





# DCMB BioComputing BootCamp Day 3, Lecture 3: Data Exploration and Visualization in R

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#### Now What?

- Scenario:
  - You understand the fundamentals of R
  - You've read your data into an R data frame
- During this session we will talk about
- Basic data summarization
- Visualize data with plots



#### Overview

- 1. Summarizing Data in R
- 2. Creating plots in R
- 3. Hierarchical clustering

### Example Data Set:

#### **Cancer Research**

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Alerts

News

Molecular and Cellular Pathobiology

Activation of Wnt/β-Catenin in Ewing Sarcoma Cells Antagonizes EWS/ETS Function and Promotes Phenotypic Transition to More Metastatic Cell States

Elisabeth A. Pedersen, Rajasree Menon, Kelly M. Bailey, Dafydd G. Thomas, Raelene A. Van Noord, Jenny Tran, Hongwei Wang, Ping Ping Qu, Antje Hoering, Eric R. Fearon, Rashmi Chugh, and Elizabeth R. Lawlor

DOI: 10.1158/0008-5472.CAN-15-3422 Published September 2016

- Ewing's sarcoma: rare bone and soft tissue cancer occurring in children and teenagers
  - 70-80% survival
- In vitro CHLA25-7TGP ES cells stimulated to overexpress WNT3A

- options(stringsAsFactors=F)
- 2. Use the read.delim() function to read in "pedersenLog2RPKM20180817.txt" file into a data frame called "data1"
- 3. Use the head() and dim() function to find out about the structure of this data file

How many rows? What are the columns?

### Quickly Calculate Simple Statistics

- R has many built in statistical functions that use fast vector and matrix operations
- No need to write a for loop, sum, and then divide by n
- Just provide a vector of data to the mean() function:
  - mean(data1\$log2RPKM)
- With one line of code you have take the mean of 97,000 values!

Exercise: Use mean(), median(), max(), min(), summary() functions on the Pedersen data

### Using the table() Function

- When exploring new datasets it is often useful to count the number of values
- table() can be used to build a contingency table of the counts of each value
  - For one column:

```
> table(data1$tx)
control WNT3A
   48585 48585
```

For multiple columns:

```
> table(data1$tx,data1$rep)

1 2 3
control 16195 16195 16195
WNT3A 16195 16195 16195
```

### Using the aggregate() Function

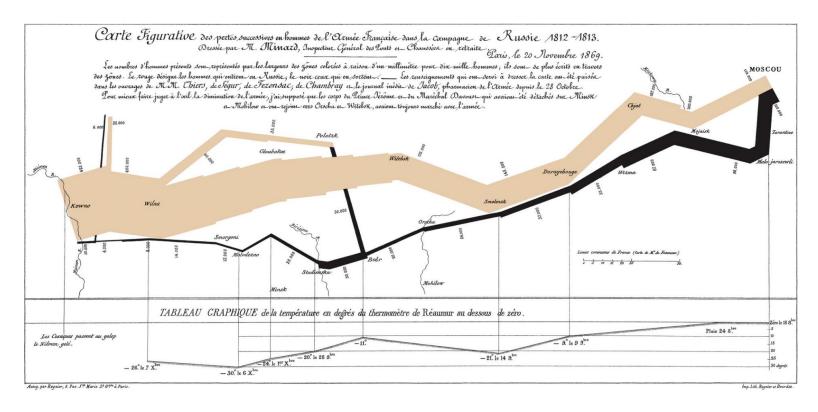
- Often times we want to perform a function on subsets of our data
  - example question: What is the mean expression for each sample?
- aggregate() splits data into subsets, computes summary statistics for each and returns the result
- aggregate() takes several arguments:

Exercise: Use aggregate() to calculate the maximum log2RPKM value per sample.

#### formula format: y ~ x1

- y is a numeric value
- x1 is a grouping variable
- possible to specify multiple groups as x1 + x2 + ...

## Data Visualization Allows Researchers to Visually Present Data



- Minard's 1869 diagram of Napoleonic France's invasion of Russia
  - Line width indicates size of army
  - Color indicates army's course to and from russia

## Data Visualization Allows Researchers to Visually Present Data

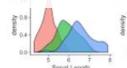
- Data visualizations should:
  - Show the data
  - Avoid distorting the data
  - Present many numbers in a small space
  - Make large data sets coherent
  - Serve a reasonably clear purpose
  - Be closely integrated with the statistical and verbal desriptions of a data set

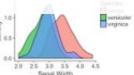
### R Base Graphics Versus ggplot2

- R comes with "base graphics" built in to support commonly used data visualizations
- Today we will focus on using an alternative data visualization framework called ggplot2
- ggplot2 is an external package that must be downloaded, installed, and loaded with the library command
- A common practice is to use ggplot2 to construct publication quality graphs but still use base graphics to quickly visualize data

### ggplot2

- ggplot2 is an R data visualization package created by Hadley Wickham
  - One of the most popular R packages
  - an alternative to R base graphics which are built into R
  - Breaks up graphs construction into additive functions
- ggplot2 documentation and cheat sheet: https://www.rdocumentation.org/packages/ggplot 2/versions/3.0.0







# Creating a Visualization with ggplot2()

- ggplot2 visualization function calls consist of several basic components:
- 1. ggplot()
- geom\_XXX()
- 3. optional layers
- 4. ggsave()
- Multiple function calls are combined together using "layers"
- aes(thetic) functions are used to map input data to plot features (e.g. x axis, y axis, colors)

```
options(stringsAsFactors=F)

library(ggplot2)

inFile = 'data.txt'
data1 = read.delim(inFile)

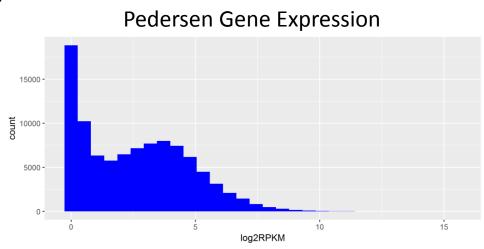
ggplot(data1,aes(x = log2RPKM)) +
geom_histogram()
ggsave('histogram.png')
```

### Visualizing Data Using Histograms

 histogram: a type of bar graph visualization in which data measurements are counted based on value

 For discrete measures it shows the frequency of values in each category

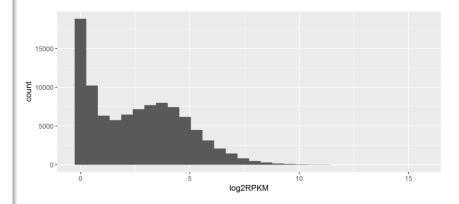
 For continuous measure it shows the frequency of values occurring in small intervals covering the whole range



# How to Create a Basic Histogram Using ggplot2

```
options(stringsAsFactors=F)
library(ggplot2)
inFile1 = 'pedersenLog2RPKM20180817.txt'
data1 = read.delim(inFile1)

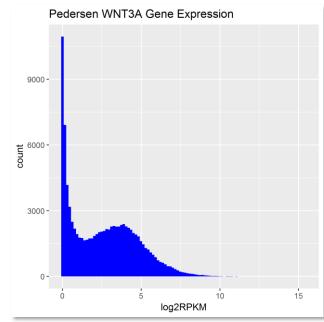
ggplot(data1,aes(x = log2RPKM)) +
  geom_histogram()
ggsave('histogram1.png')
```



Do it tourself

# Exercise: Create a histogram using the code from the previous page and update your visualization to have the following features

- 1. Change the color
  - HINT: ?geom\_histogram
  - HINT: fill = "blue"
- 2. Set the image width and height to be 5 inches
  - HINT: ?ggsave
  - HINT: height = 5
- 3. Adjust the number of bins to 100
- 4. Add a title
  - HINT: ?labs

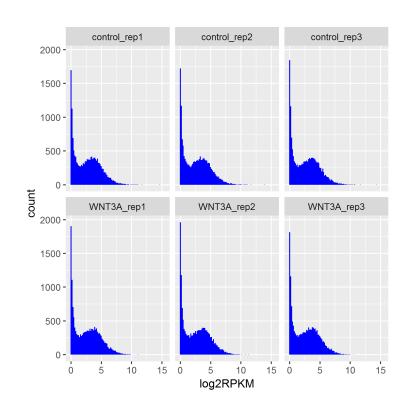


### Create Sub-plots Using Facets

- Sub-plots can easily be created using facet layers:
  - facet\_wrap()
  - facet\_grid()

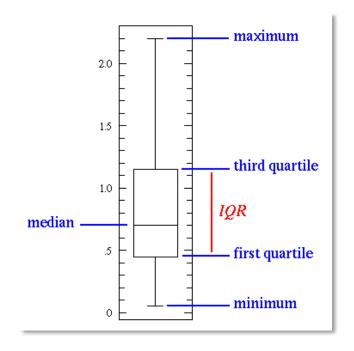
# Exercise: Update your histogram visualization to facet on sample

- Add a facet\_wrap() layer
  - HINT: + facet\_wrap(~sample)



### Visualizing Data Using Boxplots

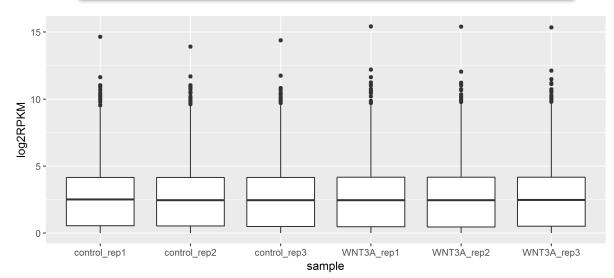
- <u>boxplot</u>: graphically represents data distributions using quartiles
- box-and-whisker plot: includes boxplots with lines extending from boxes to indicate variability outside the upper and lower quartiles
- Why it is useful?
  - Summarize the main characteristics of the data: Mean/median, quartile, spread, symmetry and outliers.
  - Efficient less complicated than histogram
  - Allows us to represent multiple data distributions in the same graph



# How to Create a Boxplot Using gplot2

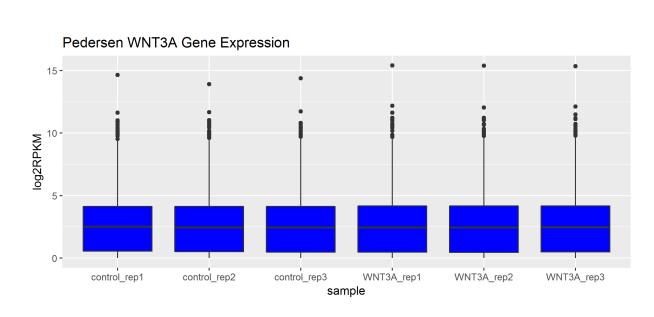
```
options(stringsAsFactors=F)
library(ggplot2)
inFile1 = 'pedersenLog2RPKM20180817.txt'
data1 = read.delim(inFile1)

ggplot(data1,aes(x = log2RPKM)) +
  geom_boxplot()
ggsave('boxplot1.png')
```



### Exercise: Create a boxplot using the code from the previous page and update your visualization to have the following features:

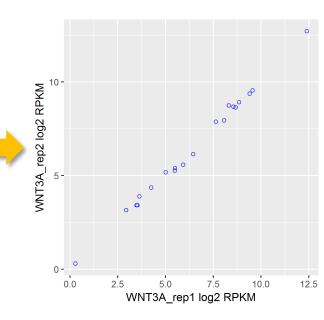
- 1. Change the fill color
  - HINT: fill = 'blue'
- 2. Add a title
  - HINT: ?labs



### Visualizing Data Using Scatter Plots

- Scatter Plots are visualizations that display two data values for the same measurement
  - <u>example</u>: two sample replicates expression values for each gene
- Data points that are not on the diagonal indicate disagreement
- We expect strong agreement between sample replicates

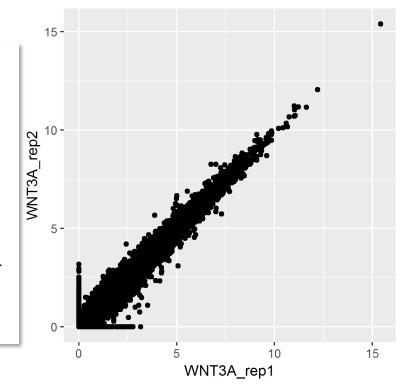
gene	WNT3A_rep1	WNT3A_rep2
A1BG	2.38	1.64
A1BG-AS1	0.83	0.58
A1CF	0.02	0.00
A2M	0.30	0.67
A2M-AS1	0.09	0.10
A2ML1	0.33	0.73
A2MP1	0.00	0.00
A4GALT	4.20	4.82
A4GNT	0.00	0.00
AAAS	5.57	5.53
AACS	2.70	2.52
AACSP1	0.13	0.15
AADAC	0.12	0.00
AADACL2	0.00	0.00
AADACL4	2.30	2.03
AADAT	0.94	1.19
AAED1	1.20	1.51
AAGAB	4.36	4.29
AAK1	1.68	1.97
AAMDC	4.41	3.78



# How to Create a Scatter Plot Using gplot2

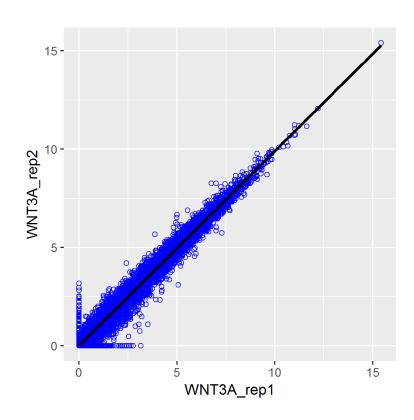
```
options(stringsAsFactors=F)
library(ggplot2)
inFile2 = 'pedersenLog2RPKM_matrix20180817.txt'
data2 = read.delim(inFile2)

ggplot(data2,aes(x = WNT3A_rep1, y = WNT3A_rep2)) +
    geom_point()
ggsave('scatter2.png')
```



### Exercise: Create a boxplot using the code from the previous page and update your visualization to have the following features:

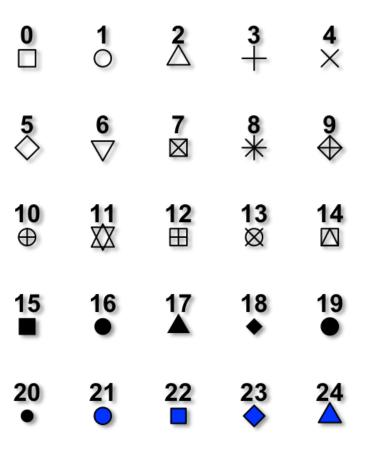
- 1. Change the color and shape of scatter plot points
  - HINT: color = 'blue'
  - HINT: shape = 1
- 2. Add a black linear regression line using a geom\_smooth layer
  - HINT: geom\_smooth(method = lm)



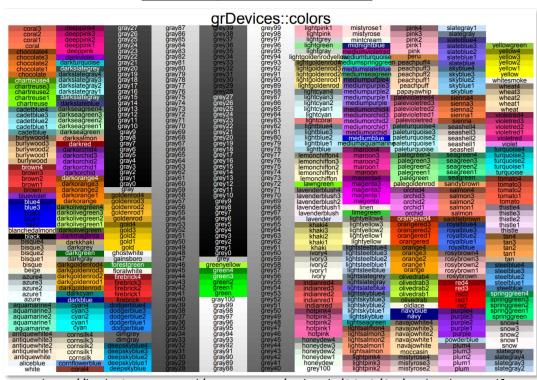
#### References

- Gentleman, Robert. R Programming for Bioinformatics. CRC Press, 2009.
- Slides Partially Sourced from Jacob Kitzman and Barry Grant

#### **R Graphics Shapes**



#### **R Graphics Colors**



http://bc.bojanorama.pl/wp-content/uploads/2013/04/rcolorsheet.pdf

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