

## Location-Scale Models for Meta-Analysis Using the metafor Package

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1

## Standard Meta-Analysis

- goal: estimate the size of the (average) effect
- random-effects model:

$$y_i = \mu + u_i + \varepsilon_i$$

for  $i = 1, \dots, k$ , where  $u_i \sim N(0, \tau^2)$  and  $\varepsilon_i \sim N(0, v_i)$

- **sampling variance:**
  - denoted by  $v_i$
  - variance in the estimates around their true effects
  - heteroscedastic by construction
- **heterogeneity:**
  - denoted by  $\tau^2$
  - variance in the true effects
  - assumed to be homoscedastic

2

## Standard Meta-Analysis

- can fit this model with the [metafor](#) package (Viechtbauer, 2010)
- ```
# install the metafor package
install.packages("metafor")
```
- example: meta-analysis on the effectiveness of the BCG vaccine against tuberculosis (Colditz et al. 1994)
- studies report number of TB+ and TB- cases for the treated (vaccinated) and control (non-vaccinated) groups
- will use this information to compute (log-transformed) risk ratios and corresponding sampling variances

3

## Example: BCG Vaccine Meta-Analysis

```
# load the metafor package
library(metafor)

# look at the BCG dataset
dat.bcg

## trial      author year tpos  tneg cpos  cneg ablat  alloc
## 1          Aronson 1948   4   119  11  128  44  random
## 2  Ferguson & Simes 1949   6   300  29  274  55  random
## 3  Rosenthal et al 1960   3   228  11  209  42  random
## 4  Hart & Sutherland 1977  62 13536 248 12619 52  random
## 5  Frimodt-Moller et al 1973  33  5036  47  5761  13  alternate
## 6  Stein & Aronson 1953  180 1361 372 1079  44  alternate
## 7  Vandiviere et al 1973   8  2537  10  619  19  random
## 8  TPT Madras 1980  505 87886 499 87892 13  random
## 9  Coetzee & Berjak 1968  29  7470  45  7232  27  random
## 10 Rosenthal et al 1961  17  1699  65  1600  42  systematic
## 11  Comstock et al 1974  186 50448 141 27197 18  systematic
## 12  Comstock & Webster 1969   5  2493   3  2338  33  systematic
## 13  Comstock et al 1976  27 16886  29 17825  33  systematic
```

4

## Example: BCG Vaccine Meta-Analysis

```
# calculate log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=tpos, bi=tneg,
             ci=cpos, di=cneg, data=dat.bcg)

dat

## trial      author year ...  alloc  yi  vi
## 1          Aronson 1948 ...  random -0.8893 0.3256
## 2  Ferguson & Simes 1949 ...  random -1.5854 0.1946
## 3  Rosenthal et al 1960 ...  random -1.3481 0.4154
## 4  Hart & Sutherland 1977 ...  random -1.4416 0.0200
## 5  Frimodt-Moller et al 1973 ...  alternate -0.2175 0.0512
## 6  Stein & Aronson 1953 ...  alternate -0.7861 0.0069
## 7  Vandiviere et al 1973 ...  random -1.6209 0.2230
## 8  TPT Madras 1980 ...  random 0.0120 0.0040
## 9  Coetzee & Berjak 1968 ...  random -0.4694 0.0564
## 10 Rosenthal et al 1961 ...  systematic -1.3713 0.0730
## 11  Comstock et al 1974 ...  systematic -0.3394 0.0124
## 12  Comstock & Webster 1969 ...  systematic 0.4459 0.5325
## 13  Comstock et al 1976 ...  systematic -0.0173 0.0714
```

5

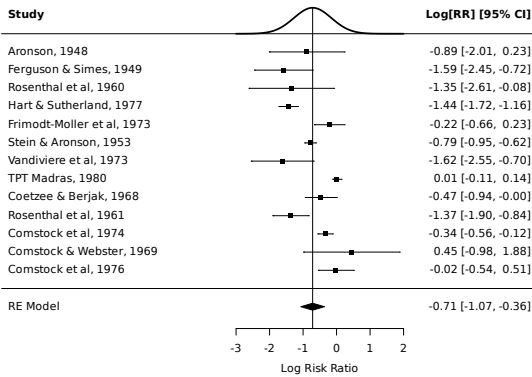
## Example: BCG Vaccine Meta-Analysis

```
# fit random-effects model (using log risk ratios and variances as input)
res <- rma(yi, vi, data=dat)
res

## Random-Effects Model (k = 13; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.3132
## tau (square root of estimated tau^2 value): 0.5597
## I^2 (total heterogeneity / total variability): 92.22%
## H^2 (total variability / sampling variability): 12.86
##
## Test for Heterogeneity:
## Q(df = 12) = 152.2330, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.7145  0.1798  -3.9744  <.0001  -1.0669  -0.3622
```

6

## Example: BCG Vaccine Meta-Analysis



7

## Meta-Regression Model

- random-effects model extended to (simple) meta-regression:

$$y_i = \beta_0 + \beta_1 x_i + u_i + \varepsilon_i$$

- of course there can be multiple moderators
- simple example: say the studies fall into two subgroups (e.g., randomized versus non-randomized studies)
- let  $x_i = 0$  for the first group (e.g., non-randomized)
- $x_i = 1$  for the second group (e.g., randomized)

8

## Example: BCG Vaccine Meta-Analysis

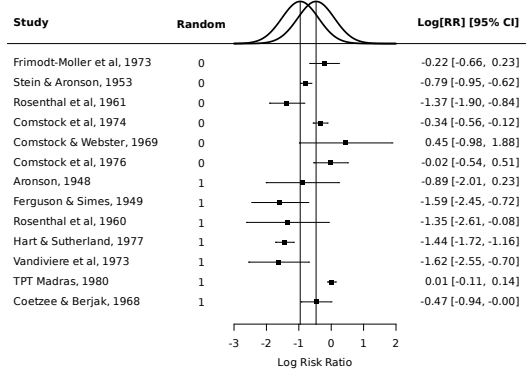
```
# dichotomize 'alloc' variable
dat$random <- ifelse(dat$alloc == "random", 1, 0)

# fit meta-regression model
res <- rma(yi, vi, mods = ~ random, data=dat)
res

## Mixed-Effects Model (k = 13; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity): 0.3184
## tau (square root of estimated tau^2 value): 0.5642
## R^2 (amount of heterogeneity accounted for): 0.00%
##
## [...]
##
## Model Results:
##
## estimate se zval pval ci.lb ci.ub
## intrcpt -0.4673 0.2574 -1.8157 0.0694 -0.9717 0.0371
## random -0.4900 0.3619 -1.3538 0.1758 -1.1994 0.2194
```

9

## Example: BCG Vaccine Meta-Analysis



10

## Meta-Analytic Location-Scale Model

- the assumption that  $\tau^2$  is homoscedastic may not be true
- can allow variance in the true effects to be a function of the study characteristics

- meta-analytic location-scale model:

$$y_i = \beta_0 + \beta_1 x_i + u_i + \varepsilon_i$$

where  $u_i \sim N(0, \tau_i^2)$  and  $\varepsilon_i \sim N(0, v_i)$  and where

$$\ln(\tau_i^2) = \alpha_0 + \alpha_1 z_i$$

- $x_i$ : location variable;  $z_i$ : scale variable
- $x_i$  may or may not be the same as  $z_i$
- and again there can be multiple location and/or scale variables
- metafor can fit such models (Viechtbauer & López-López, 2022)

11

## Example: BCG Vaccine Meta-Analysis

```
# fit meta-analytic location-scale model
res <- rma(yi, vi, mods = ~ random, scale = ~ random, data=dat)
res

## Location-Scale Model (k = 13; tau^2 estimator: REML)
##
## Model Results (Location):
##
## estimate se zval pval ci.lb ci.ub
## intrcpt -0.4813 0.2170 -2.2180 0.0266 -0.9066 -0.0560
## random -0.4897 0.3510 -1.3949 0.1630 -1.1777 0.1983
##
## Model Results (Scale):
##
## estimate se zval pval ci.lb ci.ub
## intrcpt -1.5532 0.9085 -1.7097 0.0873 -3.3337 0.2274
## random 0.6180 1.1327 0.5456 0.5853 -1.6020 2.8381
```

12

## Example: BCG Vaccine Meta-Analysis

- estimated  $\tau^2$  for non-randomized studies:

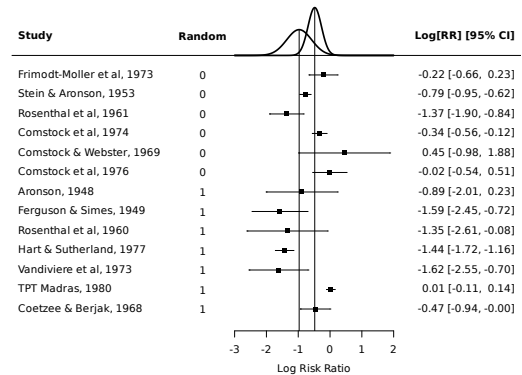
$$\exp(\alpha_0) = \exp(-1.5532) = 0.2116$$

- estimated  $\tau^2$  for randomized studies:

$$\exp(\alpha_0 + \alpha_1) = \exp(-1.5532 + 0.6180) = 0.3925$$

13

## Example: BCG Vaccine Meta-Analysis



14

## Subgrouping

- the model above yields identical results to fitting separate random-effects models within the two subgroups

```
# fit separate random-effects models within subgroups
res <- list(rma(yi, vi, data=dat, subset=random==0),
           rma(yi, vi, data=dat, subset=random==1))
tab <- data.frame(k = sapply(res, \(x) x$k),
                 estimate = sapply(res, coef),
                 se = sqrt(sapply(res, vcov)),
                 tau2 = sapply(res, \(x) x$tau2))
rownames(tab) <- c("non-random", "random")
round(tab, digits=4)

##          k estimate      se tau2
## non-random 6 -0.4813 0.2170 0.2116
## random      7 -0.9710 0.2760 0.3925
```

15

## Location-Scale Models in General

- the location-scale model is much more flexible
- can include none, one, or multiple location and scale variables
- location and scale variables can also be different
- variables can be categorical (subgroups) or quantitative
- allows testing if amount of heterogeneity is related to a scale variable or differs across subgroups (Wald-type test, likelihood ratio test, and permutation test)
- for example,  $H_0: \alpha_1 = 0$  in the example above is the same as testing  $H_0: \tau_{\text{non-random}}^2 = \tau_{\text{random}}^2$

16

## Testing Scale Variables

```
# Wald-type test
res1 <- rma(yi, vi, mods = ~ random, scale = ~ random, data=dat)
res1

##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt -1.5532 0.9085 -1.7097 0.0873 -3.3337 0.2274
## random   0.6180 1.1327  0.5456 0.5853 -1.6020 2.8381

# likelihood ratio test
res0 <- rma(yi, vi, mods = ~ random, scale = ~ 1, data=dat)
anova(res0, res1)

##          df      AIC      BIC      AICc      logLik      LRT      pval      QE
## Full      4 29.2959 30.8875 35.9626 -10.6480      138.5113
## Reduced   3 27.5948 28.7885 31.0234 -10.7974  0.2989 0.5845 138.5113

# permutation test
permutest(res1, seed=1234)

##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt -1.5532 0.9085 -1.7097 0.1830 -3.3337 0.2274
## random   0.6180 1.1327  0.5456 0.4840 -1.6020 2.8381
```

17

## A More Elaborate Example

- Bangert-Drowns et al. (2004) meta-analyzed  $k = 48$  studies examining the effectiveness of a particular intervention for improving educational achievement
- effect sizes are given as standardized mean differences
- studies differed in their size (from  $n = 16$  to  $n = 542$ ) and in the subject matter examined (mathematics:  $k = 28$ , science:  $k = 9$ , social science:  $k = 11$ )

18

## A More Elaborate Example

```
# fit meta-analytic location-scale model
res <- rma(yi, vi, mods = ~ subj + ni, scale = ~ subj + ni, data=dat)
res

## Location-Scale Model (k = 48; tau^2 estimator: REML)
##
## Model Results (Location):
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt    0.3443  0.0673   5.1179 <.0001   0.2124   0.4761
## subjSci   -0.0798  0.2040  -0.3912  0.6957  -0.4796   0.3200
## subjSoc   -0.1087  0.0829  -1.3121  0.1895  -0.2711   0.0537
## ni        -0.0006  0.0002  -2.8836  0.0039  -0.0010  -0.0002
##
## Model Results (Scale):
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt  -3.1022  0.9911  -3.1302  0.0017  -5.0447  -1.1598
## subjSci   2.2330  1.0474   2.1319  0.0330   0.1801   4.2860
## subjSoc   0.4011  1.4021   0.2861  0.7748  -2.3470   3.1492
## ni        -0.0054  0.0057  -0.9506  0.3418  -0.0165   0.0057
```

19

## A More Elaborate Example

- results suggest that:
  - larger studies tended to yield smaller effects
  - studies examining the effectiveness of the intervention on educational achievement in science subjects tended to yield more heterogeneous effects (but no evidence that the average effect itself differed for science subjects)

20

## Final Comments / Future Outlook

- location-scale models open up the possibility to examine entirely new research questions
- but tend to require larger  $k$  to obtain meaningful answers
- currently examining differences in performance of Wald-type, likelihood ratio, and permutation tests
- consider extending the possibility to fit such models to the `rma.mv()` function (for multilevel/multivariate models)

21

## References

- Bangert-Drowns, R. L., Hurlley, M. M., & Wilkinson, B. (2004). The effects of school-based writing-to-learn interventions on academic achievement: A meta-analysis. *Review of Educational Research*, 74(1), 29–58. <https://doi.org/10.3102/00346543074001029>
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- Viechtbauer, W. (2010). Conducting meta-analyses in R with the metafor package. *Journal of Statistical Software*, 36(3), 1–48. <https://doi.org/10.18637/jss.v036.i03>
- Viechtbauer, W., & López-López, J. A. (2022). Location-scale models for meta-analysis. *Research Synthesis Methods*, 13(6), 697–715. <https://doi.org/10.1002/jrsm.1562>

22

# Thank You for Your Attention!

Questions, Comments, Suggestions?

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23