Lab #1
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Basic R syntax/plots with data solutions

1.) Go to class website under Course Documents > Data Sets and download the SLE B cell data set (from Garaud et al).

Done.

2.) Unzip the text file, and read into R (Hint: using the read.table() function with a "header=T" argument and "row.names=1" argument is one method to do this).

```
sle.df = read.table('sle_b_cell.txt', header=TRUE, row.names=1)
```

3.) Look at the dimensions of the data. There should be 26 samples. If you have 27 samples, you still have the row names in the first data column, so retry 2 to set the row names to these.

```
dim(sle.df)
```

```
## [1] 34853    26
```

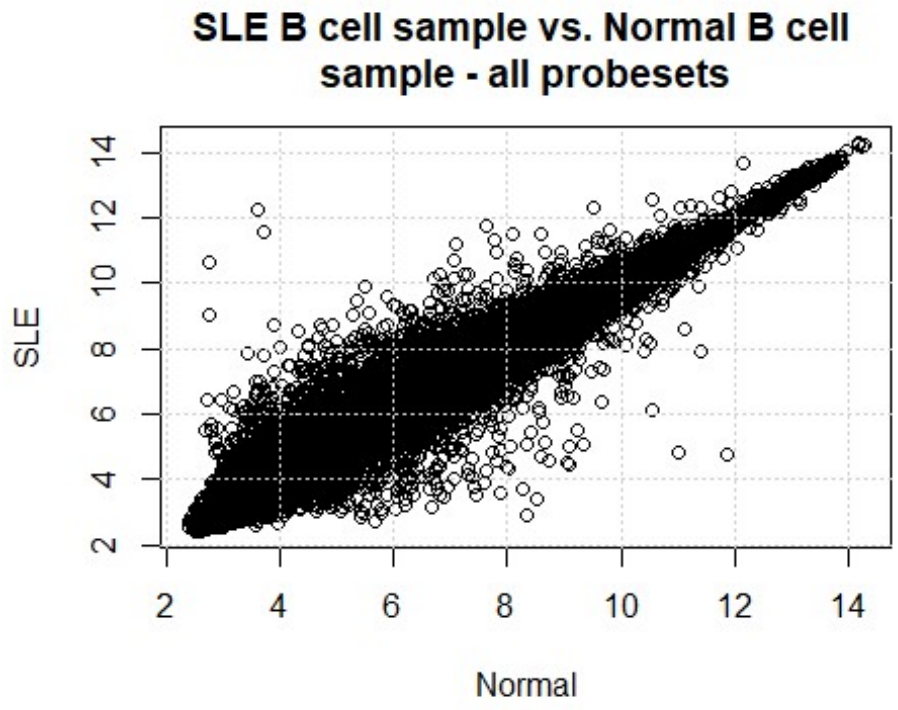
4.) Print the sample names to screen.

```
colnames(sle.df)
```

```
##  [1] "sle.1"     "sle.2"     "sle.3"     "sle.4"     "sle.5"     "sle.6"
##  [7] "sle.7"     "sle.8"     "sle.9"     "sle.10"    "sle.11"    "sle.12"
## [13] "sle.13"    "sle.14"    "sle.15"    "sle.16"    "sle.17"    "control.
1"
## [19] "control.2" "control.3" "control.4" "control.5" "control.6" "control.
7"
## [25] "control.8" "control.9"
```

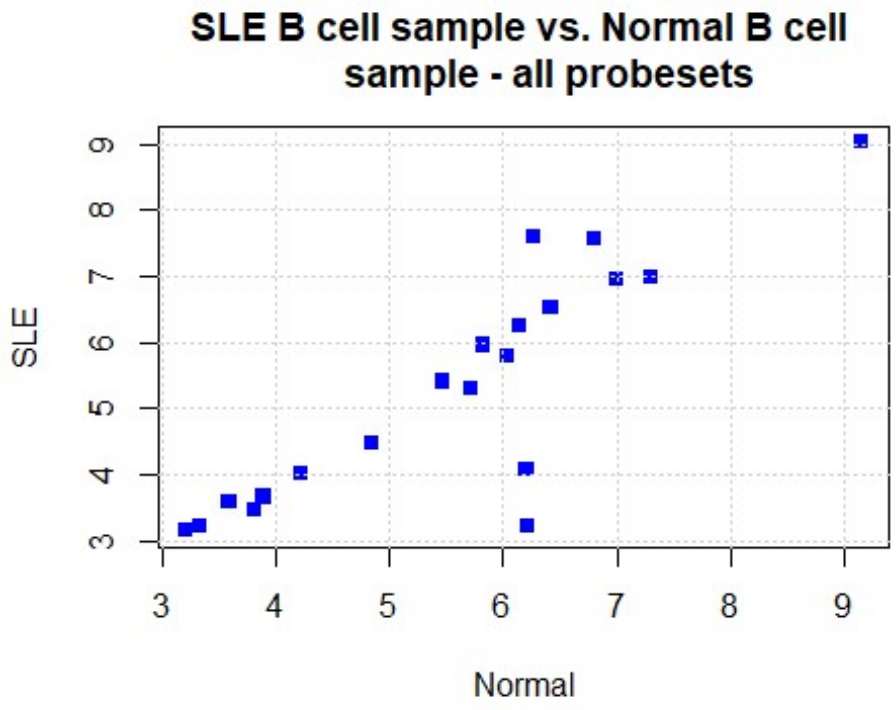
5.) Plot the second SLE patient sample versus the first normal control samples in an xy scatter plot. Remember that the first argument is the x vector. Label the x and y-axes as 'Normal' and 'SLE', respectively. Title the plot, 'SLE B cell sample vs. Normal B cell sample – all probesets'. Add grey grid lines with the function grid().

```
patient <-sle.df[,2]
control <- sle.df[,18]
plot(control, patient, type='p', main='SLE B cell sample vs. Normal B cell
        sample - all probesets', xlab='Normal', ylab='SLE')
grid()
```



6.) Now do the same plot but pick only the first 20 probesets. Use the pch=15 argument to change the shape and color the points blue with the col argument

```
plot(control[1:20], patient[1:20], type='p', main='SLE B cell sample vs. Norm
al B cell
     sample - all probesets', xlab='Normal', ylab='SLE', pch=15, col='blue')
grid()
```

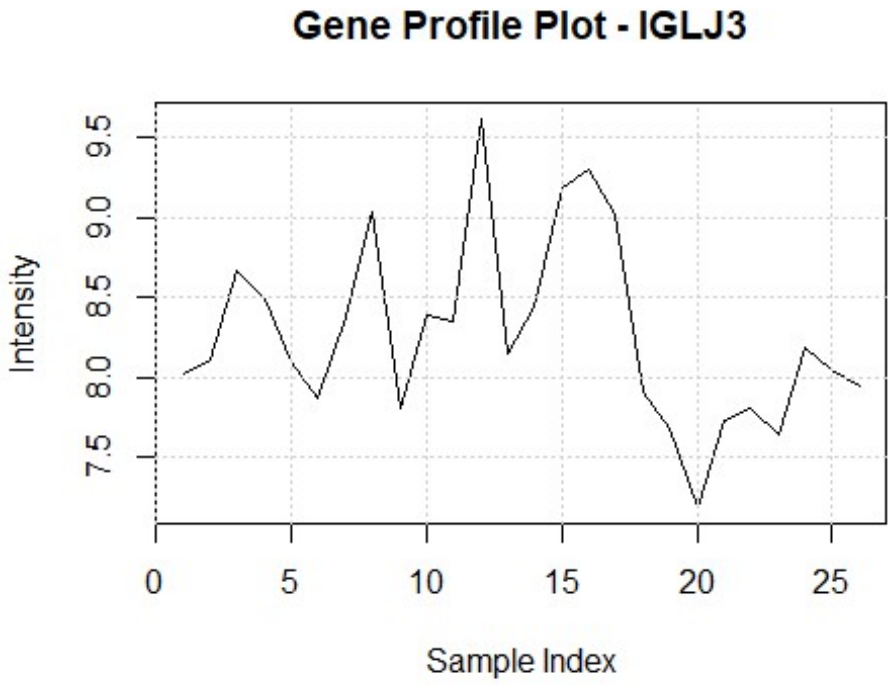


7.) Now plot the following gene in a gene profile plot, IGLJ3 (immunoglobulin lambda joining 3), which is probeset ID 211881_x_at. This type of plot has the sample indices across the x-axis and the intensities on the y-axis, so you can see a profile of the gene across experiments or arrays. First plot the ranges using the type="n" argument and the plot() function, then add the genes with the lines() function call. Add grid lines. Hint: to plot just ranges of x and y vectors, use the range() function like so:

plot(range(1:26),range(dat[geneX,]),…

Be sure to cast the gene vector to numeric before plotting.

```
IGLJ3 <- sle.df['211881_x_at',]
plot(range(1:26), range(IGLJ3),type="n", main='Gene Profile Plot - IGLJ3',
     xlab='Sample Index', ylab='Intensity')
lines(as.numeric(IGLJ3))
grid()
```



8.) Finally, another way to visualize a gene profile across conditions is to graph a boxplot with a single distribution box per condition. To do this, we need to create a factor vector that indicates the disease or normal condition like so:

f <- c(rep(“SLE”,17),rep(“Control”,9))

Then use this vector with the expression vector for IGLJ3 in the boxplot function to create the graph.

Not required, but you can increase the plot info by using the with() function and stripchart() function to add points.

```
f <- c(rep("SLE", 17),rep("Control",9))
boxplot(as.numeric(IGLJ3)~f, xlab = "Condition", ylab="Expression",
        main='Expression vs. Condition - IGLJ3')
stripchart(as.numeric(IGLJ3)~f, add = TRUE, vertical = TRUE, col="blue")
```