Chapter 4

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library(dmetar)
library(esc)
library(tidyverse)
```

The fixed effect model (FEM)

Assumes that all effect sizes come from the same population. If they differ, than only because of the sampling error ϵ_k. If all studies would survey the whole population all effect sizes would be the same

$$\hat{\theta}_k = \theta + \epsilon_k$$

We should give studies with higher precision (less error) more weight

If we want to calculate the pooled effect size under the fixed-effect model, we therefore simply use a weighted average of all studies. That is why it is also often called an inverse-variance meta-analysis.

$$w_k = \frac{1}{s_k^2}$$

$$\hat{\theta} = \frac{\sum_{k=1}^{K} \hat{\theta}_k w_k}{\sum_{k=1}^{K} w_k}$$

```
# Load data set from dmetar
data(SuicidePrevention)

# Calculate Hedges' g and the Standard Error
# - We save the study names in "study".
# - We use the pmap_dfr function to calculate the effect size
#   for each row.
SP_calc <- pmap_dfr(SuicidePrevention,
                    function(mean.e, sd.e, n.e, mean.c,
                             sd.c, n.c, author, ...){
                      esc_mean_sd(grp1m = mean.e,
                                  grp1sd = sd.e,
                                  grp1n = n.e,
                                  grp2m = mean.c,
                                  grp2sd = sd.c,
                                  grp2n = n.c,
                                  study = author,
                                  es.type = "g") %>%
                        as.data.frame()})

SP_calc |>
  mutate(w = 1/SP_calc$se^2) |>
  summarise(g = sum(w*es)/sum(w))
```

```
          g
1 -0.2311121
```

The random effects model (REM)