

SREE 2024: Science example

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```
library(metaselection)
library(metadat)
library(metafor)
```

```
## Warning: package 'metafor' was built under R version 4.4.3
```

```
## Loading required package: Matrix
```

```
## Loading required package: numDeriv
```

```
##
```

```
## Loading the 'metafor' package (version 4.8-0). For an
## introduction to the package please type: help(metafor)
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.1      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.1
## v purrr      1.0.2
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## x tidyr::pack()    masks Matrix::pack()
## x tidyr::unpack() masks Matrix::unpack()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(here)
```

```
## Warning: package 'here' was built under R version 4.4.3
```

```
## here() starts at C:/GitHub/metaselection
```

```
devtools::load_all()
```

```
## i Loading metaselection
```

Science Meta-analysis

```
sci <- read_csv(here('tests/testdata', 'ScienceMeta.csv'))
```

```
## Rows: 292 Columns: 40
## -- Column specification -----
## Delimiter: ","
## chr (11): es_id, short_cite, long_cite, intervention_delivery, intervention...
## dbl (29): study_id, yi, vi, sci_hs_bio, sci_hs_chem, sci_hs_phys, sci_k8_lif...
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
sci <- sci |>
  rename(esid = es_id, studyid = study_id) |>
  mutate(
    d = yi,
    Va = vi,
    Var_d = Va,
    sd_d = sqrt(Var_d),
    var_d = Var_d,
    p_onesided = 1 - pnorm(d / sd_d)
  )
```

Unadjusted estimate: mean only

```
sci_unadj_mean <- rma.uni(
  data = sci,
  yi = d,
  sei = sd_d,
  method = "ML"
)
sci_unadj_mean
```

```
##
## Random-Effects Model (k = 292; tau^2 estimator: ML)
##
## tau^2 (estimated amount of total heterogeneity): 0.1421 (SE = 0.0189)
## tau (square root of estimated tau^2 value): 0.3770
## I^2 (total heterogeneity / total variability): 68.18%
## H^2 (total variability / sampling variability): 3.14
##
```

```
## Test for Heterogeneity:
## Q(df = 291) = 915.8432, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.4402 0.0285 15.4445 <.0001 0.3844 0.4961 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

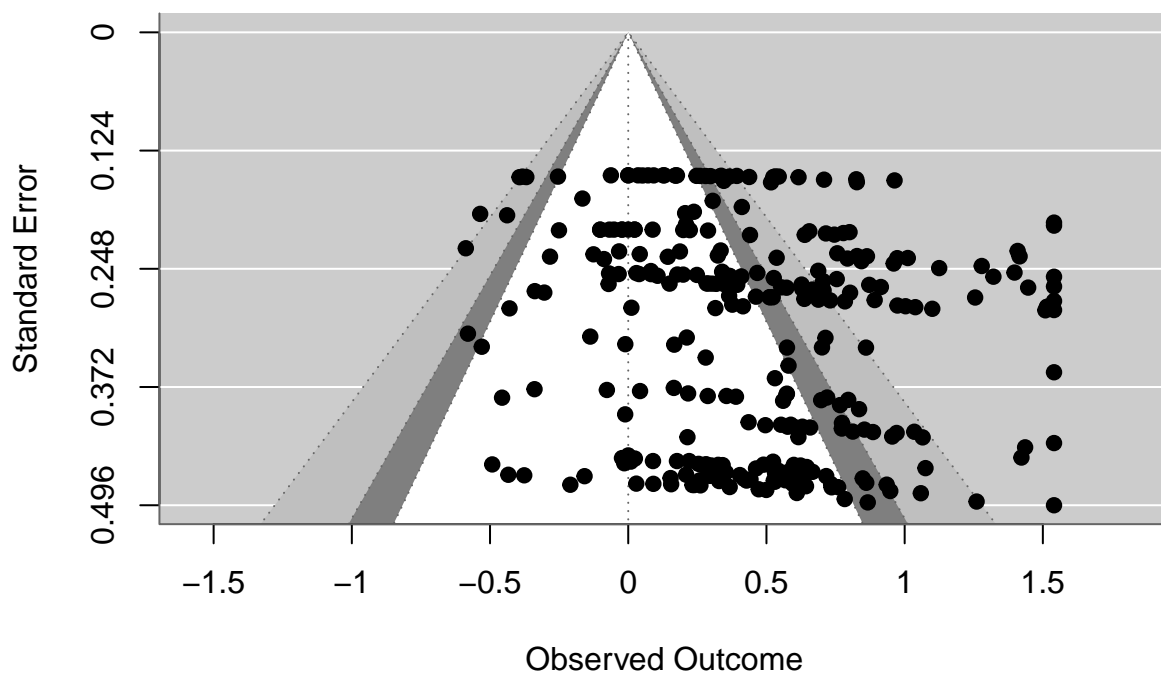
```
sci_unadj_mean_cil <- sci_unadj_mean$tau2 - 1.96*sci_unadj_mean$se.tau2
sci_unadj_mean_ciu <- sci_unadj_mean$tau2 + 1.96*sci_unadj_mean$se.tau2
sci_unadj_mean_cil; sci_unadj_mean_ciu
```

```
## [1] 0.1050343
```

```
## [1] 0.1792096
```

Forest plot

```
funnel(sci_unadj_mean, reline = 0, level = c(90, 95, 99))
```



Unadjusted estimate: moderator

```
sci_unadj_mod <- rma.uni(  
  data = sci,  
  yi = d,  
  sei = sd_d,  
  method = "ML",  
  mods = ~ outcome_type_author  
)  
sci_unadj_mod
```

```
##  
## Mixed-Effects Model (k = 292; tau^2 estimator: ML)  
##  
## tau^2 (estimated amount of residual heterogeneity):      0.1421 (SE = 0.0189)  
## tau (square root of estimated tau^2 value):             0.3770  
## I^2 (residual heterogeneity / unaccounted variability): 68.13%  
## H^2 (unaccounted variability / sampling variability):    3.14  
## R^2 (amount of heterogeneity accounted for):             0.01%  
##  
## Test for Residual Heterogeneity:  
## QE(df = 290) = 915.4359, p-val < .0001  
##  
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 1.8224, p-val = 0.1770  
##  
## Model Results:  
##  
##              estimate      se    zval    pval    ci.lb    ci.ub  
## intrcpt           0.3758  0.0556  6.7637 <.0001   0.2669   0.4848 ***  
## outcome_type_author 0.0874  0.0647  1.3500  0.1770  -0.0395   0.2143  
##  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sci_unadj_mod_cil <- sci_unadj_mod$tau2 - 1.96*sci_unadj_mod$se.tau2  
sci_unadj_mod_ciu <- sci_unadj_mod$tau2 + 1.96*sci_unadj_mod$se.tau2  
sci_unadj_mod_cil; sci_unadj_mod_ciu
```

```
## [1] 0.1050231
```

```
## [1] 0.1791935
```

Adjusted estimate in metafor: Beta model

```
sci_adj_mf <- selmodel(  
  x = sci_unadj_mod,  
  type = "beta",
```

```

steps = c(0.025, 0.975),
control=list(optimizer="nlminb"),
#verbose = "TRUE"
)

## Warning: Error when trying to invert the Hessian.

sci_adj_mf

##
## Mixed-Effects Model (k = 292; tau^2 estimator: ML)
##
## tau^2 (estimated amount of residual heterogeneity): 0.2158
## tau (square root of estimated tau^2 value):      0.4645
##
## Test for Residual Heterogeneity:
## LRT(df = 1) = 340.8744, p-val < .0001
##
## Model Results:
##
##               estimate   se   zval   pval   ci.lb   ci.ub
## intrcpt             0.2100  NA     NA     NA     NA     NA
## outcome_type_author  0.1403  NA     NA     NA     NA     NA
##
## Test for Selection Model Parameters:
## LRT(df = 2) = 9.8614, p-val = 0.0072
##
## Selection Model Results:
##
##           estimate   se   zval   pval   ci.lb   ci.ub
## delta.1      1.0947  NA     NA     NA     NA     NA
## delta.2      1.5772  NA     NA     NA     NA     NA
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

sci_adj_mf_cil <- sci_adj_mf$tau2 - 1.96*sci_adj_mf$se.tau2
sci_adj_mf_ciu <- sci_adj_mf$tau2 + 1.96*sci_adj_mf$se.tau2
sci_adj_mf_cil; sci_adj_mf_ciu

## [1] NA

## [1] NA

```

Adjusted estimate in metaselection: Beta model mean only

```

sci_adj_ms_mean <- selection_model(
  dat = sci,

```

```

yi = d,
sei = sd_d,
pi = p_onesided,
cluster = studyid,
selection_type = "beta",
steps = c(.025,.975),
make_sandwich = TRUE
)
sci_adj_ms_mean

```

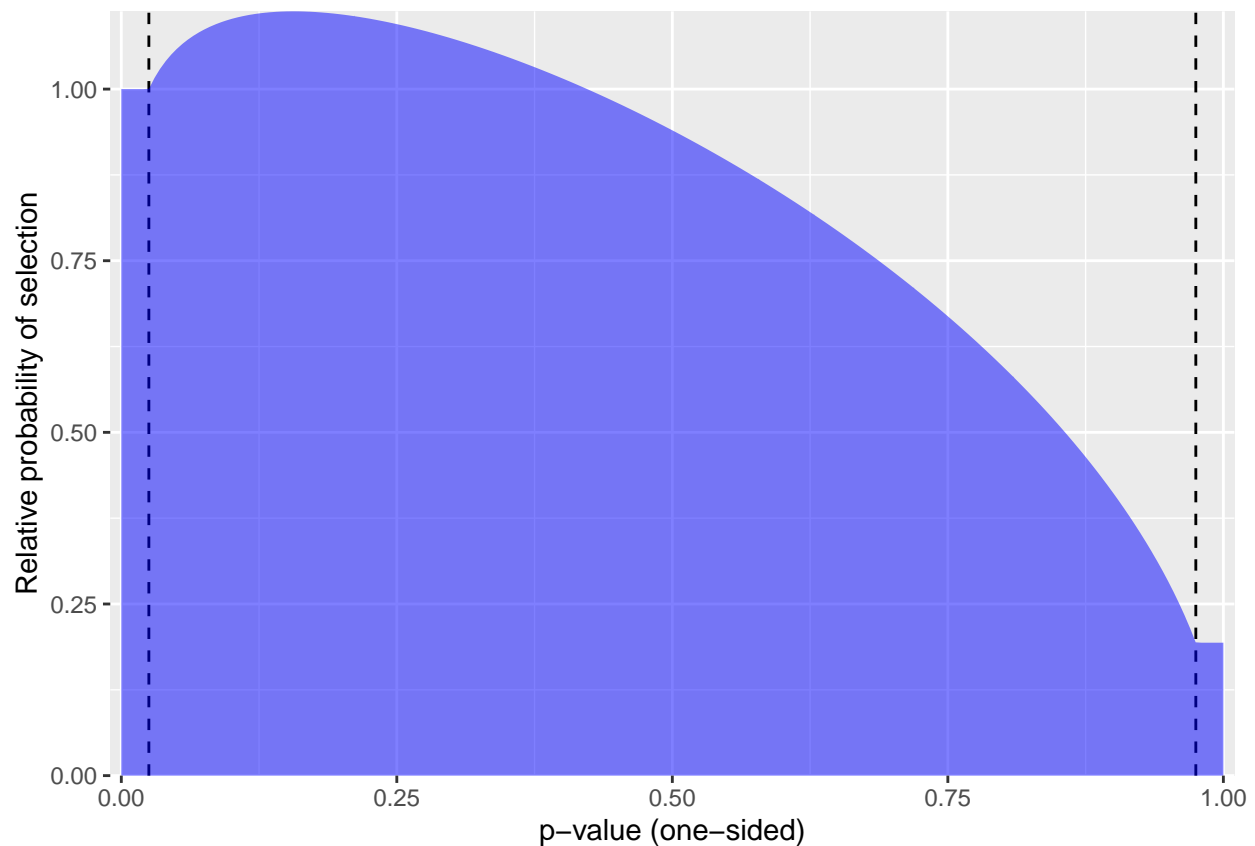
```

##      param   Est    SE p_value CI_lo CI_hi
##      beta  0.330  0.119  0.00563 0.0964 0.564
##      tau2  0.211  0.035      NA 0.1524 0.292
##      lambda1 1.102 0.160  0.50313 0.8294 1.464
##      lambda2 1.550 0.265  0.01036 1.1087 2.167

```

Selection plot: Beta model mean only

```
selection_plot(sci_adj_ms_mean)
```



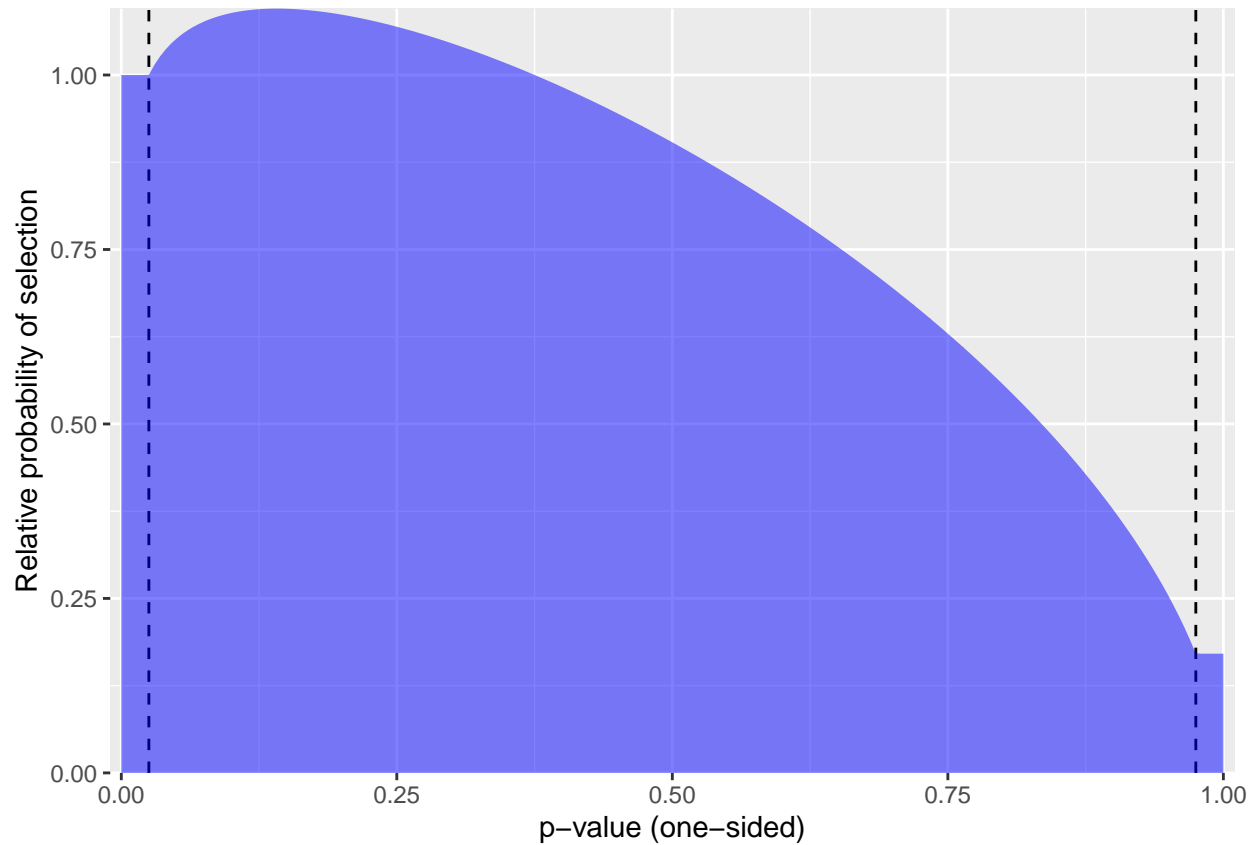
Adjusted estimate in metaselection: Beta model moderator

```
sci_adj_ms_mod <- selection_model(  
  dat = sci,  
  yi = d,  
  sei = sd_d,  
  pi = p_onesided,  
  cluster = studyid,  
  selection_type = "beta",  
  steps = c(.025,.975),  
  make_sandwich = TRUE,  
  mean_mods = ~ outcome_type_author  
)  
sci_adj_ms_mod
```

##	param	Est	SE	p_value	CI_lo	CI_hi
##	beta_(Intercept)	0.210	0.2428	0.3870	-0.266	0.686
##	beta_outcome_type_author	0.140	0.1832	0.4436	-0.219	0.499
##	tau2	0.216	0.0356	NA	0.156	0.298
##	lambda1	1.095	0.1602	0.5359	0.822	1.458
##	lambda2	1.577	0.2818	0.0108	1.111	2.239

Selection plot: Beta model moderator

```
selection_plot(sci_adj_ms_mod)
```



CHE estimate

```
V_mat <- vcalc(
  vi = vi,
  cluster = studyid,
  obs = esid,
  data = sci,
  rho = 0.5,
  sparse = TRUE
)

sci_che <- rma.mv(yi = yi,
  V = V_mat,
  random = ~ 1 | studyid / esid,
  data = sci,
  sparse = TRUE,
  digits = 3) |>
  robust(cluster = studyid, clubSandwich = TRUE)

sci_che
```

```
##
## Multivariate Meta-Analysis Model (k = 292; method: REML)
```



```
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor
## sigma^2.1 0.171 0.413   96    no      studyid
## sigma^2.2 0.037 0.192  292    no  studyid/esid
##
## Test for Heterogeneity:
## Q(df = 291) = 853.675, p-val < .001
##
## Number of estimates: 292
## Number of clusters: 96
## Estimates per cluster: 1-39 (mean: 3.04, median: 1)
##
## Model Results:
##
## estimate      se1   tval1    df1   pval1  ci.lb1  ci.ub1
##      0.453 0.053   8.587   90.95   <.001   0.349   0.558   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## 1) results based on cluster-robust inference (var-cov estimator: CR2,
##    approx t-test and confidence interval, df: Satterthwaite approx)
```

Adjusted estimate in metaselection: Step 3PSM model

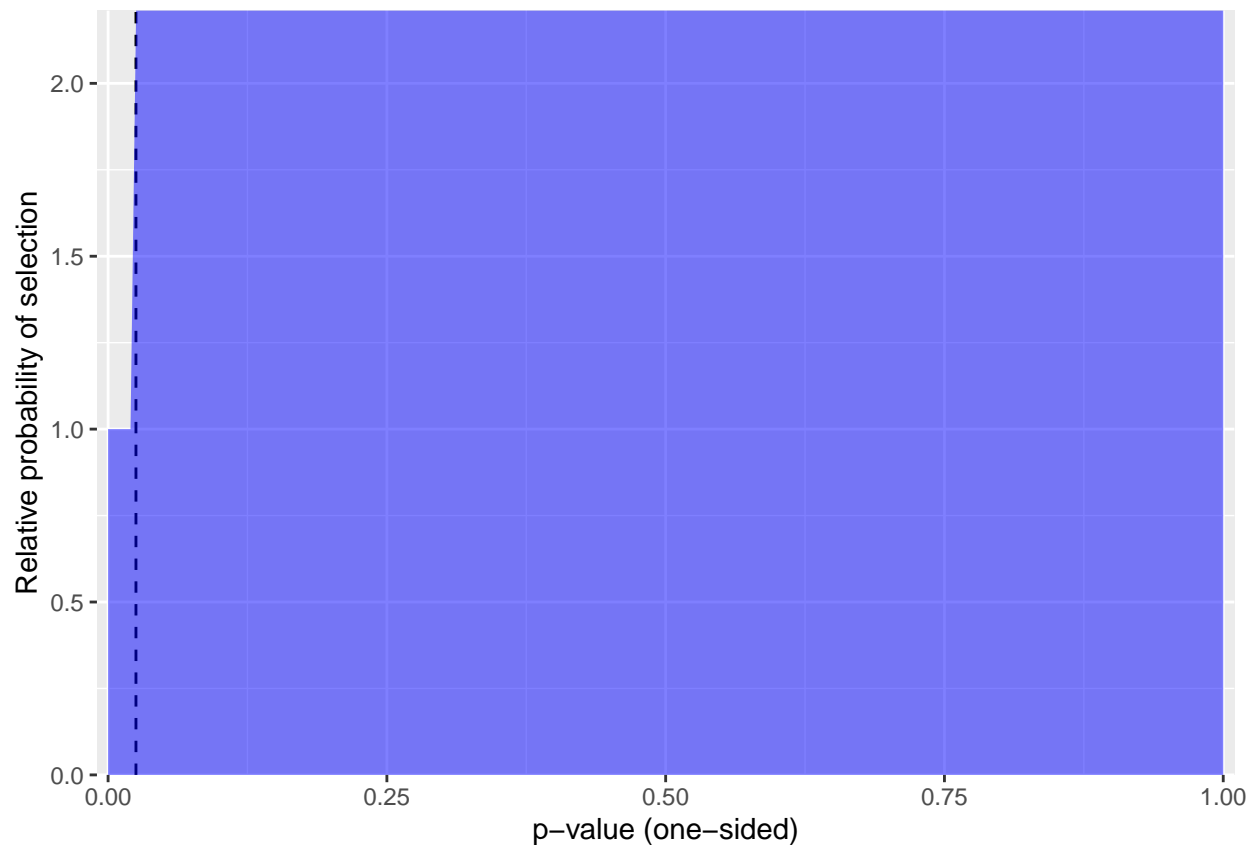
```
sci_adj_ms_step3 <- selection_model(
  dat = sci,
  yi = d,
  sei = sd_d,
  cluster = studyid,
  selection_type = "step",
  steps = 0.025
)

sci_adj_ms_step3

##      param  Est      SE  p_value CI_lo CI_hi
##      beta 0.582 0.0635 5.12e-20 0.458 0.707
##      tau2 0.157 0.0330      NA 0.104 0.237
##      lambda1 2.210 0.5647 1.90e-03 1.340 3.647
```

Selection plot: Step 3 PSM model

```
selection_plot(sci_adj_ms_step3)
```



Adjusted estimate in metaselection: Step 4PSM model

```
sci_adj_ms_step4 <- selection_model(
  dat = sci,
  yi = d,
  sei = sd_d,
  cluster = studyid,
  selection_type = "step",
  steps = c(0.025, .5)
)
```

```
sci_adj_ms_step4
```

##	param	Est	SE	p_value	CI_lo	CI_hi
##	beta	0.492	0.0744	3.61e-11	0.347	0.638
##	tau2	0.186	0.0346	NA	0.130	0.268
##	lambda1	1.933	0.5035	1.14e-02	1.160	3.221
##	lambda2	1.078	0.4599	8.61e-01	0.467	2.487

Selection plot: Step 4PSM model

```
selection_plot(sci_adj_ms_step4)
```

