install.packages("foreign")

install.packages("IsingFit")

install.packages("qgraph")

install.packages("igraph")

install.packages("bootnet")

install.packages("IsingSampler")

install.packages("compute.es")

install.packages("NetworkComparisonTest")

install.packages("mgm")

install.packages("Matrix")

install.packages("readxl")

install.packages("tidyimpute")

install.packages("cmprsk")

install.packages("devtools")

remove(list = ls())

library(foreign)

library(IsingFit)

library(qgraph)

library(igraph)

library(cmprsk)

library(bootnet)

library(IsingSampler)

library(compute.es)

library(NetworkComparisonTest)

library(mgm)

library(Matrix)

library(readxl)

library(tidyimpute)

library(Hmisc)

library(psych)

library(devtools)

### Dataset includes HLA+%, median MFI, and NK subset %s

DataKIRHIVpos <- as.data.frame(read\_excel("/Users/alexcocker/Desktop/SDY1535 HLA Network Test 3.xlsx",sheet=1,na = "."))

DataKIRHIVneg <- as.data.frame(read\_excel("/Users/alexcocker/Desktop/SDY1535 HLA Network Test 3.xlsx",sheet=2,na = "."))

KIRHIVpos <- DataKIRHIVpos[,2:16]

KIRHIVneg <- DataKIRHIVneg[,2:16]

#Correlation networks

#Run correlation

corKIRHIVpos <- cor(KIRHIVpos, use = "pairwise.complete.obs", method = "spearman")

corKIRHIVneg <- cor(KIRHIVneg, use = "pairwise.complete.obs", method = "spearman")

#View correlation r-value results

View(round(corKIRHIVpos, 2))

View(round(corKIRHIVneg, 2))

#Create correlation networks

#Graph\_pcorKIR <- qgraph(corMatKIR, bg = "transparent", graph = "cor", layout = "spring", threshold = "BH", sampleSize = nrow(DataKIR), alpha = 0.05, theme = "colorblind")

Graph\_pcorKIRHIVpos <- qgraph(corKIRHIVpos, bg = "transparent", graph = "cor", layout = "spring", threshold = "BH", sampleSize = nrow(KIRHIVpos), alpha = 0.05, theme = "colorblind", edge.labels = TRUE, edge.label.cex = 0.6, edge.label.color = "#000000", title = "HIV-1-pos", labels = colnames(corKIRHIVpos))

Graph\_pcorKIRHIVneg <- qgraph(corKIRHIVneg, bg = "transparent", graph = "cor", layout = "spring", threshold = "BH", sampleSize = nrow(KIRHIVneg), alpha = 0.05, theme = "colorblind", edge.labels = TRUE, edge.label.cex = 0.6, edge.label.color = "#000000", title = "HIV-1-neg", labels = colnames(corKIRHIVneg))

#Run Network Comparison Test

NCTKIR <- NCT(KIRHIVpos, KIRHIVneg, it = 100)

#NETWORK INVARIANCE TEST

Test statistic M: 0.2779191

p-value 0.95

GLOBAL STRENGTH INVARIANCE TEST

Global strength per group: 0.4827242 0

Test statistic S: 0.4827242

p-value 0.95

EDGE INVARIANCE TEST

NULL

CENTRALITY INVARIANCE TEST

NULL