APPENDICES

# A. R script used to run co-occurence analysis and network construction

This script counts number of pairs that significantly are related at different threshold values (*p*-value > 0.05, < 0.05, and < 0.01).

## Libraries

if (!require("WGCNA")) {  
 install.packages("WGCNA", dependencies = TRUE)  
}  
  
if(!require("apcluster")) {  
 install.packages("apcluster", dependencies = TRUE)  
}  
  
if(!require("pheatmap")) {  
 install.packages("pheatmap", dependencies = TRUE)  
}  
  
if (!require("dplyr")) {  
 install.packages("dplyr", dependencies = TRUE)  
}

# Comparison of correlation methods

# data is an data frame   
  
# spearman correlation  
cor.spearman <- cor(data, method = "spearman", use = "pairwise")  
  
# kendall correlation  
cor.kendall <- cor(data, method = "kendall", use = "pairwise")   
  
# names the object  
names(cor.spearman) <- "Spearman"  
names(cor.kendall) <- "Kendall"  
  
  
# ############################  
# flattenCorrMatrix  
# ###########################  
# reference: http://www.sthda.com/english/wiki/print.php?id=78  
# cormat : matrix of the correlation coefficients  
# pmat : matrix of the correlation p-values  
  
flattenCorrMatrix <- function(cormat, pmat) {  
 ut <- upper.tri(cormat)  
 data.frame(  
 row = rownames(cormat)[row(cormat)[ut]],  
 column = rownames(cormat)[col(cormat)[ut]],  
 cor =(cormat)[ut],  
 p = pmat[ut]  
 )  
}  
  
# counting the number of pairs that are significantly related  
  
cor.spearman <- rcorr(as.matrix(data), type = "spearman")  
cor.spearman <- flattenCorrMatrix(cor.spearman$r, cor.spearman$P)  
cor.spearman %>% filter(p > 0.05) %>% nrow()  
cor.spearman %>% filter(p < 0.05) %>% nrow()  
cor.spearman %>% filter(p < 0.01) %>% nrow()  
  
cor.kendall <- rcorr(as.matrix(data), type = "kendall")  
cor.kendall <- flattenCorrMatrix(cor.kendall$r, cor.kendall$P)  
cor.kendall %>% filter(p > 0.05) %>% nrow()  
cor.kendall %>% filter(p < 0.05) %>% nrow()  
cor.kendall %>% filter(p < 0.01) %>% nrow()