

Statistical Settings for Analyses

All analyses were done in R. The full R code is available in https://github.com/CER-METHODS/NMAstudio-app/blob/main/R_Codes/all_R_functions.R.

To allow flexibility, three data formats are supported: long, wide, and contrast. Long and wide data are automatically converted into contrast format using the pairwise function from the **meta** package. Examples for the long and wide formats are shown below:

Long format

If sm is RR or OR:

```
pair_dat <- meta::pairwise(data=dat,  
                           event=dat$r,  
                           n=dat$n,  
                           studlab=studlab, #study label  
                           treat=treat,  
                           incr=0.5,  
                           sm=sm)
```

If sm is MD or SMD:

```
pair_dat <- meta::pairwise(data=dat,  
                           mean=dat$y,  
                           sd=dat$sd,  
                           n=dat$n,  
                           studlab=studlab, #study label  
                           treat=treat,  
                           incr=0.5,  
                           sm=sm)
```

Wide format

If sm is RR or OR:

```
pair_dat <- meta::pairwise(data=dat,  
                           event=list(dat$r1, dat$r2),  
                           n=list(dat$n1, dat$n2),
```

```

studlab=studlab, #study label
treat=list(treat1,treat2),
incr=0.5,
sm=sm)

```

If sm is MD or SMD:

```

pair_dat <- meta::pairwise(data=dat,
                           mean=list(dat$y1, dat$y2),
                           sd=list(dat$sd1, dat$sd2),
                           n=list(dat$n1, dat$n2),
                           studlab=studlab, #study label
                           treat=list(treat1,treat2),
                           incr=0.5,
                           sm=sm)

```

The contrast-format data can then be used with the **netmeta** package to run a network meta-analysis, or with the **meta** package for pairwise meta-analysis. The code examples are as follows:

NMA

```

nma_temp <- netmeta(dat$TE,
                   dat$seTE,
                   dat$treat1,
                   dat$treat2,
                   dat$studlab,
                   sm = sm,
                   random = TRUE,
                   backtransf = TRUE,
                   reference.group = treatments[1])

```

Pairwise MA

```

model_temp <- metagen(dat$TE,
                     dat$seTE,
                     studlab = studlab,
                     data=dat_temp,

```

```
random = T,  
sm=sm,  
prediction=TRUE)
```