

CTD Lab Exercise

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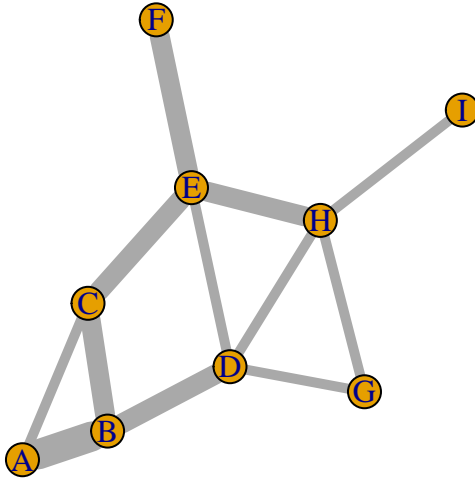
This document was rendered at 2021-03-08 20:36:47

I. Generate background knowledge graph.

I.I: Manually build graphs from adjacency matrices.

```
adj_mat = rbind(c(0,3,1,0,0,0,0,0,0), #A's neighbors
               c(3,0,2,2,0,0,0,0,0), #B's neighbors
               c(1,2,0,0,2,0,0,0,0), #C's neighbors
               c(0,2,0,0,1,0,1,1,0), #D's neighbors
               c(0,0,2,1,0,2,0,2,0), #E's neighbors
               c(0,0,0,0,2,0,0,0,0), #F's neighbors
               c(0,0,0,1,0,0,0,1,0), #G's neighbors
               c(0,0,0,1,2,0,1,0,1), #H's neighbors
               c(0,0,0,0,0,0,0,1,0) #I's neighbors
               )
rownames(adj_mat) = c("A", "B", "C", "D", "E", "F", "G", "H", "I")
colnames(adj_mat) = c("A", "B", "C", "D", "E", "F", "G", "H", "I")
# Convert adjacency matrices to igraph objects for all three graphs.
ig = graph.adjacency(adj_mat, mode="undirected", weighted=TRUE,
                    add.colnames = "name")
print(ig)

## IGRAPH beaaad3 UNW- 9 12 --
## + attr: name (v/c), weight (e/n)
## + edges from beaaad3 (vertex names):
## [1] A--B A--C B--C B--D C--E D--E D--G D--H E--F E--H G--H H--I
# Multiply edge weights by 5 to amplify edge width
# differences
plot.igraph(ig, edge.width=5*E(ig)$weight)
```



I.II: Learn a graph from data.

Note all code chunks in sections I - IV may rely on lines in previous code chunks, so do not empty your environment between code chunks.

```

# Load the Miller2015_Heparin dataset
data(Miller2015)
# Only include metabolites that are present in >90% reference samples.
fil.rate=as.numeric(Miller2015$`Times identified in all 200 samples`[-1])/200
names(fil.rate) = rownames(Miller2015)[-1]
data_mx = Miller2015[,grep("IEM_", colnames(Miller2015))]
data_mx = data_mx[which(fil.rate>0.90), ]
dim(data_mx)

```

```
## [1] 620 186
```

```

# Remove any metabolites where any profile has a z-score > 1000.
# These are likely imputed raw values that were not z-scored.
rmMets = names(which(apply(data_mx, 1, function(i) any(i>20))))
if (length(rmMets)>0) {
  data_mx = data_mx[-which(rownames(data_mx) %in% rmMets),]
}
dim(data_mx)

```

```
## [1] 196 186
```

```

# Get data from all patients with Argininemia
diags = Miller2015["diagnosis", grep("IEM", colnames(Miller2015))]
arg_data = data_mx[,which(diags=="Argininemia")]
# Add surrogate disease and surrogate reference profiles based on 1 standard
# deviation around profiles from real patients to improve rank of matrix when
# learning Gaussian Markov Random Field network on data. While surrogate
# profiles are not required, they tend to learn less complex networks
# (i.e., networks with less edges) and in faster time.
ind = which(diags=="No biochemical genetic diagnosis")
arg_data=data.surrogateProfiles(arg_data, 1, ref_data = data_mx[,ind])
dim(arg_data)

```

```
## [1] 196 260
```

```

# Learn a Gaussian Markov Random Field model using the Graphical LASSO in
# the R package "huge".
# Select the regularization parameter based on the "STARS" stability
# estimate.
#This will take 30 seconds - 1 minute.
arg = huge(t(arg_data), method="glasso")

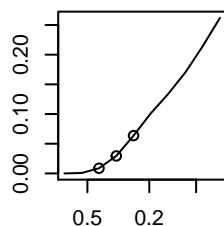
```

```
## Conducting the graphical lasso (glasso) with lossless screening...in progress: 9%
```

```
## Conducting the graphical lasso (glasso)...done.
```

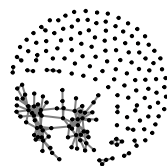
```
plot(arg)
```

arsity vs. Regularizati

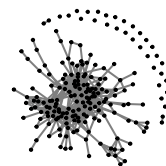


Regularization Parameter

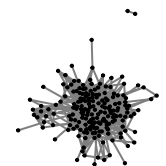
lambda = 0.421



lambda = 0.326



lambda = 0.252



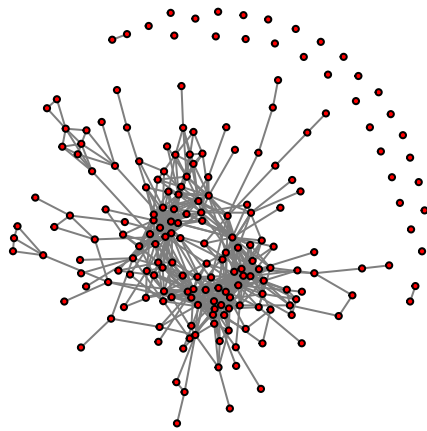
```

# This will take several minutes. For a faster option, you can use the
# "ebic" criterion instead of "stars", but we recommend "stars".

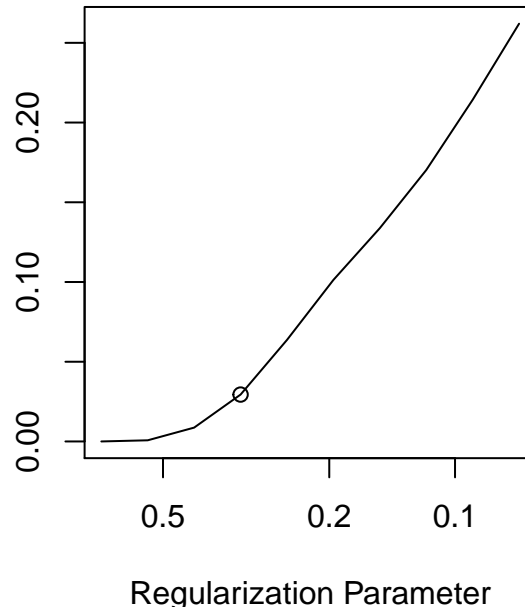
```

```
arg.select = huge.select(arg, criterion="stars")
```

```
## Conducting Subsampling...in progress:5% Conducting Subsampling...in progress:10% Conducting Subsampl  
plot(arg.select)
```



Solution path sparsity levels



```
# This is the regularization parameter the STARS method selected.  
print(arg.select$opt.lambda)
```

```
## [1] 0.3260769
```

```
# This is the corresponding inverse of the covariance matrix that corresponds  
# to the selected regularization level.
```

```
arg_icov = as.matrix(arg.select$opt.icov)
```

```
# Remove all "self" edges, as we are not interested in self-relationships.
```

```
diag(arg_icov) = 0
```

```
rownames(arg_icov) = rownames(arg_data)
```

```
colnames(arg_icov) = rownames(arg_data)
```

```
# Convert adjacency matrices to an igraph object.
```

```
ig_arg = graph.adjacency(arg_icov, mode="undirected", weighted=TRUE,  
                        add.colnames="name")
```

```
print(ig_arg)
```

```
## IGRAPH 02ae1d8 UNW- 196 562 --
```

```
## + attr: name (v/c), weight (e/n)
```

```
## + edges from 02ae1d8 (vertex names):
```

```
## [1] 1,5-anhydroglucitol (1,5-ag)--1-docosahexaenoyl-gpc (22:6)
```

```
## [2] 1,5-anhydroglucitol (1,5-ag)--pantothenate (vitamin b5)
```

```

## [3] 1,5-anhydroglucitol (1,5-ag)--x - 01911
## [4] 1-arachidonoyl-gpc (20:4) --1-docosahexaenoyl-gpc (22:6)
## [5] 1-arachidonoyl-gpc (20:4) --1-eicosatrienoyl-gpc (20:3)
## [6] 1-arachidonoyl-gpc (20:4) --1-linoleoyl-gpc (18:2)
## [7] 1-arachidonoyl-gpc (20:4) --1-stearoyl-gpc (18:0)
## [8] 1-arachidonoyl-gpc (20:4) --2-arachidonoyl-gpc (20:4)
## + ... omitted several edges

```

II. The Probability Diffusion Algorithm

II.I From a starting node.

Run the following code, then go to the directory, and open all diffusionP1Movie*.png files all at once (sorted by timestamp). Starting from the first image, view how the probability diffusion algorithm works to diffuse 100% probability to the rest of the graph. Be sure to pay attention to the recursion level listed in the title of each image, to imagine where in the call stack the algorithm is at the captured time the image was generated.

```

if (!dir.exists(sprintf("%s/images", getwd()))) {
  dir.create(sprintf("%s/images", getwd()))
}
G=vector(mode="list", length=length(V(ig)$name))
G[1:length(G)] = 0
names(G) = c("A", "B", "C", "D", "E", "F", "G", "H", "I")
startNode = "A"
visitedNodes = startNode
coords = layout.fruchterman.reingold(ig)
# Uncomment next lines if you want to generate movie images
#G_new = graph.diffuseP1(p1=1.0, sn=startNode, G=G, vNodes=visitedNodes,
#                        thresholdDiff=0.01, adj_mat=adj_mat, verbose=TRUE,
#                        out_dir = sprintf("%s/images", getwd()),
#                        r_level = 1, coords = coords)
# Inherited probabilities across all nodes should add to 1.
#sum(unlist(G_new))
# Which node inherited the highest probability from startNode?
#G_new[which.max(G_new)]

```

II.II From a starting node, after visiting previous nodes.

Now, delete all diffusionP1Movie*.png files from your current directory, and run the following code. View the new image stack in the same way we did previously.

```

# Now let's see how the probability diffusion algorithm diffuses probability
# after B has been "stepped" into.
visitedNodes = c("A", "B")
startNode = "B"
# Uncomment the next lines if you want to generate movie images
#G_new = graph.diffuseP1(p1=1.0, sn=startNode, G, vNodes=visitedNodes,
#                        thresholdDiff=0.01, adj_mat, TRUE,
#                        out_dir = sprintf("%s/images", getwd()),
#                        1, coords)
# Inherited probabilities across all nodes should add to 1.
#sum(unlist(G_new))

```


III. The Network Encoding Algorithms

III.I Multi-Node Diffusion Encoding

```
# The multi-node network walker tends to overfit on the network and is more
# computationally intensive/slow compared to the single-node network walker.
# It is therefore not recommended that you use this network walker over the
# single-node network walker. However, it is unclear if this network walker
# can be beneficial in some circumstances or application areas. We include
# it as an experimental feature only.
adj_mat = rbind(c(0,3,1,0,0,0,0,0,0), #A's neighbors
               c(3,0,2,2,0,0,0,0,0), #B's neighbors
               c(1,2,0,0,2,0,0,0,0), #C's neighbors
               c(0,2,0,0,1,0,1,1,0), #D's neighbors
               c(0,0,2,1,0,2,0,2,0), #E's neighbors
               c(0,0,0,0,2,0,0,0,0), #F's neighbors
               c(0,0,0,1,0,0,0,1,0), #G's neighbors
               c(0,0,0,1,2,0,1,0,1), #H's neighbors
               c(0,0,0,0,0,0,0,1,0) #I's neighbors
              )
rownames(adj_mat) = c("A", "B", "C", "D", "E", "F", "G", "H", "I")
colnames(adj_mat) = c("A", "B", "C", "D", "E", "F", "G", "H", "I")
# Convert adjacency matrices to igraph objects for all three graphs.
ig = graph.adjacency(adj_mat, mode="undirected", weighted=TRUE,
                    add.colnames = "name")
coords = layout.fruchterman.reingold(ig)
print(ig)

## IGRAPH bcefb28 UNW- 9 12 --
## + attr: name (v/c), weight (e/n)
## + edges from bcefb28 (vertex names):
## [1] A--B A--C B--C B--D C--E D--E D--G D--H E--F E--H G--H H--I

# Uncomment following line to generate PNGs and animate the
# multi-node encoding node ranks.
#ranks = multiNode.getNodeRanks(S = c("A", "B"), G, p1=1.0,
#                               thresholdDiff=0.01, adj_mat,
#                               log2(length(G)), FALSE,
#                               out_dir = sprintf("%s/images", getwd()),
#                               TRUE, coords)
# Get node ranks as list object, with no images generated
ranks = multiNode.getNodeRanks(S = c("A", "B"), G, p1=1.0,
                               thresholdDiff=0.01, adj_mat,
                               log2(length(G)), FALSE)
```

III.II Single-Node Diffusion Encoding

```
# This network walker tends to avoid overfitting. Of further note, since
# single-node network walker is not parameterized by the subset being
# encoded, you can pre-compute node rankings using dynamic programming.
# Pre-computing node ranks enables quick encoding of thousands of subsets
# at a time (see The Encoding Process).
```

```

S = c("A", "B")
#out_dir=sprintf("%s/images",getwd())
# Uncomment the following lines to generate PNGs and animate the
# single-node encoding node ranks.
#ranks = list()
#for (n in seq_len(length(S))) {
#  ind = which(names(G)==S[n])
#  ranks[[n]]=singleNode.getNodeRanksN(ind,G,p1=1.0,thresholdDiff=0.01,
#                                     adj_mat,S=S,num.misses=log2(length(G)),
#                                     FALSE,out_dir,TRUE,coords)
#}
#names(ranks) = S
# Get node ranks as list object, with no images generated
S = c("A", "B")
ranks = list()
for (n in 1:length(S)) {
  ind = which(names(G)==S[n])
  ranks[[n]]=singleNode.getNodeRanksN(ind,G,p1=1.0,thresholdDiff=0.01,
                                     adj_mat,S=S,
                                     num.misses=log2(length(G)),FALSE)
}
names(ranks) = S

```

IV. The Encoding Process

We're going to go back to our data using the Arginase deficiency network model, and the Miller et al (2015) dataset. ## IV.0 Re-define the Arginase deficiency network model

```

print(ig_arg)

## IGRAPH 02ae1d8 UNW- 196 562 --
## + attr: name (v/c), weight (e/n)
## + edges from 02ae1d8 (vertex names):
## [1] 1,5-anhydroglucitol (1,5-ag)--1-docosahexaenoyl-gpc (22:6)
## [2] 1,5-anhydroglucitol (1,5-ag)--pantothenate (vitamin b5)
## [3] 1,5-anhydroglucitol (1,5-ag)--x - 01911
## [4] 1-arachidonoyl-gpc (20:4) --1-docosahexaenoyl-gpc (22:6)
## [5] 1-arachidonoyl-gpc (20:4) --1-eicosatrienoyl-gpc (20:3)
## [6] 1-arachidonoyl-gpc (20:4) --1-linoleoyl-gpc (18:2)
## [7] 1-arachidonoyl-gpc (20:4) --1-stearoyl-gpc (18:0)
## [8] 1-arachidonoyl-gpc (20:4) --2-arachidonoyl-gpc (20:4)
## + ... omitted several edges

adj_mat = as.matrix(get.adjacency(ig_arg, attr="weight"))
G=vector(mode="list", length=length(V(ig_arg)$name))
G[1:length(G)] = 0
names(G) = V(ig_arg)$name

```

IV.I Choose your node subset.


```

# Maximum subset size to inspect
kmx=15
# Get our node subset associated with the $KMX highest perturbed (up or down)
# in our first Arginase deficiency sample.
S_arg = sort(abs(arg_data[,1]), decreasing=TRUE)[1:kmx]
print(S_arg)

##                x - 11381                                x - 13481
##                4.197347                                3.510904
##                2-aminobutyrate                        dihydroorotate
##                3.122232                                3.117244
##                2-arachidonoyl-gpc (20:4) 2-linoleoylglycerol (2-monolinolein)
##                2.942611                                2.862771
##                1-docosahexaenoyl-gpc (22:6)          x - 13478
##                2.754610                                2.741754
##                x - 12792                gamma-glutamyl-2-aminobutyrate
##                2.707036                                2.661916
##                1-arachidonoyl-gpc (20:4)          x - 17001
##                2.653048                                2.586215
##                x - 18914                prolylhydroxyproline
##                2.573498                                2.537495
##                1-stearoyl-gpc (18:0)
##                2.246071

```

IV.II Get k node permutations.

```

# Get the single-node encoding node ranks starting from each node in the subset
# S_arg.
ranks = list()
for (n in 1:length(S_arg)) {
  ind = which(names(G)==names(S_arg)[n])
  ranks[[n]]=singleNode.getNodeRanksN(ind,G,p1=1.0,thresholdDiff=0.01,
                                     adj_mat,S=names(S_arg),
                                     num.misses=log2(length(G)),TRUE)
}

## [1] "Node ranking 128 of 196."
## [1] "Node ranking 157 of 196."
## [1] "Node ranking 19 of 196."
## [1] "Node ranking 60 of 196."
## [1] "Node ranking 21 of 196."
## [1] "Node ranking 28 of 196."
## [1] "Node ranking 3 of 196."
## [1] "Node ranking 156 of 196."
## [1] "Node ranking 149 of 196."
## [1] "Node ranking 63 of 196."
## [1] "Node ranking 2 of 196."
## [1] "Node ranking 170 of 196."
## [1] "Node ranking 188 of 196."
## [1] "Node ranking 103 of 196."
## [1] "Node ranking 18 of 196."

```

```
names(ranks) = names(S_arg)
```

IV.III Convert to bitstrings.

```
# Get the bitstrings associated with the patient's perturbed metabolites in  
# "S_arg" based on the node ranks calculated in the previous step, "ranks".  
ptBSbyK = mle.getPtBSbyK(names(S_arg), ranks)
```

IV.IV Get encoding length of minimum length codeword.

```
ind = which(colnames(arg_data) %in% names(diags))  
data_mx.pvals=apply(arg_data[,ind], c(1,2),  
                    function(i) 2*pnorm(abs(i), lower.tail=FALSE))  
ptID = "IEM_1006"  
res = mle.getEncodingLength(ptBSbyK, t(data_mx.pvals), ptID, G)  
ind.mx = which.max(res$d.score)  
res[ind.mx,]  
  
## patientID optimalBS subsetSize opt.T  
## 11 IEM_1006 TTTTTTTTOTT 11 11  
##  
## 11 1.8e-03/6.8e-03/3.3e-03/8.0e-03/5.9e-03/9.7e-03/2.7e-05/4.5e-04/1.8e-03/7.8e-03/1.0e-02 varPvalue  
## fishers.Info IS.null IS.alt d.score  
## 11 55.8924 58.09905 18.61471 39.484
```

IV.V Get probability of node subset.

```
# This is the lower bound of the probability associated with the metabolites  
# in S_arg. The higher the probability relative to a random set of the same  
# size, the more tightly connected the metabolite set is.  
2^-res[ind.mx,"IS.alt"]
```

```
## [1] 2.491231e-06
```

```
# Note the probability printed above may seem low, but there are  
# log2(length(G), kmx) outcomes that probability is assigned between.  
# We should expect a probability for a node set of size kmx in a length(G)  
# network to have probability:  
2^-(log2(choose(length(G), kmx)))
```

```
## [1] 9.359992e-23
```

```
# You'll notice the probability associated with the metabolite set we encoded,  
# S_arg, is orders of magnitude higher than a uniform probability model. This  
# implies the metabolites in S_arg are connected in the network ig_arg more  
# than is expected by chance.
```

IV.V Get p-value of variable length encoding vs. fixed length encoding.

```
# You can interpret the probability assigned to this metabolite set by  
# comparing it to a null encoding algorithm, which uses fixed-length codes  
# for all metabolites in the set. The "d.score" is the difference in bitlength  
# between the null and alternative encoding models. Using the Algorithmic  
# Significance theorem, we can estimate the upper bounds on a p-value by  
# 2-d.score.
```

```
2-res[ind.mx,"d.score"]
```

```
## [1] 1.300564e-12
```

```
# All metabolites in S_arg
```

```
names(S_arg)
```

```
## [1] "x - 11381"  
## [2] "x - 13481"  
## [3] "2-aminobutyrate"  
## [4] "dihydroorotate"  
## [5] "2-arachidonoyl-gpc (20:4)"  
## [6] "2-linoleoylglycerol (2-monolinolein)"  
## [7] "1-docosahexaenoyl-gpc (22:6)"  
## [8] "x - 13478"  
## [9] "x - 12792"  
## [10] "gamma-glutamyl-2-aminobutyrate"  
## [11] "1-arachidonoyl-gpc (20:4)"  
## [12] "x - 17001"  
## [13] "x - 18914"  
## [14] "prolylhydroxyproline"  
## [15] "1-stearoyl-gpc (18:0)"
```

```
# Which metabolites were in the 8 metabolite subset of patient IEM_1006's  
# top 15 perturbed metabolites that had the above p-value?
```

```
ptBSbyK[[ind.mx]] # all metabolites in the bitstring
```

```
##           dihydroorotate           x - 12792  
##           1                   1  
## 2-arachidonoyl-gpc (20:4) 1-arachidonoyl-gpc (20:4)  
##           1                   1  
## 1-docosahexaenoyl-gpc (22:6) x - 17001  
##           1                   1  
##           x - 11381           x - 13481  
##           1                   1  
##           2-aminobutyrate     alpha-ketobutyrate  
##           1                   0  
## gamma-glutamyl-2-aminobutyrate x - 18914  
##           1                   1
```

```
# just the F metabolites that are in S_arg that were were "found"
```

```
names(which(ptBSbyK[[ind.mx]]==1))
```

```
## [1] "dihydroorotate"           "x - 12792"  
## [3] "2-arachidonoyl-gpc (20:4)"   "1-arachidonoyl-gpc (20:4)"  
## [5] "1-docosahexaenoyl-gpc (22:6)" "x - 17001"  
## [7] "x - 11381"                 "x - 13481"  
## [9] "2-aminobutyrate"           "gamma-glutamyl-2-aminobutyrate"
```

```
## [11] "x - 18914"
```

V. Patient Distances, Single-Node Encoding Recommended

```
data_mx=arg_data[,which(colnames(arg_data) %in% names(diags))]
data_mx=data_mx[,seq_len(8)]
S_arg=c()
for (pt in 1:ncol(data_mx)) {
  ptID=colnames(data_mx)[pt]
  S_arg=c(S_arg,names(sort(abs(data_mx[,pt]),decreasing=TRUE)[1:kmx]))
}
S_arg = unique(S_arg)
# Pre-computing node ranks from all perturbed metabolites across all patients
# is the overhead we have to pay for when using this mutual information-based
# similarity metric, but will pay off when we go to compute several pairwise
# calculations of similarity.
# It feels like a lot of overhead when run serially, but when run in parallel
# (recommended) (e.g., a computing cluster) this finishes in minutes.
ranks=list()
for (n in 1:length(S_arg)) {
  ind=which(names(G)==S_arg[n])
  ranks[[n]]=singleNode.getNodeRanksN(ind,G,p1=1.0,thresholdDiff=0.01,
  adj_mat,S=S_arg,
  num.misses=log2(length(G)),FALSE)
}
names(ranks)=S_arg
# Calculate patient bitstrings
ptBSbyK=list()
for (pt in 1:ncol(data_mx)) {
  ptID=colnames(data_mx)[pt]
  S_pt=names(sort(abs(data_mx[,pt]),decreasing=TRUE)[1:kmx])
  ptBSbyK[[ptID]]=mle.getPtBSbyK(S_pt, ranks)
}
# Now perform mutual information-based patient similarity scoring
res = list()
t = list(ncd=matrix(NA, nrow=ncol(data_mx), ncol=ncol(data_mx)))
rownames(t$ncd) = colnames(data_mx)
colnames(t$ncd) = colnames(data_mx)
for (i in 1:kmx) { res[[i]] = t }
for (pt in 1:ncol(data_mx)) {
  ptID=colnames(data_mx)[pt]
  for (pt2 in pt:ncol(data_mx)) {
    ptID2=colnames(data_mx)[pt2]
    # Because we pre-computed node ranks for all perturbed metabolites
    # across our 8 patients, this will complete very quickly.
    tmp = mle.getPtDist(ptBSbyK[[ptID]],ptID,ptBSbyK[[ptID2]],ptID2,
    data_mx,ranks,p1=1.0,thresholdDiff=0.01,adj_mat)
    for (k in 1:kmx) {
      res[[k]]$ncd[ptID, ptID2] = tmp$NCD[k]
      res[[k]]$ncd[ptID2, ptID] = tmp$NCD[k]
    }
  }
}
```

```
}
```

VI. Visualizations

```
# Multi-dimensional scaling
plot.mdsDist = function(patientDist, diagnoses, diag) {
  if (is.null(diagnoses)) {
    print("To view patient clusters, please provide clinical labels.")
    return(0)
  }
  fitDist = cmdscale(patientDist, eig=FALSE, k=2)
  x = round(fitDist[,1], 2)
  y = round(fitDist[,2], 2)
  df=data.frame(x=x,y=y,color=as.factor(diagnoses),label=colnames(patientDist))
  p=ggplot(df,aes(x,y,label=label))+geom_point(aes(colour=color),size=5)+
    geom_label(nudge_x = 0.1)
  return(p)
}

# K-nearest neighbors
plot.knnDist = function(patientDist, diagnoses, diag) {
  diagnoses = diagnoses[colnames(patientDist)]
  # Add a GREEN edge between patient nodes if k nearest neighbor is
  # correct diagnosis (either TP or TN)
  # Add a RED edge between patient nodes if k nearest neighbor is
  # incorrect diagnosis (either FP or FN)
  tp = 0
  fp = 0
  tn = 0
  fn = 0
  ig = make_empty_graph(n=ncol(patientDist), directed=TRUE)
  V(ig)$name = colnames(patientDist)
  for (pt1 in 1:length(diagnoses)) {
    diag_pt1 = diagnoses[pt1]
    ind = sort(patientDist[pt1,-pt1], decreasing = FALSE)
    ind = ind[which(ind==min(ind))]
    diag_pt_ind = diagnoses[which(names(diagnoses) %in% names(ind))]
    if (any(diag_pt_ind==diag) && diag_pt1==diag) { # True positive
      tp=tp + 1
      ind=ind[which(diag_pt_ind==diag)]
      ig=add.edges(ig,
                   edges=c(colnames(patientDist)[pt1],names(ind[1])),
                   attr=list(color="green", lty=1))
    } else if (diag_pt_ind!=diag && diag_pt1!=diag) { # True negative
      tn=tn + 1
      ig=add.edges(ig,
                   edges=c(colnames(patientDist)[pt1],names(ind[1])),
                   attr=list(color="green", lty=1))
    } else if (diag_pt_ind==diag && diag_pt1!=diag) { # False positive
      fp=fp + 1
      ig=add.edges(ig,
                   edges=c(colnames(patientDist)[pt1],names(ind[1])),

```

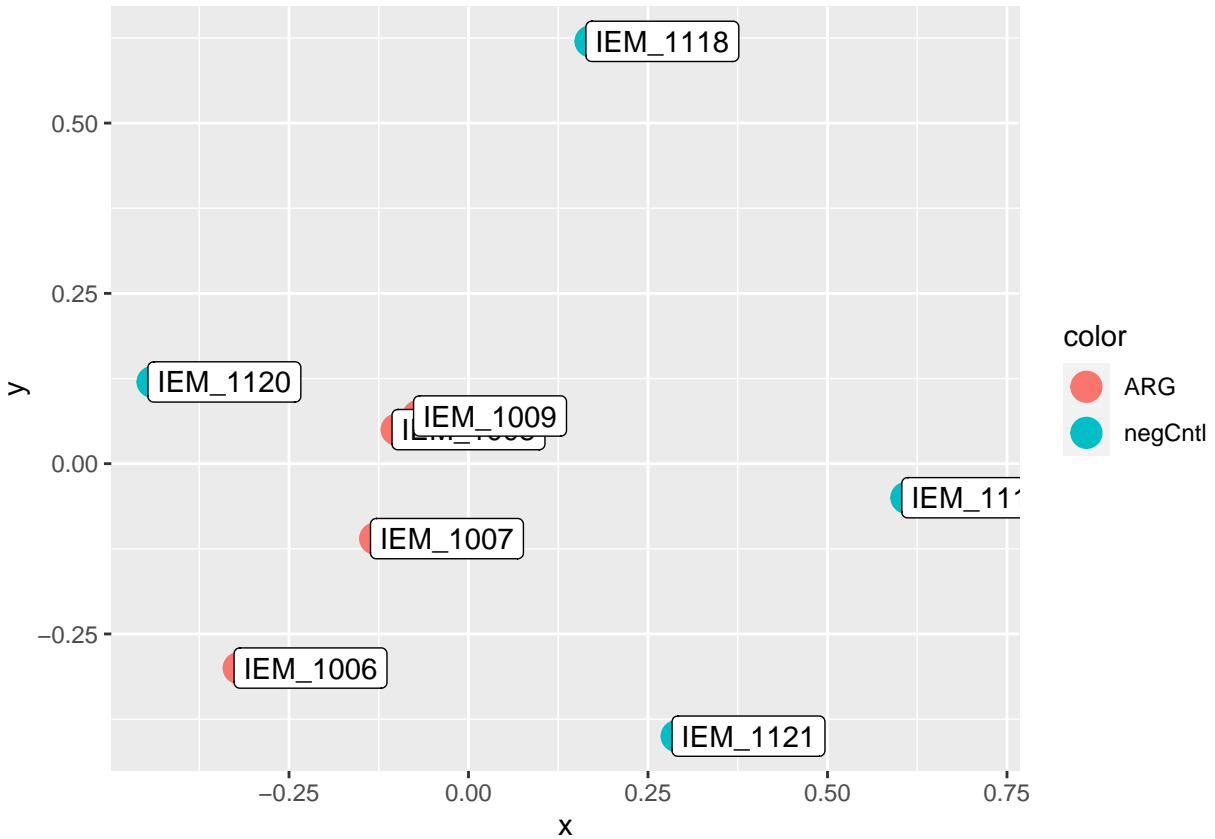
```

                                attr=list(color="red", lty=1))
  } else { # False negative
    fn=fn + 1
    ig=add.edges(ig,
                 edges=c(colnames(patientDist)[pt1],names(ind[1])),
                 attr=list(color="red", lty=1))
  }
}
print(sprintf("Tp = %d, Tn = %d, Fp = %d, Fn=%d", tp, tn, fp, fn))
sens = tp / (tp+fn)
spec = tn / (tn+fp)
print(sprintf("Sens = %.2f, Spec= %.2f", sens, spec))
V(ig)$label = rep("", length(V(ig)$name))
return(ig)
}

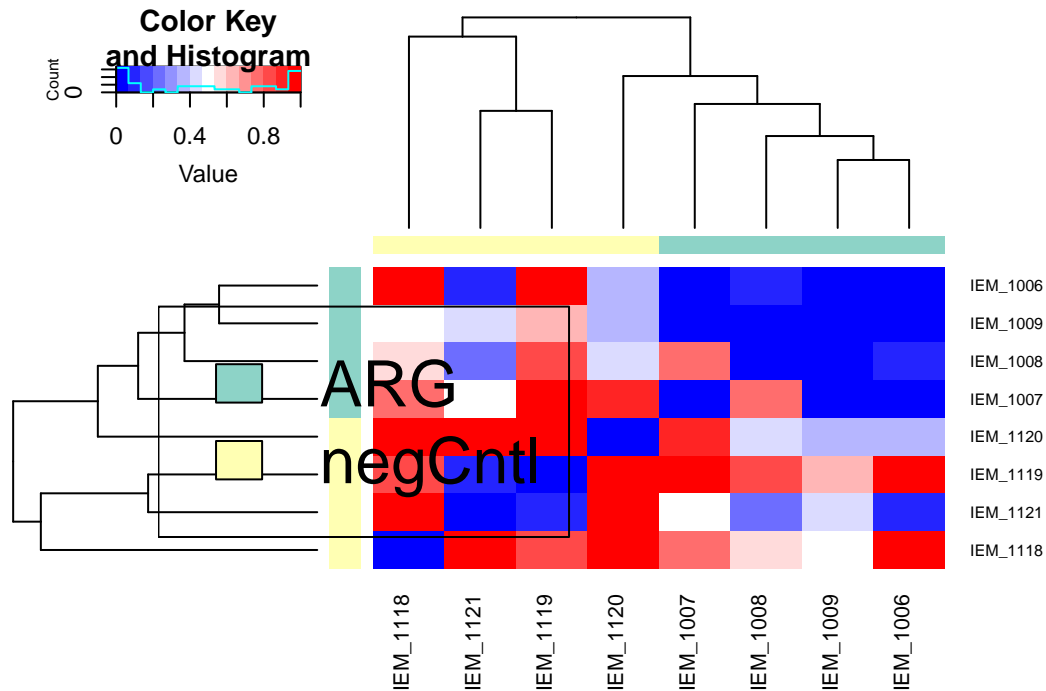
# If you have diagnostic labels associated with the colnames(data_mx),
# send them using diagnoses parameter
res_ncd = lapply(res, function(i) i$ncd)
ncd = mle.getMinPtDistance(res_ncd)
dd = colnames(data_mx)
dd[which(dd %in% names(diags)[which(diags=="Argininemia")])] = "ARG"
dd[which(dd %in% names(diags)[which(diags!="Argininemia")])] = "negCnt1"
names(dd) = colnames(res[[1]]$ncd)

colnames(ncd)=colnames(res[[1]]$ncd)
rownames(ncd)=colnames(res[[1]]$ncd)
p=plot.mdsDist(ncd, dd, NULL)
p

```



```
# Hierarchical clustering
dd_f = as.numeric(as.factor(as.character(dd)))
heatmap.2(x=ncd,dendrogram="both", Rowv=TRUE,Colv=TRUE,
          ColSideColors=c(brewer.pal(12,"Set3"),brewer.pal(9,"BrBG"))[dd_f],
          RowSideColors=c(brewer.pal(12,"Set3"),brewer.pal(9,"BrBG"))[dd_f],
          cexRow=0.75,cexCol=1, margins=c(12,12), trace="none", key=TRUE,
          col=bluered, notecol="black")
legend("left", legend=unique(sort(as.character(dd))),
      fill=c(brewer.pal(12,"Set3"), brewer.pal(9,"BrBG")), cex=2)
```



```
# K-NN
ig=plot.knnDist(ncd, dd, diag="ARG")

## [1] "Tp = 4, Tn= 2, Fp = 2, Fn=0"
## [1] "Sens = 1.00, Spec= 0.50"

grps=list()
grps[[1]]=names(dd)[which(dd=="ARG")]
grps[[2]]=names(dd)[which(dd!="ARG")]
names(grps)=names(table(dd))
plot.igraph(ig, mark.groups=grps, mark.col=c("white", "black"),
            layout=layout.circle, edge.width=3, edge.arrow.size=0.5)
```