

Practical: Network meta-analysis of rare events

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R packages

We will use the **netmeta** command to run all network meta-analyses.

```
library(meta)
library(netmeta)
```

Data

Load the data by running the following command.

```
data(Gurusamy2011)
```

The data is from a NMA regarding methods to decrease blood loss and blood transfusion requirements for patients with liver transplantation.

Have a look at the dataset. Can you calculate the total event rate across all studies and arms?

Pairwise meta-analysis using different methods

Let's start by focusing on a particular comparison, Control/Placebo vs Aprotonin.

```
p1 = pairwise(treatment, death, n, studlab = study,
              data = Gurusamy2011, sm = "OR")
p2=p1[p1$treat1=="Control/Placebo"& p1$treat2=="Aprotonin",]
```

Let us perform a series of meta-analyses, using different methods:

```
m.IV <- metabin(event.e=event1, n.e=n1, event.c=event2, n.c=n2, data = p2,
method = "Inverse", sm="OR")
m.MH <- metabin(event.e=event1, n.e=n1, event.c=event2, n.c=n2, data = p2,
method = "MH", sm="OR")
m.Peto <- metabin(event.e=event1, n.e=n1, event.c=event2, n.c=n2, data = p2,
method = "Peto", sm="OR")
```

Now look at results. Do the different methods give similar results?

Inverse variance NMA

Now run the following R commands to fit an inverse-variance network meta-analysis model.

```
IV1 = netmetabin(p1, ref = "Control/Placebo", method = "Inverse",  
                comb.random = FALSE)
```

Plot the network graph

```
netgraph(IV1, seq = "optimal", col = "black", plastic = FALSE,  
         points = TRUE, pch = 21, cex.points = 3, col.points = "black",  
         bg.points = "gray", thickness = "se.fixed",  
         multiarm = FALSE, number.of.studies = TRUE)
```

Run the following commands to see results

```
summary(IV1)
```

and get the league table

```
netleague(IV1, digits=2)
```

Mantel-Haenszel NMA

In order to run a MH-NMA run the following:

```
MH1 = netmetabin(p1, ref = "Control/Placebo")
```

and check results:

```
summary(MH1)  
netleague(MH1, digits=2)  
forest(MH1)
```

Check results with the inverse variance NMA results. Do you see any differences? Where do you attribute them?

Non-central hypergeometric NMA

Now repeat the analysis using the non-central hypergeometric NMA model:

```
NCH1 = netmetabin(p1, ref = "Control/Placebo", method = "NCH")  
summary(NCH1)  
netleague(NCH1)  
forest(NCH1)
```

Compare results with the previous analyses

Inconsistency evaluation

In order to run the SIDDE approach to inconsistency, run the following command:

```
print(netsplit(MH1), show = "both", ci = TRUE, overall = FALSE)
```

Can you interpret the results?

If you have time, repeat the analyses for a different dataset:

```
data("Dong2013")
```