Question7

Chonnikarn Charoenpanich

#Installing Biobase

```
library(Biobase)
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: parallel
```

```
##
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB
```

```
## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs
```

```
## The following objects are masked from 'package:base':
##
##     anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##     dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##     grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##     order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##     rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##     union, unique, unsplit, which.max, which.min
```

```
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.
```

Question 7

Load the Bottomly data:

```
con =url("http://bowtie-bio.sourceforge.net/recount/ExpressionSets/bodymap_eset.RData")
load(file=con)
close(con)
bm = bodymap.eset
edata = exprs(bm)
```

Which of the following code chunks will make a heatmap of the 500 most highly expressed genes (as defined by total count), without re-ordering due to clustering? Are the highly expressed samples next to each other in sample order?

Answer : a. Yes they are.

```
row_sums = rowSums(edata)
edata = edata[order(-row_sums),]
index = 1:500
heatmap(edata[index,],Rowv=NA,Colv=NA)
```
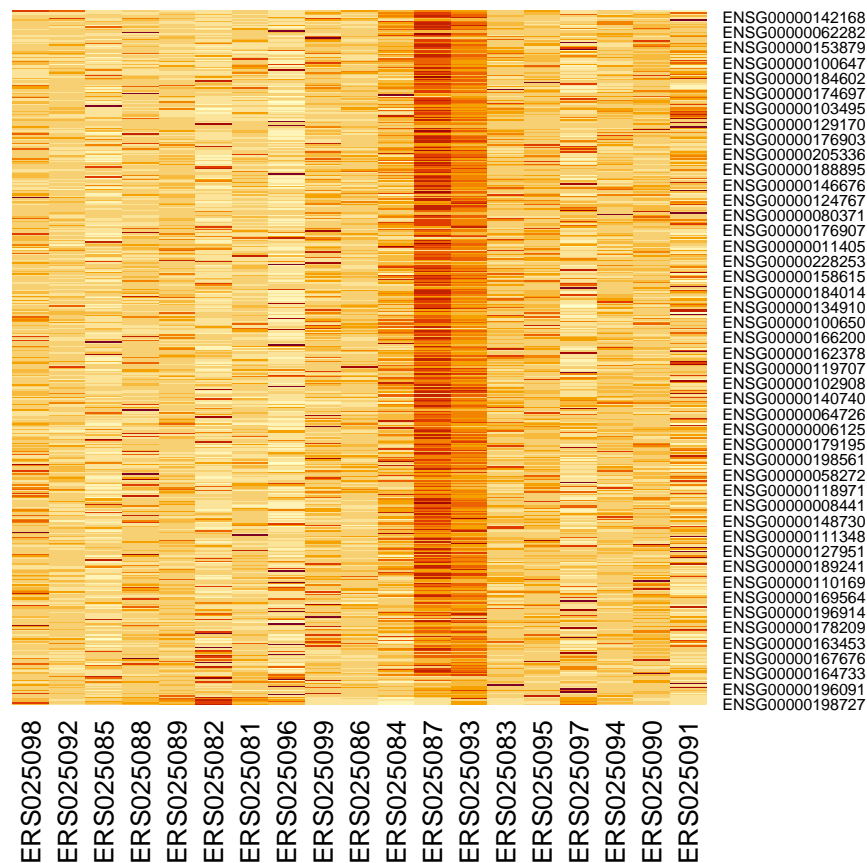

b. The highly expressed samples are not next to each other.

Error in heatmap(edata[index,], Colv = NA) : 'x' must have at least 2 rows and 2 columns

c. No they are not next to each other.

```
row_sums = rowSums(edata)
edata = edata[order(row_sums),]
index = which(rank(-row_sums) < 500 )
heatmap(edata[index,],Rowv=NA,Colv=NA)
```

```
## Warning in min(x): no non-missing arguments to min; returning Inf
```

```
## Warning in max(x): no non-missing arguments to max; returning -Inf
```


d. The highly expressed samples are not next to each other.

```
row_sums = rowSums(edata)
index = which(rank(-row_sums) < 500 )
heatmap(edata[index,],Rowv=NA,Colv=NA)
```

ENSG00000198938
ENSG00000141753
ENSG00000197102
ENSG00000173432
ENSG00000135404
ENSG00000135744
ENSG00000159403
ENSG00000189058
ENSG00000086598
ENSG00000089597
ENSG00000137642
ENSG00000178878
ENSG00000181222
ENSG00000072110
ENSG00000108861
ENSG00000129538
ENSG00000104904
ENSG00000118271
ENSG00000185591
ENSG00000167588
ENSG00000198752
ENSG00000187079
ENSG00000169926
ENSG00000159335
ENSG00000076108
ENSG00000140564
ENSG00000101474
ENSG00000136383
ENSG00000101265
ENSG00000087074
ENSG00000170540
ENSG00000114854
ENSG00000168334
ENSG00000165030
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ENSG00000132383
ENSG00000175203
ENSG00000166170
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ENSG00000107854
ENSG00000140937
ENSG00000180304
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