```
File name: recontrData-all.R
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      Comment: used to convert normal to data with 16 varialbes
##______
library(Rlab)
## OS specific directories:
mac.os <- "/Users/li11/"</pre>
linux <- "~/"
windows <- "X:/"
#root <- windows</pre>
root <- mac.os
source (paste (root, "myGit/mixturemodel/Scripts/cleaningFuncs.R", sep = ""))
source (paste (root, "myGit/mixturemodel/Scripts/simDt_functions.R", sep = ""))
source (paste (root, "myGit/mixturemodel/Scripts/reconstrDtFunctions.R", sep = ""))
parameters <- para4()</pre>
## normal sample
#dt.dir <- paste (root, "/myGit/mixturemodel/cleanedData/Normal/", sep="")</pre>
## This is for phase II
dt.dir <- paste (root, "/myGit/workingWithYicheng/phase-I-data/cleanedData/Normal/", sep="")
lab <- "n"
files <- list.files (path = dt.dir, pattern=".rda")</pre>
reconed <- reconstruct(files, parameters)</pre>
normal.temp <- reconed[,-1]</pre>
dim(t(normal.temp))[1]
label <- rep("n", dim(t(normal.temp))[1])</pre>
normal.out <- cbind(t(as.data.frame(normal.temp)), as.data.frame(label))</pre>
dim(normal.out)
##========
## olk sample
##-----
#dt.dir <- paste (root, "/myGit/mixturemodel/cleanedData/OLK/", sep="")</pre>
## This is for phase II
dt.dir <- paste (root, "/myGit/workingWithYicheng/phase-I-data/cleanedData/OLK/", sep="")</pre>
lab <- "k"
files <- list.files (path = dt.dir, pattern=".rda")</pre>
reconed <- reconstruct(files, parameters)</pre>
olk.temp <- reconed[,-1]</pre>
dim(t(olk.temp))[1]
label <- rep(lab, dim(t(olk.temp))[1])</pre>
olk.out <- cbind(t(olk.temp), as.data.frame(label))</pre>
dim(olk.out)
##=======
## oscc sample
##----
#dt.dir <- paste (root, "/myGit/mixturemodel/cleanedData/OSCC/", sep="")</pre>
## This is for phase II
dt.dir <- paste (root, "/myGit/workingWithYicheng/phase-I-data/cleanedData/OSCC/", sep="")
lab <- "c"
files <- list.files (path = dt.dir, pattern=".rda")</pre>
reconed <- reconstruct(files, parameters)</pre>
oscc.temp <- reconed[,-1]</pre>
dim(t(oscc.temp))[1]
label <- rep(lab, dim(t(oscc.temp))[1])</pre>
oscc.out <- cbind(t(oscc.temp), as.data.frame(label))</pre>
dim(oscc.out)
#setwd(paste (root, "/myGit/mixturemodel/reconData/para2/", sep=""))
#setwd(paste (root, "/myGit/mixturemodel/reconData/para3/", sep="")) #Newly tested May 9th, 2014
setwd(paste (root, "/myGit/workingWithYicheng/phase-I-data/reconData/", sep="")) #Newly tested Feb 5th, 2016
combined.recon <- rbind (oscc.out, olk.out, normal.out)</pre>
str(combined.recon)
rownames (combined.recon)
colnames (combined.recon)
write.table (combined.recon, "recon 3classes para4.txt", sep="\t", col.names = NA)
```

```
##
       reconstruction function
reconstruct <- function (files, params)
dt.return <- ""
for (k in 1:length(files))
  load(paste(dt.dir, files[k], sep=""))
 popNum = 3
  if (cleanedSample$AneuLeft == "" || length(cleanedSample$AneuLeft) == 0)
   popNum = 2
  if (cleanedSample$SP count == "")
   popNum = 1
  #Make it 8 if greater than 8
  if (popNum == 3)
  {
          cleanedSample$AneuLeft[which(cleanedSample$AneuLeft > 8)] <- 8</pre>
  }
        #if (is.na(cleanedSample$SP_count1))
  if (cleanedSample$SP_count >=5)
          ratio <- cleanedSample$FP count/cleanedSample$SP count
  }else{
   ratio <- params$oneSampleRatio[1]/params$oneSampleRatio[2]</pre>
        w.norm <- ratio/(1+ratio)</pre>
        w.mito <- 1/(1+ratio)
        x < - seq(0,2.3, by=(2.3/512))
        x < -x[-1]
  if (popNum == 3)
    y1 <- w.norm*P(x, cleanedSample$FP_mean, cleanedSample$FP_std)</pre>
    y2 <- w.mito*P(x, cleanedSample$SP_mean, cleanedSample$SP_std)
    y = y1 + y2
  }else if (popNum ==2)
    if (is.na(cleanedSample$SP_mean))
      cleanedSample$SP_std = params$fakeSP_std
      cleanedSample$SP_mean = params$fakeSP_mean
    }else if (is.na(cleanedSample$SP std))
      cleanedSample$SP_std = params$fakeSP_std
    y1 <- (w.norm*P(x, cleanedSample$FP_mean, cleanedSample$FP_std))*params$twoSampleRatio[1]
    y2 <- (w.mito*P(x, cleanedSample$SP mean, cleanedSample$SP std))*params$twoSampleRatio[1]
    y3 <- P(x, params$fake_aneu_mean, params$fake_aneu_std)*params$twoSampleRatio[2]
    y = y1 + y2 + y3
        prob.y <- c()
        pdf.y <- y/sum(y)
        prob.y[1] <- pdf.y[1]</pre>
  #Gettig the empirical cdf, very important here!!
        for (i in 2:length(y))
                temp.prob <- pdf.y[i]</pre>
                prob.y[i] <- prob.y[i-1] + temp.prob</pre>
        }
  if (popNum == 3)
          numOfAneu <- length(cleanedSample$AneuLeft)</pre>
          num2Recontr <- 9*numOfAneu</pre>
  }else{
```

```
num2Recontr <- 1000
  }
        simDt <- c()
        seed = 12345
        for (i in 1:num2Recontr)
                 x1 <- runif(1, 0, 1)
                 index <- which(prob.y < (x1 + 0.002) & prob.y > (x1 - 0.002))
                 if (length(index) < 1)
                         index <- which (prob.y < (x1 + 0.02) & prob.y > (x1 - 0.02))
                 if (length(index) < 1)
                         index <- which (prob.y < (x1 + 0.2) & prob.y > (x1 - 0.2))
                 temp <- sample( index, 1)</pre>
                 simDt[i] <- x[temp]</pre>
  if (popNum == 3)
    simDt <- c(simDt , cleanedSample$AneuLeft)</pre>
        bk = floor(max(simDt))*2
        den <- (hist(simDt, breaks=bk)$density)</pre>
        for (m in length(den):16)
        {
                den[m] <- params$filler</pre>
        dt.temp <- as.data.frame(den)</pre>
        colnames(dt.temp) <- cleanedSample$sample</pre>
        dt.return <- cbind(dt.return, dt.temp)</pre>
return (dt.return)
```