#CG cross correlation

read.csv(file.choose(), header=T,row.names = 1, sep=",")->wetchem # wet chemistry without fucose and Cel2.csv

read.csv(file.choose(), header=T,row.names = 1, sep=",")->genes # gene expression data.csv

wg.matrix <-cbind(wetchem, genes)

t(wg.matrix)-> wg.matrix.t

library(rsgcc)

wg.gcc.total<-cor.matrix(wg.matrix.t, cormethod = "GCC", cpus=3, style = "all.pairs", output= "matrix",sigmethod = "two.sided", pernum = 100000)

library(qvalue)

take.topr(wg.gcc.total[[2]],ncol(wetchem),ncol(genes))-> wg.gcc.total.p

take.topr(wg.gcc.total[[1]],ncol(wetchem),ncol(genes))-> wg.gcc.total.gcc

wg.gcc.total.p[-c(4,5,6),]-> wg.gcc.total.p.PS

wg.gcc.total.gcc[-c(4,5,6),]-> wg.gcc.total.gcc.PS

qvalue(wg.gcc.total.p)-> wg.gcc.total.q

qvalue(wg.gcc.total.p.PS) -> wg.gcc.total.q.PS

qplot(wg.gcc.total.q)

qplot(wg.gcc.total.q.PS)

gccheatmap (wg.gcc.total.gcc, wg.gcc.total.q, 0.001, 0) ->gcc.total.heatmap

gccheatmap (wg.gcc.total.gcc.PS, wg.gcc.total.q.PS, 0.001, 0) ->gcc.total.heatmap.PS

range(gcc.total.heatmap)

range(abs(gcc.total.heatmap [gcc.total.heatmap!=0]))

range(gcc.total.heatmap.PS)

range(abs(gcc.total.heatmap.PS [gcc.total.heatmap.PS!=0]))

break.pairs<-c(seq(-0.9,-0.2,by=0.7/(127)),0, seq(0.2,0.9,by=0.7/(127)))

hist(gcc.total.heatmap[gcc.total.heatmap!=0],breaks=100)

#True NULL hypothesis

wg.gcc.total.q$qvalue->q.rank.matrix

wg.gcc.total.q.PS$qvalue->q.rank.matrix.PS

matrix(rank(wg.gcc.total.q $qvalue),nrow=nrow(wg.gcc.total.q$qvalue),ncol= ncol(wg.gcc.total.q$qvalue))->q.rank.matrix

matrix(rank(wg.gcc.total.q.PS $qvalue),nrow=nrow(wg.gcc.total.q.PS$qvalue),ncol= ncol(wg.gcc.total.q.PS$qvalue))->q.rank.matrix.PS

rownames(wg.gcc.total.q$qvalue)-> rownames(q.rank.matrix)

colnames(wg.gcc.total.q$qvalue)-> colnames(q.rank.matrix)

rownames(wg.gcc.total.q.PS$qvalue)-> rownames(q.rank.matrix.PS)

colnames(wg.gcc.total.q.PS$qvalue)-> colnames(q.rank.matrix.PS)

max(q.rank.matrix)\*(1- wg.gcc.total.q$pi0)->low.boundary

max(q.rank.matrix.PS)\*(1- wg.gcc.total.q.PS $pi0)->low.boundary.PS

gcc.total.heatmap -> gcc.total.heatmap.tn

gcc.total.heatmap.PS -> gcc.total.heatmap.tn.PS

gcc.total.heatmap.tn [low.boundary.PS <q.rank.matrix]<-NA

gcc.total.heatmap.tn.PS [low.boundary <q.rank.matrix.PS]<-NA

#dendrogram for heatmap

library(rsgcc)

t(as.matrix(wetchem))-> den.wet.total.t

t(as.matrix(wetchem[,-c(4,5,6)]))-> den.wet.total.t.PS

cor.matrix(den.wet.total.t, cormethod = "GCC", cpus=3, style = "all.pairs", output= "matrix",sigmethod = "two.sided", pernum = 0) -> den.wet.total.t.matrix

cor.matrix(den.wet.total.t.PS, cormethod = "GCC", cpus=3, style = "all.pairs", output= "matrix",sigmethod = "two.sided", pernum = 0) -> den.wet.total.t.matrix.PS

as.dist(1- den.wet.total.t.matrix[[1]])->corre.distance

as.dist(1- den.wet.total.t.matrix.PS[[1]])->corre.distance.PS

intermediate.dend<-as.dendrogram(hclust(corre.distance,method="average"))

intermediate.dend.PS<-as.dendrogram(hclust(corre.distance.PS,method="average"))

library(gplots)

tiff("wet chemistry and genes gcc correlation.matrix.total.tif" , width=2200,height=2200,res=200)

heatmap.2(t(gcc.total.heatmap.tn), dendrogram="column", Rowv= FALSE, Colv= intermediate.dend, scale="none",col = bluewhitered256, margins=c(8,10),colsep=1: ncol(t(gcc.total.heatmap.tn)),rowsep=1: nrow(t(gcc.total.heatmap.tn)), sepcolor="lightgrey",trace="none",cexRow=1,cexCol=1,density.info="none", keysize=0.6,breaks= break.pairs, na.col="yellow")

dev.off()

tiff("wet chemistry and genes gcc correlation.matrix.total without diestibility.tif" , width=2200,height=2200,res=300)

heatmap.2(t(gcc.total.heatmap.tn.PS), dendrogram="column", Rowv= FALSE, Colv= intermediate.dend.PS, scale="none",col = bluewhitered256, margins=c(8,10),colsep=1: ncol(t(gcc.total.heatmap.tn.PS)),rowsep=1: nrow(t(gcc.total.heatmap.tn.PS)), sepcolor="lightgrey",trace="none",cexRow=1,cexCol=1,density.info="none", keysize=0.6,breaks= break.pairs, na.col="yellow")

dev.off()

write.csv(t(gcc.total.heatmap.tn), file = " wet chemistry and genes gcc correlation.matrix.total.csv" )

write.csv(wg.gcc.total [[1]], file = " wet chemistry and genes gcc correlation.matrix.total.complete.csv" )

write.csv(wg.gcc.total.q$qvalues, file = " wet chemistry and genes gcc correlation.matrix.total.qvalues.csv" )

write.csv(wg.gcc.total.q.PS$qvalues, file = " wet chemistry and genes gcc correlation.matrix.total.qvalues.without digestibility.csv" )