# C. Run differential network analysis in different seasons

In this appendix, the network correlation coefficients are visualized. Before performing this function, two data sets from different conditions should be selected to compare and construct a differerential network. Each data set is needed to compute correaltion coefficient using the function named cooc\_table from Appendix B first. Then, the output from each data set will be able to compare the differences using the diff\_cor function.

# Libraries

if (!require("DiffCorr")) {  
 install.packages("DiffCorr", dependencies = TRUE)  
}  
  
if (!require("igraph")) {  
 install.packages("igraph", dependencies = TRUE)  
}

# Differential season network

# df\_dry is the dataframe selected in dry season  
# df\_wet is the datafeam selected in wet season  
  
# call function cooc\_table defined in Appedix B  
  
cor\_dry <- cooc\_table(df\_dry) # dry season  
cor\_wet <- cooc\_table(df\_wet) # wet season  
  
pair.list <- cor\_dry  
# = Dry season  
cor\_dry$rho[cor\_dry$p.value > 0.05 ] <- 0  
g1 <- graph.edgelist(as.matrix(cor\_dry[1:2]), directed = FALSE)  
  
# = Wet season  
cor\_wet2$rho[cor\_df$p.value > 0.05 ] <- 0  
g2 <- graph.edgelist(as.matrix(df\_wet[1:2]), directed = FALSE)  
  
  
# = Differential network  
# g1 is network graph of dry season (condition1)  
# g2 is network graph of wet season (condition2)  
  
# create adjagency matrix from igraph object  
adj.mat1 <- as.matrix(as\_adjacency\_matrix(g1, attr = "weight")) # dry season  
  
adj.mat2 <- as.matrix(as\_adjacency\_matrix(g2, attr = "weight")) # wet season  
  
  
# compare correlation coefficient of each pair of injuries of conditionA and   
# condition B  
  
# call dfiff.corr function from 02\_co\_network\_creation.R #  
  
diff\_comb <- diff.corr(adj.mat1 , adj.mat2)  
  
# set the index that   
# if correlation coefficents of condiction A higher than B index value is positive  
# if correlation coefficents of condiction A less than B index value is negative  
diff\_comb$index <- ifelse(abs(diff\_comb$r1) - abs(diff\_comb$r2) > 0, 1, -1)  
  
# create differtial network in seasons  
  
gdif <- graph.edgelist(as.matrix(diff\_comb[1:2]), directed = FALSE)  
  
E(gdif)$weight <- as.matrix(diff\_comb$index)  
  
V(gdif)$color <- adjustcolor("khaki2", alpha.f = .8)  
V(gdif)$frame.color <- adjustcolor("khaki2", alpha.f = .8)  
V(gdif)$shape <- "circle"  
V(gdif)$size <- 25  
V(gdif)$label.color <- "black"  
V(gdif)$label.font <- 2  
V(gdif)$label.family <- "Helvetica"  
V(gdif)$label.cex <- 1.0  
gdif$layout <- layout\_with\_fr(gdif)  
  
# label edges following the result from comparison  
# Dry season - Wet season   
# Dry > Wet > 0 ; labeled with organred4 color  
# Dry < Wet < 0 ; labeled with royelblue4 color  
E(gdif)[weight > 0]$color <- adjustcolor("orangered4" , alpha.f = .8)  
E(gdif)[weight < 0]$color <- adjustcolor("royalblue4", alpha.f = .8)

# Using diff.corr function to compare differences in networks

This function perform sFisher’s *z*-test on the dataset from two different conditions. The output is data frame with a column for the dataset label, each injury pair, the correlation coefficient at condition A, *p*-value in the pair at condition A, the correlation coefficient at condition B, *p*-value in the pair at condition B, *p*-value of difference in the pair, and difference of two correlation coefficients. The result will be used for constructing differential network model with all edges in the network with differential co-occurrence significant at *p*-values < 0.05, and labelled edges by color to identify the condition that edges are represented; red edges represent differential relationship in dry season, and blue edges represented differential relationship in wet season.

diff.corr <- function(data1, data2){  
   
 ccc1 <- as.vector(data1[lower.tri(data1)])  
   
 ccc2 <- as.vector(data2[lower.tri(data2)])  
   
 n <- nrow(data1)  
   
 N <- n \* (n - 1)/2  
   
 p1 <- rep(1, N)  
   
 p2 <- rep(1, N)  
   
 pdiff <- rep(1, N)  
   
 diff <- rep(1, N)  
   
 mol.names <- rownames(data1)  
   
 p1 <- cor2.test(n1, ccc1)  
   
 p2 <- cor2.test(n2, ccc2)  
   
 pdiff <- compcorr(n1, ccc1, n2, ccc2)$pval  
 diff <- ccc1 - ccc2  
   
 pdiff[(is.na(pdiff)) == TRUE] <- 1  
   
 myindex <- which((lower.tri(data1)) == TRUE, arr.ind = TRUE)  
   
 mol.names1 <- mol.names[myindex[, 1]]  
   
 mol.names2 <- mol.names[myindex[, 2]]  
   
 fin.ind <- pdiff < 0.05  
   
 # combine data  
 res <- cbind(mol.names1[fin.ind], mol.names2[fin.ind], ccc1[fin.ind], p1[fin.ind], ccc2[fin.ind], p2[fin.ind], pdiff[fin.ind], diff[fin.ind])  
   
 # correct format the data structure  
 res <- as.data.frame(res)  
   
 # name column  
 names(res) <- c("var1", "var2", "r1", "p1", "r2", "p2", "p.difference", "difr")  
 # set class of each variable  
 res$var1 <- as.character(res$var1)  
 res$var2 <- as.character(res$var2)  
 res$r1 <- as.numeric(as.character(res$r1))  
 res$p1 <- as.numeric(as.character(res$p1))  
 res$r2 <- as.numeric(as.character(res$r2))  
 res$p2 <- as.numeric(as.character(res$p2))  
 res$p.difference <- as.numeric(as.character(res$p.difference))  
 res$difr <- as.numeric(as.character(res$difr))  
   
 return(res)  
}

# Visualising differential networks

The last step visualises the differential netowrk analysis results. Correlation coeffecients of two data sets (low yield data set and high yield data) are computed using the function named cooc\_table from Appendix B, first. Then, the output from each data set will compared for differences using the diff\_cor function. The result is used for constructing differential network models with all edges in the network with differential co-occurrence significant at *p*-values < 0.05, and select edges that are higher significantly co-occurrences at lower yield levels.

cor\_low <- cooc\_table(df\_low) # low yield level  
cor\_high <- cooc\_table(df\_high) # high yield level  
  
# = low yield data  
cor\_low$rho[cor\_dry$p.value > 0.05 ] <- 0  
g1 <- graph.edgelist(as.matrix(cor\_low[1:2]), directed = FALSE)  
E(g1)$weight <- cor\_low$rho  
  
# = high yield data  
cor\_high$rho[cor\_df$p.value > 0.05 ] <- 0  
g2 <- graph.edgelist(as.matrix(df\_high[1:2]), directed = FALSE)  
E(g2)$weight <- cor\_high$rho  
  
# = Differential network  
# g1 is network graph of low yield (condition1)  
# g2 is network graph of high yield (condition2)  
  
# create adjagency matrix from igraph object  
adj.mat1 <- as.matrix(as\_adjacency\_matrix(g1, attr = "weight")) # low yield  
  
adj.mat2 <- as.matrix(as\_adjacency\_matrix(g2, attr = "weight")) # high yield  
  
# compare correlation coefficient of each pair of injuries of conditionA and   
# condition B  
  
# call dfiff.corr function from 02\_co\_network\_creation.R #  
  
diff\_comb <- diff.corr(adj.mat1 , adj.mat2)  
  
# set the index that   
# if correlation coefficents of condition A higher than B index value is positive  
# if correlation coefficents of condition A less than B index value is negative  
diff\_comb$index <- ifelse(abs(diff\_comb$r1) - abs(diff\_comb$r2) > 0, 1, -1)  
  
# create differtial network in yield levels  
  
gdif <- graph.edgelist(as.matrix(diff\_comb[1:2]), directed = FALSE)  
  
E(gdif)$weight <- as.matrix(diff\_comb$index)  
  
V(gdif)$color <- adjustcolor("khaki2", alpha.f = .8)  
V(gdif)$frame.color <- adjustcolor("khaki2", alpha.f = .8)  
V(gdif)$shape <- "circle"  
V(gdif)$size <- 25  
V(gdif)$label.color <- "black"  
V(gdif)$label.font <- 2  
V(gdif)$label.family <- "Helvetica"  
V(gdif)$label.cex <- 1.0  
gdif$layout <- layout\_with\_fr(gdif)  
E(gdif)[weight > 0]$color <- adjustcolor("grey60" , alpha.f = .8)  
  
# this network will be considered pairs that higher significantly present at   
# low yield level because we assume that injury that highly present in low may  
# cause yield loss  
  
gdif <- delete.edges(gdif, which(E(gdif)$weight < 0))