Random-effects meta-analysis: The number of studies matters

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This document corrects the paper appendix where the printed output of the `R` function `metamany` inverted the columns `Std.Err.` and `Heterogeneity`. The Authors are grateful to Dr Karl Ove Hufthammer for noticing the bug.

Amended Appendix

The various approaches to meta-analysis compared in this paper are implemented within the different `R` packages listed in Section 4. In order to facilitate the simultaneous use of the several meta-analysis methods advocated in this paper, a single `R` function called `metamany` with a user-friendly syntax is provided in the supplementary material. Function `metamany` requires previous installation of `R` packages `metafor`,[56] `metaLik`[57] and `metatest`[50]

```
R> install.packages(metafor)
R> install.packages(metaLik)
R> install.packages(metatest)
```

Once installed the three packages above, function `metamany` can be loaded

```
R> source("metamany.R")
```

The arguments of function `metamany` are

```
metamany(y, sigma2, X = NULL, param = NULL)
```

where `y` and `sigma2` are the vectors of estimated outcomes and within-study variances, respectively. Optional input `X` allows to specify a $n \times p$ matrix of study-specific covariates (intercept excluded) for meta-regression. Optional input `param` allows to specify which parameter should be tested in meta-regression. If `param` is left unspecified, then the parameter corresponding to the last column of `X` is tested.

Local anesthesia data are available through data frame `cooper`:

```
R> cooper
      y  sigma2
1  0.00 0.03959
2 -1.71 0.07732
3 -0.19 0.02265
4 -0.58 0.01760
5 -4.27 0.16041
```

Since nonparametric methods use resampling, thereafter the random seed is fixed to allow the reproducibility of the results:

```
R> set.seed(0207)
R> metamany(y = cooper$y, sigma2 = cooper$sigma2)
```

```
Estimates:
                                 Estimate  Std.Err.  Heterogeneity
DerSimonian and Laird              -1.283     0.478      1.081
Maximum likelihood                 -1.317     0.688      2.927
Restricted maximum likelihood      -1.324     0.773      2.306


P-values:
                                    P-value
DerSimonian and Laird               0.00727
Hartung and Knapp                   0.17044
Wald test                           0.05580
Signed profile log-likelihood ratio 0.09604
Skovgaard statistic                 0.15846
Bartlett correction                 0.14441
Restricted maximum likelihood       0.08695
```

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```
Permutation test                          0.12500
```

Warning: Given the number of studies, the *p*-value of the permutation test does not allow to evaluate significance at 5% level.

Meat consumption data are available through data frame `larsson`:

```
R> larsson
        y    sigma2 type
1  -0.3425 0.017224    a
2   0.2546 0.001271    a
3   0.1740 0.000663    a
4   0.1655 0.005027    a
...
```

where variable `type` distinguishes between unprocessed red meat (`type a`) and processed meat (`type b`) consumption.

Meta-regression of meat consumption data with the random seed fixed:

```
R> set.seed(0207)
R> metamany(y = larsson$y, sigma2 = larsson$sigma2,  X = larsson$type)
```

```
Estimates:
                                 Estimate  Std.Err.  Heterogeneity
DerSimonian and Laird            0.10044   0.05218   0.00567
Maximum likelihood               0.10639   0.06117   0.01184
Restricted maximum likelihood    0.10975   0.06891   0.00850
```

```
P-values:
                                   P-value
DerSimonian and Laird              0.0543
Knapp and Hartung                  0.1459
Wald test                          0.0820
```

Signed profile log-likelihood ratio	0.0946
Skovgaard statistic	0.1454
Bartlett correction	0.1170
Restricted maximum likelihood	0.1113
Permutation test	0.1460