####################################### R code used for analyses ########################################

# The following code shows the script for our analysis. We had data from four cohorts stored in R as four separate data.frames objects called wemwbs\_ncds, wemwbs\_nihs, wemwbs\_nspn and wemwbs\_sals. The structure of each data.frame is outlined below and was the same across all cohorts.

# head(wemwbs\_ncds)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| # | ID | sex | i1 | i2 | i3 | i4 | i5 | i6 | i7 | i8 | i9 | i10 | i11 | i12 | i13 | i14 |
| # | N10001N | Female | 4 | 3 | 5 | 5 | 4 | 5 | 5 | 5 | 4 | 5 | 5 | 2 | 5 | 4 |
| # | N10002P | Male | 4 | 4 | 4 | 2 | 4 | 4 | 4 | 4 | 3 | 4 | 5 | 5 | 4 | 4 |
| # | N10007U | Female | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 5 | 5 | 5 | 5 |
| # | N10008V | Male | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 4 | 3 | 5 | 5 | 5 | 4 |
| # | N10009W | Male | 4 | 4 | 4 | 4 | 3 | 4 | 4 | 4 | 3 | 4 | 5 | 4 | 4 | 4 |
| # | N10011Q | Male | 4 | 4 | 3 | 4 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |

# sets working directory

setwd("D:/..../") # please insert the path to working directory where you want to save figures

# installs required packages

install.packages(c("qgpraph", "NetworkComparisonTest", "bootnet","networktools", "ggplot2", "gridExtra","EstimateGroupNetwork", "mgm", "reshape", "lemon", "dplyr"), dependencies=T)

# loads required packages

require(qgraph); require(NetworkComparisonTest); require(bootnet); require(networktools); require(ggplot2); require(gridExtra); require(EstimateGroupNetwork); require(mgm); require(reshape); require(lemon); require(dplyr)

# excludes individuals with missing data

wemwbs\_ncds <- na.omit(wemwbs\_ncds)

wemwbs\_nihs <- na.omit(wemwbs\_nihs)

wemwbs\_nspn <- na.omit(wemwbs\_nspn)

wemwbs\_sals <- na.omit(wemwbs\_sals)

# makes Table 1: WEMWBS item labels, wording, and item means (standard deviations) across samples

temp1 <- round(colMeans(wemwbs\_ncds[,3:16], na.rm = TRUE),2)

temp2 <- round(colMeans(wemwbs\_nihs[,3:16], na.rm = TRUE),2)

temp3 <- round(colMeans(wemwbs\_nspn[,3:16], na.rm = TRUE),2)

temp4 <- round(colMeans(wemwbs\_sals[,3:16], na.rm = TRUE),2)

temp1 <- paste(temp1, " (", round(apply(wemwbs\_ncds[,3:16], 2, sd),2), ")", sep="")

temp2 <- paste(temp2, " (", round(apply(wemwbs\_nihs[,3:16], 2, sd),2), ")", sep="")

temp3 <- paste(temp3, " (", round(apply(wemwbs\_nspn[,3:16], 2, sd),2), ")", sep="")

temp4 <- paste(temp4, " (", round(apply(wemwbs\_sals[,3:16], 2, sd),2), ")", sep="")

itemstats <- data.frame('Item label'= paste("i",1:14, sep=""), Statement=c(

"I have been feeling optimistic about the future",

"I have been feeling useful",

"I have been feeling relaxed",

"I have been feeling interested in other people",

"I have had energy to spare",

"I have been dealing with problems well",

"I have been thinking clearly",

"I have been feeling good about myself",

"I have been feeling close to other people",

"I have been feeling confident",

"I have been able to make up my own mind about things",

"I have been feeling loved",

"I have been interested in new things",

"I have been feeling cheerful"), 'NCDS'=temp1, 'NIHS'=temp2, 'NSPN'=temp3, 'SALSUS'=temp4)

itemstats

# estimates networks using mgm package and computes node predictability

temp1 <- mgm(wemwbs\_ncds[,3:16], type=rep('g', 14), lev=rep(1,14), k=2)

pred\_ncds <- predict(temp1, wemwbs\_ncds[,3:16], error.continuous='VarExpl')

temp2 <- mgm(wemwbs\_nihs[,3:16], type=rep('g', 14), lev=rep(1,14), k=2)

pred\_nihs <- predict(temp2, wemwbs\_nihs[,3:16], error.continuous='VarExpl')

temp3 <- mgm(wemwbs\_nspn[,3:16], type=rep('g', 14), lev=rep(1,14), k=2)

pred\_nspn <- predict(temp3, wemwbs\_nspn[,3:16], error.continuous='VarExpl')

temp4 <- mgm(wemwbs\_sals[,3:16], type=rep('g', 14), lev=rep(1,14), k=2)

pred\_sals <- predict(temp4, wemwbs\_sals[,3:16], error.continuous='VarExpl')

# computes fused graphical LASSO networks

groupnetwork\_kfold <- EstimateGroupNetwork(list(wemwbs\_ncds[,3:16],wemwbs\_nihs[,3:16],wemwbs\_nspn[,3:16],wemwbs\_sals[,3:16]),inputType = "list.of.dataframes", covfun = cor\_auto, method = "crossvalidation", strategy = "sequential", k = 10, seed=1234, criterion = c("ebic", "bic", "aic"), count.unique = FALSE, optimize = TRUE, optmethod = "CG", penalty = "fused", weights = "equal", penalize.diagonal = FALSE, ncores = 4, simplifyOutput = FALSE)

# makes Figure 1: Networks of WEMWBS items in four general population samples

png("Figure 1.png", width=10, height=10, units = "in", res = 600)

par(mfrow=c(2,2))

g1 <- qgraph(groupnetwork\_kfold$network[[1]], layout = "spring",theme="colorblind", pie=pred\_ncds$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g1); title("NCDS",adj=0, font.main=1, line=2.5)

g2 <- qgraph(groupnetwork\_kfold$network[[2]], layout = "spring", theme="colorblind", pie=pred\_nihs$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g2); title("NIHS",adj=0, font.main=1, line=2.5)

g3 <- qgraph(groupnetwork\_kfold$network[[3]], layout = "spring", theme="colorblind", pie=pred\_nspn$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g3); title("NSPN",adj=0, font.main=1, line=2.5)

g4 <- qgraph(groupnetwork\_kfold$network[[4]], layout = "spring", theme="colorblind", pie=pred\_sals$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g4); title("SALSUS",adj=0, font.main=1, line=2.5)

dev.off()

# assesses network differences across cohorts

comp\_ncds\_nihs <- NCT(wemwbs\_ncds[,3:16], wemwbs\_nihs[,3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, progressbar=TRUE, edges='all')

comp\_ncds\_nspn <- NCT(wemwbs\_ncds[,3:16], wemwbs\_nspn[,3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, progressbar=TRUE, edges='all')

comp\_ncds\_sals <- NCT(wemwbs\_ncds[,3:16], wemwbs\_sals[,3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, progressbar=TRUE, edges='all')

comp\_nihs\_nspn <- NCT(wemwbs\_nihs[,3:16], wemwbs\_nspn[,3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, progressbar=TRUE, edges='all')

comp\_nihs\_sals <- NCT(wemwbs\_nihs[,3:16], wemwbs\_sals[,3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, progressbar=TRUE, edges='all')

comp\_nspn\_sals <- NCT(wemwbs\_nspn[,3:16], wemwbs\_sals[,3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, progressbar=TRUE, edges='all')

comp\_ncds\_nihs$glstrinv.sep # shows network strength

comp\_ncds\_nihs$glstrinv.pval # p-value for global strength difference

comp\_ncds\_nihs$einv.pvals[comp\_ncds\_nihs$einv.pvals$`p-value`<0.05,] #shows which edges are statistically significant

comp\_ncds\_nspn$glstrinv.sep

comp\_ncds\_nspn$glstrinv.pval

comp\_ncds\_nspn$einv.pvals[comp\_ncds\_nspn$einv.pvals$`p-value`<0.05,]

comp\_ncds\_sals$glstrinv.sep

comp\_ncds\_sals$glstrinv.pval

comp\_ncds\_sals$einv.pvals[comp\_ncds\_sals$einv.pvals$`p-value`<0.05,]

comp\_nihs\_nspn$glstrinv.sep

comp\_nihs\_nspn$glstrinv.pval

comp\_nihs\_nspn$einv.pvals[comp\_nihs\_nspn$einv.pvals$`p-value`<0.05,]

comp\_nihs\_sals$glstrinv.sep

comp\_nihs\_sals$glstrinv.pval

comp\_nihs\_sals$einv.pvals[comp\_nihs\_sals$einv.pvals$`p-value`<0.05,]

comp\_nspn\_sals$glstrinv.sep

comp\_nspn\_sals$glstrinv.pval

comp\_nspn\_sals$einv.pvals[comp\_nspn\_sals$einv.pvals$`p-value`<0.05,]

# computes average layout

Layout <- averageLayout(groupnetwork\_kfold$network[[1]],groupnetwork\_kfold$network[[2]],groupnetwork\_kfold$network[[3]],groupnetwork\_kfold$network[[4]])

# makes Figure 2: Networks of WEMWBS items in four general population samples using average spring layout

png("Figure 2.png", width=10, height=10, units = "in", res = 600)

par(mfrow=c(2,2))

g1 <- qgraph(groupnetwork\_kfold$network[[1]], layout = Layout, theme="colorblind", pie=pred\_ncds$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g1); title("NCDS",adj=0, font.main=1, line=2.5)

g2 <- qgraph(groupnetwork\_kfold$network[[2]], layout = Layout, theme="colorblind", pie=pred\_nihs$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g2); title("NIHS",adj=0, font.main=1, line=2.5)

g3 <- qgraph(groupnetwork\_kfold$network[[3]], layout = Layout, theme="colorblind", pie=pred\_nspn$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g3); title("NSPN",adj=0, font.main=1, line=2.5)

g4 <- qgraph(groupnetwork\_kfold$network[[4]], layout = Layout, theme="colorblind", pie=pred\_sals$errors$Error.R2, border.width=2, vsize=10, border.color='#555555', label.color="#555555", color="#EEEEEE",DoNotPlot=TRUE); plot(g4); title("SALSUS",adj=0, font.main=1, line=2.5)

dev.off()

# bootstraps networks

set.seed("12345")

boot\_networklasso\_ncds <- bootnet(wemwbs\_ncds[,3:16], nBoots = 2500, default = "EBICglasso", type = "nonparametric", nCores = 4, verbose = TRUE, computeCentrality =TRUE,lambda.min.ratio=0.001)

boot\_networklasso\_nihs <- bootnet(wemwbs\_nihs[,3:16], nBoots = 2500, default = "EBICglasso", type = "nonparametric", nCores = 4, verbose = TRUE, computeCentrality =TRUE,lambda.min.ratio=0.001)

boot\_networklasso\_nspn <- bootnet(wemwbs\_nspn[,3:16], nBoots = 2500, default = "EBICglasso", type = "nonparametric", nCores = 4, verbose = TRUE, computeCentrality =TRUE,lambda.min.ratio=0.001)

boot\_networklasso\_sals <- bootnet(wemwbs\_sals[,3:16], nBoots = 2500, default = "EBICglasso", type = "nonparametric", nCores = 4, verbose = TRUE, computeCentrality =TRUE,lambda.min.ratio=0.001)

# makes Supplementary Figure 1: Point estimates (red) and 95% bootstrap confidence intervals (grey) of network edges (representing partial correlations between items)

png("Supplementary Figure 1.png", width=10, height=10, units = "in", res = 600)

p1 <- plot(boot\_networklasso\_ncds, statistics=c("edge"), plot="area", CIstyle="quantiles", order="sample", legend=FALSE) + ggtitle("NCDS") + theme(axis.text.y = element\_text(size=4))

p2 <- plot(boot\_networklasso\_nihs, statistics=c("edge"), plot="area", CIstyle="quantiles", order="sample", legend=FALSE) + ggtitle("NIHS") + theme(axis.text.y = element\_text(size=4))

p3 <- plot(boot\_networklasso\_nspn, statistics=c("edge"), plot="area", CIstyle="quantiles", order="sample", legend=FALSE) + ggtitle("NSPN") + theme(axis.text.y = element\_text(size=4))

p4 <- plot(boot\_networklasso\_sals, statistics=c("edge"), plot="area", CIstyle="quantiles", order="sample", legend=FALSE) + ggtitle("SALSUS") + theme(axis.text.y = element\_text(size=4))

grid.arrange(p1, p2, p3, p4, nrow =1)

dev.off()

# correlations presented in Supplementary Table 1: Spearman correlations between edges

cor(getWmat(g1)[lower.tri(getWmat(g1))], getWmat(g2)[lower.tri(getWmat(g2))], method="spearman") #0.87

cor(getWmat(g1)[lower.tri(getWmat(g1))], getWmat(g3)[lower.tri(getWmat(g3))], method="spearman") #0.79

cor(getWmat(g1)[lower.tri(getWmat(g1))], getWmat(g4)[lower.tri(getWmat(g4))], method="spearman") #0.80

cor(getWmat(g2)[lower.tri(getWmat(g2))], getWmat(g3)[lower.tri(getWmat(g3))], method="spearman") #0.75

cor(getWmat(g2)[lower.tri(getWmat(g2))], getWmat(g4)[lower.tri(getWmat(g4))], method="spearman") #0.82

cor(getWmat(g3)[lower.tri(getWmat(g3))], getWmat(g4)[lower.tri(getWmat(g4))], method="spearman") #0.83

mean(c(0.87,0.79,0.80,0.75,0.82,0.83)) #computes mean correlation (=0.81)

# makes Figure 3: Centrality indices across cohorts

strength <- as.data.frame(cbind(scale(centrality(g1)$InDegree), scale(centrality(g2)$InDegree), scale(centrality(g3)$InDegree), scale(centrality(g4)$InDegree)))

closeness <- as.data.frame(cbind(scale(centrality(g1)$Closeness), scale(centrality(g2)$Closeness), scale(centrality(g3)$Closeness), scale(centrality(g4)$Closeness)))

betweenness <- as.data.frame(cbind(scale(centrality(g1)$Betweenness), scale(centrality(g2)$Betweenness), scale(centrality(g3)$Betweenness), scale(centrality(g4)$Betweenness)))

strength <- mutate(strength, id = rownames(strength))

closeness <- mutate(closeness, id = rownames(closeness))

betweenness <- mutate(betweenness, id = rownames(betweenness))

colnames(strength)<-c("NCDS", "NIHS", "NSPN", "SALSUS", "Symptoms")

colnames(closeness)<-c("NCDS", "NIHS", "NSPN", "SALSUS", "Symptoms")

colnames(betweenness)<-c("NCDS", "NIHS", "NSPN", "SALSUS", "Symptoms")

strength\_long <- melt(strength, id="Symptoms")

strength\_long$Symptoms <- rep(1:14,4)

names(strength\_long)[2] <- "Cohorts"

closeness\_long <- melt(closeness, id="Symptoms")

closeness\_long$Symptoms <- rep(1:14,4)

names(closeness\_long)[2] <- "Cohorts"

betweenness\_long <- melt(betweenness, id="Symptoms")

betweenness\_long$Symptoms <- rep(1:14,4)

names(betweenness\_long)[2] <- "Cohorts"

png("Figure 3.png", width=6, height=6, units = "in", res = 600)

p5 <- ggplot(data=strength\_long, aes(x=Symptoms, y=value, colour=Cohorts)) + geom\_line(size=1, aes(linetype=Cohorts)) + geom\_point(shape = 21, fill = "white", size = 1.5, stroke = 1) + xlab(" ") + ylab("Centrality") + scale\_y\_continuous(limits = c(-3, 3)) + scale\_x\_continuous(breaks=c(1:14),labels=strength$Symptoms) + theme\_bw() + theme(panel.grid.minor=element\_blank(), axis.text.x = element\_text(angle = 60, hjust = 1),legend.position="none") + ggtitle("Strength") + scale\_linetype\_manual(values=c("solid", "twodash", "dotted", "dashed"))

p6 <- ggplot(data=closeness\_long, aes(x=Symptoms, y=value, colour=Cohorts)) + geom\_line(size=1, aes(linetype=Cohorts)) + geom\_point(shape = 21, fill = "white", size = 1.5, stroke = 1) + xlab(" ") + ylab("Centrality") + scale\_y\_continuous(limits = c(-3, 3)) + scale\_x\_continuous(breaks=c(1:14),labels=closeness$Symptoms) + theme\_bw() + theme(panel.grid.minor=element\_blank(), axis.text.x = element\_text(angle = 60, hjust = 1),legend.position="none") + ggtitle("Closeness") + scale\_linetype\_manual(values=c("solid", "twodash", "dotted", "dashed"))

p7 <- ggplot(data=betweenness\_long, aes(x=Symptoms, y=value, colour=Cohorts)) + geom\_line(size=1, aes(linetype=Cohorts)) + geom\_point(shape = 21, fill = "white", size = 1.5, stroke = 1) + xlab(" ") + ylab("Centrality") + scale\_y\_continuous(limits = c(-3, 3)) + scale\_x\_continuous(breaks=c(1:14),labels=betweenness$Symptoms) + theme\_bw() + theme(panel.grid.minor=element\_blank(), axis.text.x = element\_text(angle = 60, hjust = 1),legend.position="none") + ggtitle("Betweenness") + scale\_linetype\_manual(values=c("solid", "twodash", "dotted", "dashed"))

p7 <- grid\_arrange\_shared\_legend(p7, position='bottom', plot=FALSE)

grid.arrange(p5, p6, p7, nrow =3)

dev.off()

# case dropping bootstrap

set.seed("12345")

boot\_networklasso\_centrality\_ncds <- bootnet(wemwbs\_ncds[,3:16], nBoots = 2500, default = "EBICglasso", type = "case", nCores = 4, statistics = c("strength","closeness","betweenness"), model = "GGM", verbose = TRUE, computeCentrality = TRUE,lambda.min.ratio=0.001)

boot\_networklasso\_centrality\_nihs <- bootnet(wemwbs\_nihs[,3:16], nBoots = 2500, default = "EBICglasso", type = "case", nCores = 4, statistics = c("strength","closeness","betweenness"), model = "GGM", verbose = TRUE, computeCentrality = TRUE,lambda.min.ratio=0.001)

boot\_networklasso\_centrality\_nspn <- bootnet(wemwbs\_nspn[,3:16], nBoots = 2500, default = "EBICglasso", type = "case", nCores = 4, statistics = c("strength","closeness","betweenness"), model = "GGM", verbose = TRUE, computeCentrality = TRUE,lambda.min.ratio=0.001)

boot\_networklasso\_centrality\_sals <- bootnet(wemwbs\_sals[,3:16], nBoots = 2500, default = "EBICglasso", type = "case", nCores = 4, statistics = c("strength","closeness","betweenness"), model = "GGM", verbose = TRUE, computeCentrality = TRUE,lambda.min.ratio=0.001)

# makes Supplementary Figure 2: Stability of centrality indices: point estimates and corresponding 95% CIs

g\_legend<-function(a.gplot){

tmp <- ggplot\_gtable(ggplot\_build(a.gplot))

leg <- which(sapply(tmp$grobs, function(x) x$name) == "guide-box")

legend <- tmp$grobs[[leg]]

return(legend)}

p1forlegend <- plot(boot\_networklasso\_centrality\_ncds) + ylab("Correlation")

mylegend<-g\_legend(p1forlegend)

png("Supplementary Figure 2.png", width=7, height=7, units = "in", res = 600)

p1 <- plot(boot\_networklasso\_centrality\_ncds) + ylab("Correlation") + theme(legend.position="none") + ggtitle("NCDS") + scale\_y\_continuous(limits = c(0, 1))

p2 <- plot(boot\_networklasso\_centrality\_nihs) + ylab("Correlation") + theme(legend.position="none") + ggtitle("NIHS") + scale\_y\_continuous(limits = c(0, 1))

p3 <- plot(boot\_networklasso\_centrality\_nspn) + ylab("Correlation") + theme(legend.position="none") + ggtitle("NSPN") + scale\_y\_continuous(limits = c(0, 1))

p4 <- plot(boot\_networklasso\_centrality\_sals) + ylab("Correlation") + theme(legend.position="none") + ggtitle("SALSUS") + scale\_y\_continuous(limits = c(0, 1))

grid.arrange(p1, p2, p3, p4, mylegend, nrow =3)

dev.off()

# computes cs coefficients

CS\_ncds <- corStability(boot\_networklasso\_centrality\_ncds)

CS\_nihs <- corStability(boot\_networklasso\_centrality\_nihs)

CS\_nspn <- corStability(boot\_networklasso\_centrality\_nspn)

CS\_sals <- corStability(boot\_networklasso\_centrality\_sals)

# computes values in Table 2: Correlation stability coefficients

CSfinal <- rbind(CS\_ncds,CS\_nihs,CS\_nspn,CS\_sals)

rownames(CSfinal) <- c("NCDS","NIHS", "NSPN", "SALSUS")

CSfinal

# assesses gender differences

gendercomparison\_ncds <- NCT(wemwbs\_ncds[wemwbs\_ncds$sex=="Male",3:16], wemwbs\_ncds[wemwbs\_ncds$sex=="Female",3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, edges='all', progressbar=TRUE)

gendercomparison\_ncds$glstrinv.pval # p-value for global strength difference

gendercomparison\_ncds$einv.pvals$Var1[gendercomparison\_ncds$einv.pvals$`p-value`<0.05] #which items are involved in significant differences

gendercomparison\_ncds$einv.pvals$Var2[gendercomparison\_ncds$einv.pvals$`p-value`<0.05] #which items are involved in significant differences

gendercomparison\_ncds$einv.pvals$`p-value`[gendercomparison\_ncds$einv.pvals$`p-value`<0.05] #p-value

gendercomparison\_nihs <- NCT(wemwbs\_nihs[wemwbs\_nihs$sex=="Male",3:16], wemwbs\_nihs[wemwbs\_nihs$sex=="Female",3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, edges='all', progressbar=TRUE)

gendercomparison\_nihs$glstrinv.pval

gendercomparison\_nihs$einv.pvals$Var1[gendercomparison\_nihs$einv.pvals$`p-value`<0.05]

gendercomparison\_nihs$einv.pvals$Var2[gendercomparison\_nihs$einv.pvals$`p-value`<0.05]

gendercomparison\_nihs$einv.pvals$`p-value`[gendercomparison\_nihs$einv.pvals$`p-value`<0.05]

gendercomparison\_nspn <- NCT(wemwbs\_nspn[wemwbs\_nspn$sex=="Male",3:16], wemwbs\_nspn[wemwbs\_nspn$sex=="Female",3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, edges='all', progressbar=TRUE)

gendercomparison\_nspn$glstrinv.pval

gendercomparison\_nspn$einv.pvals$Var1[gendercomparison\_nspn$einv.pvals$`p-value`<0.05]

gendercomparison\_nspn$einv.pvals$Var2[gendercomparison\_nspn$einv.pvals$`p-value`<0.05]

gendercomparison\_nspn$einv.pvals$`p-value`[gendercomparison\_nspn$einv.pvals$`p-value`<0.05]

gendercomparison\_sals <- NCT(wemwbs\_sals[wemwbs\_sals$sex=="Male",3:16], wemwbs\_sals[wemwbs\_sals$sex=="Female",3:16], it=5000, binary.data=FALSE, paired=FALSE, weighted=TRUE, test.edges=TRUE, edges='all', progressbar=TRUE)

gendercomparison\_sals$glstrinv.pval

gendercomparison\_sals$einv.pvals$Var1[gendercomparison\_sals$einv.pvals$`p-value`<0.05]

gendercomparison\_sals$einv.pvals$Var2[gendercomparison\_sals$einv.pvals$`p-value`<0.05]

gendercomparison\_sals$einv.pvals$`p-value`[gendercomparison\_sals$einv.pvals$`p-value`<0.05]