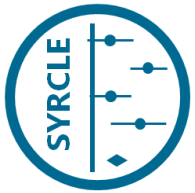
Meta-analyses in R

Cathalijn H.C. Leenaars, Ph.D.

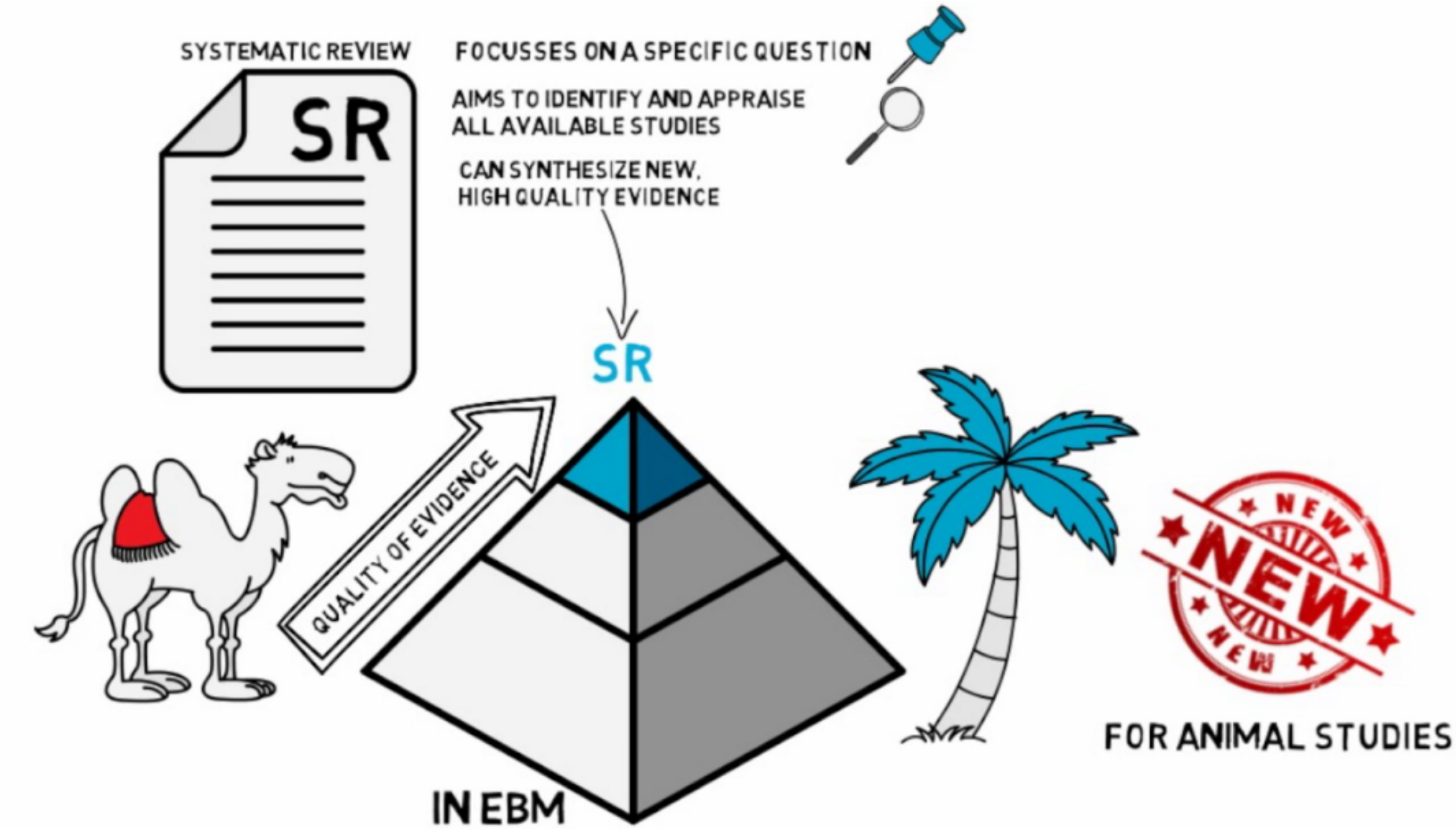


Note

This presentation has been adapted for online posting. Example plots no longer correspond to the code on the slide before.

Systematic reviews

Why do Systematic Reviews (SRs) and Meta-Analyses (MAs)?



From www.SYRCLE.nl with permission

How to do an SR?

From www.SYRCLE.nl with permission

Meta-analyses

Meta-analyses in R

- Relatively simple
- Several packages: meta, metafor, rmeta, metagear, mvmeta, netmeta

- This presentation: meta, metafor and netmeta
  - Simple MA
  - Forest plot
  - Meta-regression
  - Weighted bubble plot
  - Network meta-analysis

- Not in this presentation: Importing your data

Before you start

- Load the relevant packages
- Get your data into R
- Check if the import went well

  (`str, summary, dim, names`)
- Visualise the data to check if the structure is OK

```
1  # Load relevant packages
2  library(readxl)
3  library(meta)
4  library(metafor)
5  library(netmeta)
6
```

Simple MA function in R: metacont

- For continuous outcome data
- Comparing 2 conditions
- Fixed/ random effects
- Inverse variance weighting; SD

```
6  # simple MA with metacont function
7  ma_name <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, studlab, data=NULL,
8                      sm="MD", comb.fixed=FALSE, hakn=TRUE)
```

e → experimental; c → control

Running a meta-analysis; example output

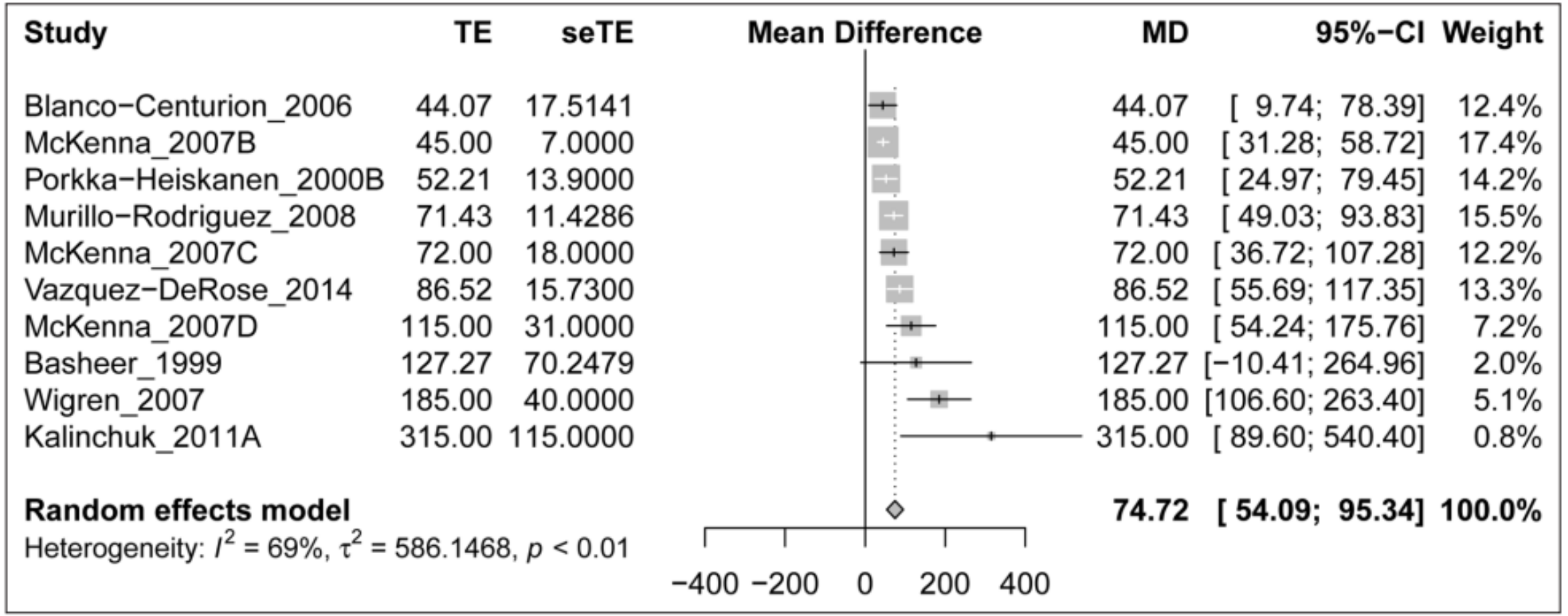
```
> metaSWS <- metacont(n_sws, SWS, SWS_SD,n_wake, W, W_SD,
+                     studlab = STUDY_ID, data=NAMDMA,
+                     comb.fixed = FALSE, comb.random = TRUE,
+                     hakn=TRUE, sm="SMD")
> metaSWS
                     SMD             95%-CI %w(random)
Orosco_95        -0.6502 [-1.9427;  0.6423]        8.1
Shouse_00        -0.8912 [-2.1036;  0.3211]        8.6
Shouse_00        -1.6756 [-3.0719; -0.2794]        7.5
Shouse_01        -1.6010 [-2.7708; -0.4311]        8.8
Shouse_01        -2.4503 [-3.8347; -1.0659]        7.6
Shouse_01        -1.3045 [-2.4141; -0.1948]        9.2
Shouse_01        -2.3671 [-3.7282; -1.0059]        7.7
Park_02          -4.6418 [-7.5342; -1.7494]        2.9
Lena_05          -0.9325 [-2.1523;  0.2872]        8.5
Lena_05          -0.8889 [-2.1009;  0.3230]        8.6
Shouse_00        -3.3766 [-5.0428; -1.7104]        6.2
Shouse_00        -2.1948 [-3.5092; -0.8804]        8.0
DeSaintHilaire_00  0.2129 [-1.0325;  1.4583]        8.4

Number of studies combined: k = 13

                         SMD             95%-CI     t p-value
Random effects model -1.5404 [-2.1902; -0.8906] -5.17  0.0002

Quantifying heterogeneity:
tau^2 = 0.5214; H = 1.46 [1.07; 2.00]; I^2 = 53.3% [12.3%; 75.1%]

Test of heterogeneity:
     Q d.f. p-value
 25.68   12  0.0119

Details on meta-analytical method:
```

Preliminary data

Creating a forest plot

```
17  #creating a forest plot
18  forest(ma_name, sortvar = Author, xlab = "Bone damage",
19         studlab = TRUE, overall = TRUE, test.overall.random = TRUE,
20         test.effect.subgroup = TRUE, leftcols = "studlab")
21
```

Example Forest Plot



https://doi.org/10.5334/jcr.171

General MA function in R: metagen

- Fixed/ random effects
- based on estimates (`TE = Treatment Estimate`)
  - MD/ SMD/ NMD → also for cross-over trials
  - Log hazard ratios
  - Risk difference
  - …
- Inverse variance weighting; SE

```
10  #MA with metagen function
11  ma_name <- metagen(TE, seTE, studlab, data=NULL, sm="MD",
12          comb.fixed=FALSE, hakn=TRUE)
13
14  #printing output
15  print(summary(ma_name), digits=2)
```

Meta-Regression

General MA function in R: rma

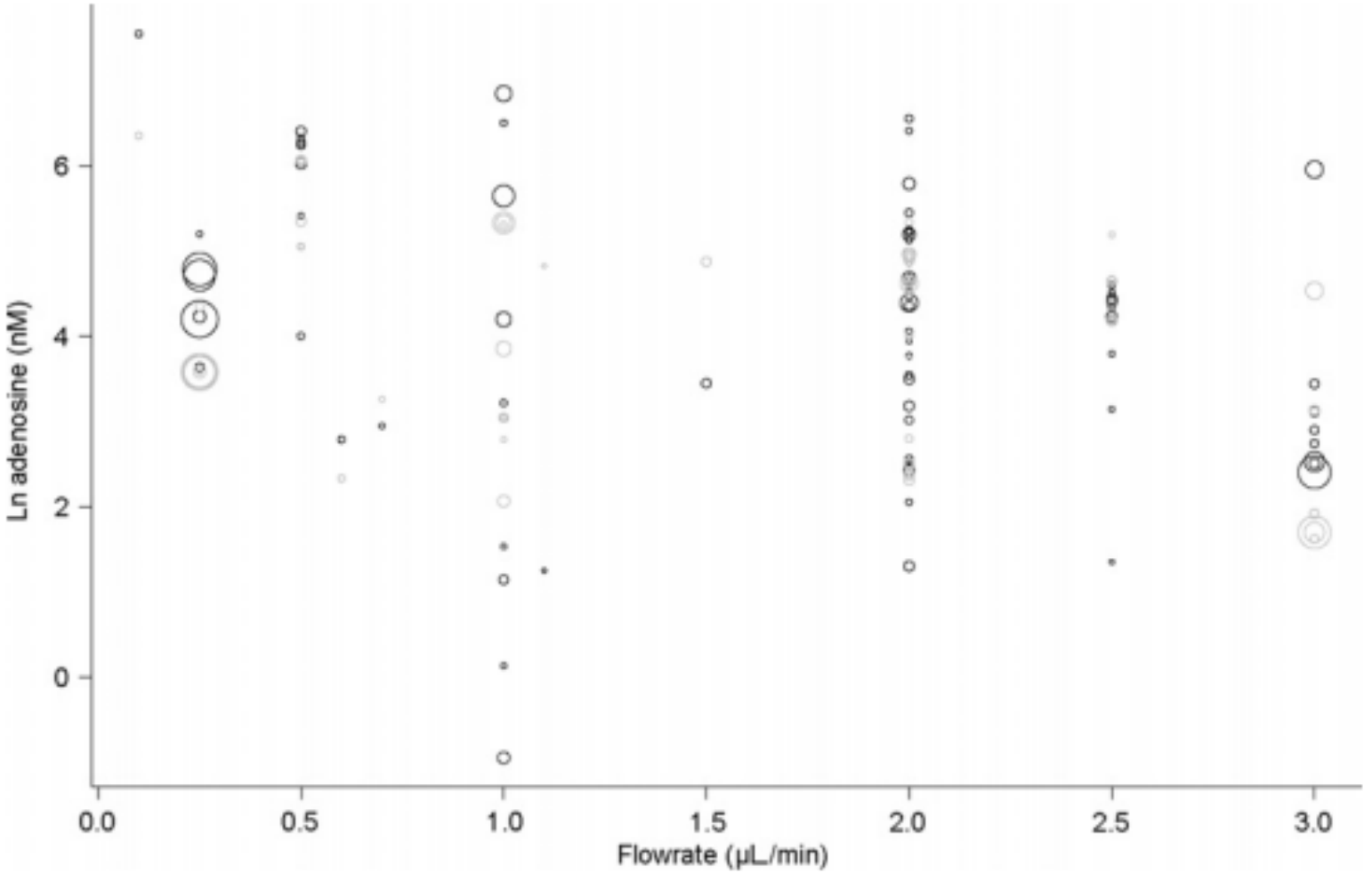
- Fixed/ random effects
- With or without moderators → meta-regression
- Inverse variance/ manual weighting

```
23  #meta-regression with rma function
24  mr_name <- rma(yi, sei, weights, mods,
25                 knha=TRUE, data)
26
```

Creating the corresponding bubble plot

```
27  # creating a bubble plot
28  # create a vector with the actual weigths
29  realweights <- weights (mr_name)
30  # make a bubble plot weight by precision
31  # note: if cex 2x larger, radius of bubble 2x larger, surface 4x
32  plot(objectname$columnforX,objectname$columnforY,cex=realweights,
33       pch=21, xlim=c(0,6), ylim=c(0,6),
34       xlab="Flowrate (µL/min)", ylab="Ln Adenosine (nM)")
```

Example bubble plot

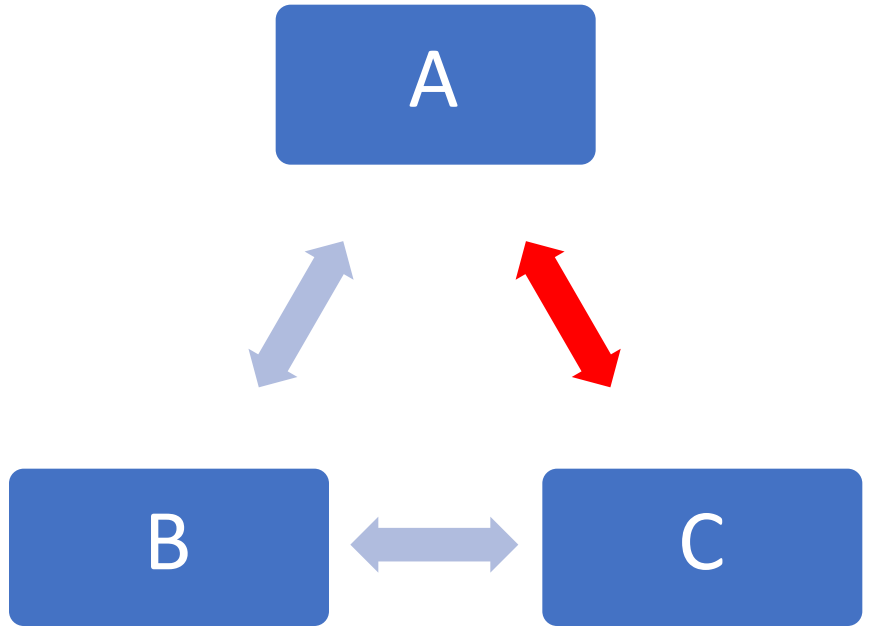


DOI: 10.1111/jnc.14552

Network Meta-analysis

Network meta-analysis

- Pairwise meta-analysis;
  compares pairs of treatments within a
  number of treatments for the same condition
- Transform your data (if needed)
- Fixed/ random effects
- based on estimates (`TE = Treatment Estimate`)
- Inverse variance weighting; SE




```
37  # Network MA
38  nm_name <-netmeta(TE, seTE, treat1, treat2, studlab, data=NULL,
39                    sm="SMD", comb.fixed=FALSE, reference.group="")
```

Resources

- Package documentation
- General R resources

- Meta-Analysis with R book (Use R!) – Schwarzer et al.