

## R Code for all analyses

```
#install.packages("meta")
#install.packages("netmeta")
#install.packages("metafor")
#install.packages("reshape")
#install.packages("calibrate")
library(reshape)
library(metafor)
library(meta)
library(netmeta)
library(calibrate)

# Read/ merge data

Level1<-read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_outcomes.csv",
header=T, fill=TRUE,na.strings=",sep=";",dec=",")
Level2_3<-read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_samples.csv",
header=T, fill=TRUE,na.strings=",sep=";",dec=",")

# Sort by Sample_ID and merge
Level1<-Level1[order(Level1$SampleID), ]
DATA1<-merge(Level2_3,Level1, by.x = "i..ReportID")

#cselect relevant studies for initial NMA

colnames(DATA1)[1] <- "studlab"

dat<- DATA1[ !(DATA1$studlab %in% c(3,5, 12, 66, 11, 105, 109, 168)), ] # in studies 3, 5,
12, 66 there was no post-treatment assessment, only follow-up data

# calculate effect sizes (SMD)

paired <- pairwise(treat = list(TR1, TR2, TR3),
  n = list(n_TR1, n_TR2, n_TR3),
  mean = list(Mt2TR1, Mt2TR2, Mt2TR3),
  sd = list(SDt2TR1, SDt2TR2, SDt2TR3),
  data = dat, studlab = studlab, sm= "SMD")

#combine effect sizes of the three subscales of the IES in studies 11 and 168

#install.packages("metaSEM")
#library(metaSEM)

#sub_11 <- subset(DATA1, studlab == "11")

#smds11 <- pairwise(treat = list(TR1, TR2),
#  # n = list(n_TR1, n_TR2),
#  # mean = list(Mt2TR1, Mt2TR2),
#  # sd = list(SDt2TR1, SDt2TR2),
#  # data = sub_11, studlab = OutcID, sm= "SMD")
```

```
#meta <- summary(meta3(y=smds11$TE, v= smds11$seTE, cluster=studlab, data=smds11))
```

```
#res.ml <- rma.mv(yi=smds11$TE, V= smds11$seTE, random = ~ 1 | studlab/OutcID,  
data=smds11)
```

```
studlab <- "11"  
treat1 <- "MBI"  
treat2 <- "WL"  
TE <- -0.48925  
seTE <- 0.28427  
age <- 51.80  
females <- 0.99  
severity <- "NA"  
income <- "high income"  
sample <- "civilian"  
arms <- 2  
self_exp <- "self-rated"  
n_TR1 <- 32  
n_TR2 <- 39  
n_total <- 71  
tr_size <- "small-moderate"  
analysis <- "ITT"
```

```
B11 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age, females, severity,  
income, sample, arms, self_exp, n_TR1, n_TR2, n_total, tr_size, analysis)
```

```
#sub_168 <- subset(DATA1, studlab == "168")
```

```
#smds168 <- pairwise(treat = list(TR1, TR2),  
# n = list(n_TR1, n_TR2),  
# mean = list(Mt2TR1, Mt2TR2),  
# sd = list(SDt2TR1, SDt2TR2),  
# data = sub_168, studlab = OutcID, sm= "SMD")
```

```
#meta <- summary(meta3(y=smds168$TE, v= smds168$seTE, cluster=studlab,  
data=smds168))
```

```
#res.ml <- rma.mv(yi=smds168$TE, V= smds168$seTE, random = ~ 1 | studlab/OutcID,  
data=smds168)
```

```
studlab <- "168"  
treat1 <- "NET"  
treat2 <- "WL"  
TE <- -1.6661  
seTE <- 0.41205  
age <- 55.73
```

```

females <- 0.77
severity <- "clinical"
income <- "low/mid.income"
sample <- "civilian"
arms <- 2
self_exp <- "self-rated"
n_TR1 <- 11
n_TR2 <- 11
n_total <- 22
tr_size <- "very small"
analysis <- "completers"

Z168 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age,
                  females, severity, severity, income, sample, arms, self_exp, n_TR1, n_TR2,
                  n_total, tr_size, analysis)

#merge all into one data frame

data <- merge_all(list(paired, B11, Z168),
                  by= c("studlab", "treat1", "treat2", "TE", "seTE", "age", "females", "severity",
                  "income",
                  "sample", "arms", "self_exp", "n_TR1", "n_TR2", "n_total", "tr_size",
                  "analysis"), all.x=TRUE, all.y=TRUE)

dat1 <- subset(data, select = c(studlab, treat1, treat2, n1, mean1, sd1, n2, mean2, sd2, TE,
seTE, OutcID, age,
                  females, severity, income, sample, arms, self_exp, n_total, tr_size,
                  analysis))
dat1<-dat1[order(dat1$OutcID), ]

#calculate the median of the number of participants per arm across all studies, range, and total

Ns <- data.frame(data$n_TR1, data$n_TR2)
merged <- reshape(Ns, varying = list(1:2), direction = "long")
median_n <- median(merged$data.n_TR1)
median_n
min(merged$data.n_TR1)
max(merged$data.n_TR1)
sum(Ns)

#### network geometry ####

#density
E <- 29
N <- 12
dens <- (2*E)/(N*(N-1))
dens

#percentage of common comparators
# = (N with >1 connections /N) x 100

```

```

n <- 12
comcomp <- (n/N)*100
comcomp

#percentage of strong edges
# = (E with >1 study /E) x 100

e <- 14
strongEd <- (e/E)*100
strongEd

##### NETWORK META ANALYSIS #####

mn1 <- netmeta(TE, seTE, treat1, treat2, studlab, data=dat1, sm="SMD", tol.multiarm =
0.0015, comb.random=TRUE, prediction = TRUE)
#print(mn1, digits=2)
print(summary(mn1), digits= 2)
league.table<- netleague(mn1, comb.random = mn1$comb.random, ci= TRUE, digits= 2)
netrank <- netrank(mn1, small.values = "good")
print(netrank, sort= TRUE, digits = 2)

#network plot
netgraph(mn1, seq=c("WL", "PE", "CPT", "CT", "EMDR", "MBI", "PCT", "SIT", "REL",
"NET", "IPT", "PsEd"))

#forest plot with treatments compared to reference group "WL"
forest(mn1, xlim=c(-1.5, 1), ref="WL",
      leftlabs="Contrast to Waitlist",
      xlab="PTSD severity difference",
      pooled="random")

#forest plot with treatments compared to reference group "PCT"
forest(mn1, xlim=c(-1.5, 1), ref="PCT",
      leftlabs="Contrast to PCT",
      xlab="PTSD severity difference",
      pooled="random")

##### Assessment of Heterogeneity and Inconsistency

#use the decomp.design function to calculate the Q statistics (within- and between-designs
(inconsistency))
round(decomp.design(mn1)$Q.decomp, 3) #here: fixed effects model used

#further decomposition of the within heterogeneity
print(decomp.design(mn1)$Q.het.design, digits=2)

#The decomp.design function also gives the between-designs Q statistic based on a random
effects model.
#This can be calculated based on a full designby-treatment interaction random effects model
# round(decomp.design(mn1)$Q.inc.random, 3)

```

```

#net heat plot (1. contribution to network estimate, 2. inconsistency decomposition)
netheat(mn1) #fixed effects model

# The contributions of each design can also be printed as follows:
round(decomp.design(mn1)$Q.inc.design, 2)

# Data frame with between-designs Q statistics (Q) of the fixxed effects model after detaching
of single designs
print(decomp.design(mn1)$Q.inc.detach, digits=3)

#local approach to test consistency assumption
print(netsplit(mn1), digits=3)

#random effects model
#netheat(mn1, random=TRUE)

##### Adressing Heterogeneity: visual examination of studies #####

# heterogenety in design EMDR versus WL
EMDR_WL <- data[which(data$treat1=="EMDR" & data$treat2=="WL"), ]
plot(EMDR_WL$TE, EMDR_WL$seTE, xlab = "SMD", ylab= "standard error", type= "p",
pch = 21, bg= "blue", col= "blue", xlim = c(-5,0), ylim = c(0,1))
textxy(EMDR_WL$TE, EMDR_WL$seTE, EMDR_WL$studlab, cex = 0.9)
MA_emdrwl <- rma(measure = "SMD", yi=TE, vi= seTE, slab = studlab, data = EMDR_WL)
baujat(MA_emdrwl, symbol= "slab")
# outlier diagnostics
influence(MA_emdrwl, 2)
plot(influence(MA_emdrwl))
forest(MA_emdrwl, showweights = TRUE)
funnel(MA_emdrwl)

# heterogeneity in CPT versus WL
CPT_WL <- data[which(data$treat1=="CPT" & data$treat2=="WL"), ]
plot(CPT_WL$TE, CPT_WL$seTE, xlab = "SMD", ylab= "standard error", type= "p", pch =
21, bg= "blue", col= "blue", xlim = c(-2,0), ylim = c(0,1))
textxy(CPT_WL$TE, CPT_WL$seTE, CPT_WL$studlab, cex = 0.9)
MA_cptwl <- rma(measure = "SMD", yi=TE, vi= seTE, slab = studlab, data = CPT_WL)
# outlier diagnostics
influence(MA_cptwl, 2)
plot(influence(MA_cptwl))

# heterogeneity in MBI versus WL
MBI_WL <- data[which(data$treat1=="MBI" & data$treat2=="WL"), ]
plot(MBI_WL$TE, MBI_WL$seTE, xlab = "SMD", ylab= "standard error", type= "p", pch =
21, bg= "blue", col= "blue", xlim = c(-2,1), ylim = c(0,1))
textxy(MBI_WL$TE, MBI_WL$seTE, MBI_WL$studlab, cex = 0.9)
MA_mbiwl <- rma(measure = "SMD", yi=TE, vi= seTE, slab = studlab, data = MBI_WL)
plot(MA_mbiwl)
# outlier diagnostics
influence(MA_mbiwl, 2)
plot(influence(MA_mbiwl))

```

```
funnel(MA_mbiwl)
```

```
# heterogeneity in NET versus WL
```

```
NET_WL <- data[which(data$treat1=="NET" & data$treat2=="WL"), ]  
plot(NET_WL$TE, NET_WL$seTE, xlab = "SMD", ylab= "standard error", type= "p", pch =  
21, bg= "blue", col= "blue", xlim = c(-5,0), ylim = c(0,1))  
textxy(NET_WL$TE, NET_WL$seTE, NET_WL$studlab, cex = 0.9)  
NET_WL  
MA_netwl <- rma(measure ="SMD", yi=TE, vi= seTE, slab = studlab, data = NET_WL)  
plot(MA_netwl)  
# outlier diagnostics  
influence(MA_netwl, 2)  
plot(influence(MA_netwl))
```

```
# heterogeneity in PE versus WL
```

```
PE_WL <- data[which(data$treat1=="PE" & data$treat2=="WL"), ]  
MA_pewl <- rma(measure ="SMD", yi=TE, vi= seTE, data = PE_WL)  
plot(MA_pewl)  
#outlier diagnostics  
influence(MA_pewl, 2)  
plot(influence(MA_pewl))
```

```
#heterogeneity in CT versus WL
```

```
CT_WL <- data[which(data$treat1=="CT" & data$treat2=="WL"), ]  
MA_ctwl <- rma(measure ="SMD", yi=TE, vi= seTE, data = CT_WL)  
#outlier diagnostics  
influence(MA_ctwl, 2)  
plot(influence(MA_ctwl))  
funnel(MA_ctwl)
```

```
#heterogeneity in PCT versus PE
```

```
PCT_PE <- data[which(data$treat1=="PE" & data$treat2=="PCT"), ]  
MA_pctPE <- rma(measure ="SMD", yi=TE, vi= seTE, data = PCT_PE)  
#outlier diagnostics  
influence(MA_pctPE, 2)  
plot(influence(MA_pctPE))
```

```
# heterogeneity in PCT versus WL
```

```
PCT_WL <- data[which(data$treat1=="PCT" & data$treat2=="WL"), ]  
MA_pctWL <- rma(measure ="SMD", yi=TE, vi= seTE, data = PCT_WL)  
#outlier diagnostics  
influence(MA_pctWL, 2)  
plot(influence(MA_pctWL))
```

```
#heterogeneity in EMDR versus PE
```

```
PE_EMDR <- data[which(data$treat1=="PE" & data$treat2=="EMDR"), ]  
MA_peemdr <- rma(measure ="SMD", yi=TE, vi= seTE, data = PE_EMDR)  
#outlier diagnostics  
influence(MA_peemdr, 2)  
plot(influence(MA_peemdr))
```

```

# heterogeneity in IPT versus WL
IPT_WL <- data[which(data$treat1=="IPT" & data$treat2=="WL"), ]
MA_ipWL <- rma(measure="SMD", yi=TE, vi=seTE, data=IPT_WL)
#outlier diagnostics
influence(MA_ipWL, 2)
plot(influence(MA_ipWL))

# visual examination of data in remaining designs (no sign. heterogeneity in the NMA)
SIT_WL <- data[which(data$treat1=="SIT" & data$treat2=="WL"), ]
PsEd_WL <- data[which(data$treat1=="PsEd" & data$treat2=="WL"), ]
REL_WL <- data[which(data$treat1=="REL" & data$treat2=="WL"), ]
CPT_CT <- data[which(data$treat1=="CPT" & data$treat2=="CT"), ]
CPT_PCT <- data[which(data$treat1=="CPT" & data$treat2=="PCT"), ]
CPT_PE <- data[which(data$treat1=="CPT" & data$treat2=="PE"), ]
CPT_PsEd <- data[which(data$treat1=="CPT" & data$treat2=="PsEd"), ]
CPT_REL <- data[which(data$treat1=="CPT" & data$treat2=="REL"), ]
CPT_SIT <- data[which(data$treat1=="CPT" & data$treat2=="SIT"), ]
CT_EMDR <- data[which(data$treat1=="CT" & data$treat2=="EMDR"), ]
CT_IPT <- data[which(data$treat1=="CT" & data$treat2=="IPT"), ]
CT_MBI <- data[which(data$treat1=="MBI" & data$treat2=="CT"), ]
CT_NET <- data[which(data$treat1=="NET" & data$treat2=="CT"), ]

### subgroup analyses ###

# moderator variable 'sample type'

civilian <- netmeta(TE, seTE, treat1, treat2, studlab, data=dat1, subset=(sample=="civilian"),
sm="SMD", tol.multiarm = 0.0015, comb.random=TRUE)
veteran <- netmeta(TE, seTE, treat1, treat2, studlab, data=dat1, subset=(sample=="veteran/military"), sm="SMD", comb.random=TRUE)
refugees <- netmeta(TE, seTE, treat1, treat2, studlab, data=dat1, subset=(sample=="refugees"), sm="SMD", comb.random=TRUE)
#mixed not included in subgroup analyses (few cases + no valid interpretation possible)

#moderator variable 'sample-level PTSD severity'
clinical <- netmeta(TE, seTE, treat1, treat2, studlab, data=dat1, subset=(severity=="clinical"),
sm="SMD", tol.multiarm = 0.0015, comb.random=TRUE)
subcl_mix <- dat1[which(dat1$severity=="subclinical" | dat1$severity=="mixed"), ]
subclin.mixed <- netmeta(TE, seTE, treat1, treat2, studlab, data=subcl_mix, sm="SMD",
comb.random=TRUE)

#trials investigating NET vs. WL: Meta-Regression of high- vs low-/middle-income countries

#NETtrials <- subset(dat1, treat1=="NET" | treat2=="WL")
#NETlowinc<- rma(measure="SMD", yi=TE, vi=seTE, mods=~relevel(factor(income),
ref="high income"), knha=TRUE, data=NETtrials)
# too few studies; therefore, this analysis (which was included in the pre-specified analysis
plan) is omitted

### #SENSITIVITY ANALYSES #####

```

```

# assess difference between ESs based on self- vs. expert-ratings in studies that report both

selfexp <- read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/self_expert.csv",
header=T, fill=TRUE, na.strings="", sep=";", dec=",")
colnames(selfexp)[1] <- "studlab"

selfrated <- subset(selfexp, self_exp == "self-rated")
selfrated <- selfrated[!(selfrated$studlab %in% c(17, 104)), ]

SMDs_self <- pairwise(treat = list(TR1, TR2, TR3),
n = list(n_TR1, n_TR2, n_TR3),
mean = list(Mt2TR1, Mt2TR2, Mt2TR3),
sd = list(SDt2TR1, SDt2TR2, SDt2TR3),
data = selfrated, studlab = studlab, sm= "SMD")

mn_self <- netmeta(TE, seTE, treat1, treat2, studlab, data= SMDs_self, sm="SMD",
comb.random=TRUE)
print(summary(mn_self))
league.tab<- netleague(mn_self, comb.random = mn1$comb.random, ci= TRUE, digits= 2)
forest(mn_self, xlim=c(-1.5, 1), ref="WL",
leftlabs="Contrast to WL",
xlab="PTSD severity difference",
pooled="random")

clinrated <- subset(selfexp, self_exp == "clinician-rated")

SMDs_exp <- pairwise(treat = list(TR1, TR2, TR3),
n = list(n_TR1, n_TR2, n_TR3),
mean = list(Mt2TR1, Mt2TR2, Mt2TR3),
sd = list(SDt2TR1, SDt2TR2, SDt2TR3),
data = clinrated, studlab = studlab, sm= "SMD")

mn_exp <- netmeta(TE, seTE, treat1, treat2, studlab, data=SMDs_exp, sm="SMD",
comb.random=TRUE)
print(summary(mn_exp))
league.tab2<- netleague(mn_exp, comb.random = mn_exp$comb.random, ci= TRUE, digits=
2)
forest(mn_exp, xlim=c(-1.5, 1), ref="WL",
leftlabs="Contrast to WL",
xlab="PTSD severity difference",
pooled="random")

# assess difference between total data sets: data set 1 with self-rated given precedence, data
set 2 with clinician-rated given precedence

selfoverclin <-
read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_out_selfoverclin.csv",
header=T, fill=TRUE, na.strings="", sep=";", dec=",")
Lev2_3<-read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_samples.csv",
header=T, fill=TRUE, na.strings="", sep=";", dec=",")
Lev1<-selfoverclin[order(selfoverclin$SampleID), ]

```



```
selfoverclin <- merge(Lev2_3, Lev1, by.x = "i..ReportID")
colnames(selfoverclin)[1] <- "studlab"
```

```
selfoverclin <- selfoverclin[!(selfoverclin$studlab %in% c(3,5, 66, 11, 12, 105, 109, 168)), ] #
in studies 3,5,66 there was no post-treatment assessment, only follow-up data
```

```
effectsizes <- pairwise(treat = list(TR1, TR2, TR3),
  n = list(n_TR1, n_TR2, n_TR3),
  mean = list(Mt2TR1, Mt2TR2, Mt2TR3),
  sd = list(SDt2TR1, SDt2TR2, SDt2TR3),
  data = selfoverclin, studlab = studlab, sm = "SMD")
```

```
studlab <- "11"
treat1 <- "MBI"
treat2 <- "WL"
TE <- -0.48925
seTE <- 0.28427
age <- 51.80
females <- 0.99
severity <- "NA"
income <- "high income"
sample <- "civilian"
arms <- 2
self_exp <- "self-rated"
n_TR1 <- 32
n_TR2 <- 39
n_total <- 71
tr_size <- "small-moderate"
analysis <- "ITT"
B11 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age, females, severity,
  income, sample, arms, self_exp, n_TR1, n_TR2, n_total, tr_size, analysis)
```

```
studlab <- "168"
treat1 <- "NET"
treat2 <- "WL"
TE <- -1.6661
seTE <- 0.41205
age <- 55.73
females <- 0.77
severity <- "clinical"
income <- "lowmid"
sample <- "civilian"
arms <- 2
self_exp <- "self-rated"
n_TR1 <- 11
n_TR2 <- 11
n_total <- 22
tr_size <- "very small"
analysis <- "completers"
Z168 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age,
```

```

      females, severity, severity, income, sample, arms, self_exp, n_TR1, n_TR2,
n_total, tr_size, analysis)

selfrated <- merge_all(list(effectsizes, B11, Z168),
      by= c("studlab", "treat1", "treat2", "TE", "seTE", "age", "females", "severity",
"income",
      "sample", "arms", "self_exp", "n_TR1", "n_TR2", "n_total", "tr_size",
"analysis"), all.x=TRUE, all.y=TRUE)
self_ov_exp <- netmeta(TE, seTE, treat1, treat2, studlab, data=selfrated, sm="SMD",
tol.multiarm = 0.0015, comb.random=TRUE)
print(summary(self_ov_exp))
netrank_self <- netrank(self_ov_exp, small.values = "good")
print(netrank_self, sort= TRUE, digits = 2)
league.tab3<- netleague(self_ov_exp, comb.random = self_ov_exp$comb.random, ci= TRUE,
digits= 2)
forest(self_ov_exp, xlim=c(-1.5, 1), ref="WL",
      leftlabs="Contrast to WL",
      xlab="PTSD severity difference",
      pooled="random")

# assess differences between NMA PP > ITT versus NMA ITT > PP

PPoverITT <-
read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_out_PPoverITT.csv",
header=T, fill=TRUE,na.strings=","sep=";",dec=",")
Lev2_3<-read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_samples.csv",
header=T, fill=TRUE,na.strings=","sep=";",dec=",")
Lev1<-PPoverITT[order(PPoverITT$SampleID), ]
PPoverITT <-merge(Lev2_3,Lev1, by.x = "i..ReportID")
colnames(PPoverITT)[1] <- "studlab"

PPoverITT<- PPoverITT[ !(PPoverITT$studlab %in% c( 11, 168)), ]

effects <- pairwise(treat = list(TR1, TR2, TR3),
      n = list(n_TR1, n_TR2, n_TR3),
      mean = list(Mt2TR1, Mt2TR2, Mt2TR3),
      sd = list(SDt2TR1, SDt2TR2, SDt2TR3),
      data = PPoverITT, studlab = studlab, sm= "SMD")

studlab <- "11"
treat1 <- "MBI"
treat2 <- "WL"
TE <- -0.48925
seTE <- 0.28427
age <- 51.80
females <- 0.99
severity <- "NA"
income <- "high income"
sample <- "civilian"
arms <-2
self_exp <- "self-rated"

```

```

n_TR1 <- 32
n_TR2 <- 39
n_total <- 71
tr_size <- "small-moderate"
analysis <- "ITT"
B11 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age, females, severity,
                  income, sample, arms, self_exp, n_TR1, n_TR2, n_total, tr_size, analysis)

studlab <- "168"
treat1 <- "NET"
treat2 <- "WL"
TE <- -1.6661
seTE <- 0.41205
age <- 55.73
females <- 0.77
severity <- "clinical"
income <- "lowmid"
sample <- "civilian"
arms <- 2
self_exp <- "self-rated"
n_TR1 <- 11
n_TR2 <- 11
n_total <- 22
tr_size <- "very small"
analysis <- "completers"
Z168 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age,
                  females, severity, severity, income, sample, arms, self_exp, n_TR1, n_TR2,
                  n_total, tr_size, analysis)

PPoverITT <- merge_all(list(effects, B11, Z168),
                      by= c("studlab", "treat1", "treat2", "TE", "seTE", "age", "females", "severity",
                          "income",
                          "sample", "arms", "self_exp", "n_TR1", "n_TR2", "n_total", "tr_size",
                          "analysis"), all.x=TRUE, all.y=TRUE)
PP_over_ITT <- netmeta(TE, seTE, treat1, treat2, studlab, data=PPoverITT, sm="SMD",
                      tol.multiarm = 0.0015, comb.random=TRUE)
print(summary(PP_over_ITT))
netrank_PP <- netrank(PP_over_ITT, small.values = "good")
print(netrank_PP, sort= TRUE, digits = 2)
league.tab4 <- netleague(PP_over_ITT, comb.random = PP_over_ITT$comb.random, ci=
TRUE, digits= 2)
forest(PP_over_ITT, xlim=c(-1.7, 0.5), ref="WL",
      leftlabs="Contrast to Waitlist",
      xlab="PTSD severity difference",
      pooled="random")

#### network meta-analysis of studies with a moderate risk of bias and/or high primary study
quality #####

```

```

highPSQ <-
read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_out_PSQfilter.csv",
header=T, fill=TRUE,na.strings=","sep=";",dec=",")
L2_3<-read.csv("C:/Users/rebec/Documents/Masterarbeit/Kodierung/data_samples.csv",
header=T, fill=TRUE,na.strings=","sep=";",dec=",")
L1<-highPSQ[order(highPSQ$SampleID), ]
highPSQ <-merge(L2_3,L1, by.x = "i..ReportID")
colnames(highPSQ)[1] <- "studlab"

highPSQ<- highPSQ[ !(highPSQ$studlab %in% c( 11, 168)), ]

effects <- pairwise(treat = list(TR1, TR2, TR3),
                    n = list(n_TR1, n_TR2, n_TR3),
                    mean = list(Mt2TR1, Mt2TR2, Mt2TR3),
                    sd = list(SDt2TR1, SDt2TR2, SDt2TR3),
                    data = highPSQ, studlab = studlab, sm= "SMD")

studlab <- "11"
treat1 <- "MBI"
treat2 <- "WL"
TE <- -0.48925
seTE <- 0.28427
age <- 51.80
females <- 0.99
severity <- "NA"
income <- "high income"
sample <- "civilian"
arms <-2
self_exp <- "self-rated"
n_TR1 <- 32
n_TR2 <-39
n_total <-71
tr_size <- "small-moderate"
analysis <- "ITT"
B11 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age, females, severity,
                 income, sample, arms, self_exp, n_TR1, n_TR2, n_total, tr_size, analysis)

studlab <- "168"
treat1 <- "NET"
treat2 <- "WL"
TE <- -1.6661
seTE <- 0.41205
age <- 55.73
females <- 0.77
severity <- "clinical"
income <- "lowmid"
sample <- "civilian"
arms <-2
self_exp <- "self-rated"
n_TR1 <- 11
n_TR2 <-11
n_total <-22

```

```

tr_size <- "very small"
analysis <- "completers"
Z168 <- data.frame(studlab, treat1, treat2, TE, seTE=round(seTE, 2), age,
  females, severity, severity, income, sample, arms, self_exp, n_TR1, n_TR2,
  n_total, tr_size, analysis)

high.psq <- merge_all(list(effects, B11, Z168),
  by= c("studlab", "treat1", "treat2", "TE", "seTE", "age", "females", "severity",
  "income",
  "sample", "arms", "self_exp", "n_TR1", "n_TR2", "n_total", "tr_size",
  "analysis"), all.x=TRUE, all.y=TRUE)

high.psq.nma <- netmeta(TE, seTE, treat1, treat2, studlab, data= high.psq, sm="SMD",
  comb.random=TRUE)
print(summary(high.psq.nma))

netgraph(high.psq.nma)
forest(high.psq.nma, xlim=c(-1.7, 0.5), ref="WL",
  leftlabs="Contrast to Waitlist",
  xlab="PTSD severity difference",
  pooled="random")
print(decomp.design(high.psq.nma)$Q.het.design, digits=2)
netheat(high.psq.nma)
round(decomp.design(high.psq.nma)$Q.inc.design, 2)
decomp.design(high.psq.nma)$Q.inc.detach
netrank.psq <- netrank(high.psq.nma, small.values = "good")
print(netrank.psq, sort= TRUE, digits = 2)

#### OUTLIER DETECTION IN THE INITIAL NMA ####

install.packages("devtools")
devtools::install_github("petropouloumaria/NMAoutlier")
library(NMAoutlier)

# omit the 3-arm-study with inconsistent treatment effects (because argument 'tol.multiarm'
cannot be applied in this package)
dat1<- dat1[ !(dat1$studlab== "34"), ]

# outlier detection using NMAoutlier function
outliers <- NMAoutlier(TE, seTE, treat1, treat2, studlab, data= dat1, sm= "SMD")

# visualization of results
fwdplot(outliers,"cook")
fwdplot(outliers,"estand", 4) # standardized residuals for study 4
fwdplot(outliers, "ratio")
fwdplot(outliers,"heterog")
fwdplot(outliers,"Q")
fwdplot(outliers, "nsplit")
fwdplotest(outliers)
ord <- c("EMDR", "CPT", "CT", "IPT", "PE", "SIT", "NET", "MBI", "REL", "PCT", "PsEd",
"WL")

```

```

library(metafor)
funnel(mn1, order= ord, pooled = "random", linreg= TRUE, pch= c(1:10), col = 1:6)

##### NMA after exclusion of outliers #####

# exclusion of outliers at design level in pairwise Meta-analysis: Studies with extreme effects
are studies 68 and 167

outlier.exclusion1 <- dat1[ !(dat1$studlab %in% c(68,167)), ]
mn3 <- netmeta(TE, seTE, treat1, treat2, studlab, data= outlier.exclusion1, sm="SMD",
tol.multiarm = 0.0015, comb.random=TRUE)
print(summary(mn3), digits=2)
netleague(mn3, digits=2)
forest(mn3, xlim=c(-1.7, 0.5), ref="WL",
      leftlabs="Contrast to Waitlist",
      xlab="PTSD severity difference",
      pooled="random")
# heterogeneity statistics
print(decomp.design(mn3)$Q.het.design, digits=2)
netheat(mn3)
#treatment rankings
netrank1 <- netrank(mn3, small.values = "good")
print(netrank1, sort= TRUE, digits = 2)

# exclusion of outliers on NMA-level: excluding studies 107, 158, 87

outlier.exclusion2 <- dat1[ !(dat1$studlab %in% c(107, 22, 87)), ]
mn4 <- netmeta(TE, seTE, treat1, treat2, studlab, data= outlier.exclusion2, sm="SMD",
tol.multiarm = 0.0015, comb.random=TRUE)
print(summary(mn4), digits=2)
netleague(mn4, digits=2)
forest(mn4, xlim=c(-1.7, 0.5), ref="WL",
      leftlabs="Contrast to Waitlist",
      xlab="PTSD severity difference",
      pooled="random")
# heterogeneity statistics
print(decomp.design(mn4)$Q.het.design, digits=2)
netheat(mn4)
#treatment rankings
netrank2 <- netrank(mn4, small.values = "good")
print(netrank2, sort= TRUE, digits = 2)

# exclusion of all outliers at all levels

outlier.exclusion3 <- dat1[ !(dat1$studlab %in% c(68, 167,107, 22, 87)), ]
mn5 <- netmeta(TE, seTE, treat1, treat2, studlab, data= outlier.exclusion3, sm="SMD",
tol.multiarm = 0.0015, comb.random=TRUE)
print(summary(mn5), digits=2)
netleague(mn5, digits=2)
forest(mn5, xlim=c(-1.7, 0.5), ref="WL",
      leftlabs="Contrast to Waitlist",

```

```

      xlab="PTSD severity difference",
      pooled="random")
# heterogeneity statistics
print(decomp.design(mn5)$Q.het.design, digits=2)
netheat(mn5)
#treatment rankings
netrank3 <- netrank(mn5, small.values = "good")
print(netrank3, sort= TRUE, digits = 2)

##### further information to assess the quality and certainty of evidence #####

# contributions of individual studies to estimates in the network

options(max.print = 100000000)
netimpact(mn1, verbose = FALSE)

netmeasures(mn1, random = mn1$comb.random, warn= TRUE)

# direct evidence proportion, mean pathlength and minimal parallelism
# (= measures of indirectness and robustness of estimates in the NMA)

devtools::install_github("MathiasHarrer/dmetar")
library(dmetar)
direct.evidence.plot(x= mn1)

##### to further assess transitivity in the network: visual examination of distributions of effect
modifiers

#sample type 1
veterans <- subset(dat1, sample == "veteran/military")
refugees <- subset(dat1, sample == "refugees")
civilians <- subset(dat1, sample == "civilian")

# sample type 2
clinical <- subset(dat1, severity == "clinical")
subclinical <- subset(dat1, severity == "subclinical")
mixed.clin <- subset(dat1, severity == "mixed")

# analysis
per.protocol<- subset(dat1, analysis == "completers")
ITT <- subset(dat1, analysis == "ITT")

#trial size
moderate <- subset(dat1, tr_size == "small-moderate")
large <- subset(dat1, tr_size == "large")
very.small <- subset(dat1, tr_size == "very small")

```