

Labs: Trees, Hierarchical Clustering, Heatmaps

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Data Analytics

ITWS-4600/ITWS-6600/MATP-4450/CSCI-4960

Group 2, Lab-3, Oct 10th 2023

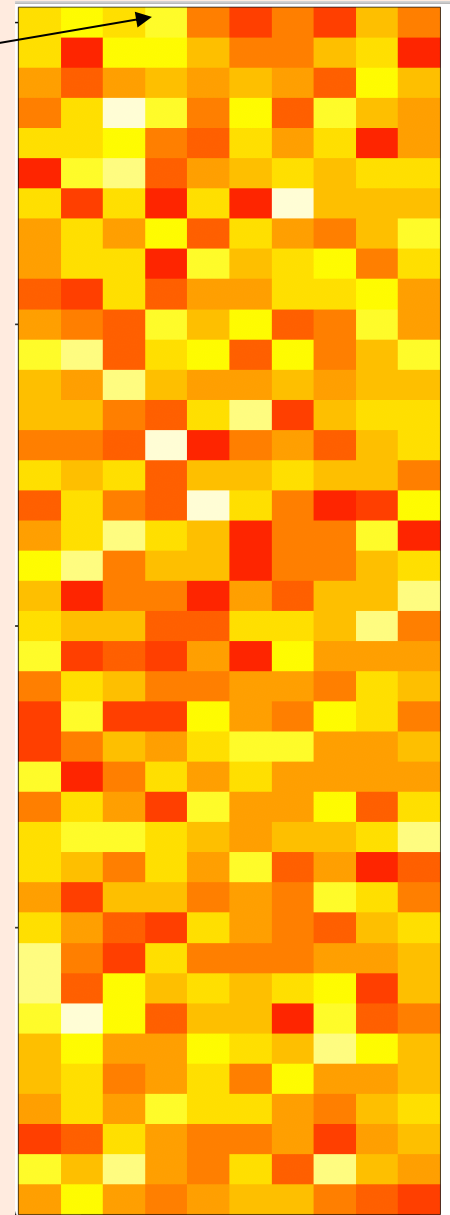
Heatmap(), image() and hierarchical clustering example

```
# creating a matrix data with random numbers
# and plotting the matrix using the image() function
# you will see there, it does not have a real pattern in the plot.
set.seed(12345)
help(par)
# par can be used to set or query graphical parameters.
# Parameters can be set by specifying them as arguments
# to par in tag = value form, or by passing them as a list of tagged values.
par(mar = rep(0.2,4))
data_Matrix <- matrix(rnorm(400), nrow = 40)
image(1:10, 1:40, t(data_Matrix)[,nrow(data_Matrix):1])
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Heatmap(), image() and hierarchical clustering example ...

There are 40 rows and 10 columns



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image(1:10, 1:40, t(data_Matrix)[,nrow(data_Matrix):1])
```

Heatmap(), image() and hierarchical clustering example ...

now we can run a hierarchical cluster
analysis on the dataset

we will use the heatmap() function that is
available in R

help("heatmap") # read the documentation for
the heatmap() function that is available in
#RStudio

#Read the documentation for rep()
help(rep)

Heatmap(), image() and hierarchical clustering example ...

```
par(mar=rep(0.2,4))
```

```
heatmap(data_Matrix)
```

When we run the heatmap() here, we get the dendrograms printed on the both columns and the rows and still there is no real immerging pattern that is interesting to us,

#it is because there is no real interesting pattern underlying in the data we generated.

```
par(mar=rep(0.2,4))
```

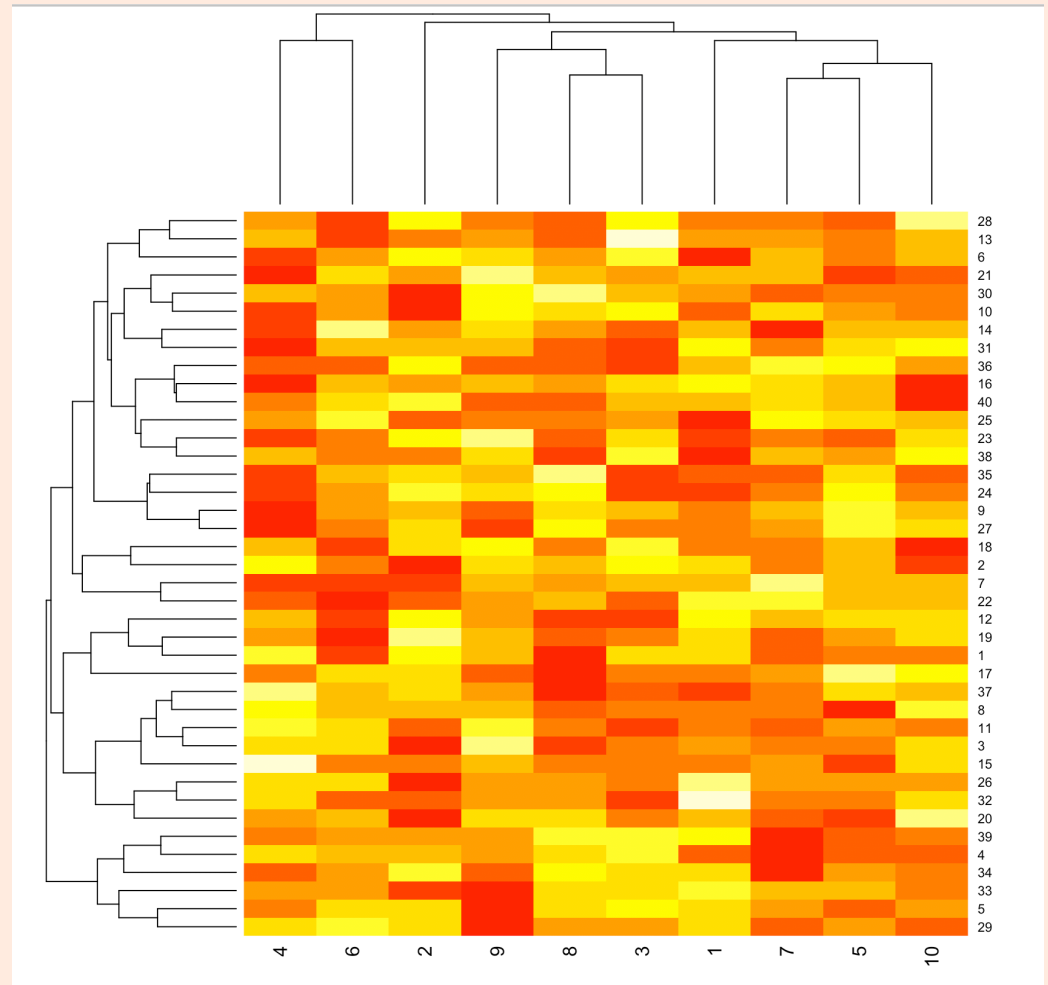
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Heatmap(), image() and hierarchical clustering example ...

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par(mar=rep(0.2,4))  
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```

Dendrograms printed
on columns
and rows



Now we will add a pattern to the data by doing a random coin flip.

we will use the rbinom() function along with a for-loop.

help("rbinom") # read the documentation for the rbinom() function that

is available in RStudio

Heatmap(), image() and hierarchical clustering example ...

```
set.seed(678910)
for(i in 1:40){
  # flipping a coin and getting the data
  coin_Flip <- rbinom(1, size = 1, prob = 0.5)
  # if the coin is "Heads", add a common pattern to that row,
  if(coin_Flip){
    data_Matrix[i, ] <- data_Matrix[i, ] + rep(c(0,3), each =5)
  }
}
```

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for(i in 1:40){
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  }
}
```


what I did here is, I looped through all the rows and, on a random row, I flipped a coin.
during the coin flip, if it turns out to be one (true), then, just added a pattern to my data in a way that the five of the columns have a mean of zero and others have mean of three.

```
set.seed(678910) # set seed.  
for(i in 1:40){  
  # flipping a coin and getting the data  
  coin_Flip <- rbinom(1, size = 1, prob = 0.5)  
  # if the coin is "Heads", add a common pattern to that row,  
  if(coin_Flip){  
    data_Matrix[i, ] <- data_Matrix[i, ] + rep(c(0,3), each = 5)  
  }  
}
```

Heatmap(), image() and hierarchical clustering example ...

Now we will plot the data

Now we can see that the right hand five columns have more yellow in them,

which means they have a higher value and the left hand five columns that are little bit more in red color which means they have a lower value.

it is because some of the rows have a mean of three in the right hand side, and

some of the rows have mean of zero. Now we have introduced some pattern to it.

Heatmap(), image() and hierarchical clustering example ...

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par(mar= rep(0.2, 4))
```

```
image(1:10, 1:40, t(data_Matrix)[, nrow(data_Matrix):1])
```

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# which means they have a higher value and the left hand five columns that are
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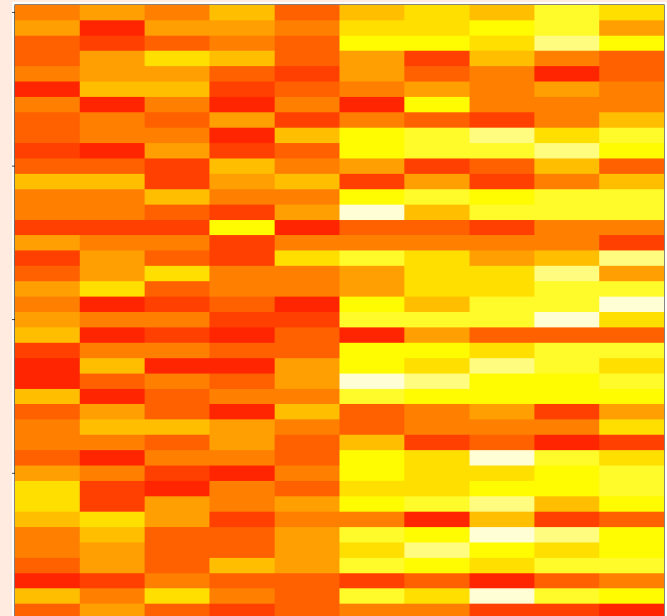
```
# some of the rows have mean of zero. Now we have introduce some pattern to it.
```

```
par(mar= rep(0.2, 4))
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image(1:10, 1:40, t(data_Matrix)[, nrow(data_Matrix):1])
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Heatmap(), image() and hierarchical clustering example ...

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# which means they have a higher value and the left hand five columns that are  
# more little bit more red color which means they have a lower value.  
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# some of the rows have mean of zero. Now we have introduce some pattern to it.  
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image(1:10, 1:40, t(data_Matrix)[, nrow(data_Matrix):1])
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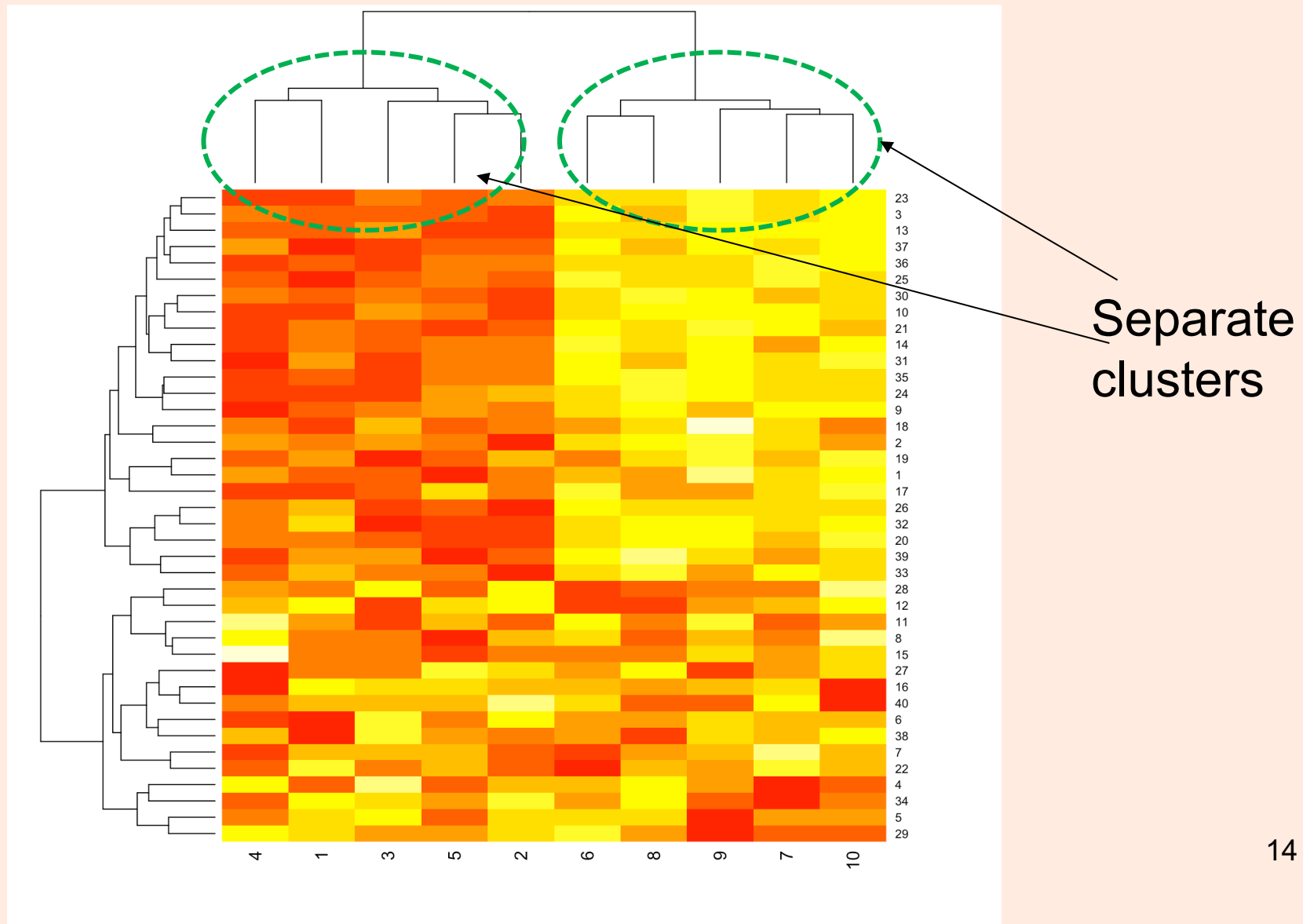
Heatmap(), image() and hierarchical clustering example ...

now we will run the heatmap() function on the data, we can see that, two
#sets of columns are easily separated.

```
par(mar=rep(0.2, 4))  
heatmap(data_Matrix)
```

```
# now we will run the heatmap() function on the data, we can see that, two sets of columns are  
# easily separated out.  
par(mar=rep(0.2, 4))  
heatmap(data_Matrix)
```

Heatmap(), image() and hierarchical clustering example ...

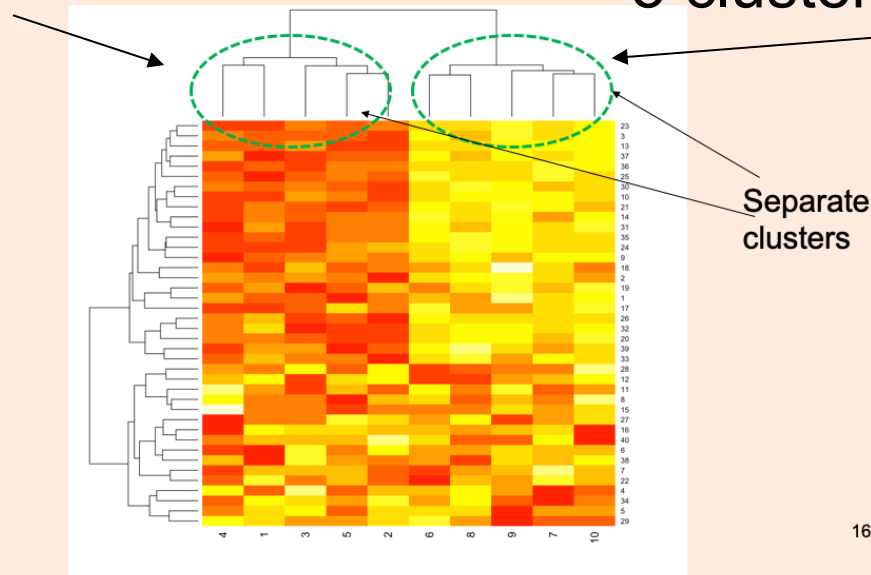


Heatmap(), image() and hierarchical clustering example ...

- # The dendrogram is on the top of the of the matrix, (which is on the top of the columns),
- # has clearly splits into two separate clusters.
- # five on the left, and five on the right
- # on the rows, there is no real pattern that goes along the rows

5 cluster to the Left

5 cluster to the Right



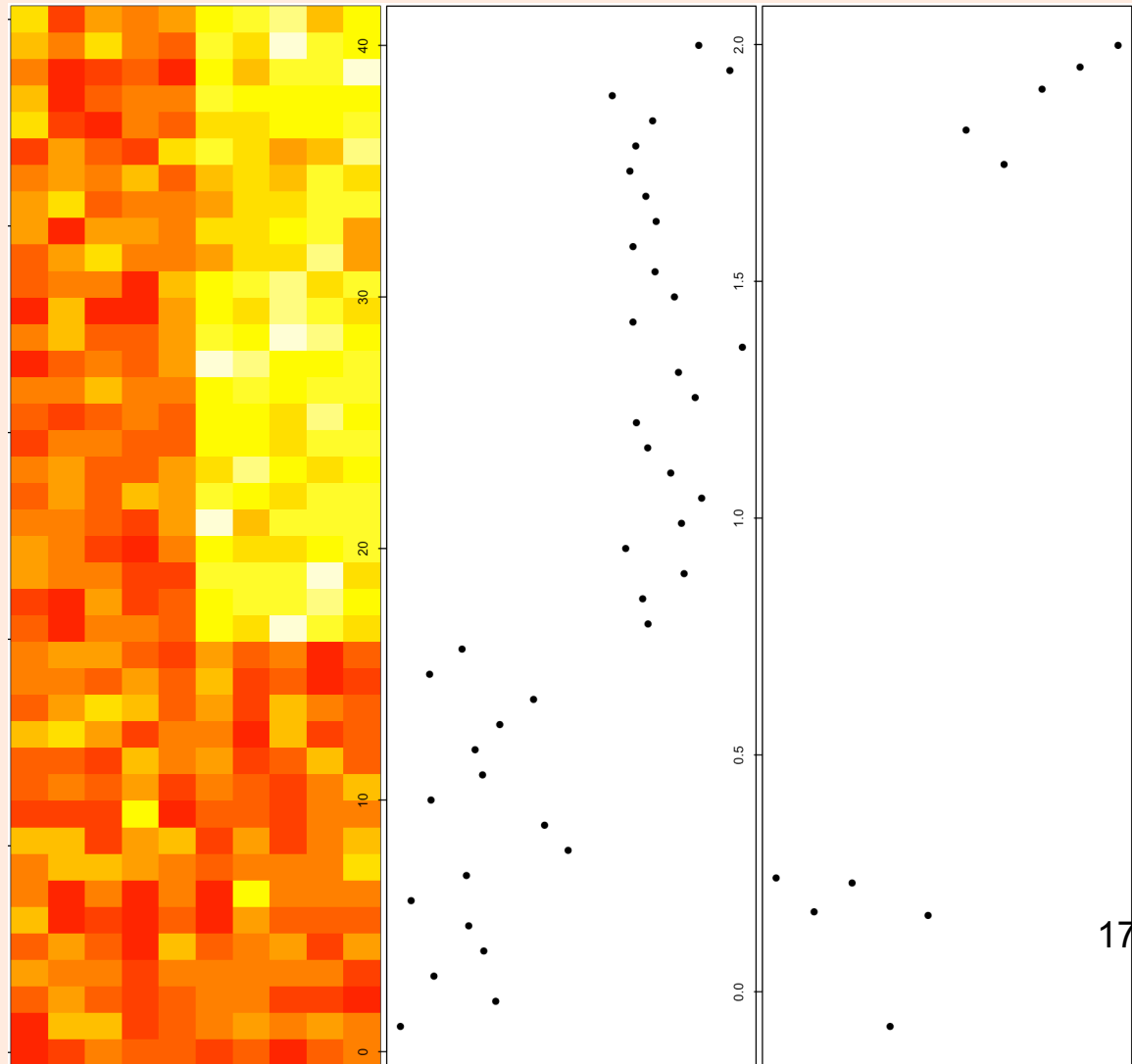
Let's take a closer look at the patterns in rows and columns by looking at the marginal

means of the rows and columns.

ten different columns mean and forty different rows means

```
# Let's take a closer look at the patterns in rows and columns by looking at the marginal
# means of the rows and columns.
# ten different columns mean and forty different rows means
hh <- hclust(dist(data_Matrix))
data_Matrix_Ordered <- data_Matrix[hh$order,]
par(mfrow = c(1,3))
image(t(data_Matrix_Ordered)[, nrow(data_Matrix_Ordered):1])
plot(rowMeans(data_Matrix_Ordered), 40:1, , xlab = "The Row Mean", ylab = "Row", pch=19)
plot(colMeans(data_Matrix_Ordered), xlab = "Column", ylab = "Column Mean", pch = 19)
```


Pay attention to the number of dots on the middle and right-hand side plot



Interpretation...

left plot has the original data reordered according to the hierarchical cluster analysis of the rows.

Middle plot has the mean of each row. (there are 40 rows and therefore 40 dots representing the mean)

right hand side plot has the means of each column (there are 10 columns and therefore 10 dots representing the mean)

Scripts – work through these

Reminder to finish these code

examples See in folder group2/ Lab1

Go over the following scrips,

Lab1_bronx1.R.

Lab1_bronx2.R

Lab1_ctree2.R

Lab1_kknn1.R

Lab1_kknn2.R

Lab1_kknn3.R

Lab1_kmeans1.R

Lab1_nyt.R

Search before you ask! You might need to search your code errors online when you are debugging your code!.

script fragments in R available on the web site:

<https://rpi.box.com/s/2xx9ul1fmc6bf5ff8h4jreae69emikmf>

NOTE: you are allowed to work in small groups and discuss during this lab.

Scripts – work through these

Next...

See in folder group2/ Lab3

Go over the following scrips,

Lab3_ctree1.R

Lab3_ctree2.R

Lab3_ctree3.R

.....

And the remaining code snippets in

group2/Lab 2 and Lab3

Search before you ask! You might need to search your code errors online when you are debugging your code!

script fragments in R available on the web site:

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NOTE: you are allowed to work in small groups and discuss during this lab.

Trees for the Titanic

`data(Titanic)`

`rpart`, `ctree`, `hclust`, for:

`Survived ~ .`

Read the titanic dataset documentation in Rdocumentation:
<https://www.rdocumentation.org/packages/titanic/versions/0.1.0>

One-on-One with the instructor

- Today and next week: Project Dataset Documentation:
- **Mandatory One-on-One with the instructor.**
- Meet with the instructor to document the project datasets during today's lab.