

script.r

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```
filesToRead <- dir("../ExpressionResults/",pattern = "*\\.txt",full.names=T)
fileRead <- vector("list",length=length(filesToRead))
for(i in 1:length(filesToRead)){
  fileRead[[i]] <- read.delim(filesToRead[i],header=F,sep="\t")
  colnames(fileRead[[i]]) <- c("GeneNames",basename(filesToRead[i]))
}
mergedTable <- NULL
for(i in fileRead){
  if(is.null(mergedTable)){
    mergedTable <- i
  }else{
    mergedTable <- merge(mergedTable,i,by=1,all=T)
  }

  print(nrow(mergedTable))
}
```

```
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
## [1] 2000
```

```
mergedTable[1:3,]
```

```
##   GeneNames ExpressionResults_Sample1.txt ExpressionResults_Sample10.txt
## 1   Gene_1                3.448466                7.665488
## 2   Gene_10               5.314180                7.813501
## 3   Gene_100              5.591612                5.186500
##   ExpressionResults_Sample2.txt ExpressionResults_Sample3.txt
## 1                5.250063                5.968927
## 2                5.361170                5.305980
## 3                6.840497                5.197710
##   ExpressionResults_Sample4.txt ExpressionResults_Sample5.txt
## 1                6.868251                5.367100
## 2                6.742855                5.957786
## 3                5.922931                6.813154
##   ExpressionResults_Sample6.txt ExpressionResults_Sample7.txt
## 1                5.189686                3.882930
## 2                6.293098                7.361497
## 3                6.228178                5.831575
```

```
## ExpressionResults_Sample8.txt ExpressionResults_Sample9.txt
## 1 5.329258 6.167451
## 2 6.649428 6.213910
## 3 6.653152 3.992555
```

```
Annotation <- read.table("../ExpressionResults/Annotation.ann",sep="\t",h=T)
annotatedExpression <- merge(Annotation,mergedTable,by=1,all.x=F,all.y=T)
annotatedExpression[1:2,]
```

```
## GeneName Ensembl Pathway ExpressionResults_Sample1.txt
## 1 Gene_1 Ens_1001 DNA_Binding 3.448466
## 2 Gene_10 Ens_10010 DNA_Binding 5.314180
## ExpressionResults_Sample10.txt ExpressionResults_Sample2.txt
## 1 7.665488 5.250063
## 2 7.813501 5.361170
## ExpressionResults_Sample3.txt ExpressionResults_Sample4.txt
## 1 5.968927 6.868251
## 2 5.305980 6.742855
## ExpressionResults_Sample5.txt ExpressionResults_Sample6.txt
## 1 5.367100 5.189686
## 2 5.957786 6.293098
## ExpressionResults_Sample7.txt ExpressionResults_Sample8.txt
## 1 3.882930 5.329258
## 2 7.361497 6.649428
## ExpressionResults_Sample9.txt
## 1 6.167451
## 2 6.213910
```

```
table(Annotation$Pathway)
```

```
##
## DNA_Binding Glycolysis TGFb WntSignaling
## 1000 500 300 200
```

```
summary(Annotation$Pathway)
```

```
## DNA_Binding Glycolysis TGFb WntSignaling NA's
## 1000 500 300 200 3000
```

```
cor(annotatedExpression[,grep("ExpressionResults",colnames(annotatedExpression))])
```

```
## ExpressionResults_Sample1.txt
## ExpressionResults_Sample1.txt 1.0000000
## ExpressionResults_Sample10.txt 0.8620963
## ExpressionResults_Sample2.txt 0.8662458
## ExpressionResults_Sample3.txt 0.8681681
## ExpressionResults_Sample4.txt 0.8616757
## ExpressionResults_Sample5.txt 0.8643865
## ExpressionResults_Sample6.txt 0.8712424
## ExpressionResults_Sample7.txt 0.8625237
## ExpressionResults_Sample8.txt 0.8618539
```

```

## ExpressionResults_Sample9.txt 0.8686308
## ExpressionResults_Sample10.txt
## ExpressionResults_Sample1.txt 0.8620963
## ExpressionResults_Sample10.txt 1.0000000
## ExpressionResults_Sample2.txt 0.8662233
## ExpressionResults_Sample3.txt 0.8681699
## ExpressionResults_Sample4.txt 0.8701285
## ExpressionResults_Sample5.txt 0.8703278
## ExpressionResults_Sample6.txt 0.8683173
## ExpressionResults_Sample7.txt 0.8698833
## ExpressionResults_Sample8.txt 0.8660971
## ExpressionResults_Sample9.txt 0.8685996
## ExpressionResults_Sample2.txt
## ExpressionResults_Sample1.txt 0.8662458
## ExpressionResults_Sample10.txt 0.8662233
## ExpressionResults_Sample2.txt 1.0000000
## ExpressionResults_Sample3.txt 0.8724322
## ExpressionResults_Sample4.txt 0.8707259
## ExpressionResults_Sample5.txt 0.8715251
## ExpressionResults_Sample6.txt 0.8685840
## ExpressionResults_Sample7.txt 0.8697635
## ExpressionResults_Sample8.txt 0.8697318
## ExpressionResults_Sample9.txt 0.8757107
## ExpressionResults_Sample3.txt
## ExpressionResults_Sample1.txt 0.8681681
## ExpressionResults_Sample10.txt 0.8681699
## ExpressionResults_Sample2.txt 0.8724322
## ExpressionResults_Sample3.txt 1.0000000
## ExpressionResults_Sample4.txt 0.8679524
## ExpressionResults_Sample5.txt 0.8660294
## ExpressionResults_Sample6.txt 0.8699042
## ExpressionResults_Sample7.txt 0.8637106
## ExpressionResults_Sample8.txt 0.8656122
## ExpressionResults_Sample9.txt 0.8704524
## ExpressionResults_Sample4.txt
## ExpressionResults_Sample1.txt 0.8616757
## ExpressionResults_Sample10.txt 0.8701285
## ExpressionResults_Sample2.txt 0.8707259
## ExpressionResults_Sample3.txt 0.8679524
## ExpressionResults_Sample4.txt 1.0000000
## ExpressionResults_Sample5.txt 0.8749856
## ExpressionResults_Sample6.txt 0.8745045
## ExpressionResults_Sample7.txt 0.8670132
## ExpressionResults_Sample8.txt 0.8703234
## ExpressionResults_Sample9.txt 0.8697739
## ExpressionResults_Sample5.txt
## ExpressionResults_Sample1.txt 0.8643865
## ExpressionResults_Sample10.txt 0.8703278
## ExpressionResults_Sample2.txt 0.8715251
## ExpressionResults_Sample3.txt 0.8660294
## ExpressionResults_Sample4.txt 0.8749856
## ExpressionResults_Sample5.txt 1.0000000
## ExpressionResults_Sample6.txt 0.8645176
## ExpressionResults_Sample7.txt 0.8707010

```

```

## ExpressionResults_Sample8.txt          0.8716815
## ExpressionResults_Sample9.txt          0.8764503
##                                     ExpressionResults_Sample6.txt
## ExpressionResults_Sample1.txt          0.8712424
## ExpressionResults_Sample10.txt         0.8683173
## ExpressionResults_Sample2.txt          0.8685840
## ExpressionResults_Sample3.txt          0.8699042
## ExpressionResults_Sample4.txt          0.8745045
## ExpressionResults_Sample5.txt          0.8645176
## ExpressionResults_Sample6.txt          1.0000000
## ExpressionResults_Sample7.txt          0.8721725
## ExpressionResults_Sample8.txt          0.8725429
## ExpressionResults_Sample9.txt          0.8722234
##                                     ExpressionResults_Sample7.txt
## ExpressionResults_Sample1.txt          0.8625237
## ExpressionResults_Sample10.txt         0.8698833
## ExpressionResults_Sample2.txt          0.8697635
## ExpressionResults_Sample3.txt          0.8637106
## ExpressionResults_Sample4.txt          0.8670132
## ExpressionResults_Sample5.txt          0.8707010
## ExpressionResults_Sample6.txt          0.8721725
## ExpressionResults_Sample7.txt          1.0000000
## ExpressionResults_Sample8.txt          0.8584981
## ExpressionResults_Sample9.txt          0.8675662
##                                     ExpressionResults_Sample8.txt
## ExpressionResults_Sample1.txt          0.8618539
## ExpressionResults_Sample10.txt         0.8660971
## ExpressionResults_Sample2.txt          0.8697318
## ExpressionResults_Sample3.txt          0.8656122
## ExpressionResults_Sample4.txt          0.8703234
## ExpressionResults_Sample5.txt          0.8716815
## ExpressionResults_Sample6.txt          0.8725429
## ExpressionResults_Sample7.txt          0.8584981
## ExpressionResults_Sample8.txt          1.0000000
## ExpressionResults_Sample9.txt          0.8692940
##                                     ExpressionResults_Sample9.txt
## ExpressionResults_Sample1.txt          0.8686308
## ExpressionResults_Sample10.txt         0.8685996
## ExpressionResults_Sample2.txt          0.8757107
## ExpressionResults_Sample3.txt          0.8704524
## ExpressionResults_Sample4.txt          0.8697739
## ExpressionResults_Sample5.txt          0.8764503
## ExpressionResults_Sample6.txt          0.8722234
## ExpressionResults_Sample7.txt          0.8675662
## ExpressionResults_Sample8.txt          0.8692940
## ExpressionResults_Sample9.txt          1.0000000

```

```

indexGroupOne <- grep("[1-5].txt",colnames(annotatedExpression))
indexGroupTwo <- grep("[6-9,0].txt",colnames(annotatedExpression))
ttestResults <- apply(annotatedExpression,1,function(x) t.test(as.numeric(x[indexGroupOne]),as.numeric(
str(ttestResults[[1]]))

```

```
## List of 9
```

```
## $ statistic : Named num -0.318
## .. attr(*, "names")= chr "t"
## $ parameter : Named num 7.92
## .. attr(*, "names")= chr "df"
## $ p.value : num 0.759
## $ conf.int : atomic [1:2] -2.2 1.67
## .. attr(*, "conf.level")= num 0.95
## $ estimate : Named num [1:2] 5.38 5.65
## .. attr(*, "names")= chr [1:2] "mean of x" "mean of y"
## $ null.value : Named num 0
## .. attr(*, "names")= chr "difference in means"
## $ alternative: chr "two.sided"
## $ method : chr "Welch Two Sample t-test"
## $ data.name : chr "as.numeric(x[indexGroupOne]) and as.numeric(x[indexGroupTwo])"
## - attr(*, "class")= chr "htest"
```

```
testResult <- sapply(ttestResults,function(x) c(log2(x$estimate[2]) - log2(x$estimate[1]), x$statistic,
testResult <- t(testResult)
colnames(testResult) <- c("logFC","tStatistic","pValue")
annotatedResult <- cbind(annotatedExpression[,1:3],testResult)
annotatedResult <- annotatedResult[order(annotatedResult$tStatistic),]
annotatedResult[1:2,]
```

```
##      GeneName      Ensembl      Pathway      logFC tStatistic      pValue
## 1491 Gene_54    Ens_10054 DNA_Binding 0.2631082      -5.3950 0.0007161659
## 1716 Gene_742  Ens_100742 Glycolysis 0.2311226      -4.5044 0.0029789595
```

```
#write.table(annotatedResult,file="annotatedResults.csv",sep=" ",row.names=F,col.names=F)
```