0.42 [-0.20, 1 0.48 [-0.03, 0
& Kawahara, 2017	22 50 22 50		0.48 (-0.03, 0
& Kawahara, 2017 rantino, 2019		<u>, </u>	0.48 (-0.12, 1
rantino, 2019 8. Kawahara, 2017 rantino, 2019 rantino, 2019 illa et al., 2020	22 22		0.50 (-0.08, 1
& Kawahara, 2017 rantino, 2019 rantino, 2019 illa et al., 2020 julla, 2019	22 22 41 16		
& Kawahara, 2017 rantino, 2019 rantino, 2019 illa et al., 2020 julla, 2019 illa et al., 2020	22 22 41 16 21 20		0.57 [-0.05, 1
& Kawahara, 2017 randino, 2019 randino, 2019 solita et al., 2020 pulla, 2019 solita et al., 2020 randino, 2019	22 22 41 16 21 20 22 25	—	0.57 [-0.05, 1 0.58 [-0.01, 1
& Kawahara, 2017 rantino, 2019 rantino, 2019 rila et al., 2020 pulla, 2019 rila et al., 2020 rantino, 2019 rantino, 2019	22 22 41 16 21 20 22 25 22 25		0.57 (-0.05, 1 0.58 (-0.01, 1 0.67 (0.08, 1
& Kawahara, 2017 rantino, 2019 rantino, 2019 sila et al., 2020 guila, 2019 sila et al., 2020 rantino, 2019 rantino, 2019 rantino, 2019 hannes et al., 2019	22 22 41 16 21 20 22 25 22 25 21 18		0.57 (-0.05, 1 0.58 (-0.01, 1 0.67 (0.08, 1 0.81 (0.16, 1
& Kawahara, 2017 rantino, 2019 rantino, 2019 rila et al., 2020 suila, 2019 rila et al., 2020 rantino, 2019 rantino, 2019	22 22 41 16 21 20 22 25 22 25		0.57 (-0.05, 1 0.58 (-0.01, 1 0.67 (0.08, 1

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 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.

```
### Saving the Forest Plot as a Separate File (Optional) -----
# Save the forest plot as a PDF file
# Name the pdf file of the forest plot
pdf(file = "mlmforestplot.pdf", width = 15, height = 40)
# Same forest plot code as above
forest(
       mlmmetaresults,
       order = "obs",
       ylim = c(-3, 140),
       ilab = cbind(n p, n a),
       ilab.xpos = c(-3, -2.55),
       slab = paste(author, year_published, sep = ", "),
       xlim = c(-5, 3),
       alim = c(-2, 2),
       steps = 9,
       efac = 0.3,
       header = FALSE,
       xlab = "Hedge's g"
)
text(x = -4.6, y = 139, "Author(s) Year", font = 2)
text(x = -2.8, y = 139.6, "Sample Size", font = 2)
text(c(x = -3, x = -2.55), y = 139, c("Presence", "Absence"), font = 2)
text(x = 2.7, y = 139, "g [95\% CI]", font = 2)
# Close the forest plot and finalise it as a saved file
dev.off()
## pdf
```

Tests for Publication Bias

##

2

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:

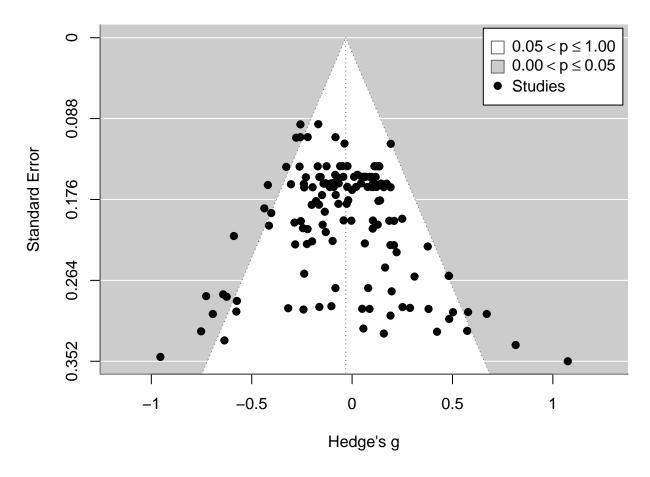
Funnel Plot

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.

- 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 mlmmetaresults 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, "Hedge's g".
- 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 = "Hedge's g")
```



Optional: Saving the Funnel Plot as a Separate File

- 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.

```
### Saving the Funnel Plot as a Separate File (Optional) -----
# 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 = "mlmfunnelplot.pdf", width = 8, height = 5)

# Same funnel plot code as above
```

```
par(mar = c(4, 4, 0.3, 1))
funnel(mlmmetaresults, legend = TRUE, xlab = "Hedge's g")

# 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 multilevelmeta\$sei_corrected variable is created to store the corrected standard error for each effect size, calculated using the formula $\sqrt{\frac{(n_p+n_a)}{(n_p\cdot n_a)}}$. Using Egger' test (unadjusted) on SMDs results in inflated Type 1 error as SMD and SE are not independent. Hence, use corrected formula for SE.
- The lmer() function is used to fit a linear mixed-effects model, where the effect size weighted by the corrected 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 / sei_corrected) expression indicates that the effect size (yi) is divided by the corrected standard error (sei_corrected), which is used to weight the effect sizes in the model.
- The I(1 / sei_corrected) expression indicates that the inverse of the corrected standard error is included in the model as a predictor.
- The 1 | lab_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.

Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]

```
## Formula: I(yi/sei_corrected) ~ 1 + I(1/sei_corrected) + (1 | lab_id)
##
      Data: multilevelmeta
##
## REML criterion at convergence: 444.7
##
## Scaled residuals:
##
      Min
                10 Median
                                30
                                       Max
## -2.6417 -0.7225 0.0334 0.7713
                                    2.6991
##
## Random effects:
   Groups
             Name
                         Variance Std.Dev.
   lab_id
             (Intercept) 0.445
                                  0.667
##
## Residual
                         1.335
                                  1.155
## Number of obs: 136, groups:
                               lab_id, 22
##
## Fixed effects:
##
                      Estimate Std. Error
                                               df t value Pr(>|t|)
## (Intercept)
                        0.6753
                                   0.4536 61.7763
                                                     1.49
                                                              0.142
                                                             0.042 *
                       -0.1803
                                   0.0874 79.4062
                                                    -2.06
## I(1/sei_corrected)
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Moderation Analysis

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

For continuous moderators, use meta-regression. Specifically, the modsfunction specifies the moderator variable (for continuous moderators).

For categorical moderators, use subgroup analysis. Specifically, the **subset** argument is used to specify the subset of data for categorical moderators, allowing for separate analyses for each category.

Explanation of the Code

- The rma.mv() function is used to perform the moderation analysis.
- 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 | lab_id / ID indicates that random intercepts are included for both the lab and individual studies, accounting for the nested structure of the data.
- The mods argument specifies the moderator variable (for continuous moderators).
- The subset argument is used to specify the subset of data for categorical moderators, allowing for separate analyses for each category.
- The method argument specifies the method used to estimate heterogeneity, in this case, "REML" (Restricted Maximum Likelihood).
- The data argument specifies the dataset to be used for the analysis.
- The summary() function is used to display the results of the meta-analysis, including the overall effect size estimate and its confidence interval.

Note that if convergence issues arise, the control argument 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.

```
### Moderation Analysis -----
# Categorical variable (i.e., publication type)
rma.mv(
      yi = yi,
      V = vi,
      random = ~ 1 | lab_id / ID,
      # Specify categorical moderator (i.e., Journal Article)
      subset = (publication == "Journal article"),
      data = multilevelmeta,
      # To address convergence issues (if it exists)
      control = list(rel.tol=1e-8)
)
##
## Multivariate Meta-Analysis Model (k = 66; method: REML)
## Variance Components:
##
##
              estim
                       sqrt nlvls fixed
                                             factor
## sigma^2.1 0.0270 0.1644
                             14
                                       no
                                              lab id
## sigma^2.2 0.0000 0.0000
                                66
                                       no lab_id/ID
##
## Test for Heterogeneity:
## Q(df = 65) = 100.7856, p-val = 0.0029
##
## Model Results:
##
## estimate
              se
                       zval
                               pval
                                       ci.lb ci.ub
## -0.0476 0.0571 -0.8328 0.4050 -0.1596 0.0644
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
rma.mv(
      yi = yi,
      V = vi,
      random = ~ 1 | lab_id / ID,
      # Specify categorical moderator (i.e., Thesis/dissertation)
      subset = (publication == "Thesis/dissertation"),
      data = multilevelmeta
)
## Multivariate Meta-Analysis Model (k = 68; method: REML)
## Variance Components:
##
##
              estim
                       sqrt nlvls fixed
                                              factor
## sigma^2.1 0.0321 0.1792
                               8
                                       no
                                              lab_id
## sigma^2.2 0.0029 0.0543
                                68
                                       no lab id/ID
##
## Test for Heterogeneity:
## Q(df = 67) = 100.9032, p-val = 0.0047
##
```

```
## Model Results:
##
## estimate
                se
                      zval
                              pval
                                      ci.lb
    0.0131 0.0872 0.1506 0.8803 -0.1578 0.1841
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
rma.mv(
      yi = yi,
      V = vi,
      random = ~ 1 | lab_id / ID,
      # Specify categorical moderator (i.e., Conference)
      subset = (publication == "Conference"),
      data = multilevelmeta
)
## Warning: Single-level factor(s) found in 'random' argument. Corresponding
## 'sigma2' value(s) fixed to 0.
##
## Multivariate Meta-Analysis Model (k = 2; method: REML)
## Variance Components:
##
                       sqrt nlvls fixed
                                             factor
              estim
## sigma^2.1 0.0000 0.0000
                                             lab_id
                                 1
                                     yes
## sigma^2.2 0.2598 0.5097
                                 2 no lab_id/ID
##
## Test for Heterogeneity:
## Q(df = 1) = 4.3422, p-val = 0.0372
## Model Results:
##
## estimate se
                       zval
                               pval
                                      ci.lb ci.ub
## -0.2118 0.4108 -0.5155 0.6062 -1.0170 0.5934
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# Continuous variable (i.e., female proportion)
rma.mv(
      yi = yi,
      V = vi,
      random = ~ 1 | lab_id / ID,
      # Specify continuous moderator (i.e., female proportion)
      mods = ~ female_proportion,
      method = "REML",
      data = multilevelmeta
) |>
      summary()
## Multivariate Meta-Analysis Model (k = 136; method: REML)
##
    logLik Deviance
##
                          AIC
                                     BIC
                                             AICc
```

```
##
     5.4145 -10.8291
                         -2.8291
                                    8.7623
                                             -2.5190
##
  Variance Components:
##
##
##
               estim
                         sqrt
                               nlvls
                                      fixed
                                                factor
             0.0246
                      0.1567
                                  22
## sigma^2.1
                                                lab id
                                         no
                      0.0000
## sigma^2.2
              0.0000
                                 136
                                         no
                                             lab id/ID
##
## Test for Residual Heterogeneity:
  QE(df = 134) = 200.0850, p-val = 0.0002
## Test of Moderators (coefficient 2):
  QM(df = 1) = 5.1951, p-val = 0.0227
##
## Model Results:
##
##
                                                    pval
                                                             ci.lb
                       estimate
                                                                      ci.ub
                                     se
                                            zval
## intrcpt
                       -0.3041
                                 0.1286
                                         -2.3650
                                                  0.0180
                                                           -0.5562
                                                                    -0.0521
                        0.4104
                                 0.1801
                                          2.2793
                                                  0.0227
                                                            0.0575
                                                                     0.7634
## female_proportion
##
## Signif. codes: 0 '***' 0.001 '**' 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 both presence of smartphones and absence of smartphones groups
- Custom headers for the plot
- Custom labels for the studies
- Summary effect sizes for each moderator

- 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 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 both the presence of smartphones and absence of smartphones groups.

- The cbind() function combines multiple columns side-by-side. In this case, the sample sizes of the groups (n p and n a) will appear side-by-side in 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_published" columns. The sep argument specifies the separator between the columns, which is set to "," in this case. Hence, the label will be in the format "Author(s), Year" (e.g., "Smith, 2020").
- 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 x argument specifying the horizontal arrangement of the columns and the y specifying the vertical arrangement of the columns.
- The pos argument specifies the position of the text relative to the specified coordinates.
- The font argument adjusts the font size.
- 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 random argument specifies the random effects structure, where ~ 1 | lab_id / 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 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.

```
rows = c(143:79, 75:7, 3:2),
       # Add y-axis limits
       ylim = c(-3, 147),
       # Add sample size information for presence and absence of smartphones groups
       # -4.2 for presence of smartphones (n_p)
       # -3.6 for absence of smartphones (n a)
       ilab = cbind(n_p, n_a),
       ilab.xpos = c(-4.2, -3.6),
       # Label studies on the forest plot
       slab = paste(author, year_published, 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 = 11,
       # 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, "Hedge's g"
       xlab = "Hedge's g"
# 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 type (Moderator Analysis)
\# - "Journal article" at y = 7
\# - "Thesis/Dissertations" at y = 15
\# - "Non-Conference" at y = 21
text(
       x = -7,
       y = c(4, 76, 144),
       pos = 4,
       c("Conference", "Thesis/dissertation", "Journal article"),
       font = 2
)
# Moderation analysis
res.j = rma.mv(
       yi,
       vi,
       random = ~ 1 | lab_id / ID,
```

```
subset = (publication == "Journal article"),
       data = multilevelmeta,
       # To address convergence issues (if it exists)
       control = list(rel.tol=1e-8)
res.t = rma.mv(
      уi,
       vi,
       random = ~ 1 | lab_id / ID,
       subset = (publication == "Thesis/dissertation"),
       data = multilevelmeta
)
res.c = rma.mv(
      уi,
       vi,
       random = ~ 1 | lab_id / ID,
       subset = (publication == "Conference"),
       data = multilevelmeta
)
## Warning: Single-level factor(s) found in 'random' argument. Corresponding
## 'sigma2' value(s) fixed to 0.
# Add summary effect sizes for each of the moderators
addpoly(res.c, row = 1) # summary effect for "Conference" group
addpoly(res.t, row = 6) # summary effect for "Thesis/Dissertation" group
addpoly(res.j, row = 78) # summary effect for "Journal article" group
# Add"Author(s) Year" header
text(x = -6.5, y = 146, "Author(s) Year", font = 2)
# Add "Sample Size" header
text(x = -3.9, y = 146.7, "Sample Size", font = 2)
# Add specific sample size column headers, "Presence" and "Absence"
# x = -4.2 for for presence of smartphones
# x = -3.6 for absence of smartphones
# y = 146  for both
text(c(x = -4.2, x = -3.6), y = 146, c("Presence", "Absence"), font = 2)
# Add "g [95% CI]" header
text(x = 3.6, y = 146, "g [95\% CI]", font = 2)
```

Journal article Blowmonia et al., 2023 Thomason et al., 2013 Thomason et al., 2014 Thomason et al., 2014 Thomason et al., 2014 Andrean et al., 2014 Andrean et al., 2014 Andrean et al., 2014 Thomason et al., 2014 Thomason et al., 2017 Thomason et al., 2017 Thomason et al., 2019 Thomason et al., 2019 Thomason et al., 2019 The all and	21 22 23 24 40 40 48 40 48 40 49 40 40 40 40 40 40 40 40 40 40 40 40 40	51 77 74 18 18 24 25 27 18 18 18 24 27 18 18 18 24 27 18 18 18 28 28 29 20 20 20 20 20 20 20 20 20 20 20 20 20		-271-1-30, -0271-1-30, -0281-1
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No. or al., 2022 Tritler et al., 2077 Tritler et al., 2079 Trit	50 41 167 167 167 167 167 167 167 167 167 16	50 39 1757 1934 5 39 46 178 54 44 44 153 177 175 175 175 175 175 175 175 175 175		-201 CAR. 0. 10 CAR. 0
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Interest et al., 2017 Interest et al., 2019	167 158 41 48 167 58 40 48 40 58 40 58 70 70 77 70 27 70 58 58 70 70 70 70 70 71 70 70 71 70 70 70 70 70 70 70 70 70 70 70 70 70	178 353 46 46 47 178 189 189 189 189 189 189 189 189 189 18		-28[-6.4], -6.2 -28[-6.4], -6.
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Trees et al., 2017 Trees et al., 2019 Trees et al.,	48 40 40 4167 58 40 40 4167 58 40 40 4167 58 40 40 4167 58 40 40 4167 58 4167 70 58 4167 70 50 41 41 42 41 41 41 41 41 41 41 41 41 41 41 41 41	46 170 64 42 42 42 42 42 42 42 42 42 42 42 42 42		-22 [c.m. c.] -23 [c.m. c.] -24 [c.m. c.] -25 [c.m. c.
Water et al., 2017 Water State (1977) Water	167 58 40 40 40 58 40 50 50 50 50 50 50 50 50 50 50 50 50 50	178 64 42 42 53 54 54 55 55 55 55 55 55 55 55 55 55 55		-22[-64, -64] -20[-68, 0] -20[
Times and a 2017 What of all	40 167 58 40 20 21 21 21 21 21 21 21 21 21 21 21 21 21	42 343 343 44 65 65 65 65 65 65 65 65 65 65 65 65 65		-00[-0.8, 0.7, 0.7, 0.7, 0.7, 0.7, 0.7, 0.7, 0.7
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Stone, 2020 Salley, 2018	21	18		0.81 [0.16, 1.4
	19	18	←	-0.95 [-1.64, -0.2
Ruiz Pardo, 2022	27 75	24 85	F	-0.57 [-1.13, -0.0 -0.42 [-0.73, -0.1
Stahl, 2018	51	47		-0.41 [-0.81, -0.0
Ruiz Pardo, 2022	75	162	· ⊢	-0.33 [-0.60, -0.0
Tarantino, 2019 Ruiz Pando, 2022	22 75	25 85		-0.32 [-0.89, 0.0 -0.30 [-0.62, 0.0
Ruiz Pardo, 2022	75	162	' ⊢- -j	-0.26 [-0.54, 0.0
Stahl, 2018 Aguila, 2019	46 41	48		-0.24 [-0.65, 0.1 -0.24 [-0.82, 0.1
Ruiz Pardo, 2022	75	16 85		-0.24 [-0.55, 0.0
Tarantino, 2019	22	50		-0.24 [-0.74, 0.2
Ruiz Pando, 2022 Ruiz Pando, 2022	75 85	77 90		-0.24 [-0.58, 0.0 -0.23 [-0.53, 0.0
Ruiz Pardo, 2022	75	77	⊢	-0.20 [-0.52, 0.1
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Ruiz Pando, 2022	85	90	⊢ +	-0.08 [-0.37, 0.2
Ruiz Pando, 2022 Ruiz Pando, 2022	75 75	85 162	<u> </u>	-0.07 [-0.38, 0.2 -0.06 [-0.33, 0.2
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Ruiz Pardo, 2022	85	90	i -i-i	0.01 [-0.29, 0.3
Ruiz Pardo, 2022 Ruiz Pardo, 2022	75 75	77 85		0.02 [-0.30, 0.5
Ruiz Pardo, 2022	85	90	=	0.05 [-0.25, 0.3
Aguila, 2019 Buiz Panto, 2022	41 85	16 90	 	0.05 [-0.53, 0.6
Ruiz Pando, 2022	85 85	90		0.06 [-0.24, 0.1 0.07 [-0.23, 0.1
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Aguila, 2019	41	16		0.50 [-0.08, 1.0
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Optional: Saving the Forest Plot of Moderators as a Separate File

- 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
# Adjust the width and height of the pdf file
pdf(file = "mlmforestplotwithmoderators.pdf", width = 15, height = 45)
# Same forest plot code as above
forest(
       mlmmetaresults,
       rows = c(143:79, 75:7, 3:2),
       ylim = c(-3, 147),
       ilab = cbind(n_p, n_a),
       ilab.xpos = c(-4.2, -3.6),
       slab = paste(author, year_published, sep = ", "),
       xlim = c(-7, 4),
       alim = c(-1.5, 1.5),
       steps = 11,
       efac = 0.3,
       header = FALSE,
       xlab = "Hedge's g"
)
text(
       x = -7,
       y = c(4, 76, 144),
       pos = 4,
       c("Conference", "Thesis/dissertation", "Journal article"),
       font = 2
res.j = rma.mv(
       yi,
       vi,
       random = ~ 1 | lab_id / ID,
       subset = (publication == "Journal article"),
       data = multilevelmeta,
       control = list(rel.tol=1e-8)
)
```

```
res.t = rma.mv(
       yi,
       vi,
       random = ~ 1 | lab_id / ID,
       subset = (publication == "Thesis/dissertation"),
       data = multilevelmeta
)
res.c = rma.mv(
       yi,
       ٧i,
       random = ~ 1 | lab_id / ID,
      subset = (publication == "Conference"),
       data = multilevelmeta
)
## Warning: Single-level factor(s) found in 'random' argument. Corresponding
## 'sigma2' value(s) fixed to 0.
addpoly(res.c, row = 1)
addpoly(res.t, row = 6)
addpoly(res.j, row = 78)
text(x = -6.5, y = 146, "Author(s) Year", font = 2)
text(x = -3.9, y = 146.7, "Sample Size", font = 2)
text(c(x = -4.2, x = -3.6), y = 146, c("Presence", "Absence"), font = 2)
text(x = 3.6, y = 146, "g [95\% CI]", font = 2)
# Close the forest plot and finalise it as a saved file
dev.off()
## pdf
##
   2
```

End of Code