Simulate effect sizes

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Introduction

In this report, we look at estimators for the population effect at the meta-analysis level. We generate effect sizes at the study level and then fit a random effects model. We estimate the between study heterogeneity using the DerSimonian & Laird estimator, the Hedges' estimator and Restricted Maximum Likelihood. These estimates are used to estimate the population effect. We will increase the amount of between-study heterogeneity to see its effect on the estimates of the population effect.

Data generating model

Consider an observed (standardized) effect Y_i for study $i = 1, \ldots, K$. We assume the following model:

$$Y_i = X\beta + u_i + \varepsilon_i,$$

where

$$u_i \sim N\left(0, \sigma_*^2\right) \varepsilon_i \sim N\left(0, \sigma_i^2\right).$$

Here β represents the population effect, X the design matrix at the meta-analysis level, u a random effect and ε a within-study error. Note that X will be a vector of length K with 1's.

Model parameters

We set $\beta = 0.9$ and let the between-study variance (σ_*^2) increase in 4 Monte-Carlo simulation settings. More particularly, we have: $\sigma_*^2 \in \{0, 1, 4, 9\}$. We set the number of studies K to 500.

```
# True ES
Tes <- 0.9
# Number of studies
nstud <- 500
# X vector of 1's
X <- matrix(1, nrow = nstud)
# Between study variability
sigm2U <- c(0, 1, 4, 9)</pre>
```

To select the within-study variance components of each study, we do the following. First we sample a number of subjects for each study. This is a number between 100 and 300. Using this sample size and the true value for β (the population effect size), we calculate the true within-study variance for each study (i.e. σ_i^2).

```
# Sample number of subjects
nsubS <- sample(x = 100:300, size = nstud, replace = TRUE)
# Alternative: each study the same sample size
#nsubS <- rep(30, nstud)
# Calculate true value for the variance
sigm2E <- NeuRRoStat::varHedgeT(g = Tes, N = nsubS)</pre>
```

Note that we have a large number of subjects and studies which is needed to see if we have unbiased estimates.

Model estimation

We use the **R** package metafor to fit the random-effects models. To esimate σ_*^2 , we will use the DerSimonian & Laird esimator, the Hedges' estimator and a Restricted Maximimum Likelihood approach. Note that the model fitting procedure uses weights where these are the inverse of the sum of the within- and estimated between-study variability. Furthermore, we use the NeuRRoStat package to estimate σ_*^2 with the DerSimonian & Laird estimator. However, I checked its result and it is equal to the one using the metafor package.

Monte-Carlo

Settings

We set the number of simulations to 10.00.

```
# Number of simulations
nsim <- 1000</pre>
```

We loop over the 4 possible values for the between-study herogeneity. The following code in \mathbf{R} is an example of one simulation iteration for one value for σ_*^2 (e.g. j=1). We generate K effect sizes, then calculate the within-study variance (using the formula of Hedges) of each effect size.

```
# Generate data
Y <- X %*% Tes + rnorm(n = nstud, mean = 0, sd = sqrt(sigm2U[j])) +
   rnorm(n = nstud, mean = 0, sd = sqrt(sigm2E))

# Weights of each study
vi <- NeuRRoStat::varHedgeT(g = Y, N = nsubS)</pre>
```

Execution

Here we run the simulation.

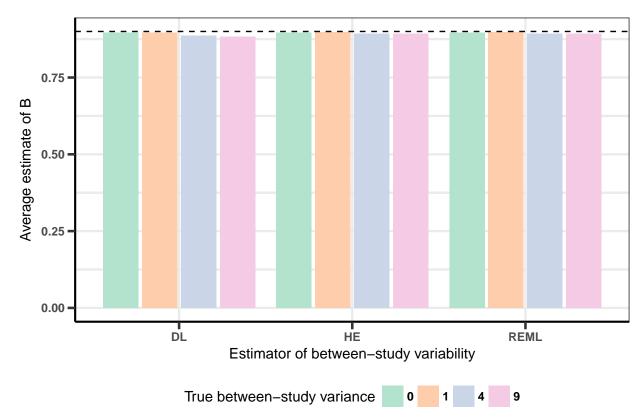
```
# Empty data frame
results <- data.frame() %>%
  as tibble()
# For loop over the simulations
for(i in 1:nsim){
  # For loop over the amount of between-study heterogeneity
  for(j in 1:length(sigm2U)){
    # Generate data
    Y \leftarrow X \%\% Tes + rnorm(n = nstud, mean = 0, sd = sqrt(sigm2U[j])) +
      rnorm(n = nstud, mean = 0, sd = sqrt(sigm2E))
    # Weights of each study
    vi <- NeuRRoStat::varHedgeT(g = Y, N = nsubS)</pre>
    # Fit the model using rma + HE or REML estimator for tau2
    fitHE <- metafor::rma(yi = Y, vi = vi, method = 'HE')
    fitREML <- metafor::rma(yi = Y, vi = vi, method = 'REML')</pre>
    # Between study variability: DL estimator
    tau2_DL <- NeuRRoStat::tau(Y = Y, W = (1/vi), k = length(Y))</pre>
    # HE estimator
```

```
tau2_HE <- c(fitHE$tau2)</pre>
    # REML estimator
    tau2_REML <- c(fitREML$tau2)</pre>
    # Weights
    W <- diag(c(1/(vi + tau2_DL)))</pre>
    # Estimate for B using various estimators for tau
    \# First one = DerSimonian and Laird
    B_DL \leftarrow EstB(X = X, W = W, Y = Y)
      # controle: rma(yi = Y, vi = vi, method = 'DL') \longrightarrow klopt
    # One using Hedges
    B HE <- c(fitHE$beta)
    # One using REML
    B_REML <- c(fitREML$beta)</pre>
    # Save in data frame
    results <- data.frame('B' = c(B_DL, B_HE, B_REML),
               'TrueB' = Tes,
               'tau2' = c(tau2_DL, tau2_HE, tau2_REML),
               'TrueTau2' = sigm2U[j],
               'estimatorBS' = c('DL', 'HE', 'REML')
                ) %>% as_tibble() %>%
      bind_rows(results, .)
  }
}
```

Results

Estimator for population effect

We will first plot the average (over all simulations) of the estimates for β . We do this for each value of between-study variability and each of the three estimators for the latter. The dashed line corresponds to the true value of β .



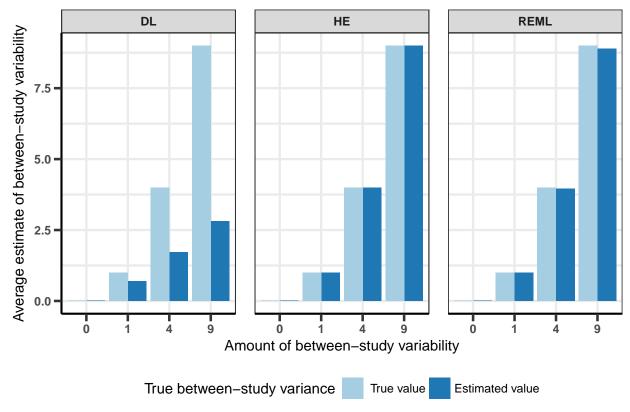
Averaged over 1000 simulations. Dashed line = true value.

It seems to be off using DL!

```
results %>%
  group_by(estimatorBS, TrueTau2) %>%
  summarise(AvgEstB = mean(B),
            TrueB = mean(TrueB))
# A tibble: 12 x 4
# Groups:
            estimatorBS [?]
   estimatorBS TrueTau2 AvgEstB TrueB
   <fct>
                   <dbl>
                            <dbl> <dbl>
 1 DL
                       0
                            0.895
                                    0.9
 2 DL
                           0.895
                                    0.9
                       1
 3 DL
                       4
                           0.887
                                    0.9
 4 DL
                       9
                           0.883
                                    0.9
 5 HE
                       0
                           0.895
                                    0.9
 6 HE
                       1
                           0.898
                                    0.9
 7 HE
                           0.893
                                    0.9
 8 HE
                       9
                           0.893
                                    0.9
 9 REML
                       0
                           0.895
                                    0.9
10 REML
                       1
                           0.898
                                    0.9
11 REML
                       4
                           0.893
                                    0.9
12 REML
                            0.893
                                    0.9
```

Estimator for between-study variance

We repeat the same for the estimates of between-study variability.



Averaged over 1000 simulations.

In a table, we have:

```
results %>%
  dplyr::select(-B,-TrueB) %>%
  group_by(TrueTau2, estimatorBS) %>%
  summarise(AvgEstTau2 = mean(tau2))
# A tibble: 12 \times 3
# Groups:
            TrueTau2 [?]
   TrueTau2 estimatorBS AvgEstTau2
      <dbl> <fct>
                              <dbl>
 1
          O DL
                           0.000170
          O HE
 2
                           0.000192
 3
          O REML
                           0.000175
 4
          1 DL
                           0.689
5
          1 HE
                           1.00
 6
          1 REML
                           0.990
 7
          4 DL
                           1.72
 8
          4 HE
                           4.00
9
          4 REML
                           3.95
          9 DL
                           2.81
10
                           8.99
          9 HE
11
12
          9 REML
                           8.89
```