

HW1_BMI882

I first downloaded the file from the “Everything” in the source materials.

Next, I found their source code for Fig1b is located at `./RNowebSource/examiningDoxorubicinInDetail.Rnw`

Then, I copied the data required `/RawData/PottiNatMed` for the source code into my workingdir and directly copy the code needed and paste it here. It takes me some time to figure out the blocks do I need to copy.

loadGenes

```
doxorubicinGenes <-  
  read.table(file.path("RawData", "PottiNatMed",  
                        "GeneListsNov07", "Adria(final).txt"),  
             sep="\t", header=TRUE)  
dim(doxorubicinGenes)  
  
## [1] 80 3  
  
doxorubicinGenes[1:3,]  
  
##   Probe.Set.ID                               Gene.Title  
## 1    1051_g_at                               melan-A  
## 2    110_at chondroitin sulfate proteoglycan 4 (melanoma-associated)  
## 3    1319_at                               discoidin domain receptor family, member 2  
##   Gene.Symbol  
## 1      MLANA  
## 2      CSPG4  
## 3      DDR2  
  
doxorubicinGenes <- as.character(doxorubicinGenes[, "Probe.Set.ID"])  
doxorubicinGenes[1:3]  
  
## [1] "1051_g_at" "110_at"      "1319_at"
```

loadDoxo07

```
tempDoxorubicin07Header1 <-  
  read.table(file.path("RawData", "PottiNatMed", "Adria_ALL.txt"), sep="\t",  
             nrows=1, header=FALSE)  
tempDoxorubicin07Header1 <- as.vector(t(tempDoxorubicin07Header1));  
  
tempDoxorubicin07Header2 <-  
  read.table(file.path("RawData", "PottiNatMed", "Adria_ALL.txt"), sep="\t",  
             skip=1, nrows=1, header=FALSE)  
tempDoxorubicin07Header2 <- as.vector(t(tempDoxorubicin07Header2));  
  
tempDoxorubicin07Header1[1:25]  
  
## [1] "Adria0"      "0"           "0"           "0"           "0"
```

```
## [6] "0"          "0"          "0"          "0"          "0"
## [11] "Adria1"      "1"          "1"          "1"          "1"
## [16] "1"          "1"          "1"          "1"          "1"
## [21] "1"          "1"          "Validation2" "2"          "2"

tempDoxorubicin07Header2[1:25]

## [1] "Resistant" "Resistant" "Resistant" "Resistant" "Resistant" "Resistant"
## [7] "Resistant" "Resistant" "Resistant" "Resistant" "Sens"       "Sens"
## [13] "Sens"       "Sens"       "Sens"       "Sens"       "Sens"       "Sens"
## [19] "Sens"       "Sens"       "Sens"       "Sens"       "NR"         "NR"
## [25] "Resp"

table(tempDoxorubicin07Header1)

## tempDoxorubicin07Header1
##           0           1           2      Adria0      Adria1 Validation2
##           9          11          120           1           1           2

table(tempDoxorubicin07Header2)

## tempDoxorubicin07Header2
##           NR Resistant      Resp      Sens
##           99          10          23          12
```

buildDoxo07Info

```
tempSampleNames <-
  c(paste("Training", c(1:22), sep=""),
    paste("Test", c(1:122), sep=""))

tempGroup <- c(rep("Training", 22), rep("Test", 122))
tempStatus <- tempDoxorubicin07Header2
tempStatus[tempStatus == "Sens"] <- "Sensitive"
tempStatus[tempStatus == "NR"] <- "Resistant"
tempStatus[tempStatus == "Resp"] <- "Sensitive"

doxorubicin07Info <-
  data.frame(sampleGroup = tempGroup,
             status       = tempStatus,
             row.names    = tempSampleNames)

doxorubicin07Info[c(1:2,22:25),]

##           sampleGroup      status
## Training1      Training Resistant
## Training2      Training Resistant
## Training22     Training Sensitive
## Test1          Test Resistant
## Test2          Test Resistant
## Test3          Test Sensitive

#rm(doxorubicin07Header1, doxorubicin07Header2, tempGroup, tempStatus)
rm(list=ls(pattern="^temp"))
```

loadDoxo07Numbers

```
doxorubicin07Numbers <-  
  read.table(file.path("RawData", "PottiNatMed", "Adria_ALL.txt"), sep="\t",  
             skip=2, header=FALSE)  
  
colnames(doxorubicin07Numbers) <- rownames(doxorubicin07Info)  
  
doxorubicin07Numbers[1:4, c(1:2, 22:25)]  
  
##   Training1 Training2 Training22 Test1 Test2 Test3  
## 1      1.18      1.12      1.22  0.60  3.53  2.16  
## 2      1.75      4.02      0.63  0.71  0.63  0.30  
## 3      0.13      0.35      2.54  0.97  0.29  1.67  
## 4      0.19      0.42      0.94  0.71  1.86  3.11
```

getDoxoCors

```
doxorubicin07Cors <- cor(doxorubicin07Numbers)  
sum(doxorubicin07Cors > 0.9999)
```

```
## [1] 256
```

```
sum(diag(doxorubicin07Cors) > 0.9999)
```

```
## [1] 144
```

plotDoxoHighCors, fig=TRUE

```
doxorubicin07HighCors <- (doxorubicin07Cors > 0.9999)  
  
same07Status <- matrix(rep(doxorubicin07Info[, "status"], 144), 144, 144)  
same07Status <- (same07Status == t(same07Status))  
  
temp07Ties <- which(doxorubicin07HighCors & same07Status, arr.ind=TRUE)  
temp07Ties <- temp07Ties[temp07Ties[, 1] != temp07Ties[, 2], ]  
temp07BadTies <- which(doxorubicin07HighCors & (!same07Status), arr.ind=TRUE)  
  
plot(1:144, 1:144, pch=".", cex=3,  
     xlim=c(0.5, 144.5), ylim=c(0.5, 144.5),  
     xaxs="i", yaxs="i",  
     xlab="Column in Adria_ALL.txt",  
     ylab="Column in Adria_ALL.txt",  
     main="Identical Columns in Adria_ALL.txt",  
     )  
points(temp07Ties[, 1], temp07Ties[, 2], pch=21, bg="white", lwd=1)  
points(temp07BadTies[, 1], temp07BadTies[, 2], pch=24, bg="red", lwd=2)  
abline(h=22.5, v=22.5)  
  
abline(v=32, lty="dashed")
```

Identical Columns in Adria_ALL.txt

