

# Is There an Association Between Survey Characteristics and Representativeness? A Meta-Analysis

Mon Oct 02 10:26:25 2017

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#####  
##### Carina Cornesse  
#####  
##### SFB 884 "Political Economy of Reforms", University of Mannheim  
#####  
##### and GESIS - Leibniz Institute for the Social Sciences  
#####  
##### and  
#####  
##### Michael Bosnjak  
#####  
##### ZPID - Leibniz Institute for Psychology Information  
##### and University of Trier  
#####
```

```
rm(list = ls())
```

```
## load the R-Indicator dataset
```

```
Metaanalyse_R <-
```

```
read.table("A:/A8/research/WORK/3_Metaanalyse/Representativeness/3_Data/R_Ind  
icators/Meta_Analysis_R_20170307.txt", header=TRUE,  
           sep="\t")
```

```
## load the Median Absolute Bias dataset
```

```
Metaanalyse_Benchmarks <-
```

```
read.table("A:/A8/research/WORK/3_Metaanalyse/Representativeness/3_Data/Bench  
marks/Meta_Analysis_MAB_20170623.txt", header=TRUE,  
           sep="\t")
```

```
## load the Mean Absolute Bias dataset
```

```
Metaanalyse_Benchmarks_mean <-
```

```
read.table("A:/A8/research/WORK/3_Metaanalyse/Representativeness/3_Data/Bench  
marks/Meta_Analysis_MeanAB_20170628.txt", header=TRUE,  
           sep="\t")
```

```
## load the metafor package
```

```
# install.packages('metafor') when using metafor for the first time
```

```
library(metafor)
```

```
## Warning: package 'metafor' was built under R version 3.3.2
```

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

```

## Loading 'metafor' package (version 1.9-9). For an overview
## and introduction to the package please type: help(metafor).

#####
#####      General findings      #####
##### (section 5.1 in the paper) #####
#####

#### R-Indicators ####

## Null-model with outlier inclusion
res_imp <- rma(measure="GEN", yi=es, vi=vi_imp, data=Metaanalyse_R)

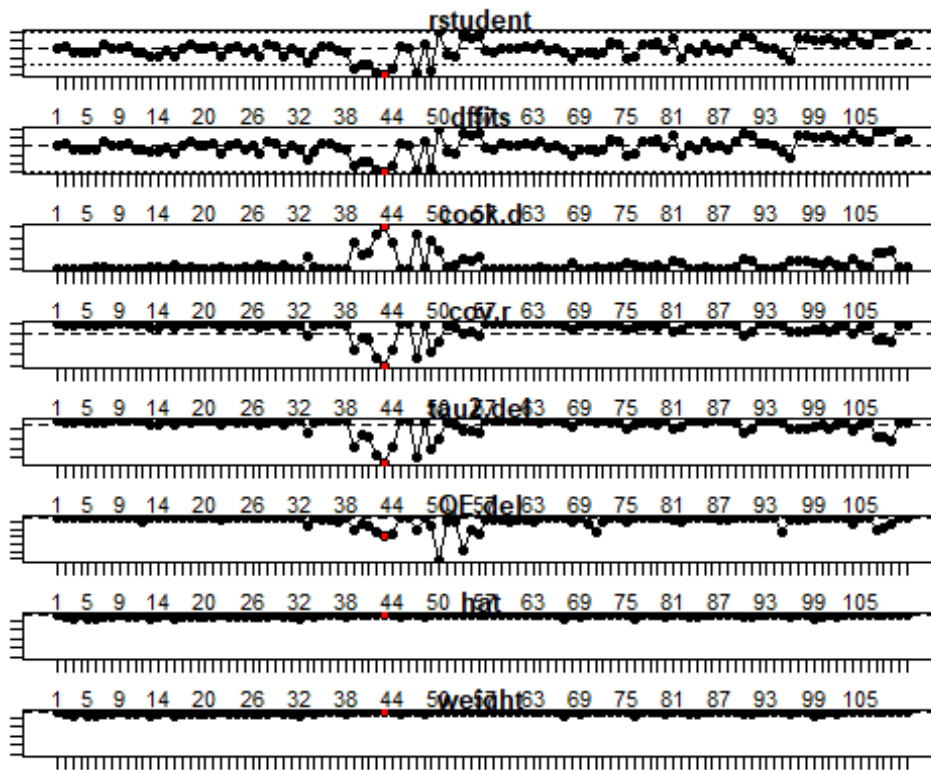
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R): Studies with NAs omitted from model fitting.

res_imp

##
## Random-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0052 (SE = 0.0007)
## tau (square root of estimated tau^2 value):      0.0723
## I^2 (total heterogeneity / total variability):   99.58%
## H^2 (total variability / sampling variability):  239.91
##
## Test for Heterogeneity:
## Q(df = 109) = 23289.4638, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
## 0.8370      0.0070 120.0313    <.0001    0.8234    0.8507
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res_imp)
par(mar=c(1,1,1,1))
plot(inf, layout=c(8,1))

```



# identified outlier: study No.43

```
## Null-model with outlier exclusion (as presented in the paper)
R.without.outliers.re <- subset(Metaanalyse_R, subset =
(Metaanalyse_R$`X_mi_id`!=43))
res_imp.no.outliers <- rma(measure="GEN", yi=es, vi=vi_imp,
data=R.without.outliers.re)

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## R.without.outliers.re): Studies with NAs omitted from model fitting.

res_imp.no.outliers

##
## Random-Effects Model (k = 109; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0053 (SE = 0.0007)
## tau (square root of estimated tau^2 value): 0.0725
## I^2 (total heterogeneity / total variability): 99.58%
## H^2 (total variability / sampling variability): 238.34
##
## Test for Heterogeneity:
## Q(df = 108) = 23286.3547, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.8366      0.0070 119.0569 <.0001 0.8228 0.8504 ***
```

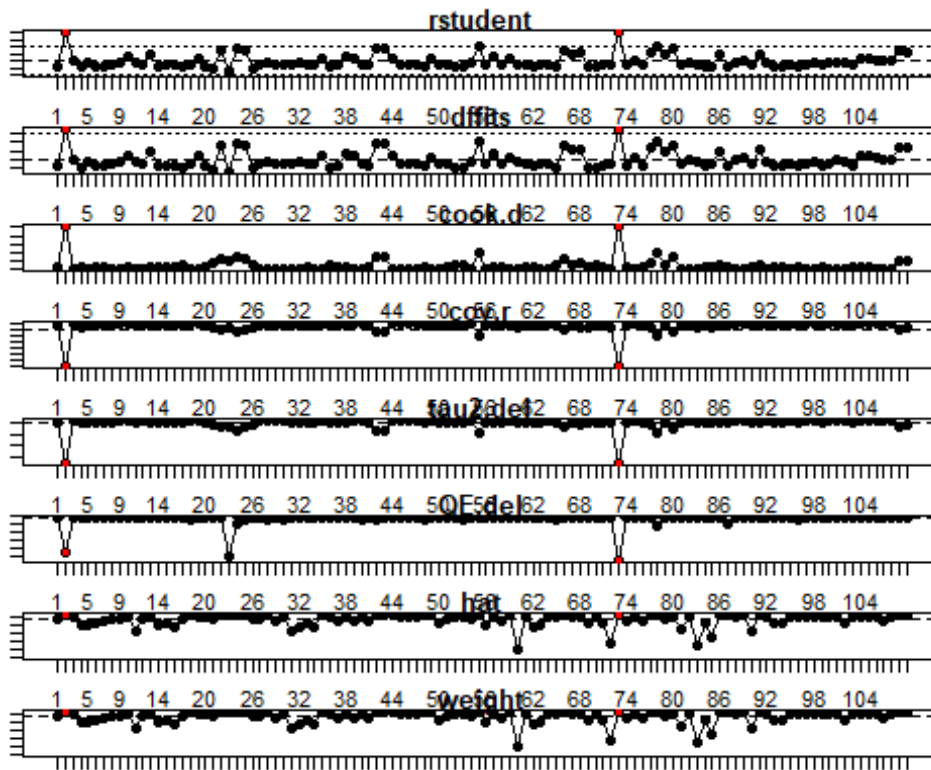
```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Median Absolute Bias ####

## Null-model with outlier inclusion
res <- rma(measure="GEN", yi=es, vi=vi, data=Metaanalyse_Benchmarks)
res

##
## Random-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 12.4664 (SE = 1.8853)
## tau (square root of estimated tau^2 value):      3.5308
## I^2 (total heterogeneity / total variability):   97.69%
## H^2 (total variability / sampling variability):  43.31
##
## Test for Heterogeneity:
## Q(df = 109) = 10914.8610, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##  4.4906    0.3581  12.5410    <.0001    3.7888    5.1924      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res)
plot(inf, layout=c(8,1))
```



```
## identified outliers: studies No. 2 & 72

## Null-model with outlier exclusion (as presented in the paper)
Benchmarks.without.outliers <- subset(Metaanalyse_Benchmarks,
                                       subset =
(Metaanalyse_Benchmarks$id_h != 2 &
Metaanalyse_Benchmarks$id_h != 72))

res_imp.without.outliers <- rma(measure="GEN", yi=es, vi=vi,
data=Benchmarks.without.outliers)
res_imp.without.outliers

##
## Random-Effects Model (k = 108; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 10.7688 (SE = 1.6591)
## tau (square root of estimated tau^2 value):      3.2816
## I^2 (total heterogeneity / total variability):   97.23%
## H^2 (total variability / sampling variability):  36.16
##
## Test for Heterogeneity:
## Q(df = 107) = 8710.9501, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    4.3882    0.3375   13.0030    <.0001    3.7267    5.0496    ***
```

```

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

##### 
##### Moderator analyses #####
##### (Section 5.2 in the paper) #####
##### 

#### Probabilty vs. nonprobability surveys: R-Indicator findings ####

## No mixed-effects models, because k(nonprob)=0

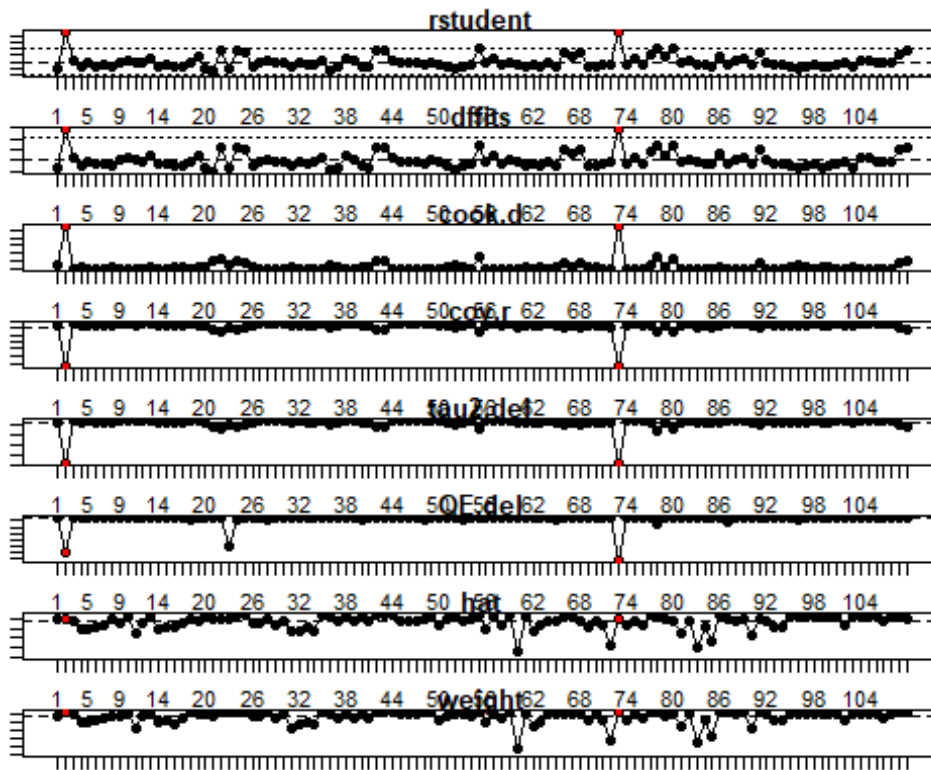
#### Probabilty vs. nonprobability surveys: MAB findings ####

## Mixed effects model with outlier inclusion
res.metareg.sample <- rma(measure="GEN", yi=es, vi=vi, mods = sample,
data=Metaanalyse_Benchmarks)
res.metareg.sample

##
## Mixed-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      12.0622 (SE =
1.8380)
## tau (square root of estimated tau^2 value):              3.4731
## I^2 (residual heterogeneity / unaccounted variability): 97.53%
## H^2 (unaccounted variability / sampling variability):    40.52
## R^2 (amount of heterogeneity accounted for):              3.24%
##
## Test for Residual Heterogeneity:
## QE(df = 108) = 10719.3472, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 5.1748, p-val = 0.0229
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      5.3439  0.5131  10.4156 <.0001    4.3383    6.3494 ***
## mods        -1.6073  0.7066  -2.2748  0.0229   -2.9922   -0.2225  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res.metareg.sample)
plot(inf, layout=c(8,1))

```



```
## identified outliers: studies No. 2 & 73
```

```
## Mixed effects model with outlier exclusion
```

```
Benchmarks.without.outliers.sample <- subset(Metaanalyse_Benchmarks,
                                              subset =
```

```
(Metaanalyse_Benchmarks$id_h != 2
```

```
&
```

```
Metaanalyse_Benchmarks$id_h != 73))
```

```
res.metareg.mixed.no.outlier <- rma(measure="GEN", yi=es, vi=vi, mods =
sample, data=Benchmarks.without.outliers.sample)
```

```
res.metareg.mixed.no.outlier
```

```
##
```

```
## Mixed-Effects Model (k = 108; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of residual heterogeneity):      7.9147 (SE =
1.2695)
```

```
## tau (square root of estimated tau^2 value):             2.8133
```

```
## I^2 (residual heterogeneity / unaccounted variability): 95.86%
```

```
## H^2 (unaccounted variability / sampling variability):    24.17
```

```
## R^2 (amount of heterogeneity accounted for):            10.93%
```

```
##
```

```
## Test for Residual Heterogeneity:
```

```
## QE(df = 106) = 3674.7639, p-val < .0001
```

```
##
```

```
## Test of Moderators (coefficient(s) 2):
```

```
## QM(df = 1) = 13.5499, p-val = 0.0002
```

```
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      5.3948  0.4218  12.7906 <.0001   4.5682   6.2215 ***
## mods        -2.1758  0.5911  -3.6810  0.0002  -3.3343  -1.0173 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Response rate: R-Indicator findings ####

## Mixed effects model with outlier inclusion
res.metareg.rr.imp <- rma(measure="GEN", yi=es, vi=vi_imp, mods = rr,
data=Metaanalyse_R)

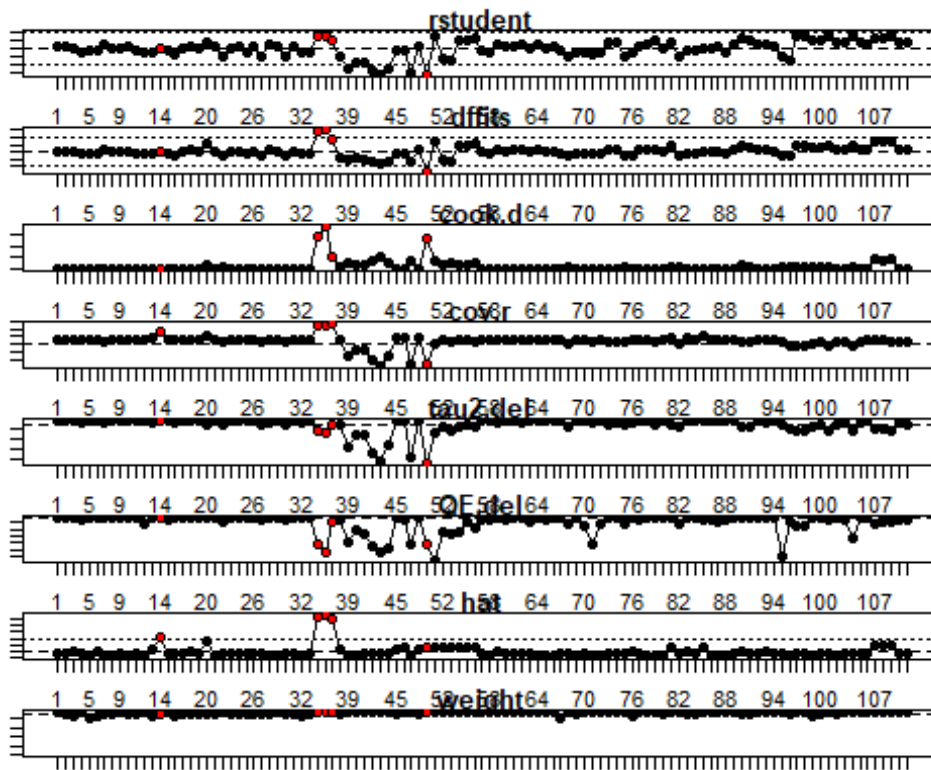
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = rr, data =
## Metaanalyse_R): Studies with NAs omitted from model fitting.

res.metareg.rr.imp

##
## Mixed-Effects Model (k = 109; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0.0047 (SE =
0.0007)
## tau (square root of estimated tau^2 value):              0.0688
## I^2 (residual heterogeneity / unaccounted variability):  99.53%
## H^2 (unaccounted variability / sampling variability):     212.52
## R^2 (amount of heterogeneity accounted for):              8.30%
##
## Test for Residual Heterogeneity:
## QE(df = 107) = 16329.3300, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 10.7250, p-val = 0.0011
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      0.7426  0.0299  24.8204 <.0001   0.6839   0.8012 ***
## mods         0.0014  0.0004   3.2749  0.0011   0.0006   0.0022 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res.metareg.rr.imp)
plot(inf, layout=c(8,1))
```





```
## identified outliers: studies No. 14, 35, 36, 37, 49
```

```
## Mixed effects model with outlier exclusion
```

```
R.without.outliers.rr <- subset(Metaanalyse_R,
                                subset = ( Metaanalyse_R$`X_mi_id`!=14 &
                                             Metaanalyse_R$`X_mi_id`!=35 &
                                             Metaanalyse_R$`X_mi_id`!=36 &
                                             Metaanalyse_R$`X_mi_id`!=37 &
                                             Metaanalyse_R$`X_mi_id`!=49))
```

```
res.metareg.rr.imp.no.outliers <- rma(measure="GEN", yi=es, vi=vi_imp, mods =
rr, data=R.without.outliers.rr)
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = rr, data =
## R.without.outliers.rr): Studies with NAs omitted from model fitting.
```

```
res.metareg.rr.imp.no.outliers
```

```
##
```

```
## Mixed-Effects Model (k = 104; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of residual heterogeneity):      0.0049 (SE =
0.0007)
```

```
## tau (square root of estimated tau^2 value):             0.0699
```

```
## I^2 (residual heterogeneity / unaccounted variability): 99.56%
```

```
## H^2 (unaccounted variability / sampling variability):    226.20
```

```
## R^2 (amount of heterogeneity accounted for):             8.18%
```

```
##
```

```

## Test for Residual Heterogeneity:
## QE(df = 102) = 16281.1696, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 10.1218, p-val = 0.0015
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      0.7391  0.0317  23.3208 <.0001  0.6770  0.8012 ***
## mods         0.0014  0.0004   3.1815  0.0015  0.0005  0.0023 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Response rate: MAB findings ####

## Mixed effects model with outlier inclusion
res.metareg.rr <- rma(measure="GEN", yi=es, vi=vi, mods = rr,
data=Metaanalyse_Benchmarks)

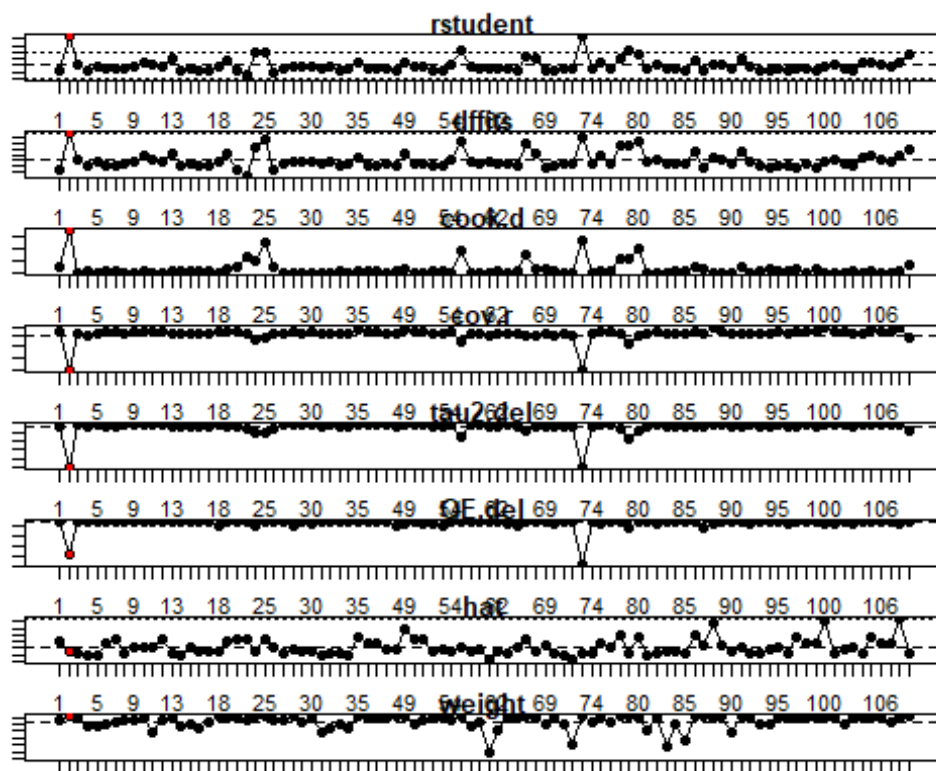
## Warning in rma(measure = "GEN", yi = es, vi = vi, mods = rr, data =
## Metaanalyse_Benchmarks): Studies with NAs omitted from model fitting.

res.metareg.rr

##
## Mixed-Effects Model (k = 92; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      12.2759 (SE =
2.0679)
## tau (square root of estimated tau^2 value):              3.5037
## I^2 (residual heterogeneity / unaccounted variability):  97.43%
## H^2 (unaccounted variability / sampling variability):     38.93
## R^2 (amount of heterogeneity accounted for):              0.28%
##
## Test for Residual Heterogeneity:
## QE(df = 90) = 7757.7143, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 1.5479, p-val = 0.2134
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      4.9525  0.7079   6.9956 <.0001   3.5649   6.3400 ***
## mods        -0.0175  0.0141  -1.2442  0.2134  -0.0452   0.0101
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
## Identification of outliers: Influence Plot
inf <- influence(res.metareg.rr)
plot(inf, layout=c(8,1))
```



```
## identified outliers: studies No. 2 & 73
```

```
## Mixed effects model with outlier exclusion
```

```
Benchmarks.without.outliers.rr <- subset(Metaanalyse_Benchmarks,
                                          subset =
(Metaanalyse_Benchmarks$id_h != 73 &
Metaanalyse_Benchmarks$id_h != 2))
```

```
res.metareg.rr <- rma(measure="GEN", yi=es, vi=vi, mods = rr,
data=Benchmarks.without.outliers.rr)
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi, mods = rr, data =
## Benchmarks.without.outliers.rr): Studies with NAs omitted from model
## fitting.
```

```
res.metareg.rr
```

```
##
```

```
## Mixed-Effects Model (k = 90; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of residual heterogeneity): 7.6001 (SE =
1.3637)
```

```
## tau (square root of estimated tau^2 value): 2.7568
```

```
## I^2 (residual heterogeneity / unaccounted variability): 95.29%
```

```

## H^2 (unaccounted variability / sampling variability): 21.21
## R^2 (amount of heterogeneity accounted for): 2.22%
##
## Test for Residual Heterogeneity:
## QE(df = 88) = 3510.1156, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 3.2285, p-val = 0.0724
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      4.7958  0.5687   8.4334 <.0001   3.6812  5.9104 ***
## mods       -0.0205  0.0114  -1.7968  0.0724  -0.0428  0.0019 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Mixed vs. single mode: R-Indicator findings ####

## Mixed effects model with outlier inclusion
res.metareg.mixed.imp <- rma(measure="GEN", yi=es, vi=vi_imp, mods = mixed,
data=Metaanalyse_R)

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = mixed, data =
## Metaanalyse_R): Studies with NAs omitted from model fitting.

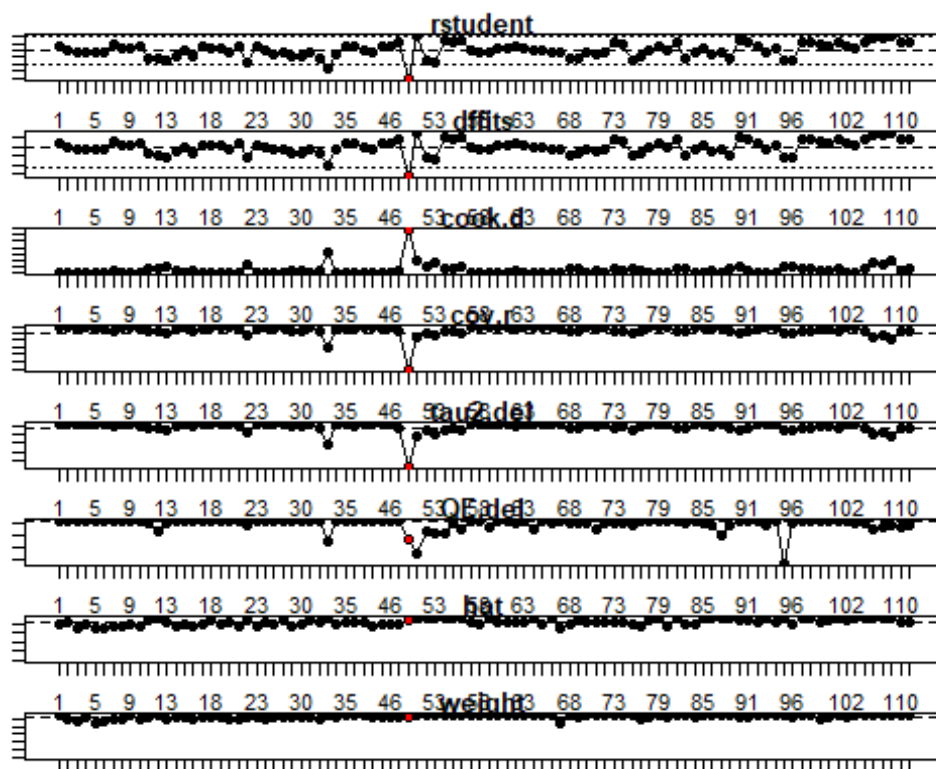
res.metareg.mixed.imp

##
## Mixed-Effects Model (k = 96; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity): 0.0031 (SE =
0.0005)
## tau (square root of estimated tau^2 value): 0.0555
## I^2 (residual heterogeneity / unaccounted variability): 99.30%
## H^2 (unaccounted variability / sampling variability): 142.06
## R^2 (amount of heterogeneity accounted for): 13.22%
##
## Test for Residual Heterogeneity:
## QE(df = 94) = 11566.8032, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 15.1236, p-val = 0.0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      0.8256  0.0080  103.6655 <.0001   0.8100  0.8412 ***
## mods         0.0451  0.0116   3.8889  0.0001   0.0224  0.0678 ***
##

```

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

## Identification of outliers: Influence Plot
inf <- influence(res.metareg.mixed.imp)
plot(inf, layout=c(8,1))
```



```
## identified outliers: study No. 49
```

```
## Mixed effects model with outlier exclusion
```

```
R.without.outliers.mode <- subset(Metaanalyse_R, subset =
(Metaanalyse_R$`X_mi_id`!=49))
```

```
res.metareg.mixed.imp.no.outliers <- rma(measure="GEN", yi=es, vi=vi_imp,
mods = mixed, data=R.without.outliers.mode)
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = mixed, data =
## R.without.outliers.mode): Studies with NAs omitted from model fitting.
```

```
res.metareg.mixed.imp.no.outliers
```

```
##
```

```
## Mixed-Effects Model (k = 96; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of residual heterogeneity):      0.0031 (SE =
0.0005)
```

```
## tau (square root of estimated tau^2 value):             0.0555
```

```
## I^2 (residual heterogeneity / unaccounted variability): 99.30%
```

```
## H^2 (unaccounted variability / sampling variability):    142.06
```

```

## R^2 (amount of heterogeneity accounted for):          13.22%
##
## Test for Residual Heterogeneity:
## QE(df = 94) = 11566.8032, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 15.1236, p-val = 0.0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      0.8256  0.0080  103.6655  <.0001   0.8100   0.8412   ***
## mods         0.0451  0.0116   3.8889   0.0001   0.0224   0.0678   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Mixed vs. single mode: MAB findings ####

## No mixed-effects models, because k(mixed)=2

#### Web vs. other single mode: R-Indicator findings ####

## No mixed-effects models, because k(web)=1

#### Web vs. other single mode: MAB findings ####

## Mixed effects model with outlier inclusion
res.metareg.web <- rma(measure="GEN", yi=es, vi=vi, mods = web,
data=Metaanalyse_Benchmarks)

## Warning in rma(measure = "GEN", yi = es, vi = vi, mods = web, data =
## Metaanalyse_Benchmarks): Studies with NAs omitted from model fitting.

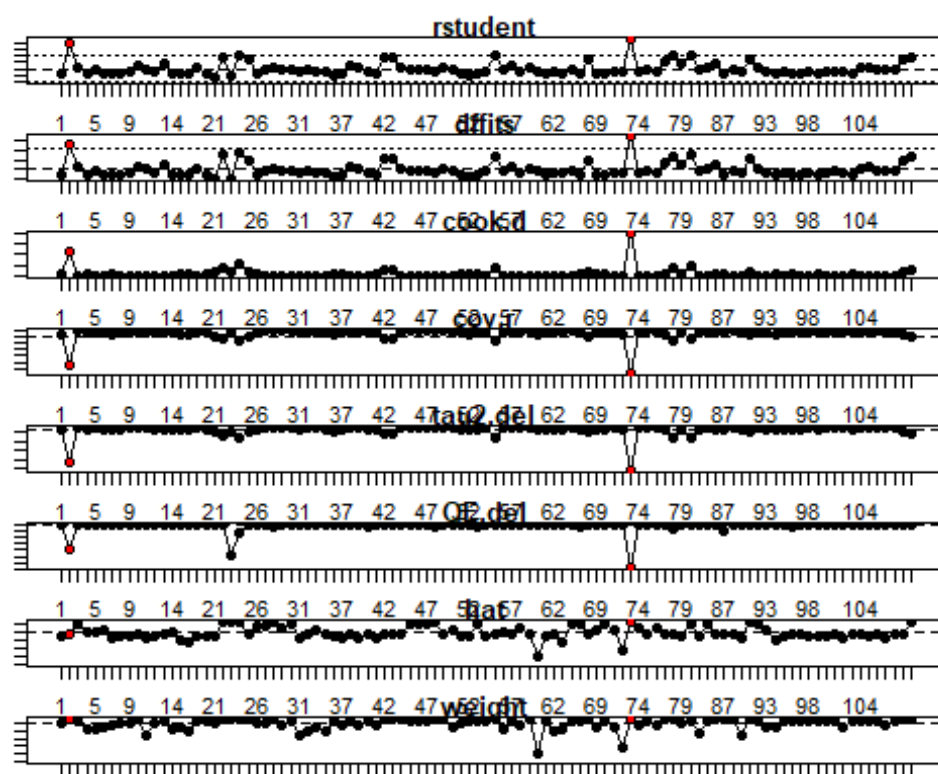
res.metareg.web

##
## Mixed-Effects Model (k = 101; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      12.5837 (SE =
1.9845)
## tau (square root of estimated tau^2 value):              3.5473
## I^2 (residual heterogeneity / unaccounted variability):  97.71%
## H^2 (unaccounted variability / sampling variability):     43.72
## R^2 (amount of heterogeneity accounted for):              2.14%
##
## Test for Residual Heterogeneity:
## QE(df = 99) = 10489.8603, p-val < .0001
##

```

```
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 3.6365, p-val = 0.0565
##
## Model Results:
##
##           estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt    3.6576  0.5775  6.3338  <.0001  2.5258  4.7894 ***
## mods       1.4446  0.7575  1.9070  0.0565 -0.0402  2.9293 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res.metareg.web)
plot(inf, layout=c(8,1))
```



```
## identified outliers: studies No. 2 & 73

## Mixed effects model with outlier exclusion
Benchmarks.without.outliers.web <- subset(Metaanalyse_Benchmarks,
                                           subset =
(Metaanalyse_Benchmarks$id_h != 73
                                     &
Metaanalyse_Benchmarks$id_h != 2))

res.metareg.web <- rma(measure="GEN", yi=es, vi=vi, mods = web,
data=Benchmarks.without.outliers.web)
```

```

## Warning in rma(measure = "GEN", yi = es, vi = vi, mods = web, data =
## Benchmarks.without.outliers.web): Studies with NAs omitted from model
## fitting.

res.metareg.web

##
## Mixed-Effects Model (k = 99; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      8.6193 (SE =
1.4239)
## tau (square root of estimated tau^2 value):              2.9359
## I^2 (residual heterogeneity / unaccounted variability): 96.29%
## H^2 (unaccounted variability / sampling variability):    26.95
## R^2 (amount of heterogeneity accounted for):              4.37%
##
## Test for Residual Heterogeneity:
## QE(df = 97) = 5152.1127, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 5.8315, p-val = 0.0157
##
## Model Results:
##
##           estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      3.3294  0.4979  6.6867  <.0001  2.3535  4.3052  ***
## mods         1.5658  0.6484  2.4148  0.0157  0.2950  2.8367   *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Auxiliary variables: R-Indicator findings ####

## Mixed effects model with outlier inclusion
res.metareg.auxvars.imp <- rma(measure="GEN", yi=es, vi=vi_imp, mods =
auxvars, data=Metaanalyse_R)

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = auxvars, data
## = Metaanalyse_R): Studies with NAs omitted from model fitting.

res.metareg.auxvars.imp

##
## Mixed-Effects Model (k = 106; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0.0049 (SE =
0.0007)
## tau (square root of estimated tau^2 value):              0.0700
## I^2 (residual heterogeneity / unaccounted variability): 99.54%
## H^2 (unaccounted variability / sampling variability):    215.56
## R^2 (amount of heterogeneity accounted for):              0.00%
##

```





```

res.metareg.auxvars.imp <- rma(measure="GEN", yi=es, vi=vi_imp, mods =
auxvars, data=R.without.outliers.auxvars)

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = auxvars, data
## = R.without.outliers.auxvars): Studies with NAs omitted from model
fitting.

res.metareg.auxvars.imp

##
## Mixed-Effects Model (k = 104; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0.0049 (SE =
0.0007)
## tau (square root of estimated tau^2 value):              0.0702
## I^2 (residual heterogeneity / unaccounted variability): 99.53%
## H^2 (unaccounted variability / sampling variability):    212.56
## R^2 (amount of heterogeneity accounted for):              0.00%
##
## Test for Residual Heterogeneity:
## QE(df = 102) = 16150.0866, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0466, p-val = 0.8291
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      0.8345   0.0123  67.7500 <.0001    0.8104    0.8587 ***
## mods        -0.0005   0.0023  -0.2159  0.8291   -0.0051    0.0041
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Auxiliary variables: R-Indicator findings ####

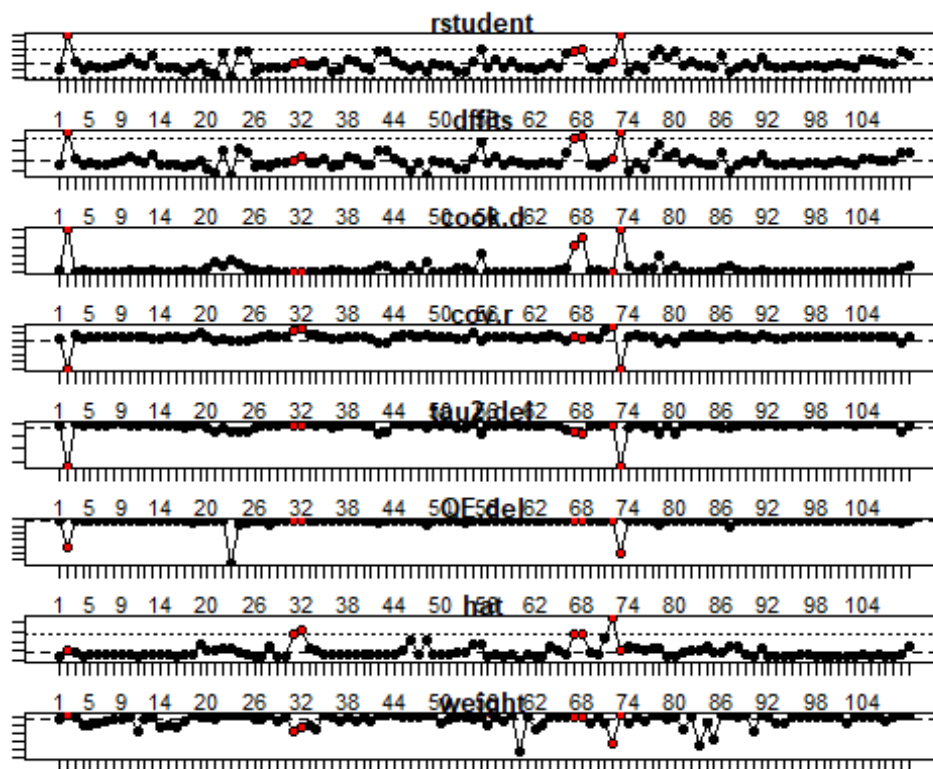
## Mixed effects model with outlier inclusion
res.metareg.auxvars <- rma(measure="GEN", yi=es, vi=vi, mods = numvars,
data=Metaanalyse_Benchmarks)
res.metareg.auxvars

##
## Mixed-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      11.8557 (SE =
1.8082)
## tau (square root of estimated tau^2 value):              3.4432
## I^2 (residual heterogeneity / unaccounted variability): 97.55%
## H^2 (unaccounted variability / sampling variability):    40.79
## R^2 (amount of heterogeneity accounted for):              4.90%
##
## Test for Residual Heterogeneity:

```

```
## QE(df = 108) = 10414.2495, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 6.7644, p-val = 0.0093
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      6.4656  0.8331   7.7611 <.0001   4.8328   8.0985 ***
## mods       -0.1156  0.0445  -2.6009  0.0093  -0.2027  -0.0285 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res.metareg.auxvars)
plot(inf, layout=c(8,1))
```



```
## identified outliers: studies No. 2,31,32,68,72,73

## Mixed effects model with outlier exclusion
Benchmarks.without.outliers.auxvars <- subset(Metaanalyse_Benchmarks,
                                              subset =
(Metaanalyse_Benchmarks$id_h !=2
                                              &
Metaanalyse_Benchmarks$id_h !=31
                                              &
Metaanalyse_Benchmarks$id_h !=32
```

```

&
Metaanalyse_Benchmarks$`id_h`!=68
&
Metaanalyse_Benchmarks$`id_h`!=72
&
Metaanalyse_Benchmarks$`id_h`!=73))

res.metareg.auxvars <- rma(measure="GEN", yi=es, vi=vi, mods = numvars,
data=Benchmarks.without.outliers.auxvars)
res.metareg.auxvars

##
## Mixed-Effects Model (k = 104; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      8.5431 (SE =
1.3734)
## tau (square root of estimated tau^2 value):             2.9229
## I^2 (residual heterogeneity / unaccounted variability): 96.35%
## H^2 (unaccounted variability / sampling variability):    27.41
## R^2 (amount of heterogeneity accounted for):             3.81%
##
## Test for Residual Heterogeneity:
## QE(df = 102) = 5574.6691, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 5.2655, p-val = 0.0218
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      5.9477  0.7993   7.4410 <.0001    4.3811    7.5144 ***
## mods        -0.1028  0.0448  -2.2947  0.0218   -0.1906   -0.0150  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### #####
#### Graphs of subgroup comparisons ####
#### #####

#### Probabilty vs. nonprobability surveys: R-Indicator findings ####

## No descriptive comparison of subgroups: prob. vs. nonprob. survey, because
k(nonprob)=0

#### Probabilty vs. nonprobability surveys: MAB findings ####

## Descriptive comparison of subgroups
res.subset.sample.non <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(sample=="0"))

```

```

res.subset.sample.prob <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(sample=="1"))
res.subset.sample.non

##
## Random-Effects Model (k = 49; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 10.4850 (SE = 2.3007)
## tau (square root of estimated tau^2 value):      3.2381
## I^2 (total heterogeneity / total variability):    97.59%
## H^2 (total variability / sampling variability):   41.45
##
## Test for Heterogeneity:
## Q(df = 48) = 2102.8223, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    5.3592    0.4804   11.1546    <.0001    4.4175    6.3008      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.subset.sample.non

##
## Random-Effects Model (k = 61; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 13.3546 (SE = 2.8201)
## tau (square root of estimated tau^2 value):      3.6544
## I^2 (total heterogeneity / total variability):    97.41%
## H^2 (total variability / sampling variability):   38.54
##
## Test for Heterogeneity:
## Q(df = 60) = 8616.5249, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    3.7175    0.5080    7.3176    <.0001    2.7218    4.7133      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Figure 2: Subgroup comparison results by probability versus
nonprobability surveys as a moderator

## Figure 2: R-Indicators

par(mfrow = c(1,2))

res_imp <- rma(measure="GEN", yi=es, vi=vi_imp, data=Metaanalyse_R)

```

```

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R): Studies with NAs omitted from model fitting.

res_imp

##
## Random-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0052 (SE = 0.0007)
## tau (square root of estimated tau^2 value):      0.0723
## I^2 (total heterogeneity / total variability):   99.58%
## H^2 (total variability / sampling variability):  239.91
##
## Test for Heterogeneity:
## Q(df = 109) = 23289.4638, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
##    0.8370    0.0070 120.0313    <.0001    0.8234    0.8507
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

boxplot(x = c(res_imp[1], 8),
        horizontal = F,
        main = "R-Indicators",
        names = c("Prob. (k = 110)", "Nonprob."),
        ylim = c(0.6,1),
        las = 1,
        pch = ".",
        width = NULL,
        border = "white",
        cex.axis = 0.8)

points(y = c(res_imp[1], 0),
       x = c(1,2),
       pch = 19,
       cex = 1)

# Vertical lines
lines(c(1,1),
      c(res_imp$ci.lb,res_imp$ci.ub))

lines(c(0.95,1.05),
      c(res_imp$ci.ub,res_imp$ci.ub))

lines(c(0.95,1.05),
      c(res_imp$ci.lb,res_imp$ci.lb))

```

```
## Figure 2: MAB
```

```
boxplot(x = c(res.subset.sample.prob[1], res.subset.sample.non[1]),
        horizontal = F,
        main = "MAB",
        names = c("Prob. (k = 61)", "Nonprob. (k = 49)"),
        ylim = c(7,0),
        las = 1,
        pch = ".",
        width = NULL,
        border = "white",
        cex.axis = 0.8)
```

```
points(y = c(res.subset.sample.prob[1], res.subset.sample.non[1]),
       x = c(1,2),
       pch = 19,
       cex = 1)
```

```
# Vertical lines
```

```
lines(c(2,2),
      c(res.subset.sample.non$ci.lb,res.subset.sample.non$ci.ub))
```

```
lines(c(1,1),
      c(res.subset.sample.prob$ci.lb,res.subset.sample.prob$ci.ub))
```

```
# Horizontal Lines: Nonprob
```

```
lines(c(1.9,2.1),
      c(res.subset.sample.non$ci.ub,res.subset.sample.non$ci.ub))
```

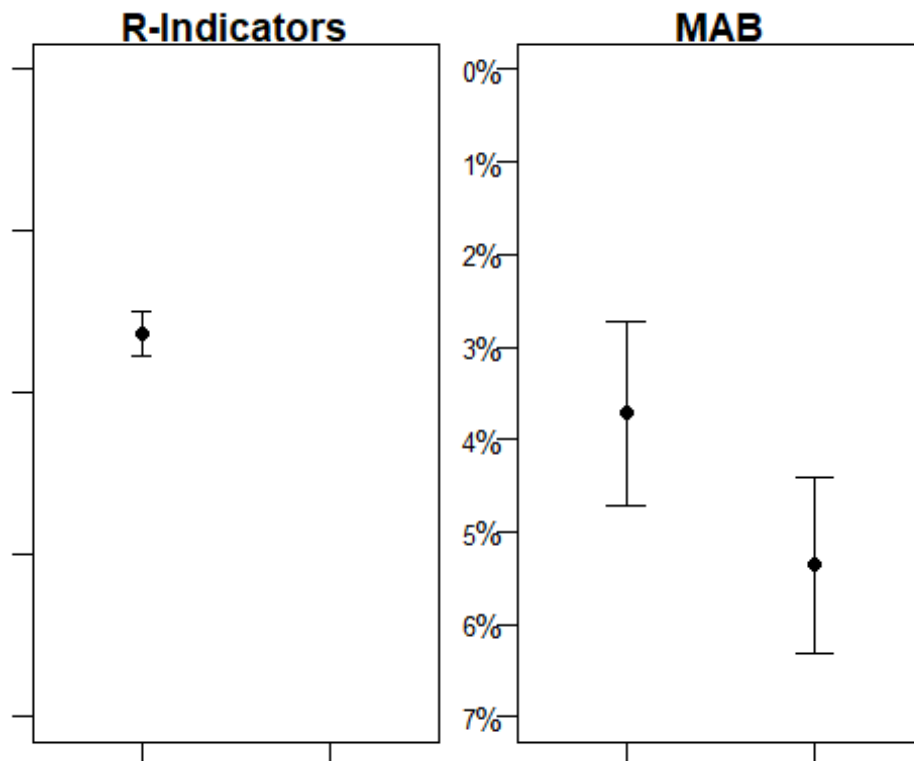
```
lines(c(1.9,2.1),
      c(res.subset.sample.non$ci.lb,res.subset.sample.non$ci.lb))
```

```
# Horizontal Lines: Prob
```

```
lines(c(0.9,1.1),
      c(res.subset.sample.prob$ci.ub,res.subset.sample.prob$ci.ub))
```

```
lines(c(0.9,1.1),
      c(res.subset.sample.prob$ci.lb,res.subset.sample.prob$ci.lb))
```

```
axis(side = 2, labels = c("%","%", "%", "%", "%", "%", "%", "%"),
     tick = FALSE,
     line = NA,
     at = c(0,1,2,3,4,5,6,7),
     padj = 0.49,
     hadj = 0.1,
     las = 1,
     cex = 0.3,
     col.ticks = "white")
```



#### Mixed vs. single mode: R-Indicator findings ####

## Descriptive comparison of subgroups

```
res.subset.mixed.imp <- rma(measure="GEN", yi=es, vi=vi_imp,
data=Metaanalyse_R, subset=(mixed=="1"))
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R, : Studies with NAs omitted from model fitting.
```

```
res.subset.single.imp <- rma(measure="GEN", yi=es, vi=vi_imp,
data=Metaanalyse_R, subset=(mixed=="0"))
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R, : Studies with NAs omitted from model fitting.
```

```
res.subset.mixed.imp
```

```
##
```

```
## Random-Effects Model (k = 45; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of total heterogeneity): 0.0050 (SE = 0.0011)
```

```
## tau (square root of estimated tau^2 value): 0.0704
```

```
## I^2 (total heterogeneity / total variability): 99.68%
```

```
## H^2 (total variability / sampling variability): 313.17
```

```
##
```

```
## Test for Heterogeneity:
```

```
## Q(df = 44) = 9861.7171, p-val < .0001
```

```
##
```

```
## Model Results:
```



```

##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.8705 0.0106 82.0655 <.0001 0.8497 0.8913 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.subset.single.imp

##
## Random-Effects Model (k = 51; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0014 (SE = 0.0003)
## tau (square root of estimated tau^2 value):      0.0371
## I^2 (total heterogeneity / total variability):   97.68%
## H^2 (total variability / sampling variability):  43.09
##
## Test for Heterogeneity:
## Q(df = 50) = 1705.0862, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.8261 0.0055 151.2927 <.0001 0.8154 0.8368 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Mixed vs. single mode: MAB findings ####

## Descriptive comparison of subgroups
res.subset.mixed <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(mixed=="1"))

## Warning in rma(measure = "GEN", yi = es, vi = vi, data =
## Metaanalyse_Benchmarks, : Studies with NAs omitted from model fitting.

res.subset.single <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(mixed=="0"))

## Warning in rma(measure = "GEN", yi = es, vi = vi, data =
## Metaanalyse_Benchmarks, : Studies with NAs omitted from model fitting.

res.subset.mixed

##
## Random-Effects Model (k = 8; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 9.7605 (SE = 6.6032)
## tau (square root of estimated tau^2 value):      3.1242
## I^2 (total heterogeneity / total variability):   93.47%
## H^2 (total variability / sampling variability):  15.31
##

```

```

## Test for Heterogeneity:
## Q(df = 7) = 77.8820, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
## 4.5302      1.2682      3.5723      0.0004      2.0447      7.0157
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.subset.single

##
## Random-Effects Model (k = 101; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 12.8586 (SE = 2.0140)
## tau (square root of estimated tau^2 value):      3.5859
## I^2 (total heterogeneity / total variability):    97.85%
## H^2 (total variability / sampling variability):   46.46
##
## Test for Heterogeneity:
## Q(df = 100) = 10688.2412, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
## 4.4935      0.3775     11.9048      <.0001      3.7537      5.2333
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Figure 3: Subgroup comparison results by mixed-mode versus single-mode
surveys as a moderator

## Figure 3: R-Indicators

par(mfrow = c(1,2))

boxplot(x = c(res.subset.mixed.imp[1], res.subset.single.imp[1]),
        horizontal = F,
        main = "R-Indicators",
        names = c("Mixed (k = 45)", "Single (k = 51)"),
        ylim = c(0.6,1),
        las = 1,
        pch = ".",
        width = NULL,
        border = "white",
        cex.axis = 0.8)

points(y = c(res.subset.mixed.imp[1], res.subset.single.imp[1]),

```

```

    x = c(1,2),
    pch = 19,
    cex = 1)

# Vertical lines
lines(c(1,1),
      c(res.subset.mixed.imp$ci.lb,res.subset.mixed.imp$ci.ub))

lines(c(2,2),
      c(res.subset.single.imp$ci.lb,res.subset.single.imp$ci.ub))

# Horizontal lines: Mixed
lines(c(0.95,1.05),
      c(res.subset.mixed.imp$ci.ub,res.subset.mixed.imp$ci.ub))

lines(c(0.95,1.05),
      c(res.subset.mixed.imp$ci.lb,res.subset.mixed.imp$ci.lb))

# Horizontal lines: Single
lines(c(1.95,2.05),
      c(res.subset.single.imp$ci.ub,res.subset.single.imp$ci.ub))

lines(c(1.95,2.05),
      c(res.subset.single.imp$ci.lb,res.subset.single.imp$ci.lb))

## Figure 3: MAB

boxplot(x = c(res.subset.mixed[1], res.subset.single[1]),
        horizontal = F,
        main = "MAB",
        names = c("Mixed (k = 8)", "Single (k = 101)"),
        ylim = c(7,0),
        las = 1,
        pch = ".",
        width = NULL,
        border = "white",
        cex.axis = 0.8)

points(y = c(res.subset.mixed[1], res.subset.single[1]),
       x = c(1,2),
       pch = 19,
       cex = 1)

# Vertical lines
lines(c(1,1),
      c(res.subset.mixed$ci.lb,res.subset.mixed$ci.ub))

```

```

lines(c(2,2),
      c(res.subset.single$ci.lb,res.subset.single$ci.ub))

# Horizontal Lines: Mixed

lines(c(0.95,1.05),
      c(res.subset.mixed$ci.ub,res.subset.mixed$ci.ub))

lines(c(0.95,1.05),
      c(res.subset.mixed$ci.lb,res.subset.mixed$ci.lb))

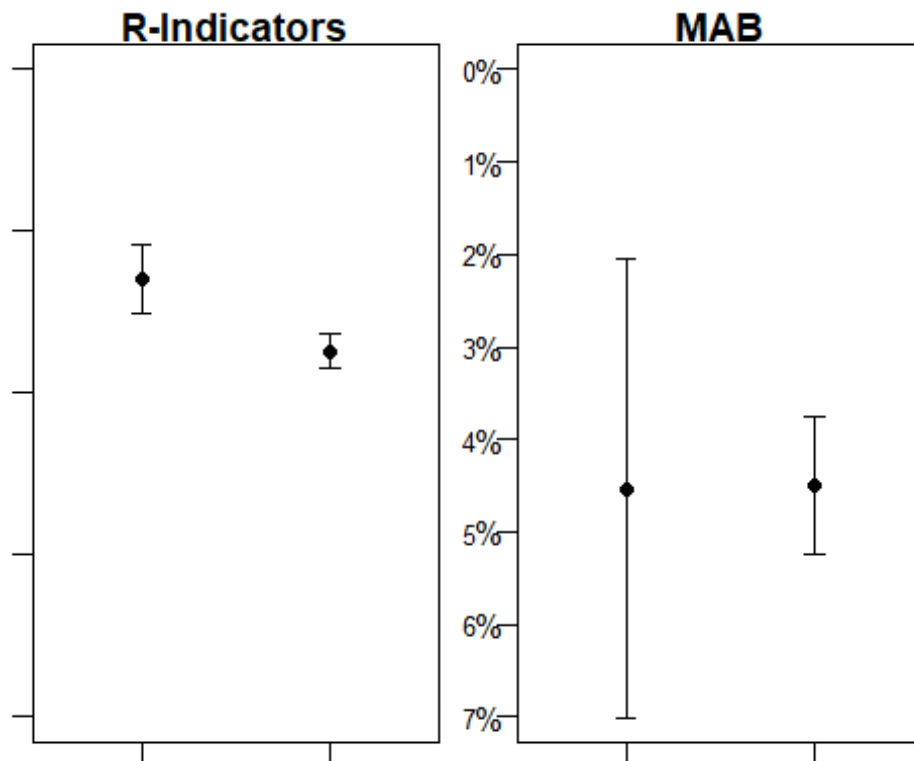
# Horizontal Lines: Single

lines(c(1.95,2.05),
      c(res.subset.single$ci.ub,res.subset.single$ci.ub))

lines(c(1.95,2.05),
      c(res.subset.single$ci.lb,res.subset.single$ci.lb))

axis(side = 2, labels = c("%","%", "%","%", "%","%", "%","%"),
     tick = FALSE,
     line = NA,
     at = c(0,1,2,3,4,5,6,7),
     padj = 0.49,
     hadj = 0.1,
     las = 1,
     cex = 0.3,
     col.ticks = "white")

```



#### Web vs. other single mode: R-Indicator findings ####

## Descriptive comparison of subgroups

```
res.subset.web.imp <- rma(measure="GEN", yi=es, vi=vi_imp,
data=Metaanalyse_R, subset=(web=="1"))
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R, : Studies with NAs omitted from model fitting.
```

```
res.subset.other.imp <- rma(measure="GEN", yi=es, vi=vi_imp,
data=Metaanalyse_R, subset=(web=="0"))
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R, : Studies with NAs omitted from model fitting.
```

```
res.subset.web.imp
```

```
##
```

```
## Fixed-Effects Model (k = 1)
```

```
##
```

```
## Test for Heterogeneity:
```

```
## Q(df = 0) = 0.0000, p-val = 1.0000
```

```
##
```

```
## Model Results:
```

```
##
```

```
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.7800    0.0153   50.9600    <.0001    0.7500    0.8100
```

\*\*\*

```
##
```

```

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

res.subset.other.imp

##
## Random-Effects Model (k = 50; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0014 (SE = 0.0003)
## tau (square root of estimated tau^2 value):      0.0369
## I^2 (total heterogeneity / total variability):   97.70%
## H^2 (total variability / sampling variability):  43.47
##
## Test for Heterogeneity:
## Q(df = 49) = 1687.8542, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.8270    0.0055 150.6129    <.0001    0.8162    0.8377      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Web vs. other single mode: MAB findings ####

## Descriptive comparison of subgroups
res.subset.web <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(web=="1"))

## Warning in rma(measure = "GEN", yi = es, vi = vi, data =
## Metaanalyse_Benchmarks, : Studies with NAs omitted from model fitting.

res.subset.other <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(web=="0"))

## Warning in rma(measure = "GEN", yi = es, vi = vi, data =
## Metaanalyse_Benchmarks, : Studies with NAs omitted from model fitting.

res.subset.web

##
## Random-Effects Model (k = 56; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 12.3639 (SE = 2.5195)
## tau (square root of estimated tau^2 value):      3.5162
## I^2 (total heterogeneity / total variability):   97.71%
## H^2 (total variability / sampling variability):  43.67
##
## Test for Heterogeneity:
## Q(df = 55) = 4283.1555, p-val < .0001
##
## Model Results:

```

```

##
## estimate      se      zval      pval      ci.lb      ci.ub
## 5.1041 0.4863 10.4967 <.0001 4.1510 6.0571 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.subset.other

##
## Random-Effects Model (k = 45; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 12.8688 (SE = 3.2016)
## tau (square root of estimated tau^2 value):      3.5873
## I^2 (total heterogeneity / total variability):   97.72%
## H^2 (total variability / sampling variability):   43.78
##
## Test for Heterogeneity:
## Q(df = 44) = 6206.7048, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 3.6534 0.5832 6.2649 <.0001 2.5104 4.7964 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Figure 4: Subgroup comparison results by web surveys versus other
single-mode surveys as a moderator

## Figure 4: R-Indicators
par(mfrow = c(1,2))

boxplot(x = c(res.subset.web.imp[1], res.subset.other.imp[1]),
        horizontal = F,
        main = "R-Indicators",
        names = c("Web (k = 1)", "Other (k = 50)"),
        ylim = c(0.6,1),
        las = 1,
        pch = ".",
        width = NULL,
        border = "white",
        cex.axis = 0.8)

points(y = c(res.subset.web.imp[1], res.subset.other.imp[1]),
       x = c(1,2),
       pch = 19,
       cex = 1)

# Vertical Lines

```

```

lines(c(1,1),
      c(res.subset.web.imp$ci.lb,res.subset.web.imp$ci.ub))

lines(c(2,2),
      c(res.subset.other.imp$ci.lb,res.subset.other.imp$ci.ub))

# Horizontal lines: Web

lines(c(0.95,1.05),
      c(res.subset.web.imp$ci.ub,res.subset.web.imp$ci.ub))

lines(c(0.95,1.05),
      c(res.subset.web.imp$ci.lb,res.subset.web.imp$ci.lb))

# Horizontal lines: Other

lines(c(1.95,2.05),
      c(res.subset.other.imp$ci.ub,res.subset.other.imp$ci.ub))

lines(c(1.95,2.05),
      c(res.subset.other.imp$ci.lb,res.subset.other.imp$ci.lb))

## Figure 4: MAB

boxplot(x = c(res.subset.web[1], res.subset.other[1]),
        horizontal = F,
        main = "MAB",
        names = c("Web (k = 56)", "Other (k = 55)"),
        ylim = c(7,0),
        las = 1,
        pch = ".",
        width = NULL,
        border = "white",
        cex.axis = 0.8)

points(y = c(res.subset.web[1], res.subset.other[1]),
       x = c(1,2),
       pch = 19,
       cex = 1)

# Vertical lines
lines(c(1,1),
      c(res.subset.web$ci.lb,res.subset.web$ci.ub))

lines(c(2,2),
      c(res.subset.other$ci.lb,res.subset.other$ci.ub))

# Horizontal lines: web

```



```

lines(c(0.95,1.05),
      c(res.subset.web$ci.ub,res.subset.web$ci.ub))

lines(c(0.95,1.05),
      c(res.subset.web$ci.lb,res.subset.web$ci.lb))

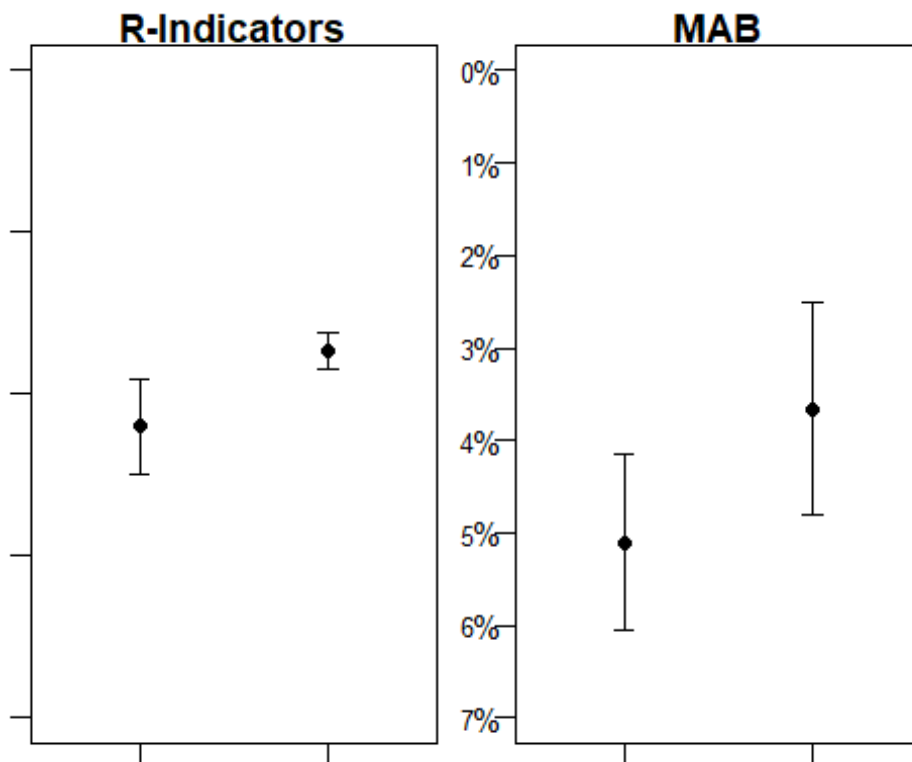
# Horizontal lines: Other

lines(c(1.95,2.05),
      c(res.subset.other$ci.ub,res.subset.other$ci.ub))

lines(c(1.95,2.05),
      c(res.subset.other$ci.lb,res.subset.other$ci.lb))

axis(side = 2, labels = c("%","%", "%", "%", "%", "%", "%", "%"),
     tick = FALSE,
     line = NA,
     at = c(0,1,2,3,4,5,6,7),
     padj = 0.49,
     hadj = 0.1,
     las = 1,
     cex = 0.3,
     col.ticks = "white")

```



```

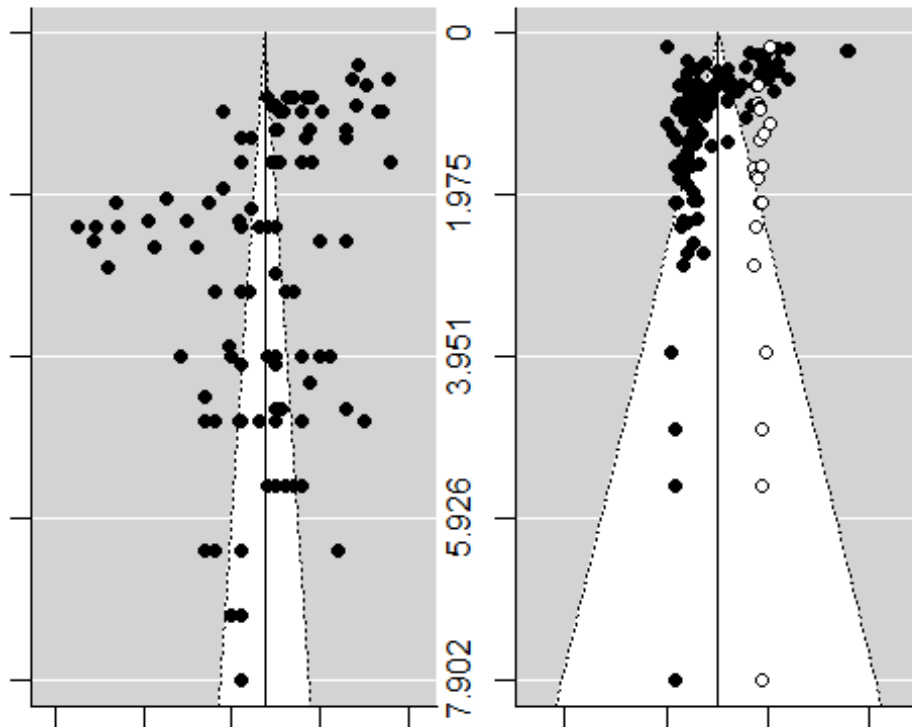
#####
##### Further analyses #####
##### (not reported in the paper) #####
#####

```

```
#### Sensitivity analysis: Trim & Fill funnel plot
```

```
## R-Indicator findings
taf <- trimfill(res_imp)
funnel(taf)
```

```
## MAB findings
taf <- trimfill(res)
funnel(taf)
```



```
#### Weighted vs. unweighted data: MAB only
```

```
res.subset.weighted.no <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(weighted=="0"))
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi, data =
## Metaanalyse_Benchmarks, : Studies with NAs omitted from model fitting.
```

```
res.subset.weighted.yes <- rma(measure="GEN", yi=es, vi=vi,
data=Metaanalyse_Benchmarks, subset=(weighted=="1"))
```

```
## Warning in rma(measure = "GEN", yi = es, vi = vi, data =
## Metaanalyse_Benchmarks, : Studies with NAs omitted from model fitting.
```

```
res.subset.weighted.no
```

```
##
```

```
## Random-Effects Model (k = 67; tau^2 estimator: REML)
```

```
##
```

```

## tau^2 (estimated amount of total heterogeneity): 15.0696 (SE = 2.8225)
## tau (square root of estimated tau^2 value):      3.8820
## I^2 (total heterogeneity / total variability):   98.47%
## H^2 (total variability / sampling variability):  65.38
##
## Test for Heterogeneity:
## Q(df = 66) = 6710.0447, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 5.5002    0.4930  11.1564    <.0001    4.5339    6.4665      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.subset.weighted.yes

##
## Random-Effects Model (k = 30; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 2.4247 (SE = 0.9114)
## tau (square root of estimated tau^2 value):      1.5571
## I^2 (total heterogeneity / total variability):   83.19%
## H^2 (total variability / sampling variability):  5.95
##
## Test for Heterogeneity:
## Q(df = 29) = 416.1709, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 2.5706    0.3473   7.4008    <.0001    1.8898    3.2514      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.metareg.weighted <- rma(measure="GEN", yi=es, vi=vi, mods = weighted,
data=Metaanalyse_Benchmarks)

## Warning in rma(measure = "GEN", yi = es, vi = vi, mods = weighted, data =
## Metaanalyse_Benchmarks): Studies with NAs omitted from model fitting.

res.metareg.weighted

##
## Mixed-Effects Model (k = 97; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity): 11.2453 (SE =
1.8047)
## tau (square root of estimated tau^2 value):      3.3534
## I^2 (residual heterogeneity / unaccounted variability): 97.58%

```

```

## H^2 (unaccounted variability / sampling variability): 41.38
## R^2 (amount of heterogeneity accounted for): 14.51%
##
## Test for Residual Heterogeneity:
## QE(df = 95) = 7126.2156, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 15.8189, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      5.5495  0.4305  12.8906 <.0001   4.7057   6.3932 ***
## mods        -3.1125  0.7826  -3.9773 <.0001  -4.6464  -1.5787 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#### Business surveys vs. non-business surveys: R-Indicators only
res.subset.business.no <- rma(measure="GEN", yi=es, vi=vi_imp,
data=Metaanalyse_R, subset=(business=="0"))

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, data =
## Metaanalyse_R, : Studies with NAs omitted from model fitting.

res.subset.business.yes <- rma(measure="GEN", yi=es, vi=vi_imp,
data=Metaanalyse_R, subset=(business=="1"))
res.subset.business.no

##
## Random-Effects Model (k = 22; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.0056 (SE = 0.0018)
## tau (square root of estimated tau^2 value): 0.0751
## I^2 (total heterogeneity / total variability): 99.83%
## H^2 (total variability / sampling variability): 586.53
##
## Test for Heterogeneity:
## Q(df = 21) = 6974.7025, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.8803  0.0161  54.6912 <.0001   0.8488   0.9119 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.subset.business.yes

##
## Random-Effects Model (k = 88; tau^2 estimator: REML)

```

```
##
## tau^2 (estimated amount of total heterogeneity): 0.0046 (SE = 0.0007)
## tau (square root of estimated tau^2 value):      0.0677
## I^2 (total heterogeneity / total variability):   99.28%
## H^2 (total variability / sampling variability):  138.61
##
## Test for Heterogeneity:
## Q(df = 87) = 10745.8560, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.8260    0.0073 112.6998    <.0001    0.8117    0.8404      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.metareg.business <- rma(measure="GEN", yi=es, vi=vi_imp, mods = business,
data=Metaanalyse_R)

## Warning in rma(measure = "GEN", yi = es, vi = vi_imp, mods = business,
data
## = Metaanalyse_R): Studies with NAs omitted from model fitting.

res.metareg.business

##
## Mixed-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0.0048 (SE =
0.0007)
## tau (square root of estimated tau^2 value):              0.0692
## I^2 (residual heterogeneity / unaccounted variability): 99.53%
## H^2 (unaccounted variability / sampling variability):    213.60
## R^2 (amount of heterogeneity accounted for):              8.24%
##
## Test for Residual Heterogeneity:
## QE(df = 108) = 17720.5585, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 10.6529, p-val = 0.0011
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt    0.8803    0.0149  59.2794    <.0001    0.8512    0.9094      ***
## mods      -0.0543    0.0166  -3.2639    0.0011   -0.0869   -0.0217      **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#### Descriptive statistics
## number of auxiliary variables
table(Metaanalyse_R$auxvars)

##
##  1  2  3  4  5  6  7 14
## 10 15 25 26  6 13  5  7

table(Metaanalyse_Benchmarks$numvars)

##
##  3  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 21 22 23 24 25 26 28 30 34
##  2  3  4  4  5  2  1  2  2 11  5  8  3  1  2 18  4 13  1  2  2  2  3  3  3
## 36 39 56
##  1  2  1

## mean difference in auxiliary variables across probability vs.
nonprobability samples
t.test(numvars ~ sample, Metaanalyse_Benchmarks)

##
##  Welch Two Sample t-test
##
## data:  numvars by sample
## t = -1.1565, df = 103.33, p-value = 0.2502
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -4.948335  1.302969
## sample estimates:
## mean in group 0 mean in group 1
##      16.73469      18.55738

## crosstable: sample type and mixed mode
table(Metaanalyse_Benchmarks$sample, Metaanalyse_Benchmarks$mixed)

##
##      0  1
## 0 47  2
## 1 54  6

# In the benchmark data are 47 nonprob. single-mode studies, 54 prob. single-
mode studies, 2 nonprob. mixed-mode studies, and 6 prob. mixed-mode studies
table(Metaanalyse_R$sample, Metaanalyse_R$mixed)

##
##      0  1
## 1 51 46

# In the R-Indicator data are 0 nonprob. single-mode study, 0 nonprob. mixed-
mode studies, 51 prob. single-mode studies, and 46 prob. mixed-mode studies

## crosstable: sample type and web mode
table(Metaanalyse_Benchmarks$sample, Metaanalyse_Benchmarks$web)
```

```
##
##      0  1
##    0  2 45
##    1 43 11

# In the benchmark data are 2 nonprob. non-web studies, 45 nonprob. web
# studies, 43 prob. non-web studies and 11 prob. web studies.
table(Metaanalyse_R$sample, Metaanalyse_R$web)

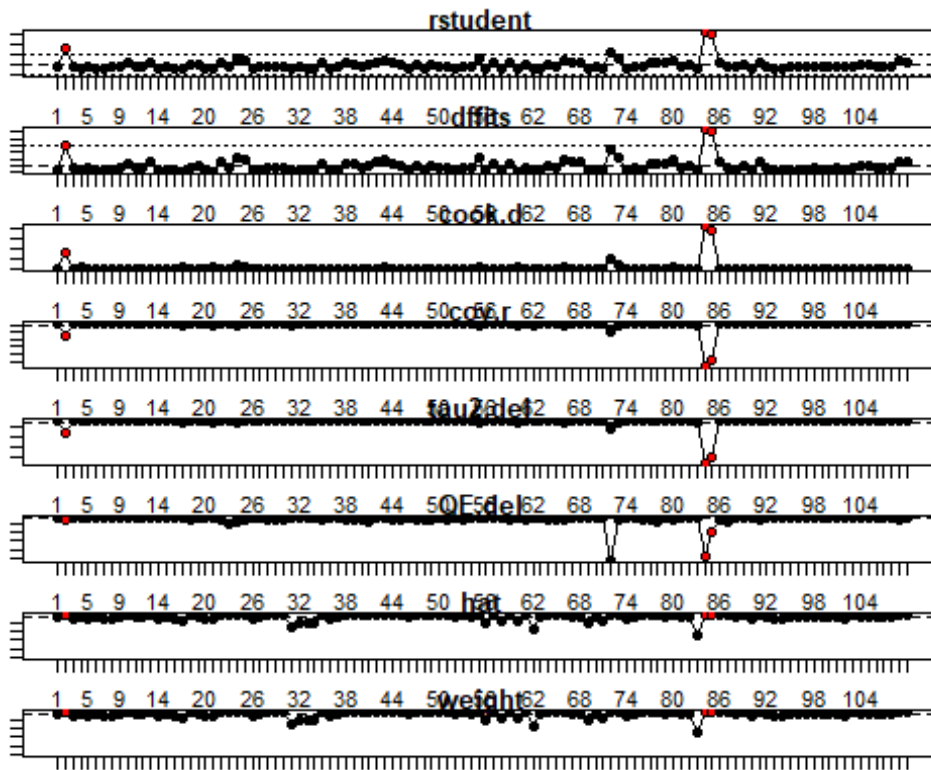
##
##      0  1
##    1 50  1

# In the R-Indicator data are 0 nonprob. studies, 50 prob. non-web and 1
# prob. web study.

#### Sensitivity analysis: Mean Absolute Bias
## Null-model with outlier inclusion
res <- rma(measure="GEN", yi=es, vi=vi, data=Metaanalyse_Benchmarks_mean)
res

##
## Random-Effects Model (k = 110; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 29.0235 (SE = 4.1431)
## tau (square root of estimated tau^2 value):      5.3873
## I^2 (total heterogeneity / total variability):   99.79%
## H^2 (total variability / sampling variability):  484.92
##
## Test for Heterogeneity:
## Q(df = 109) = 196423.7168, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
##    6.1997    0.5280   11.7416    <.0001    5.1648    7.2346
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Identification of outliers: Influence Plot
inf <- influence(res)
plot(inf, layout=c(8,1))
```



```
## identified outliers: studies No. 2, 84, 85

## Null-model with outlier exclusion
Benchmarks.without.outliers.mean <- subset(Metaanalyse_Benchmarks_mean,
                                             subset =
(Metaanalyse_Benchmarks_mean$id_h != 2 &
Metaanalyse_Benchmarks_mean$id_h != 84 &
Metaanalyse_Benchmarks_mean$id_h != 85))

res_mean.without.outliers <- rma(measure="GEN", yi=es, vi=vi,
data=Benchmarks.without.outliers.mean)
res_mean.without.outliers

##
## Random-Effects Model (k = 107; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 9.7225 (SE = 1.5212)
## tau (square root of estimated tau^2 value):      3.1181
## I^2 (total heterogeneity / total variability):    96.75%
## H^2 (total variability / sampling variability):   30.79
##
## Test for Heterogeneity:
## Q(df = 106) = 20226.8424, p-val < .0001
##
## Model Results:
##
```



```
## estimate      se      zval      pval      ci.lb      ci.ub
##    5.6374    0.3235  17.4246    <.0001    5.0033    6.2715      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```