Exercise 8
Basic graphs

Create the script exercise8.R (in R Studio: File ->) and save it to the "Rintro/day4" directory: you will save all the commands of exercise 8 in that script.
Remember you can comment the code using #.

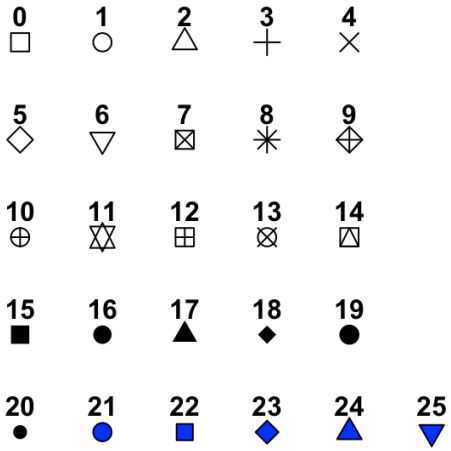
Exercise 8a – scatter plot

1. Read in file "/users/bi/sbonnin/gene_counts.txt" in object **genes.**
Note: this file contains a header.

2. Create a scatter plot showing **sample1** (x-axis) vs **sample2** (y-axis) of **genes**.
plot()

3. Change the point type and colors.
*Note: see options **pch** and **col.***

*example of **pch:***



*For **col**, you can use:*
- integers (1, 2, 3 etc.) but limited to 8 different colors!
*- or pick up the name of a color using: **colors**(); for color picked randomly, you can use sample(colors(), 1).*

4. Change axis labels to "**Sample 1**" and "**Sample 2**".
*Note: see options **xlab** and **ylab**.*

5. Add a title to the plot.
*Note: see option **main**.*

6. Add a **red** vertical line at the **median** expression value of sample 1. Do it in two steps:
   a. calculate the median expression of genes in sample 1.
   median()
   b. plot a vertical line using **abline**().
*Note: **plot**(….) must be called before **abline()** is called. abline is not an argument but a function!*
See abline help page.

Exercise 8b – bar plot + pie chart

1. Read in file "/users/bi/sbonnin/gene_counts_significance.txt" in object **de**.
Note: this file contains a header.

2. The column **updown** describes whether a gene is up- (enriched) or down- (depleted) regulated, or not regulated (none)..
Produce a **barplot** that displays this information: how many genes are enriched, depleted, or not regulated.
barplot(table())

3. Color the bars of the boxplot, each in a different color: up in red, down in blue, none in grey.

4. Now use option **names.arg** in **barplot**() to rename the bars.

5. The **las** argument allows you to rotate labels for a better visibility.
Try value 2 for las: what happens?

6. Create a pie chart of the same information (up, down, none)
pie(table())
*Note: Try arguments **color**, **main** and **labels**.*

Exercise 8c – histogram

1. Use **genes** object from exercise 8a to create a **histogram** of the gene expression distribution of sample 1.
hist()

2. Repeat the histogram but change argument **breaks** to 50.
What is the difference?

3. Color this histogram in light blue.
Note: there is color called "lightblue"

4. "Zoom" in the histogram: show only the distribution of expression values from 7 to 12 (x-axis).
*Note: use **xlim** option. Adjust also **ylim** if necessary for a better visibility.*

5. Save plot in a pdf file.
a. Try with RStudio Plots window (Export)
b. Try in the console:
pdf(…)
hist(…)
dev.off()

Exercise 9.
Introduction to ggplot2.

Create the script exercise9.R (in R Studio: File ->) and save it to the "Rintro/day4" directory: you will save all the commands of exercise 8 in that script.
Remember you can comment the code using #.

Exercise 9a – scatter plot

1. Load **ggplot2** package.

2. Using **de** object from Exercise 9, create a simple scatter plot for plotting gene expression of sample 1 and sample 2.
Note: remember the structure:
ggplot(data=, aes(x=, y=)) + geom_point()

3. Color points according to the **updown** column. Save in object **p**.
Note: remember the structure:
*p <- ggplot(data=, aes(x=, y=, **color=**)) + geom_point()*

4. Change colors of the points to blue, grey and red. Save to p2.
*p2 <- p + **scale_color_manual**()*

5. Save p2 into a jpeg file.
a. Try with RStudio Plots window (Export)
b. Try in the console:
jpeg(…)
plot(…)
dev.off()

Exercise 9b – box plot

1. Convert **de** from a wide format to a long format, save in **de_long**.
*Note: remember **melt** function from **reshape2** package. Don't forget to load reshape2 package!*
de_long <- melt(de)

2. Produce a boxplot of the expression of sample 1 and sample 2 (each sample should be represented by a box)
ggplot(data=, aes(x=, y=)) + geom_boxplot()

3. Modify the previous boxplot so as to obtain 3 "sub"-boxplots per sample, each representing the expression of either UP, DOWN or NONE genes.
ggplot(data=, aes(x=, y=, color=)) + geom_boxplot()

Exercise 9c – bar plot

1. Produce a bar plot of how many UP/DOWN/NONE genes are in **de**.
ggplot(data=, aes(x=)) + geom_bar()

2. Add an horizontal line at counts **1000** (y-axis).

geom_hline()

3. Swap x and y axis.
coord_flip()

4. Add a title to the graph.
ggtitle()

Exercise 9d – histogram

1. Create a simple histogram using **de_long** (using the column "value").
ggplot(data=, aes(x=)) + geom_histogram()

2. Notice that you get the following warning message *"stat_bin()` using `bins = 30`. Pick better value with `binwidth`."*
Change **bins** parameter of **geom_histogram**() to **50**.

3. This histogram plots expression values for both sample1 and sample2.
Change the plot so as to obtain 2 histograms on the same plot: one corresponding to sample1, one corresponding to sample2.
*ggplot(data=, aes(x=, **fill**=)) + geom_histogram()*

4. By default, geom_histogram produces a stacked histogram.
Change the position of the bars to **dodge**.
*ggplot(data=, aes(x=, **fill**=)) + geom_histogram(position=…)*

5. Finally, change the colors of the bars to colors of your choice.
scale_fill_manual()
Note: Try the rainbow() function for coloring!

6. Zoom in the plot: reduce the x-axis to values from 7 to 12.
xlim() layer.