How Effective Are Reading Comprehension Interventions for Children with ASD? A Meta-Analysis of Single-Case Design Studies

Effect Size Pooling, Test for Moderators, and Publication Bias

Suplemental Materialss

January 11, 2021

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1 Preparation

1.1 Packages

1.1.1 General

```r
library(tidyverse)       # Easily Install and Load the 'Tidyverse'
library(broom)           # Convert Statistical Analysis Objects into Tidy Tibbles
library(purrr)           # Functional Programming Tools
library(readxl)          # Read Excel Files
library(glue)            # Interpreted String Literals
library(xtable)          # Export Tables to LaTeX or HTML
library(pander)          # Tables
```

1.1.2 Specific

```r
library(nlme)            # Linear and Nonlinear Mixed Effects Models
library(scdhlm)          # Estimating Hierarchical Linear Models for Single-Case Designs
library(robumeta)        # Robust Variance Meta-Regression
library(metafor)         # Meta-Analysis Package for R
library(SingleCaseES)    # Single Case Desing Study Effect Sizes
library(clubSandwich)    # Robust variance
```

1.2 Dataset

1.2.1 Import

```
data_raw <- readxl::read_excel("Data Collection and Organization/SCD_MetaA_MLM_data (1).xlsx")
```

1.2.2 Wrangle

care for categorical variables

```
data_clean <- data_raw %>%
  dplyr::rename(personID = person_id) %>%
  tidyr::separate(personID,
                  into = c("study", "id", "outcome"),
                  remove = FALSE) %>%
  dplyr::mutate(outcome = ifelse(is.na(outcome), 1, as.numeric(outcome))) %>%
  # dplyr::filter(round == 1) %>%
  dplyr::mutate(study_name = study  %>%
                  fct_recode("Bethune & Wood (2013)"         = "1",
                             "Knight et al. (2015)"          = "2",
                             "Alison et al. (2017)"          = "3",
                             "Stringfield et al. (2011)"     = "4",
                             "Solis et al. (2016)"           = "5",  # remove for ES
                             "Howorth et al. (2016)"         = "6",
                             "Carnahan & Williamson (2014)"  = "7",  # keep first AB cycle
                             "Singh et al. (2017)"           = "8",  # not used for BC_SMD
                             "Williamson et al. (2015)"      = "9",
                             "Carnahan et al. (2016)"        = "10",
                             "Cadette (2016)"                = "11",  # keep round 1->ES (paper after d
                             "Chovanes (2018*)"              = "12",  # exclude 2 subjects, not used fo
                             "Koh (2013*)"                   = "13",
                             "Schatz (2017*)"                = "14",
                             "Kim et al. (2018)"             = "15",
                             "Browder et al. (2017)"         = "16",
                             "Ozsayin (2017*)"               = "17") %>%
                  fct_relevel(sort)) %>%
  dplyr::mutate(type = ifelse(study == "5",  "AB", "MB")) %>%
  dplyr::mutate(wwc  = factor(wwc,
                              levels = c(0, 1),
                              labels = c("met with reservations",
                                         "met fully"))) %>%
  dplyr::mutate(age_cat = cut(age,
                              breaks = c(6, 12, 18),
                              include.lowest = TRUE)) %>%
  dplyr::mutate(dx = factor(dx,
                            levels = c(0, 1),
                            labels = c("ASD",
                                       "ASD+Other"))) %>%
  dplyr::mutate(race_ethnic = factor(race_ethnic,
                                     levels = c(0, 1, 2, 3, 4),
                                     labels = c("Latino",
                                                "White",
                                                "Black",
                                                "Asian",
                                                "Indian"))) %>%
```

```r
  dplyr::mutate(cog_cat = cut(cog_ability,
                              breaks = c(50, 79, 110))) %>%
  dplyr::mutate(status = factor(status,
                                levels = c(0, 1, 2),
                                labels = c("baseline",
                                           "intervention",
                                           "maintenance")))  %>%
  dplyr::filter(study != "7" | (study == "7" & session_day <= 8)) %>%
  dplyr::group_by(personID) %>%
  dplyr::mutate(phaseA = ifelse(status == "baseline", session_day, 0)) %>%
  dplyr::mutate(lastA = max(phaseA)) %>%
  dplyr::mutate(total_obs = max(session_day)) %>%
  dplyr::mutate(intervention = as.numeric(session_day > lastA)) %>%
  dplyr::ungroup() %>%
  dplyr::mutate(time = session_day - lastA) %>%
  dplyr::mutate(score_per = score/max_poss) %>%
  dplyr::mutate(num_cor = score_per * max_poss,
                num_inc = max_poss - num_cor) %>%
  dplyr::mutate(published = ifelse(study %in% c("12", "13", "14", "17"),
                                   "Gray Literature",
                                   "Publication") %>%
                  factor) %>%
  dplyr::select(study, study_name,
                type, wwc, published,
                id, personID, outcome,
                age, age_cat, dx, race_ethnic, cog_ability, cog_cat,
                total_iv_sess, total_obs, lastA,
                session_day, time, status, intervention,
                score, max_poss, outcome_type, score_per, num_cor, num_inc)

tibble::glimpse(data_clean)
```

```
Rows: 943
Columns: 27
$ study         <chr> "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1"...
$ study_name    <fct> Bethune & Wood (2013), Bethune & Wood (2013), Bethune...
$ type          <chr> "MB", "MB", "MB", "MB", "MB", "MB", "MB", "MB", "MB",...
$ wwc           <fct> met with reservations, met with reservations, met wit...
$ published     <fct> Publication, Publication, Publication, Publication, P...
$ id            <chr> "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1"...
$ personID      <chr> "1_1", "1_1", "1_1", "1_1", "1_1", "1_1", "1_1", "1_1...
$ outcome       <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,...
$ age           <dbl> 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 10, 1...
$ age_cat       <fct> "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6...
$ dx            <fct> ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD...
$ race_ethnic   <fct> Latino, Latino, Latino, Latino, Latino, Latino, Latin...
$ cog_ability   <dbl> 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 9...
$ cog_cat       <fct> "(79,110]", "(79,110]", "(79,110]", "(79,110]", "(79,...
$ total_iv_sess <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5,...
$ total_obs     <dbl> 28, 28, 28, 28, 28, 28, 28, 28, 28, 28, 28, 28, 28, 2...
$ lastA         <dbl> 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 9, 9,...
$ session_day   <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 17, 22, 25, 28...
$ time          <dbl> -5, -4, -3, -2, -1, 0, 1, 2, 3, 4, 5, 7, 11, 16, 19, ...
$ status        <fct> baseline, baseline, baseline, baseline, baseline, bas...
```

```
$ intervention  <dbl> 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0,...
$ score         <dbl> 4, 1, 5, 4, 5, 4, 7, 7, 7, 8, 7, 8, 8, 7, 7, 8, 3, 3,...
$ max_poss      <dbl> 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8,...
$ outcome_type  <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
$ score_per     <dbl> 0.500, 0.125, 0.625, 0.500, 0.625, 0.500, 0.875, 0.87...
$ num_cor       <dbl> 4, 1, 5, 4, 5, 4, 7, 7, 7, 8, 7, 8, 8, 7, 7, 8, 3, 3,...
$ num_inc       <dbl> 4, 7, 3, 4, 3, 4, 1, 1, 1, 0, 1, 0, 0, 1, 1, 0, 5, 5,...
```

```
data_clean %>%
  dplyr::group_by(study_name, id) %>%
  dplyr::slice(1) %>%
  dplyr::group_by(study_name) %>%
  dplyr::mutate(n = n()) %>%
  dplyr::slice(1) %>%
  dplyr::arrange(study_name) %>%
  dplyr::select(study, study_name, type, published, n) %>%
  pander::pander(caption = "List of Studies")
```

Table 1: List of Studies

study	study_name	type	published	n
3	Alison et al. (2017)	MB	Publication	3
1	Bethune & Wood (2013)	MB	Publication	3
16	Browder et al. (2017)	MB	Publication	3
11	Cadette (2016)	MB	Publication	3
7	Carnahan & Williamson (2014)	MB	Publication	3
10	Carnahan et al. (2016)	MB	Publication	3
12	Chovanes (2018*)	MB	Gray Literature	3
6	Howorth et al. (2016)	MB	Publication	4
15	Kim et al. (2018)	MB	Publication	3
2	Knight et al. (2015)	MB	Publication	4
13	Koh (2013*)	MB	Gray Literature	3
17	Ozsayin (2017*)	MB	Gray Literature	4
14	Schatz (2017*)	MB	Gray Literature	3
8	Singh et al. (2017)	MB	Publication	1
5	Solis et al. (2016)	AB	Publication	4
4	Stringfield et al. (2011)	MB	Publication	3
9	Williamson et al. (2015)	MB	Publication	3

1.2.3 Reduce

Long format = one line per observation

```r
data_es <- data_clean %>%
  dplyr::filter(status %in% c("baseline", "intervention")) %>%
  dplyr::filter(study != "5") %>%
  dplyr::filter(!personID %in% c("12_1", "12_2"))

tibble::glimpse(data_es)
```

```
Rows: 823
Columns: 27
$ study         <chr> "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1"...
$ study_name    <fct> Bethune & Wood (2013), Bethune & Wood (2013), Bethune...
$ type          <chr> "MB", "MB", "MB", "MB", "MB", "MB", "MB", "MB", "MB",...
$ wwc           <fct> met with reservations, met with reservations, met wit...
$ published     <fct> Publication, Publication, Publication, Publication, P...
$ id            <chr> "1", "1", "1", "1", "1", "1", "1", "1", "1", "1", "1"...
$ personID      <chr> "1_1", "1_1", "1_1", "1_1", "1_1", "1_1", "1_1", "1_1...
$ outcome       <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,...
$ age           <dbl> 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 10, 10, 10, 10, 10, ...
$ age_cat       <fct> "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6...
$ dx            <fct> ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD...
$ race_ethnic   <fct> Latino, Latino, Latino, Latino, Latino, Latino, Latin...
$ cog_ability   <dbl> 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 67, 67, 6...
$ cog_cat       <fct> "(79,110]", "(79,110]", "(79,110]", "(79,110]", "(79,...
$ total_iv_sess <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5,...
$ total_obs     <dbl> 28, 28, 28, 28, 28, 28, 28, 28, 28, 28, 28, 29, 29, 2...
$ lastA         <dbl> 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 9, 9, 9, 9, 9, 9, 9,...
$ session_day   <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 3, 4, 5, 6, 7, 8, ...
$ time          <dbl> -5, -4, -3, -2, -1, 0, 1, 2, 3, 4, 5, -6, -5, -4, -3,...
$ status        <fct> baseline, baseline, baseline, baseline, baseline, bas...
$ intervention  <dbl> 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0,...
$ score         <dbl> 4, 1, 5, 4, 5, 4, 7, 7, 7, 8, 7, 3, 3, 3, 2, 4, 2, 2,...
$ max_poss      <dbl> 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8,...
$ outcome_type  <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
$ score_per     <dbl> 0.500, 0.125, 0.625, 0.500, 0.625, 0.500, 0.875, 0.87...
$ num_cor       <dbl> 4, 1, 5, 4, 5, 4, 7, 7, 7, 8, 7, 3, 3, 3, 2, 4, 2, 2,...
$ num_inc       <dbl> 4, 7, 3, 4, 3, 4, 1, 1, 1, 0, 1, 5, 5, 5, 6, 4, 6, 6,...
```

1.2.4 Restructure

Wide format = one line per participant

```
data_wide <- data_es %>%
  dplyr::group_by(personID) %>%
  dplyr::mutate(line = row_number()) %>%
  dplyr::filter(line == 1) %>%
  dplyr::select(personID, outcome,
                age, age_cat,
                dx,
                race_ethnic,
                cog_ability, cog_cat,
                total_iv_sess,
                wwc, published)

tibble::glimpse(data_wide)
```

```
Rows: 53
Columns: 11
Groups: personID [53]
$ personID      <chr> "1_1", "1_2", "1_3", "2_1", "2_2", "2_3", "2_4", "3_1...
$ outcome       <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,...
$ age           <dbl> 8, 10, 10, 11, 11, 12, 14, 8, 8, 10, 11, 8, 8, 10, 11...
$ age_cat       <fct> "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6...
$ dx            <fct> ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD...
$ race_ethnic   <fct> Latino, White, Black, Black, Black, Black, Black, Bla...
$ cog_ability   <dbl> 94, 67, 90, 55, 53, 63, 67, NA, NA, NA, NA, NA, NA, 9...
$ cog_cat       <fct> "(79,110]", "(50,79]", "(79,110]", "(50,79]", "(50,79...
$ total_iv_sess <dbl> 5, 5, 7, 15, 11, 10, 9, 16, 12, 9, 23, 16, 13, 6, 6, ...
$ wwc           <fct> met with reservations, met with reservations, met wit...
$ published     <fct> Publication, Publication, Publication, Publication, P...
```

2 Between-Case Effect Size (BC-SMD)

design comparable

2.1 Moment Estimation

Hedges, Pustejovsky, & Shadish (2013)

assumes no trend in BL or intervention

EFFECT SIZE : * `delta_hat` corrected effect size estimate * `V_delta_hat` estimated variance of delta_hat

```
bc_smd <- function(df){
  es <- scdhlm::effect_size_MB(outcome   = df$score_per,
                               treatment = df$status,
                               id        = df$personID,
                               time      = df$session_day)
  es %>%
    unlist()
}
```

2.1.1 By Study

```
data_bcsmd <- data_es %>%
  dplyr::filter(type == "MB",
                study != "8",
                study != "12") %>%
  dplyr::group_by(study) %>%
  dplyr::mutate(n_sub = n_distinct(id)) %>%
  dplyr::group_by(study, study_name, n_sub) %>%
  tidyr::nest() %>%
  dplyr::mutate(fit  = purrr::map(data, bc_smd)) %>%
  dplyr::mutate(tidy = purrr::map(fit, broom::tidy)) %>%
  tidyr::unnest(tidy) %>%
  dplyr::select(-data, -fit) %>%
  tidyr::pivot_wider(names_from  = names,
                     values_from = x)
```

```
data_bcsmd %>%
  dplyr::ungroup() %>%
  dplyr::arrange(study_name) %>%
  dplyr::select("Study Citation" = study_name,
                "Subjects"       = n_sub,
                "Observations"   = g_dotdot,
                "Estimate"       = delta_hat,
                "Variance"       = V_delta_hat) %>%
  xtable::xtable(digits = c(0, 0, 0, 0, 3, 3),
                 align = c("l", "l", "c", "c", "r", "r"),
                 caption = "Design Comparable Effect Sizes: BC-SMD, Momemt Estimation Method (assumes n
  print(booktabs = TRUE,
        comment = FALSE,
        include.rownames = FALSE,
        caption.placement = "top")
```

Table 2: Design Comparable Effect Sizes: BC-SMD, Momemt Estimation Method (assumes no time trend during baseline or intervention phases)

Study Citation	Subjects	Observations	Estimate	Variance
Alison et al. (2017)	3	63	2.287	0.723
Bethune & Wood (2013)	3	38	2.284	0.578
Browder et al. (2017)	3	41	3.201	2.327
Cadette (2016)	3	129	2.868	0.200
Carnahan & Williamson (2014)	3	24	2.595	0.701
Carnahan et al. (2016)	3	35	4.538	0.921
Howorth et al. (2016)	4	40	1.231	0.261
Kim et al. (2018)	3	39	8.577	4.898
Knight et al. (2015)	4	72	1.426	0.114
Koh (2013*)	3	33	0.511	0.341
Ozsayin (2017*)	4	59	1.091	0.591
Schatz (2017*)	3	72	1.687	0.170
Stringfield et al. (2011)	3	96	3.726	0.283
Williamson et al. (2015)	3	50	2.010	1.808

2.1.2 Overall

- Meta-regression models using robust variance estimation (RVE) methods
- Estimate correlated and hierarchical effects models using the original (Hedges, Tipton and Johnson, 2010) and small-sample corrected (Tipton, 2013) RVE methods

```r
robumeta::robu(formula = delta_hat ~ 1,
               data = data_bcsmd,
               studynum = study_name,
               var.eff.size = V_delta_hat)
```

```
RVE: Correlated Effects Model with Small-Sample Corrections

Model: delta_hat ~ 1

Number of studies = 14
Number of outcomes = 14 (min = 1 , mean = 1 , median = 1 , max = 1 )
Rho = 0.8
I.sq = 71.16328
Tau.sq = 0.9533298

               Estimate StdErr t-value  dfs   P(|t|>) 95% CI.L 95% CI.U Sig
1 X.Intercept.     2.28  0.338    6.76 11.5 0.0000254     1.54     3.02 ***
---
Signif. codes: < .01 *** < .05 ** < .10 *
---
Note: If df < 4, do not trust the results
```

2.1.3 Forest Plot

```
data_bcsmd %>%
  ggplot(aes(y = delta_hat,
             x = fct_rev(study_name))) +
  geom_hline(yintercept = 0,
             alpha = .2,
             size = 2) +
  geom_point(aes(size = g_dotdot),
             shape = 15) +
  geom_errorbar(aes(ymin = delta_hat - 1.96*sqrt(V_delta_hat),
                    ymax = delta_hat + 1.96*sqrt(V_delta_hat)),
                width = 0) +
  theme_bw() +
  coord_flip() +
  labs(x = NULL,
       y = "BC-SMD Estimate",
       size = "Obs.",
       caption = "Note:\nAssumes no time trend during baseline\nor intervention phases.") +
  theme(legend.position = "none")
```

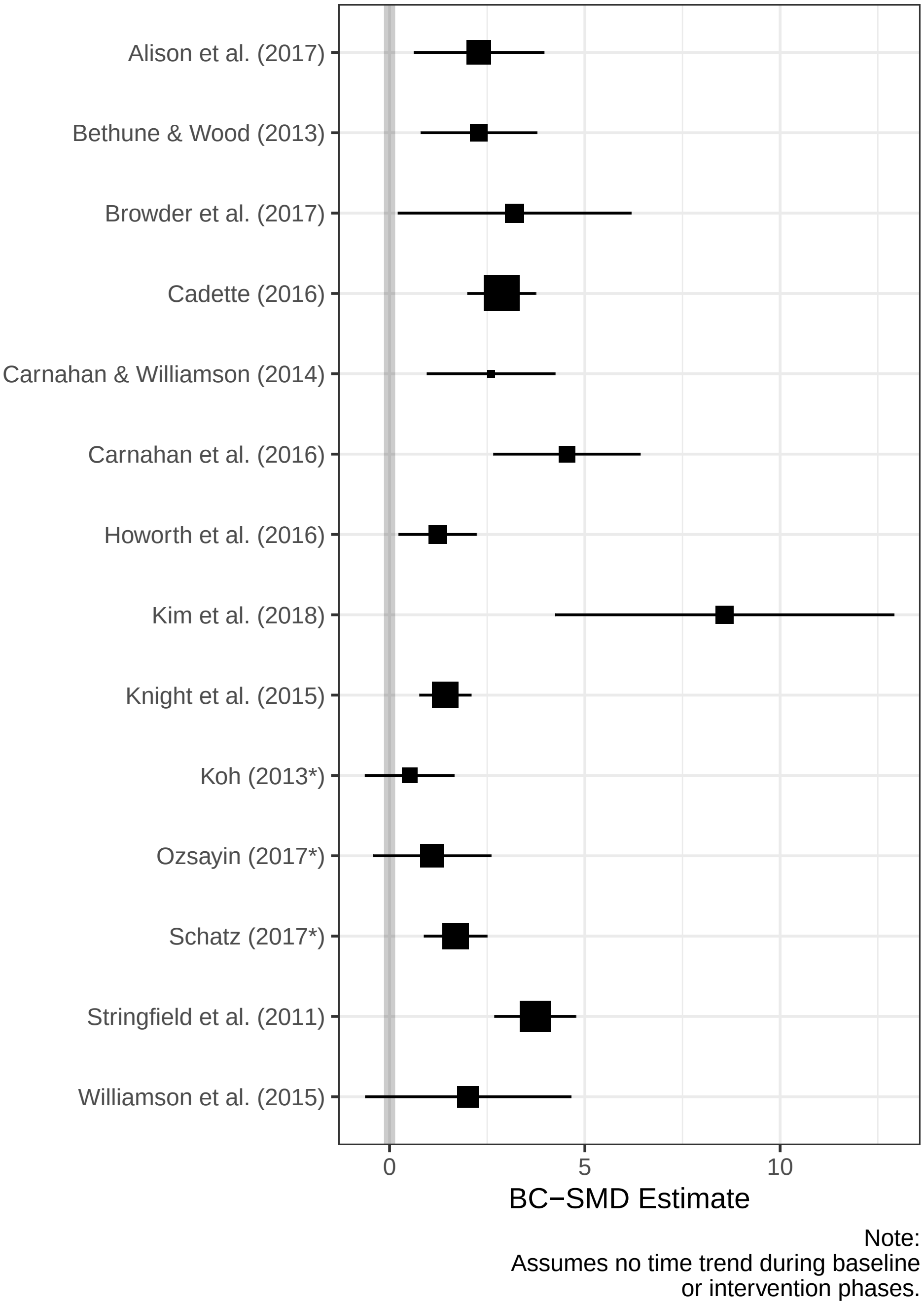

Figure 1: Forest Plot of Design Comparable Effect Sizes: BC-SMD, Momemt Estimation Method

2.2 REML estimation

Pustejovsky, Hedges, & Shaddish (2014)

```
extract_g <- function(x){
  x[c("g_AB", "V_g_AB")]
}
```

2.2.1 By Study

```
data_dcsmd <- data_es %>%
  dplyr::filter(type  == "MB",
                study != "8",
                study != "12") %>%
  dplyr::group_by(study_name) %>%
  dplyr::mutate(g_dotdot = n()) %>%
  dplyr::mutate(n_sub = n_distinct(id)) %>%
  dplyr::group_by(study, study_name, n_sub, g_dotdot) %>%
  tidyr::nest_legacy() %>%
  dplyr::mutate(mlm = map(data,
                          ~nlme::lme(fixed  = score_per ~ intervention + intervention:time,
                                     random =  ~ 1 |personID,
                                     correlation = corAR1(0, ~ time|personID),
                                     data = .))) %>%
  dplyr::mutate(fit_g = purrr::map(mlm,
                                   ~scdhlm::g_REML(.,
                                                   p_const = c(0, 1, 10),
                                                   r_const = c(1, 0, 1),
                                                   returnModel = FALSE))) %>%
  dplyr::mutate(test = purrr::map(fit_g, ~extract_g(.))) %>%
  tidyr::unnest_wider(test, simplify = TRUE)
```

```
data_dcsmd %>%
  dplyr::ungroup() %>%
  dplyr::arrange(study_name) %>%
  dplyr::select("Study Citation" = study_name,
                "Subjects"       = n_sub,
                "Observations"   = g_dotdot,
                "Estimate"       = g_AB,
                "Variance"       = V_g_AB) %>%
  xtable::xtable(digits = c(0, 0, 0, 0, 3, 3),
                 align = c("l", "l", "c", "c", "r", "r"),
                 caption = "Design Comparable Effect Size: BC-SMD, REML Estimation Method (assuming no
  print(booktabs = TRUE,
        comment = FALSE,
        include.rownames = FALSE,
        caption.placement = "top")
```

2.2.2 Overall

- Meta-regression models using robust variance estimation (RVE) methods
- Estimate correlated and hierarchical effects models using the original (Hedges, Tipton and Johnson, 2010) and small-sample corrected (Tipton, 2013) RVE methods

Table 3: Design Comparable Effect Size: BC-SMD, REML Estimation Method (assuming no time trend during baseline but a time trend during intervention phase)

Study Citation	Subjects	Observations	Estimate	Variance
Alison et al. (2017)	3	63	2.776	0.332
Bethune & Wood (2013)	3	38	3.947	1.062
Browder et al. (2017)	3	41	5.739	0.852
Cadette (2016)	3	129	1.891	0.088
Carnahan & Williamson (2014)	3	24	3.170	2.242
Carnahan et al. (2016)	3	35	6.427	1.686
Howorth et al. (2016)	4	40	1.538	0.177
Kim et al. (2018)	3	39	8.294	2.874
Knight et al. (2015)	4	72	1.556	0.101
Koh (2013*)	3	33	0.781	0.877
Ozsayin (2017*)	4	59	1.670	0.844
Schatz (2017*)	3	72	1.285	0.339
Stringfield et al. (2011)	3	96	4.077	0.152
Williamson et al. (2015)	3	50	2.355	2.231

```r
robumeta::robu(formula = g_AB ~ 1,
               data = data_dcsmd,
               studynum = study_name,
               var.eff.size = V_g_AB)
```

```
RVE: Correlated Effects Model with Small-Sample Corrections

Model: g_AB ~ 1

Number of studies = 14
Number of outcomes = 14 (min = 1 , mean = 1 , median = 1 , max = 1 )
Rho = 0.8
I.sq = 83.22254
Tau.sq = 1.670859

               Estimate StdErr t-value  dfs   P(|t|>) 95% CI.L 95% CI.U Sig
1 X.Intercept.     2.91  0.486    5.99 11.9 0.0000648     1.85     3.97 ***
---
Signif. codes: < .01 *** < .05 ** < .10 *
---
Note: If df < 4, do not trust the results
```

2.2.3 Forest Plot

```
data_dcsmd %>%
  ggplot(aes(y = g_AB,
             x = fct_rev(study_name))) +
  geom_hline(yintercept = 0, alpha = .2, size = 2) +
  geom_point(aes(size = g_dotdot),
             shape = 15) +
  geom_errorbar(aes(ymin = g_AB - 1.96*sqrt(V_g_AB),
                    ymax = g_AB + 1.96*sqrt(V_g_AB)),
                width = 0) +
  theme_bw() +
  coord_flip() +
  labs(x = NULL,
       y = "BC-SMD Estimate (after 10 sessions)",
       size = "Obs.",
       caption = "Note:\nAssumes no time trend during baseline phase,\nbut allows for a time trend duri
  theme(legend.position = "none")
```

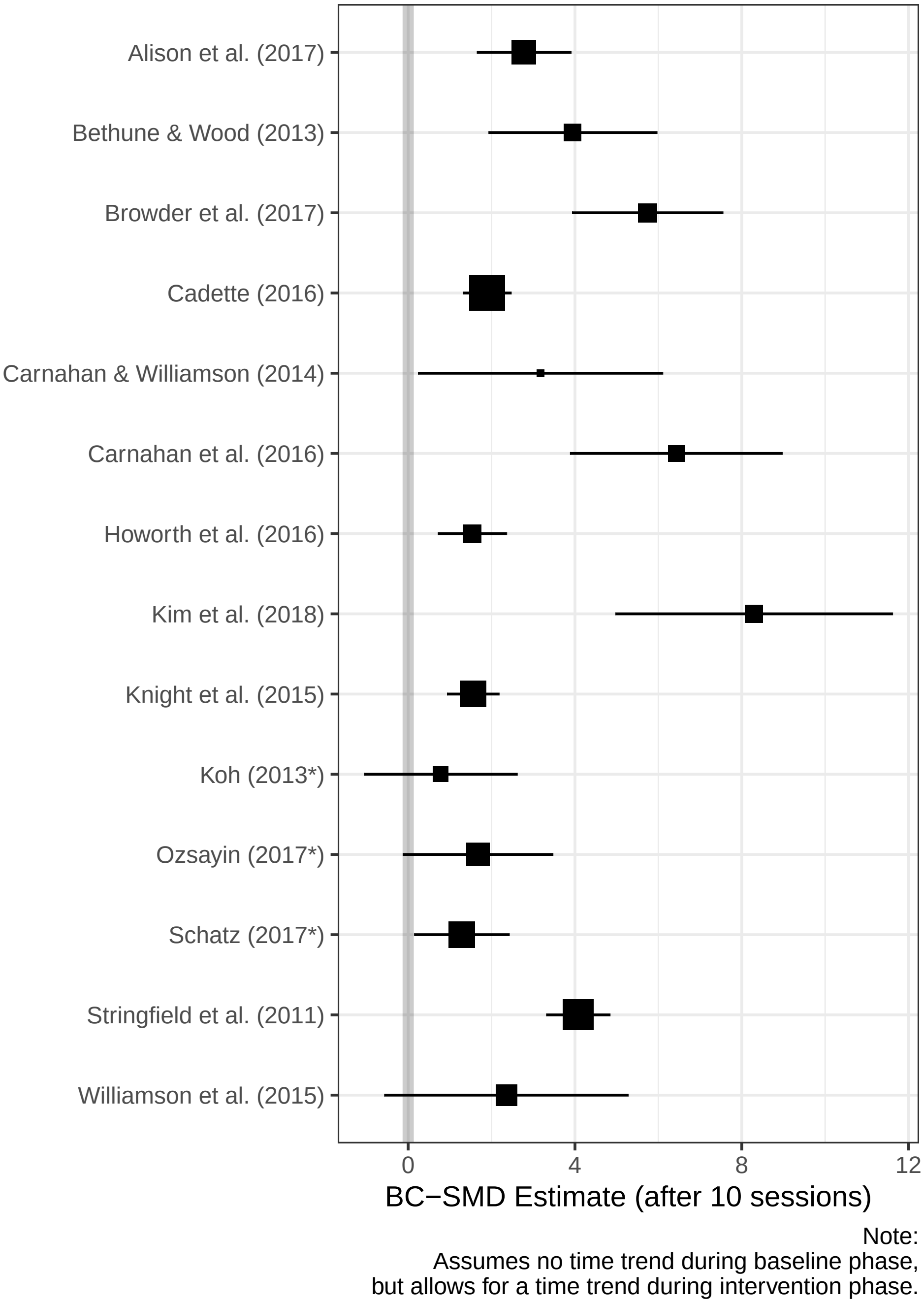

Figure 2: Forest Plot of Design Comparable Effect Sizes: BC-SMD, REML Estimation Method

2.3 Publication Bias (REML based)

The `metafor` package provides a comprehensive collection of functions for conducting meta-analyses in `R`. The package includes functions for calculating various effect size or outcome measures frequently used in meta-analyses (e.g., risk differences, risk ratios, odds ratios, standardized mean differences, Fisher's r-to-z-transformed correlation coefficients) and then allows the user to fit fixed-, random-, and **mixed-effects models** to these data. By including **study-level covariates ('moderators')** in these models, so-called **'meta-regression'** analyses can be carried out.

2.3.1 Random Effects Model

```r
data_dcsmd %>%
  metafor::rma(yi = g_AB,
               vi = V_g_AB,
               data = .,
               slab = study_name)
```

```
Random-Effects Model (k = 14; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 2.8924 (SE = 1.4307)
tau (square root of estimated tau^2 value):      1.7007
I^2 (total heterogeneity / total variability):   89.57%
H^2 (total variability / sampling variability):  9.59

Test for Heterogeneity:
Q(df = 13) = 77.4849, p-val < .0001

Model Results:

estimate      se    zval    pval   ci.lb   ci.ub
  3.0060  0.5145  5.8428  <.0001  1.9976  4.0143  ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.3.2 Funnel Plot

For **random-effects models** (i.e., models not involving moderators), the plot shows the individual observed effect sizes or outcomes on the x-axis against the corresponding standard errors (i.e., the square root of the sampling variances) on the y-axis. A vertical line indicates the estimate based on the model. A pseudo confidence interval region is drawn around this value with bounds equal to ±1.96 SE, where SE is the standard error value from the y-axis (assuming level of 95%).

```
metafor::rma(yi   = g_AB,
             vi   = V_g_AB,
             data = data_dcsmd,
             slab = study_name) %>%
  metafor::funnel(xlab = "BC-SMD Estimate (after 10 sessions)")
```

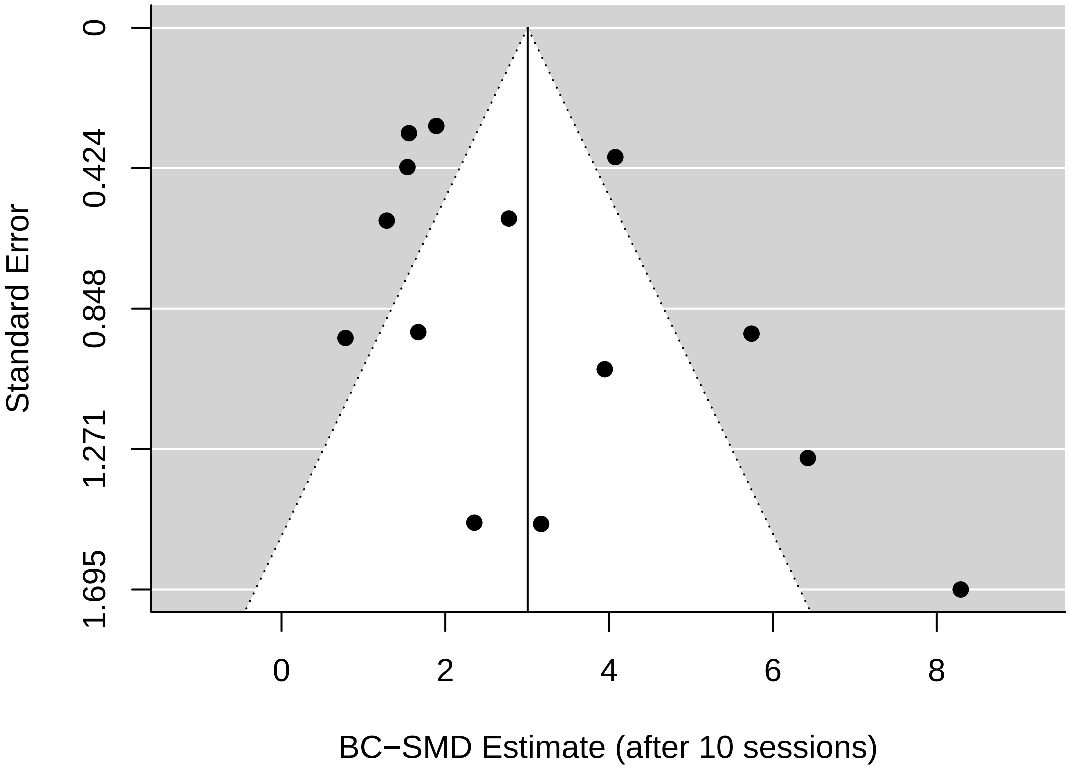

Figure 3: Publication Bias: Funnel Plot, BC-SMD (REML based)

2.3.3 Egger's Regression Test

Various tests for **funnel plot asymmetry** have been suggested in the literature, including the rank correlation test by Begg and Mazumdar (1994) and the **regression test by Egger et al. (1997)**. Extensions, modifications, and further developments of the regression test are described (among others) by Macaskill, Walter, and Irwig (2001), Sterne and Egger (2005), Harbord, Egger, and Sterne (2006), Peters et al. (2006), Rücker et al. (2008), and Moreno et al. (2009).

All of the tests do not directly test for publication bias, but for a* relationship between the observed outcomes and the chosen predictor*. If such a relationship is present, then this usually implies asymmetry in the funnel plot, which in turn may be an indication of publication bias. However, it is important to keep in mind that there can be other reasons besides publication bias that could lead to asymmetry in the funnel plot.

Check for Funnel Plot Asymmetry

```
metafor::rma(yi   = g_AB,
             vi   = V_g_AB,
             data = data_dcsmd,
             slab = study_name) %>%
  metafor::regtest()
```

```
Regression Test for Funnel Plot Asymmetry

model:     mixed-effects meta-regression model
predictor: standard error

test for funnel plot asymmetry: z = 2.3191, p = 0.0204
```

3 Within-Case Effect Size (LRRi)

3.1 Log Response Rate Increase

The **Response Ratio** parameter = ratio of the mean level of the outcome during **phase B** to the mean level of the outcome during **phase A**.

The **log response ratio** = natural logarithm of the response ratio. This effect size is appropriate for outcomes measured on a ratio scale *(so that zero corresponds to the true absence of the outcome)*.

There are two versions of the LRR.

- The LRR-increasing (LRRi) is defined so that positive values correspond to therapeutic improvements.
- The LRR-decreasing (LRRd) is defined so that negative values correspond to therapeutic improvements.

For outcomes measured as frequency counts or rates, the two versions will have the same magnitude but opposite sign; for outcomes measured as percentages or proportions, the LRRd and LRRi will differ in both sign and magnitude (Pustejovsky, 2018).

Without bias correction, the log response ratio is estimated as the natural logarithm of the phase B sample mean, minus the natural logarithm of the phase A sample mean. A **delta-method bias correction** to the estimator is used by default.

The **standard error of LRR** is calculated based on a delta-method approximation, allowing for the possibility of different degrees of dispersion in each phase. The confidence interval for LRR is based on a large-sample (z) approximation.

```
data_lrr <- data_es %>%
  dplyr::arrange(study_name, id, status, session_day) %>%
  SingleCaseES::batch_calc_ES(grouping       = c(study_name, personID),
                              condition      = status,
                              outcome        = score_per,
                              session_number = session_day,
                              baseline_phase = "baseline",
                              ES             = "LRRi",
                              improvement    = "increase",
                              scale          = "proportion",
                              interval       = max_poss,
                              bias_correct   = TRUE,
                              confidence     = .95) %>%
  dplyr::left_join(data_wide, by = "personID")

tibble::glimpse(data_lrr)
```

```
Rows: 53
Columns: 17
$ study_name    <fct> Alison et al. (2017), Alison et al. (2017), Alison et...
$ personID      <chr> "3_1", "3_2", "3_3", "1_1", "1_2", "1_3", "16_1", "16...
$ ES            <chr> "LRRi", "LRRi", "LRRi", "LRRi", "LRRi", "LRRi", "LRRi...
$ Est           <dbl> 1.4282134, 1.3884312, 1.9803347, 0.6184447, 0.8541821...
$ SE            <dbl> 0.33870834, 0.27229817, 0.39568113, 0.15920513, 0.122...
$ CI_lower      <dbl> 0.76435727, 0.85473663, 1.20481395, 0.30640842, 0.614...
$ CI_upper      <dbl> 2.0920696, 1.9221258, 2.7558555, 0.9304811, 1.0941203...
$ outcome       <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 3, 1, 2, 3, 1, 2, 3,...
$ age           <dbl> 8, 8, 10, 8, 10, 10, 8, 9, 10, 15, 15, 15, 17, 17, 17...
$ age_cat       <fct> "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6,12]", "[6...
$ dx            <fct> ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD, ASD+Othe...
$ race_ethnic   <fct> Black, Latino, Latino, Latino, White, Black, Latino, ...
```

```
$ cog_ability   <dbl> NA, NA, NA, 94, 67, 90, 58, 70, 64, NA, NA, NA, NA, N...
$ cog_cat       <fct> NA, NA, NA, "(79,110]", "(50,79]", "(79,110]", "(50,7...
$ total_iv_sess <dbl> 16, 12, 9, 5, 5, 7, 12, 6, 6, 12, 14, 7, 13, 10, 7, 1...
$ wwc           <fct> met with reservations, met with reservations, met wit...
$ published     <fct> Publication, Publication, Publication, Publication, P...
```

```
data_lrr %>%
  tidyr::separate(col = personID,
                  into = c("study_num", "person_num")) %>%
  ggplot(aes(y = Est,
             x = person_num)) +
  geom_hline(yintercept = 0, alpha = .2, size = 2) +
  geom_point(aes(size = total_iv_sess),
             shape = 15) +
  geom_errorbar(aes(ymin = CI_lower,
                    ymax = CI_upper),
                width = 0) +
  theme_bw() +
  coord_flip() +
  labs(x = "Participant Number within Study",
       y = "Log Resonse Ratio, Increase (LRR-i)",
       size = "Obs.") +
  theme(legend.position = "none") +
  facet_grid(study_name ~ .,
             space = "free",
             scale = "free") +
  theme(strip.text.y = element_text(angle = 360))
```

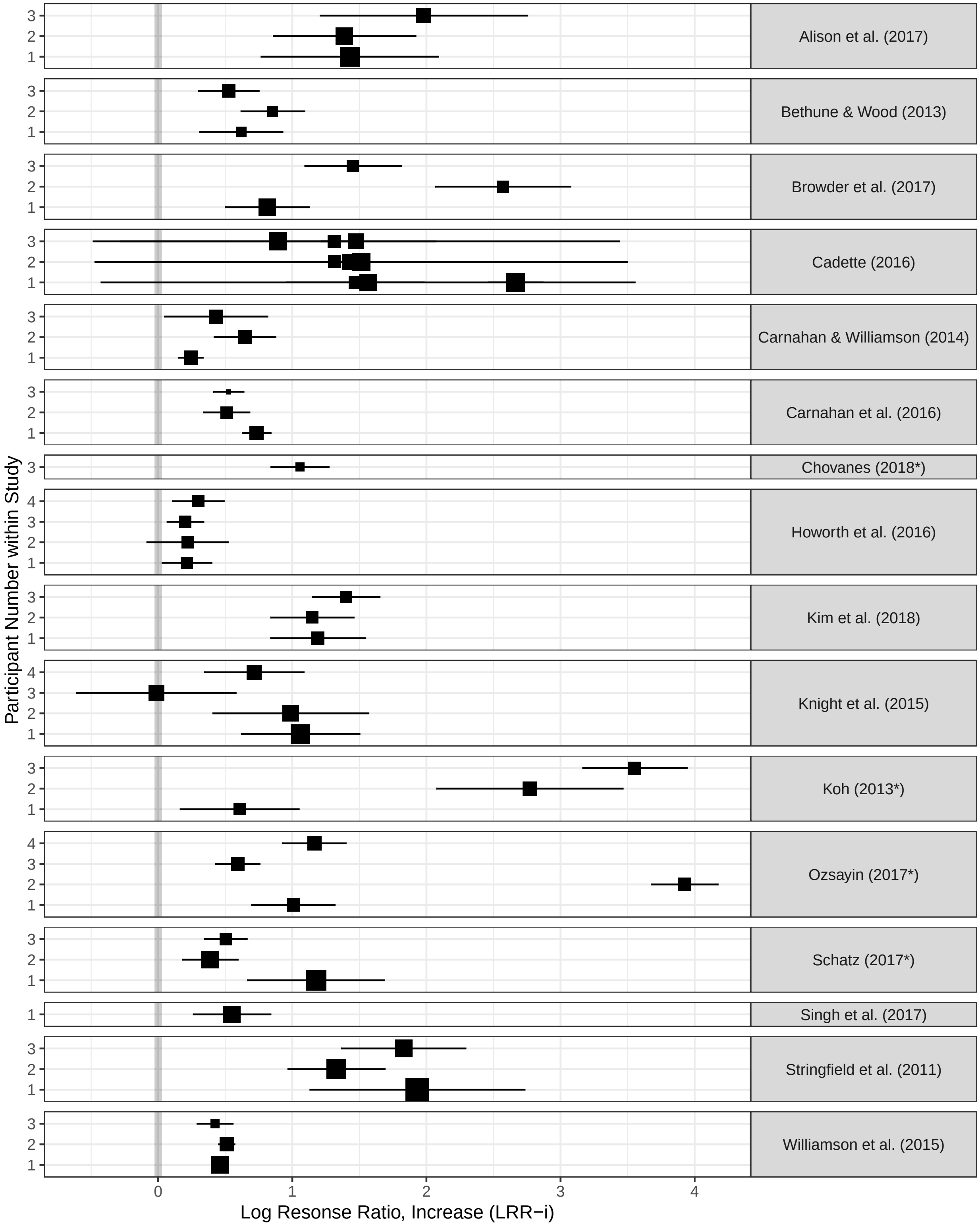

Figure 4: Forest Plot of Within-Case Effect Sizes: LRRi

3.2 Overall

Meta-Analysis via Multivariate/Multilevel Linear (Mixed-Effects) Models

```
meta_d <- data_lrr %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 1,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

The p-values and confidence intervals here use the z-distrubution (assume large sample)

```
summary(meta_d)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-61.9340  123.8680  129.8680  135.7218  130.3680

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2293  0.4788     16     no  study_name
sigma^2.2  0.4368  0.6609     53     no    personID

Test for Heterogeneity:
Q(df = 52) = 2051.4375, p-val < .0001

Model Results:

estimate      se    zval    pval   ci.lb   ci.ub
  1.0730  0.1569  6.8408  <.0001  0.7656  1.3804  ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Test all or selected regression coefficients in a fitted model `clubSandwich::coef_test` reports t-tests for each coefficient estimate in a fitted linear regression model, using a sandwich estimator for the standard errors and a small sample correction for the p-value. The small-sample correction is based on a Satterthwaite approximation or a saddlepoint approximation.

The p-value and confidence intervals here use the t-distribution with Satterthwaite degrees of freedom (small sample correction)

```
meta_d %>%
  clubSandwich::coef_test(vcov = "CR2",
                          test = "Satterthwaite") %>%
  dplyr::mutate(CI_L      = beta - SE * qt(.975, df = df),
                CI_U      = beta + SE * qt(0.975, df = df),
                per_change_est = 100*(exp(beta) - 1),
                per_change_95l = 100*(exp(CI_L) - 1),
                per_change_95u = 100*(exp(CI_U) - 1))
```

```
  Coef. Estimate    SE t-stat d.f. p-val (Satt) Sig.
1     1     1.07 0.157   6.84 14.5       <0.001  ***
```

```
with(meta_d, b[[1]] + c(-1,1) * sqrt(sigma2[1]))
```

```
[1] 0.5941832 1.5518028
```

```
with(meta_d, exp(b[[1]] + c(-1,1) * sqrt(sigma2[1])) - 1)
```

```
[1] 0.8115506 3.7199717
```

LRRi: The overall group contingencies was estimated as 1.07, 95% CI: [0.74, 1.41], which corresponds to an increase in comprehension of 192%, 95% CI: [109%, 309%].

The between-study variance in average effects was estimated as $\widehat{\tau^2} = 0.229$. This is a substantial degree of heterogeneity in effects across studies.

ADditionally, the within-study variance in individual-specific treatment effects was estimates as of $\widehat{\omega^2} = 0.437$, which is substantially larger than the between-study varaince.

3.3 Meta Regression: Test For Moderators

```
meta_regress_table <- function(fit_rma, cap = "Caption"){

  term_names <- rownames(fit_rma$beta)

  fit_rma %>%
  clubSandwich::coef_test(vcov = "CR2",
                          test = "Satterthwaite") %>%
  dplyr::mutate(CI_L           = beta - SE * qt(0.975, df = df),
                CI_U           = beta + SE * qt(0.975, df = df),
                per_change_est = 100*(exp(beta) - 1),
                per_change_95l = 100*(exp(CI_L) - 1),
                per_change_95u = 100*(exp(CI_U) - 1)) %>%
    dplyr::mutate(terms = term_names) %>%
    dplyr::select("Term"               = terms,
                  "Percent Increase" = per_change_est,
                  "Lower 95 CI"      = per_change_95l,
                  "Upper 95 CI"      = per_change_95u,
                  "Sig."             = p_Satt) %>%
    xtable::xtable(caption = cap,
                   digits = c(0, 0, 0, 0, 0, 3),
                   align = c("l", "l", "c", "r", "l", "r")) %>%
    print(booktabs = TRUE,
          comment = FALSE,
          include.rownames = FALSE,
          caption.placement = "top")
}
```

3.3.1 Overall

```
data_lrr %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

studies	cases
16	53

3.3.2 Published or Gray Literature

Without intercept

> *Note: For the Cadette (2016) paper, the 3 participants were measured on 3 outcomes and are treated as 9 separate cases*

```
data_lrr %>%
  dplyr::group_by(published) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

`summarise()` ungrouping output (override with `.groups` argument)

published	studies	cases
Gray Literature	4	11
Publication	12	42

```
meta_d_pub_int <- data_lrr %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 0 + published,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_pub_int)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-59.9387  119.8775  127.8775  135.6048  128.7471

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2004  0.4477     16     no  study_name
sigma^2.2  0.4383  0.6620     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 1857.9673, p-val < .0001

Test of Moderators (coefficients 1:2):
QM(df = 2) = 52.7004, p-val < .0001

Model Results:

                          estimate      se    zval    pval   ci.lb   ci.ub
publishedGray Literature    1.4697  0.3126  4.7021  <.0001  0.8571  2.0823  ***
publishedPublication        0.9531  0.1723  5.5309  <.0001  0.6153  1.2908  ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_pub_int,
                   cap = "Test for Moderators: Percent Increase in LRRi for Publication or Gray Literatu
```

Table 6: Test for Moderators: Percent Increase in LRRi for Publication or Gray Literature

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
publishedGray Literature	335	24	1420	0.034
publishedPublication	159	81	272	0.000

With intercept

```
meta_d_pub <- data_lrr %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 1 + published,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_pub)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-59.9387  119.8775  127.8775  135.6048  128.7471

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2004  0.4477     16     no  study_name
sigma^2.2  0.4383  0.6620     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 1857.9673, p-val < .0001

Test of Moderators (coefficient 2):
QM(df = 1) = 2.0952, p-val = 0.1478

Model Results:

                      estimate      se     zval    pval    ci.lb   ci.ub
intrcpt                 1.4697  0.3126   4.7021  <.0001   0.8571  2.0823  ***
publishedPublication   -0.5166  0.3569  -1.4475  0.1478  -1.2162  0.1829

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3.3.3 Race

```
data_lrr %>%
  dplyr::filter(race_ethnic %in% c("Asian", "Black", "Latino", "White")) %>%
  group_by(race_ethnic) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

`summarise()` ungrouping output (override with `.groups` argument)

race_ethnic	studies	cases
Latino	5	6
White	7	13
Black	6	12
Asian	2	4

```
meta_d_race <- data_lrr %>%
  dplyr::filter(race_ethnic %in% c("Asian", "Black", "Latino", "White")) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 0 + race_ethnic,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_race)
```

```
Multivariate Meta-Analysis Model (k = 35; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-39.7188   79.4376   91.4376  100.0415   94.9376

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.3051  0.5524     10     no  study_name
sigma^2.2  0.5220  0.7225     35     no    personID

Test for Residual Heterogeneity:
QE(df = 31) = 1031.4481, p-val < .0001

Test of Moderators (coefficients 1:4):
QM(df = 4) = 40.4074, p-val < .0001

Model Results:

                   estimate      se    zval    pval   ci.lb   ci.ub
race_ethnicLatino    1.1930  0.3824  3.1195  0.0018  0.4434  1.9425   **
race_ethnicWhite     1.7068  0.2930  5.8253  <.0001  1.1325  2.2811  ***
race_ethnicBlack     1.0433  0.3191  3.2697  0.0011  0.4179  1.6688   **
race_ethnicAsian     1.1126  0.5117  2.1742  0.0297  0.1097  2.1156    *
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_race,
                   cap = "Test for Moderators: Percent Increase in LRRi for Ethnicity")
```

Table 8: Test for Moderators: Percent Increase in LRRi for Ethnicity

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
race_ethnicLatino	230	38	688	0.018
race_ethnicWhite	451	126	1243	0.003
race_ethnicBlack	184	59	407	0.006
race_ethnicAsian	204	-51	1799	0.090

3.3.4 Age, continuous

```r
data_lrr %>%
  dplyr::filter(complete.cases(age)) %>%
  dplyr::summarise(studies = n_distinct(study_name),
                   cases = n()) %>%
  pander::pander()
```

studies	cases
16	53

```r
meta_d_age <- data_lrr %>%
  dplyr::filter(complete.cases(age)) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 1 + I(age - 12),
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```r
summary(meta_d_age)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-60.2512  120.5023  128.5023  136.2296  129.3719

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2121  0.4605     16     no  study_name
sigma^2.2  0.4399  0.6632     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 1899.4334, p-val < .0001

Test of Moderators (coefficient 2):
QM(df = 1) = 1.3709, p-val = 0.2417

Model Results:

             estimate      se     zval    pval    ci.lb   ci.ub
intrcpt        1.0591  0.1540   6.8793  <.0001   0.7574  1.3609  ***
I(age - 12)   -0.0565  0.0482  -1.1708  0.2417  -0.1510  0.0381

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
meta_regress_table(meta_d_age,
                   cap = "Test for Moderators: Percent Increase in LRRi for Age, years from 12")
```

Table 10: Test for Moderators: Percent Increase in LRRi for Age, years from 12

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
intrcpt	188	107	301	0.000
I(age - 12)	-5	-12	2	0.126

3.3.5 Age, categorical

```
data_lrr %>%
  dplyr::filter(complete.cases(age_cat)) %>%
  group_by(age_cat) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

`summarise()` ungrouping output (override with `.groups` argument)

age_cat	studies	cases
[6,12]	10	30
(12,18]	8	23

```
meta_d_age_cat <- data_lrr %>%
  dplyr::filter(complete.cases(age_cat)) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 0 + age_cat,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_age_cat)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-60.1635  120.3270  128.3270  136.0543  129.1965

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2013  0.4486     16     no  study_name
sigma^2.2  0.4427  0.6653     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 1926.3150, p-val < .0001

Test of Moderators (coefficients 1:2):
QM(df = 2) = 51.9858, p-val < .0001

Model Results:

                estimate      se    zval    pval   ci.lb   ci.ub
age_cat[6,12]     1.2246  0.1908  6.4170  <.0001  0.8506  1.5986  ***
age_cat(12,18]    0.8539  0.2269  3.7629  0.0002  0.4091  1.2987  ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_age_cat,
                   cap = "Test for Moderators: Percent Increase in LRRi for Age, over or under 12")
```

Table 12: Test for Moderators: Percent Increase in LRRi for Age, over or under 12

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
age_cat[6,12]	240	111	449	0.000
age_cat(12,18]	135	52	264	0.003

3.3.6 Diagnosis

```
data_lrr %>%
  dplyr::filter(complete.cases(dx)) %>%
  group_by(dx) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

`summarise()` ungrouping output (override with `.groups` argument)

dx	studies	cases
ASD	14	40
ASD+Other	3	13

```
meta_d_dx <- data_lrr %>%
  dplyr::filter(complete.cases(dx)) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 0 + dx,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_dx)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-60.8095  121.6190  129.6190  137.3463  130.4886

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2501  0.5001     16     no  study_name
sigma^2.2  0.4398  0.6632     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 1823.5441, p-val < .0001

Test of Moderators (coefficients 1:2):
QM(df = 2) = 44.2561, p-val < .0001

Model Results:

             estimate      se    zval    pval   ci.lb   ci.ub
dxASD          1.0748  0.1735  6.1939  <.0001  0.7347  1.4150  ***
dxASD+Other    1.0621  0.3695  2.8745  0.0040  0.3379  1.7864   **

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_dx,
                   cap = "Test for Moderators: Percent Increase in LRRi for Diagnosis")
```

Table 14: Test for Moderators: Percent Increase in LRRi for Diagnosis

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
dxASD	193	104	321	0.000
dxASD+Other	189	-36	1199	0.091

3.3.7 Cognative Ability

```
data_lrr %>%
  dplyr::filter(complete.cases(cog_ability)) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

studies	cases
7	19

```
data_lrr %>%
  dplyr::filter(complete.cases(cog_ability)) %>%
  dplyr::pull(cog_ability) %>%
  mean()
```

```
[1] 78.84211
```

```
meta_d_cog <- data_lrr %>%
  dplyr::filter(complete.cases(cog_ability)) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 1 + I((cog_ability - 82.4)/10),
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_cog)
```

```
Multivariate Meta-Analysis Model (k = 19; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-21.0714   42.1428   50.1428   53.4756   53.4761

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.4675  0.6838      7     no  study_name
sigma^2.2  0.4268  0.6533     19     no    personID

Test for Residual Heterogeneity:
QE(df = 17) = 364.7611, p-val < .0001

Test of Moderators (coefficient 2):
QM(df = 1) = 2.3602, p-val = 0.1245

Model Results:

                            estimate      se     zval    pval    ci.lb   ci.ub
intrcpt                       0.8765  0.3134   2.7969  0.0052   0.2623  1.4908
I((cog_ability - 82.4)/10)   -0.2087  0.1359  -1.5363  0.1245  -0.4750  0.0576

intrcpt                     **
I((cog_ability - 82.4)/10)
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_cog,
                   cap = "Test for Moderators: Percent Increase in LRRi for Cognative Ability, per 10 p
```

Table 16: Test for Moderators: Percent Increase in LRRi for Cognative Ability, per 10 points from 82.4 (M)

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
intrcpt	140	20	382	0.023
I((cog_ability - 82.4)/10)	-19	-39	8	0.106

3.3.8 Length of Intervention, Continuous

```r
data_lrr %>%
  dplyr::filter(complete.cases(total_iv_sess)) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

studies	cases
16	53

```r
data_lrr %>%
  dplyr::filter(complete.cases(total_iv_sess)) %>%
  dplyr::pull(total_iv_sess) %>%
  summary()
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      3       6       8       9      12      23
```

```r
meta_d_sess <- data_lrr %>%
  dplyr::filter(complete.cases(total_iv_sess)) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 1 + I((total_iv_sess - 9)),
                 V = var,
                 random = list(~ 1 | study_name,
                               ~ 1 | personID),
                 data = .)
```

```r
summary(meta_d_sess)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-60.5929  121.1858  129.1858  136.9131  130.0553

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2172  0.4660     16     no  study_name
sigma^2.2  0.4403  0.6636     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 2036.8481, p-val < .0001

Test of Moderators (coefficient 2):
QM(df = 1) = 1.0740, p-val = 0.3001

Model Results:

                        estimate      se    zval    pval    ci.lb   ci.ub
intrcpt                   1.0818  0.1548  6.9885  <.0001   0.7784  1.3852  ***
I((total_iv_sess - 9))    0.0330  0.0319  1.0363  0.3001  -0.0294  0.0955

---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_sess,
                   cap = "Test for Moderators: Percent Increase in LRRi for Duration of Intervention, se
```

Table 18: Test for Moderators: Percent Increase in LRRi for Duration of Intervention, session beyond 9

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
intrcpt	195	113	309	0.000
I((total_iv_sess - 9))	3	-2	9	0.156

3.3.9 Method Quality

```
data_lrr %>%
  dplyr::filter(complete.cases(wwc)) %>%
  dplyr::group_by(wwc) %>%
  summarise(studies = n_distinct(study_name),
            cases = n()) %>%
  pander::pander()
```

`summarise()` ungrouping output (override with `.groups` argument)

wwc	studies	cases
met with reservations	10	33
met fully	6	20

```
meta_d_wwc <- data_lrr %>%
  dplyr::filter(complete.cases(wwc)) %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ 0 + wwc,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .)
```

```
summary(meta_d_wwc)
```

```
Multivariate Meta-Analysis Model (k = 53; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-53.9822  107.9643  115.9643  123.6916  116.8339

Variance Components:

            estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.0000  0.0000     16     no  study_name
sigma^2.2  0.4346  0.6592     53     no    personID

Test for Residual Heterogeneity:
QE(df = 51) = 1062.3623, p-val < .0001

Test of Moderators (coefficients 1:2):
QM(df = 2) = 150.4114, p-val < .0001

Model Results:

                          estimate      se     zval    pval   ci.lb   ci.ub
wwcmet with reservations    1.4851  0.1259  11.7990  <.0001  1.2384  1.7318
wwcmet fully                0.5057  0.1511   3.3460  0.0008  0.2095  0.8020

wwcmet with reservations  ***
wwcmet fully              ***

---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
meta_regress_table(meta_d_wwc,
                   cap = "Test for Moderators: Percent Increase in LRRi for Method Quality, WWC")
```

Table 20: Test for Moderators: Percent Increase in LRRi for Method Quality, WWC

Term	Percent Increase	Lower 95 CI	Upper 95 CI	Sig.
wwcmet with reservations	342	221	508	0.000
wwcmet fully	66	35	104	0.002

3.3.10 Combine

```r
data_lrr %>%
  dplyr::mutate(var = SE^2) %>%
  metafor::rma.mv(Est ~ race_ethnic + age_cat + dx + wwc,
                  V = var,
                  random = list(~ 1 | study_name,
                                ~ 1 | personID),
                  data = .) %>%
  summary()
```

```
Multivariate Meta-Analysis Model (k = 36; method: REML)

  logLik  Deviance       AIC       BIC      AICc
-35.1603   70.3205   90.3205  103.6426  103.2617

Variance Components:

           estim    sqrt  nlvls  fixed      factor
sigma^2.1  0.2454  0.4954     10     no  study_name
sigma^2.2  0.5462  0.7391     36     no    personID

Test for Residual Heterogeneity:
QE(df = 28) = 739.7887, p-val < .0001

Test of Moderators (coefficients 2:8):
QM(df = 7) = 8.2507, p-val = 0.3110

Model Results:

                   estimate      se     zval    pval    ci.lb   ci.ub
intrcpt              1.3345  0.3843   3.4725  0.0005   0.5813  2.0878  ***
race_ethnicWhite     0.6073  0.4520   1.3435  0.1791  -0.2786  1.4932
race_ethnicBlack     0.0074  0.4446   0.0167  0.9867  -0.8639  0.8787
race_ethnicAsian    -0.0260  0.6365  -0.0408  0.9674  -1.2735  1.2216
race_ethnicIndian   -1.0231  0.8648  -1.1830  0.2368  -2.7181  0.6720
age_cat(12,18]      -0.1072  0.5152  -0.2081  0.8351  -1.1171  0.9026
dxASD+Other         -0.0798  0.6650  -0.1199  0.9045  -1.3832  1.2237
wwcmet fully        -0.8571  0.5566  -1.5401  0.1235  -1.9480  0.2337

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4 Package Citations

```r
citation() %>% print(bibtex = FALSE)
```

```
To cite R in publications use:

  R Core Team (2020). R: A language and environment for statistical
  computing. R Foundation for Statistical Computing, Vienna, Austria.
  URL https://www.R-project.org/.

We have invested a lot of time and effort in creating R, please cite it
when using it for data analysis. See also 'citation("pkgname")' for
citing R packages.
```

```r
citation("scdhlm") %>% print(bibtex = FALSE)
```

```
James E. Pustejovsky (2016). _scdhlm: Estimating hierarchical linear
models for single-case designs_. University of Texas at Austin, Austin,
TX. R package version 0.3, <URL: http://github.com/jepusto/scdhlm>.
```

```r
citation("robumeta") %>% print(bibtex = FALSE)
```

```
To cite package 'robumeta' in publications use:

  Zachary Fisher, Elizabeth Tipton and Hou Zhipeng (2017). robumeta:
  Robust Variance Meta-Regression. R package version 2.0.
  https://CRAN.R-project.org/package=robumeta
```

```r
citation("SingleCaseES") %>% print(bibtex = FALSE)
```

```
To cite package 'SingleCaseES' in publications use:

  James E. Pustejovsky and Daniel M. Swan (2019). SingleCaseES: A
  Calculator for Single-Case Effect Sizes. R package version 0.4.3.
  https://CRAN.R-project.org/package=SingleCaseES
```

```r
citation("metafor") %>% print(bibtex = FALSE)
```

```
To cite the metafor package in publications, please use:

  Viechtbauer, W. (2010). Conducting meta-analyses in R with the
  metafor package. Journal of Statistical Software, 36(3), 1-48. URL:
  https://www.jstatsoft.org/v36/i03/
```

```r
citation("clubSandwich") %>% print(bibtex = FALSE)
```

```
To cite package 'clubSandwich' in publications use:

  James Pustejovsky (2020). clubSandwich: Cluster-Robust (Sandwich)
  Variance Estimators with Small-Sample Corrections. R package version
  0.5.0. https://CRAN.R-project.org/package=clubSandwich
```