

rmarkdowntest.R

Mcdade

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```
setwd("C:/Users/Mcdade/Desktop/EUFLOW")
RNASEQDATA<-read.csv(file="RNASEQDATA.csv",header=TRUE)
RPPADATA<-read.csv(file="RPPADATA.original.csv",header=TRUE)
EvaluationExperimentSet<-RNASEQDATA
#EvaluationExperimentSet<-rbind(RNASEQDATA,RANDOMSET)
ReferenceSet<-RPPADATA
```

```
require(IdMappingAnalysis)
```

```
## Loading required package: IdMappingAnalysis
```

```
## Warning: package 'IdMappingAnalysis' was built under R version 3.2.2
```

```
## Loading required package: R.oo
```

```
## Loading required package: R.methodsS3
```

```
## R.methodsS3 v1.7.0 (2015-02-19) successfully loaded. See ?R.methodsS3 for help.
```

```
## R.oo v1.19.0 (2015-02-27) successfully loaded. See ?R.oo for help.
```

```
##
```

```
## Attaching package: 'R.oo'
```

```
## The following objects are masked from 'package:methods':
```

```
##
```

```
##      getClasses, getMethods
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      attach, detach, gc, load, save
```

```
## Loading required package: rChoiceDialogs
```

```
## Loading required package: rJava
```

```
## Warning: package 'rJava' was built under R version 3.2.3
```

```
##
```

```
## Attaching package: 'rJava'
```

```
## The following object is masked from 'package:R.oo':
##
##      clone
```

```
## This is rChoiceDialogs 1.0.6 2014-09-05
```

```
## This is IdMappingAnalysis 1.14.0 2013-05-24
```

```
# #require(mvbutils)
options(stringsAsFactors = FALSE)

.assign.status<-function(x,status,data.type,version){
  if (status == "workflow_option")
    status_tag<-paste(row.names(x),"_WFO","_",as.character(data.type),"_",as.character(version),sep="")
  if (status == "driver")
    status_tag<-paste(row.names(x),"_DRIVER",sep="")
  return(status_tag)
}

WorkflowEvaluationData<-function(EvaluationExperimentSet,ReferenceSet){

  names(EvaluationExperimentSet)[1]<- "Symbol"
  names(ReferenceSet)[1]<- "Symbol"
  row.names(EvaluationExperimentSet)<-EvaluationExperimentSet$Symbol
  row.names(ReferenceSet)<-ReferenceSet$Symbol
  WorkflowList<-strsplit(row.names(EvaluationExperimentSet),"_")
  WorkflowNameVector<-sapply(WorkflowList, "[", 1)
  WorkflowOptionVector<-sapply(WorkflowList, "[", 2)
  #WorkflowNumber<-substr(WorkflowOptionVector,nchar(WorkflowOptionVector),nchar(WorkflowOptionVector)-1)
  return(list(ReferenceSet,(split(EvaluationExperimentSet,WorkflowOptionVector))))

}

Workflow.Data<-WorkflowEvaluationData(EvaluationExperimentSet,ReferenceSet)

merge.tag.options<-function(Workflow.Data,ReferenceTag="P",EvaluationTag="RS"){
  EvaluationList<-Workflow.Data[[2]]
  Merged.options<-Workflow.Data[[1]]
  row.names(Merged.options)<- .assign.status(Merged.options,status="driver",ReferenceTag,1)
  for(o in c(1:length(EvaluationList))) {
    Evaluation_dataframe<-as.data.frame(EvaluationList[[o]])
    SymbolList<-strsplit(row.names(Evaluation_dataframe),"_")
    row.names(Evaluation_dataframe)<-sapply(SymbolList, "[", 1)
    row.names(Evaluation_dataframe)<- .assign.status(Evaluation_dataframe,status="workflow_option",EvaluationTag,1)
    Merged.options=rbind(Merged.options,Evaluation_dataframe)
  }
}
```

```

    }
    return(Merged.options)
}

Merged.options<-merge.tag.options(Workflow.Data)

#count.options<-function(x) {
#   paste(row.names(workflow_options_data[sapply(strsplit(row.names(workflow_options_data),"_"), "[",
#}]

make.workflow.map <- function(Merged.options){
  drivers<-row.names(Merged.options[sapply(strsplit(row.names(Merged.options),"_"), "[", 2) == "DRIVER"])
  workflow_options_data<-Merged.options[sapply(strsplit(row.names(Merged.options),"_"), "[", 2) == "WORKFLOW_OPTIONS"]
  count.options<-function(x) {
    paste(row.names(workflow_options_data[sapply(strsplit(row.names(workflow_options_data),"_"), "[",
  })
  #workflow_options<-row.names(workflow_options_data[sapply(strsplit(row.names(workflow_options_data),
  imax<-max(unique(sapply(strsplit(row.names(workflow_options_data),"_"), "[", 4)),na.rm = TRUE)
  #imin<-min(unique(sapply(strsplit(row.names(workflow_options_data),"_"), "[", 4)),na.rm = TRUE)
  #workflow_options_merged<-paste(count.options(workflow_options_data,1),count.options(workflow_options_data,2))
  workflow_options_matrix<-sapply(1:imax,count.options)
  #workflow_options_merged<-paste(row.names(workflow_options_data[sapply(strsplit(row.names(workflow_options_data),
  workflow_options_merged<-sapply(1:dim(workflow_options_matrix)[1],function(i){paste0(as.character(workflow_options_matrix[i,]),
  WorkflowMap<-data.frame(drivers,workflow_options_merged)
  ###when your ready class(Merged.options)<- "WorkflowMap"
  return(WorkflowMap)
}

Model.quality.list<-function(Merged.options){
  WorkflowMap.object<-make.workflow.map(Merged.options)
  IdMap.example<-IdMap(DF=WorkflowMap.object,name="Workflowmap.object", primaryKey="drivers",secondaryIDs=
  secondaryIDs<-unlist(strsplit(WorkflowMap.object$workflow_options_merged,""))
  uniquePairs_workflow <- as.UniquePairs.IdMap(IdMap.example,secondaryIDs)
  reference<-Merged.options[sapply(strsplit(row.names(Merged.options),"_"), "[",2) == "DRIVER",]
  names(reference)[names(reference)=="Symbol"] <- "drivers"
  reference$drivers<-row.names(reference)
  evaluation<-Merged.options[sapply(strsplit(row.names(Merged.options),"_"), "[",2) != "DRIVER",]
  names(evaluation)[names(evaluation)=="Symbol"] <- "workflow_options_merged"
  evaluation$workflow_options_merged<-row.names(evaluation)
  Model.quality.object<-CorrData(uniquePairs_workflow,reference,evaluation)
  return(Model.quality.object)
}

Model.quality.object<-Model.quality.list(Merged.options)

Workflow.Criterion<-function(Model.quality.object){
  Model.quality<- Corr(Model.quality.object,method="spearman",verbose=TRUE)
  return(Model.quality)
}

```

```
Model.Quality<-Workflow.Criterion(Model.quality.object)
```

```
## Performing correlations...
```

```
fit2clusters.workflow<-function(Y, Ysigsq,
                                bootModel,
                                piStart = c(0.5, 0.5),
                                VStart = c(0.1,0.1),
                                psiStart = c(0,0.1),
                                NinnerLoop = 1,
                                nReps=500,
                                psi0Constraint,
                                VOConstraint,
                                sameV=FALSE,
                                estimatesOnly=TRUE,
                                printMe = TRUE,
                                plotMe = TRUE,
                                testMe=FALSE,
                                Ntest = 5000,
                                seed) {
  ### EM algorithm for 2 clusters,
  ### with constraints on the cluster means and variances, and known data variances
  if(testMe) {
    if(missing(seed)) .Random.seed <- Random.seed.save
    else if(!is.na(seed)) .Random.seed <- seed
    # NA ==> a new dataset.
    simPsi = c(0, 0.4) ##
    simPi = c(2/3, 1/3)
    simData = data.frame(G = 1+rbinom(Ntest, 1, simPi[2]))
    simV = c(0.05^2, 0.05^2)
    simData$Ysigsq = rgamma(Ntest, 10, 400)
    simData$sd = sqrt(simV[simData$G] +simData$Ysigsq)
    simData = within(simData, Y <- simPsi[G] + rnorm(Ntest)*sqrt(simV[G]) + rnorm(Ntest)*sqrt(Ysigsq))
    print(summary(simData$Y))
    Y = simData$Y
    Ysigsq = simData$Ysigsq
  }
  ##### Beginning of EM algorithm #####
  piStar = piStart
  VStar = VStart
  psiStar = psiStart
  stopMe = FALSE
  iRep = 0
  while(1) {
    iRep = iRep + 1
    # catn(" ", " ", missing(VOConstraint))
    if(!missing(VOConstraint))
      VStar[1] = VOConstraint
    if(!missing(psi0Constraint))
      psiStar[1] = psi0Constraint
    # print(psiStar)
    piStarOdds = piStar[2]/piStar[1]
```

```

piStarOddsGK = piStarOdds *
  dnorm(Y, psiStar[2], sqrt(VStar[2] + Ysigsq)) /
  dnorm(Y, psiStar[1], sqrt(VStar[1] + Ysigsq))
piStarGK = cbind(1/(1+piStarOddsGK), piStarOddsGK/(1+piStarOddsGK))
EstarN = apply(piStarGK, 2, sum)
piStar = apply(piStarGK, 2, mean)
psiHat = psiStar
VHat = VStar
for(iRepInner in 1:NinnerLoop) {
  varHatTotal = colSums(outer(Y, psiHat, "-")^2 * piStarGK)
  sigsqTotal = Ysigsq %*% piStarGK
  VHat = pmax(0, varHatTotal - sigsqTotal) / EstarN
  if(!missing(VOConstraint))
    VHat[1] = VOConstraint
  psiHat = colSums( Y %*% (piStarGK
    / outer(Ysigsq, VHat, "+"))) /
    colSums( piStarGK
    / outer(Ysigsq, VHat, "+"))
  if(!missing(psiOConstraint))
    psiHat[1] = psiOConstraint
  if(sameV)
    VHat[1] = VHat[2] = mean(VHat[1], VHat[2])
  if(max(abs(psiHat-psiStar), abs(VHat-VStar)) < 1e-7)
    stopMe = TRUE;
  psiHat -> psiStar
  VHat -> VStar
}
if(iRep >= nReps) stopMe = TRUE
if(stopMe) break
}
cat(iRep, ifelse(iRep==nReps, ". Loop exhausted.", ". Converged."), "\n")

if(plotMe) {
  options(echo=F)
  plot(col="blue", type = "l", main = "Mixture density", Ytemp<-seq(-1,1,length=100),
    xlab= as.character(names(bootModel[3])), cex.lab = 1.5, ylab="Density", sub = as.character
    piStar[1]*dnorm(Ytemp, psiStar[1], sqrt(VStar[1] + mean(Ysigsq)))
    +
    piStar[2]*dnorm(Ytemp, psiStar[2], sqrt(VStar[2] + mean(Ysigsq)))
  )
  for(g in 1:2) lines(col="blue", lty=2, Ytemp<-seq(-1,1,length=100),
    piStar[g]*dnorm(Ytemp, psiStar[g], sqrt(VStar[g] + mean(Ysigsq))))
  lines(density(Y), lwd=2, col="black")
  abline(v = 0)
  abline(v = 0.38352)
  ### Should we make a better choice than the means of the Ysigsq?
  if(testMe) lines(col="red", Ytemp<-seq(-1,1,length=100),
    piStar[1]*dnorm(Ytemp, simPsi[1], sqrt(simV[1] + mean(simData$Ysigsq)))
    +
    piStar[2]*dnorm(Ytemp, simPsi[2], sqrt(simV[2] + mean(simData$Ysigsq)))
  )
  legend(x=par("usr")[1], y=par("usr")[4],
    legend=c(ifelse(testMe, "truth", "")),

```

```

        "data smooth", "estimate", " x or 0 component", " + component"),
        col=c("red", "black", "blue", "blue", "blue"),
        lty=c(ifelse(testMe, 1,0),1,1,2,2),
        lwd=c(1,2,1,1,1)
    )
    options(echo=T)
}
estimates = c(pi1=piStar[2], psi0=psiHat[1],
              psi1=psiHat[2], Var0=VStar[1], Var1=VStar[2])

posteriorOdds =
  piStar[2]*dnorm(Y, psiHat[2], sqrt(VStar[2] + Ysigsq)) /
  piStar[1]/dnorm(Y, psiHat[1], sqrt(VStar[1] + Ysigsq))
postProb = posteriorOdds/(1+posteriorOdds)
postProbVar = Ysigsq * (postProb*(1-postProb))^2 *
  ((Y-psiHat[1])/(VStar[1]+Ysigsq) - (Y-psiHat[2])/(VStar[2]+Ysigsq))^2

if(testMe) {
  simTruth = c(pi1=simPi[2], psi0=simPsi[1],
               psi1=simPsi[2], Var0=simV[1], Var1=simV[2])
  estimates = data.frame(row.names=c("true","estimated"),
                         rbind(simTruth, estimates))
}
if(estimatesOnly) return(estimates)
else {
  attr(x=posteriorOdds, which="estimates") = estimates
  return(data.frame(posteriorOdds,postProbVar))
}
}

```

```

Workflow.posteriorestimate<-function(Model.quality.object,Model.Quality,postProb=NULL,postProbVar=NULL){
  bootstrap<-Bootstrap(Model.quality.object,Fisher=TRUE,verbose=TRUE)
  bootModel<-as.data.frame(bootstrap)
  bootModel<-bootModel[complete.cases(bootModel),]
  pairs<-bootModel[,1:2]
  #bootModel<-bootModel[c(1:96,99:134),]
  EMtest<-fit2clusters.workflow(bootModel$corr, bootModel$sd^2,bootModel,psi0Constraint=0, sameV=T,es
  #again part of the EMtest
  postProbs<-as.vector(EMtest[[1]]/(1+EMtest[[1]])) #not needed at the output is a datafrmae from fi
  postProbVar <-as.vector(EMtest[[2]])
  bootMergedWithPairs = merge(data.frame(postProbs=postProbs, postProbVar=postProbVar,bootModel), pairs
  return(bootMergedWithPairs)
}

```

```

Posterior.dataframe<-Workflow.posteriorestimate(Model.quality.object,Model.Quality)

```

```

## Performing bootstrap R= 200 on correlations...
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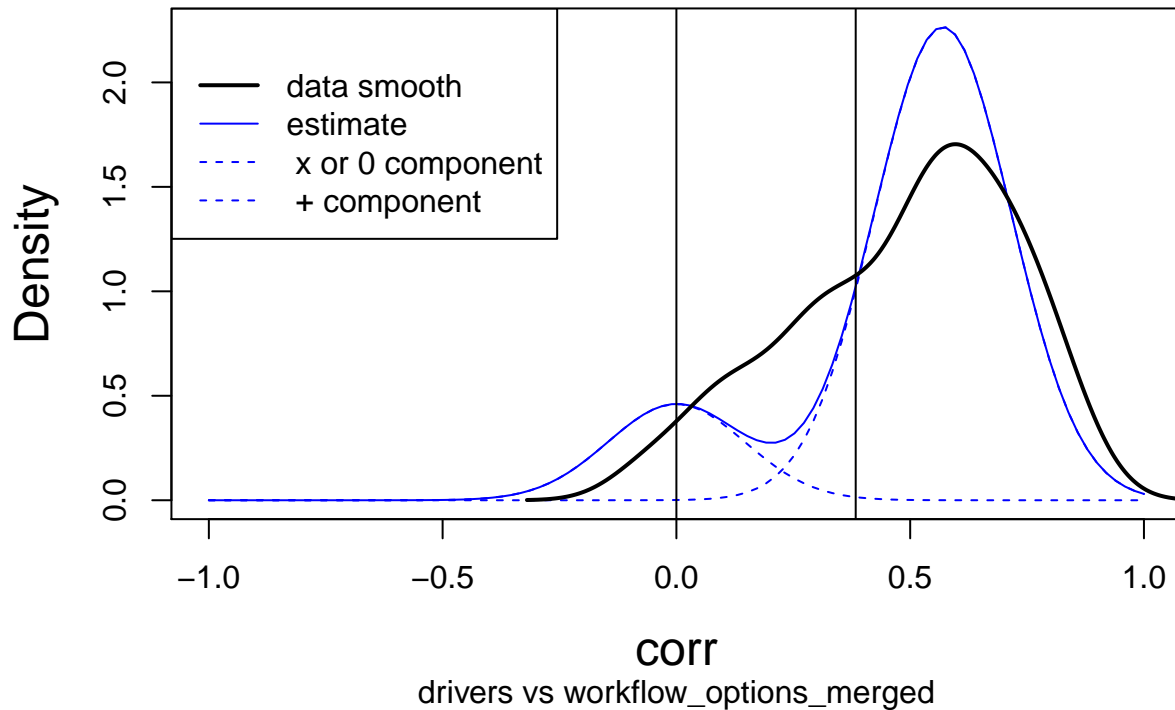
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35 . Converged.

Mixture density



```
expectedUtility<-function(dataset, label="", Lfp=1,Utp=1,deltaPlus=1,guarantee=1e-5)
{
  postProbVar = pmax(dataset$postProbVar, guarantee)
  PrPlus = sum(dataset$postProbs/postProbVar)/
    sum(1/postProbVar)
  result = data.frame(label=label,
    Utp=Utp, Lfp=Lfp, deltaPlus=deltaPlus,
    nPairs=nrow(dataset),
    PrPlus= PrPlus,
    PrTrue= PrTrue<-PrPlus / deltaPlus,
    PrFalse= PrFalse<-1 - PrTrue,
    Utrue= Utrue<-PrTrue * Utp,
    Lfalse= Lfalse<-PrFalse * Lfp,
    Eutility1= Utrue-Lfalse,
    Eutility= nrow(dataset)*(Utrue-Lfalse))
  rownames(result) = label
  return(result)
}
```

```
Workflow.Evaluation.table<-function(Posterior.dataframe,Lfp=1,Utp=1,deltaPlus=1,guarantee=1e-5){
  WorkflowStats<-data.frame(sapply(strsplit(Posterior.dataframe$workflow_options_merged,"_"), "[",1),s
  colnames(WorkflowStats)[1]<-"Marker"
  colnames(WorkflowStats)[2]<-"WorkflowID"
  og<-expectedUtility(label="Use All", dataset=WorkflowStats,Lfp=Lfp,Utp=Utp,deltaPlus=deltaPlus,guar
  for(p in unique(WorkflowStats$WorkflowID)){
    set<-expectedUtility(label=as.character(WorkflowStats$WorkflowID[as.numeric(p)]), dataset=Workf
```

```

    og=rbind(og,set)
  }
  return(og)
}

```

```
Workflow.Evaluation.table(Posterior.dataframe)
```

```

##           label Utp Lfp deltaPlus nPairs    PrPlus    PrTrue    PrFalse
## Use All Use All  1   1          1    133 0.9543752 0.9543752 0.04562483
## 1           1   1   1          1     67 0.9390894 0.9390894 0.06091061
## 2           2   1   1          1     66 0.9698081 0.9698081 0.03019194
##           Utrue    Lfalse Eutility1  Eutility
## Use All 0.9543752 0.04562483 0.9087503 120.86380
## 1      0.9390894 0.06091061 0.8781788  58.83798
## 2      0.9698081 0.03019194 0.9396161  62.01466

```