# Explore and visualize your data using Graphpad Prism

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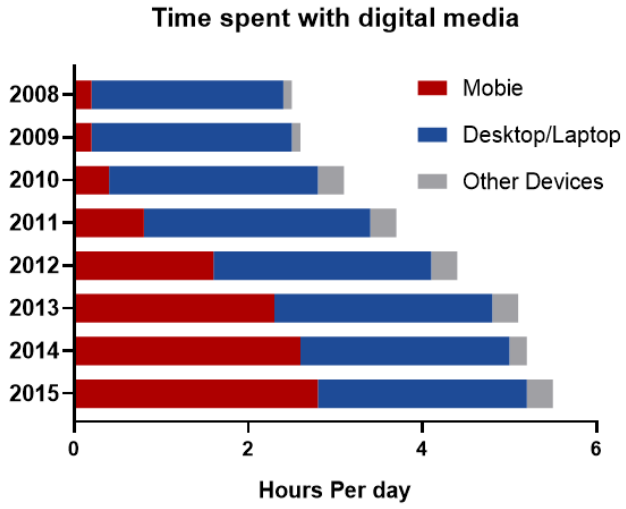
“The simple graph has brought more information to the data analyst’s mind than any other device.” – John Tukey

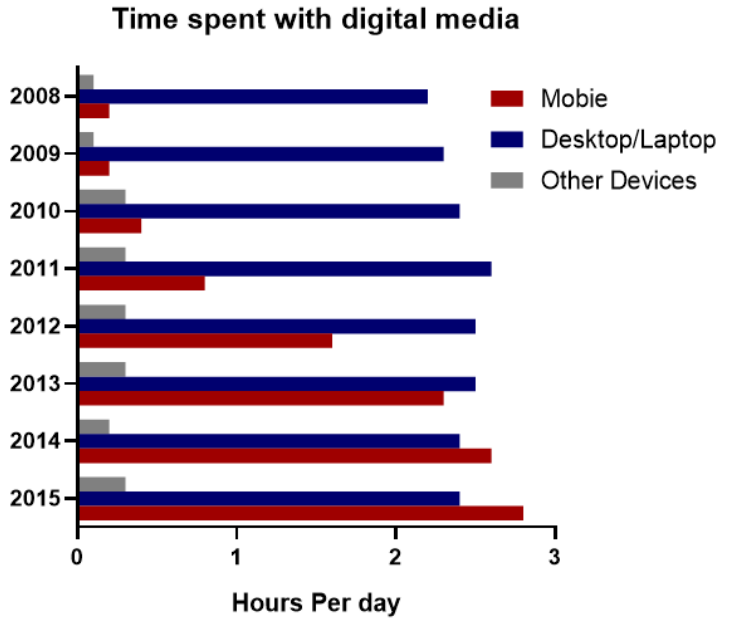
# Graph help us interpret scientific data more efficiently

**Time spent with digital media**

| Year | Mobie | Desktop/Laptop | Other Devices |
|---|---|---|---|
| 2015 | 2.8 | 2.4 | 0.3 |
| 2014 | 2.6 | 2.4 | 0.2 |
| 2013 | 2.3 | 2.5 | 0.3 |
| 2012 | 1.6 | 2.5 | 0.3 |
| 2011 | 0.8 | 2.6 | 0.3 |
| 2010 | 0.4 | 2.4 | 0.3 |
| 2009 | 0.2 | 2.3 | 0.1 |
| 2008 | 0.2 | 2.2 | 0.1 |

## When to use what



# Choose the most appropriate graph for your data


https://www.data-to-viz.com/

## Why Graphpad Prism?

- Easy and fast
- Commonly used statistical methods
- Graphs and data are automatically updated in real time
- Reusable graph template
- … …

# Three steps to generate a graph

- ❑ Prepare data
- ❑ Perform analysis
- ❑ Choose the type of graph

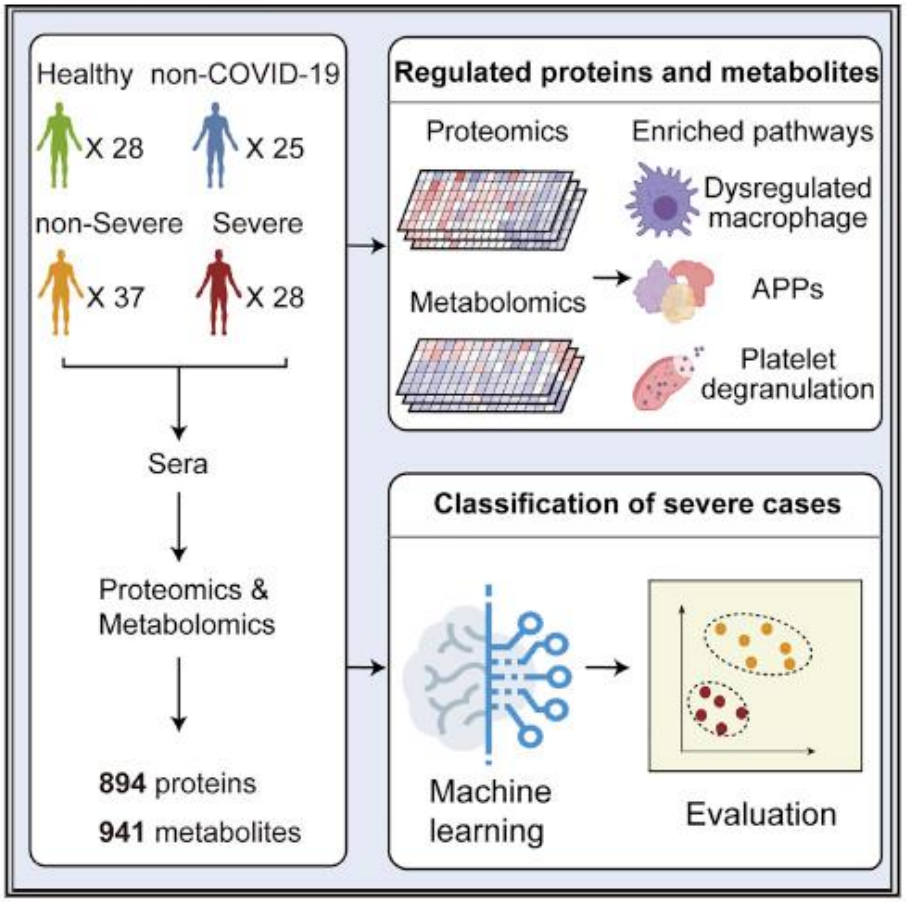
# Dataset for practice

Cell

Article

## Proteomic and Metabolomic Characterization of COVID-19 Patient Sera

### Graphical Abstract

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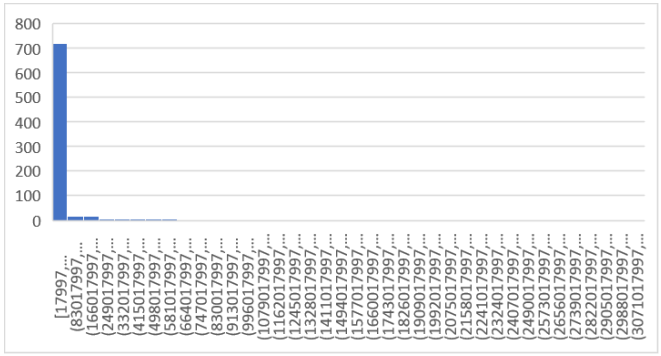
### In Brief

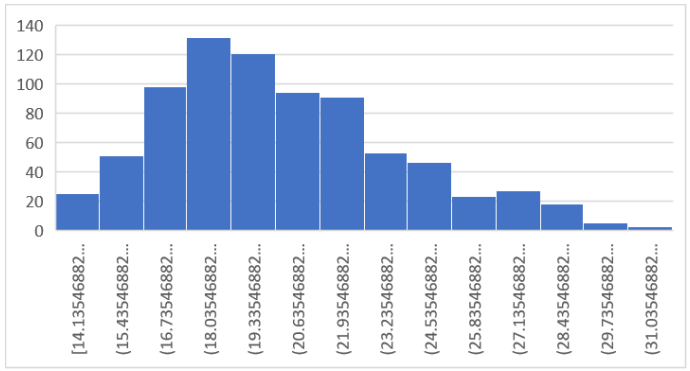
Proteomic and metabolomic analysis of COVID-19 sera identifies differentially expressed factors that correlate with disease severity and highlights dysregulation of multiple immune and metabolic components in clinically severe patients.

- ❑ Distribution of metabolites' concentration
- ❑ Correlation of metabolomics across patients
- ❑ T-test (comparison of two groups)
- ❑ One-way anova (comparing more groups)

# Practice: Transform the data to log2 scale

1. “log2” changes the distribution to normal-like distribution




2. “log2” brings the up- and down-regulated genes/metabolites to same scale

Control = 20
Treatment = 160

Fold change = 8

Log2 fold change = 3

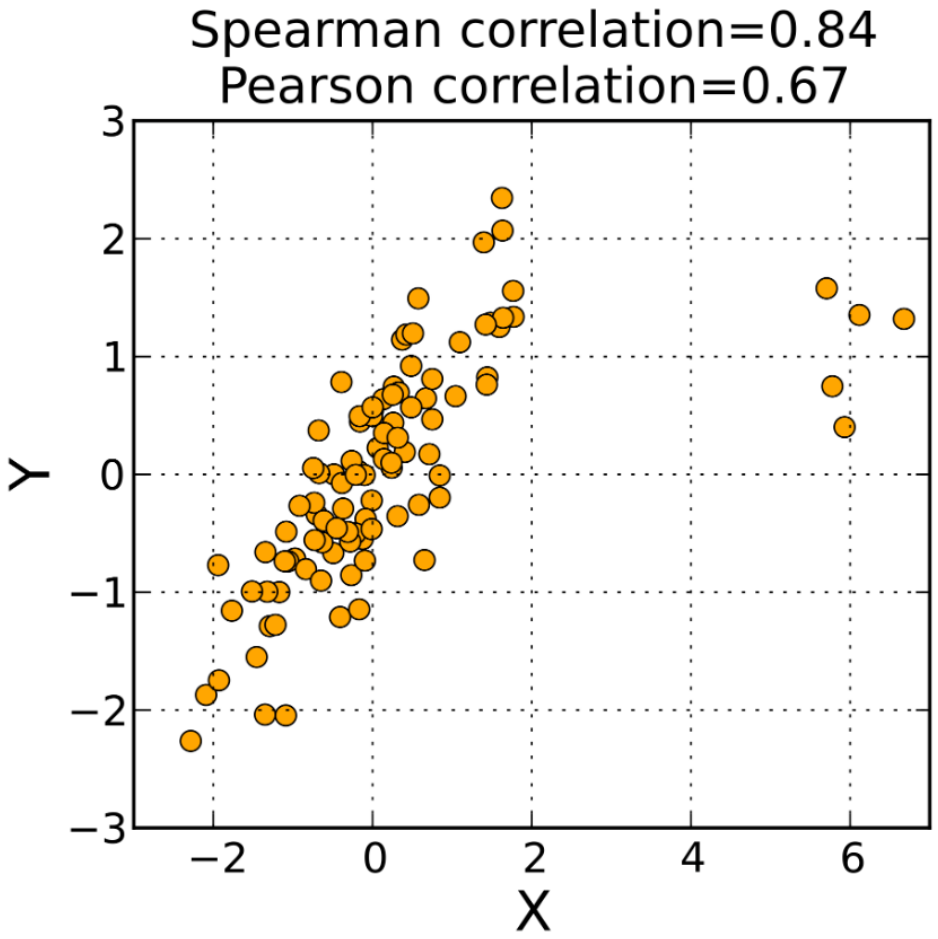
Control = 160
Treatment = 20

Fold change = 0.125

Log2 fold change = -3

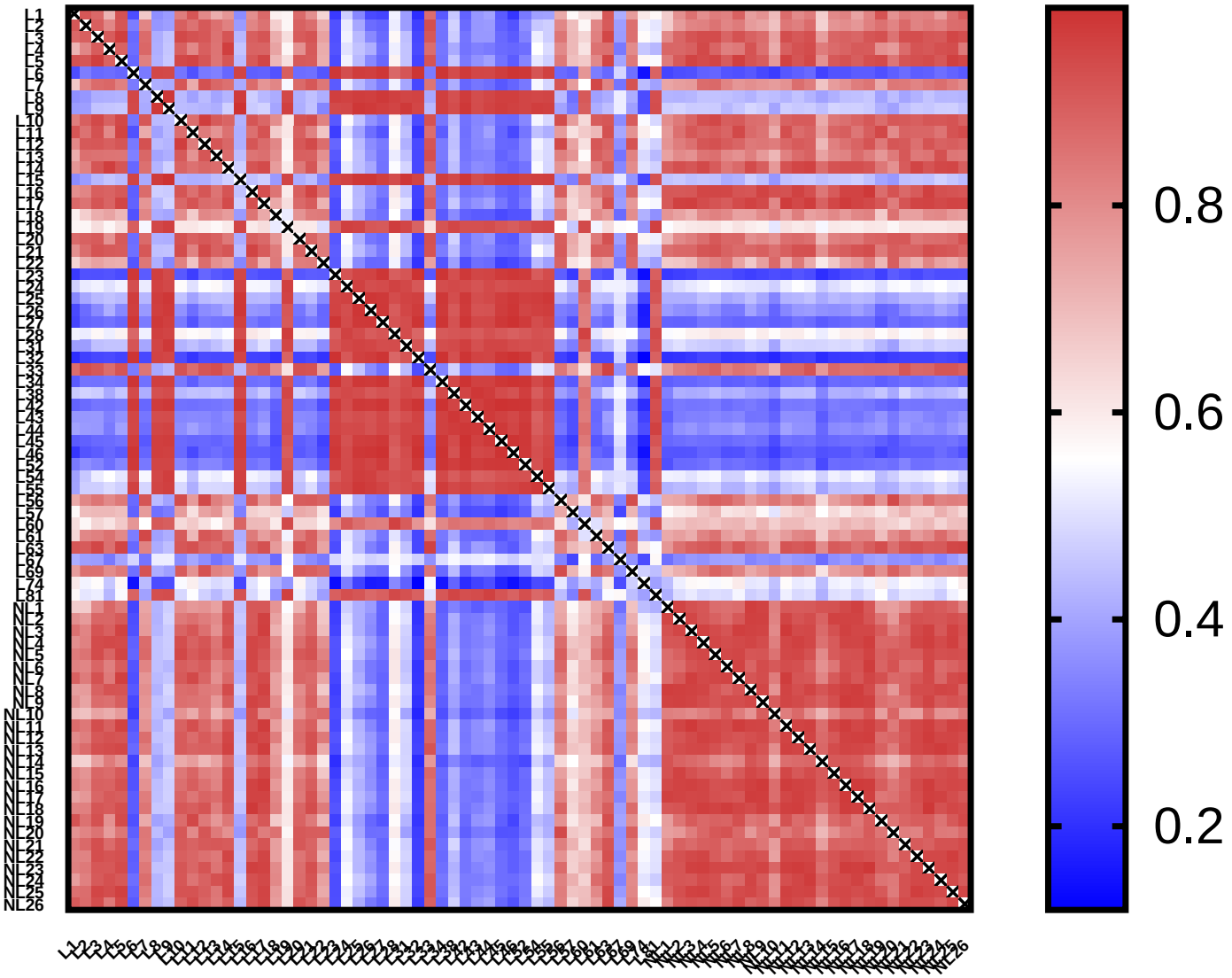
# Practice: calculate correlation

**Correlation (pearson or spearman?)**

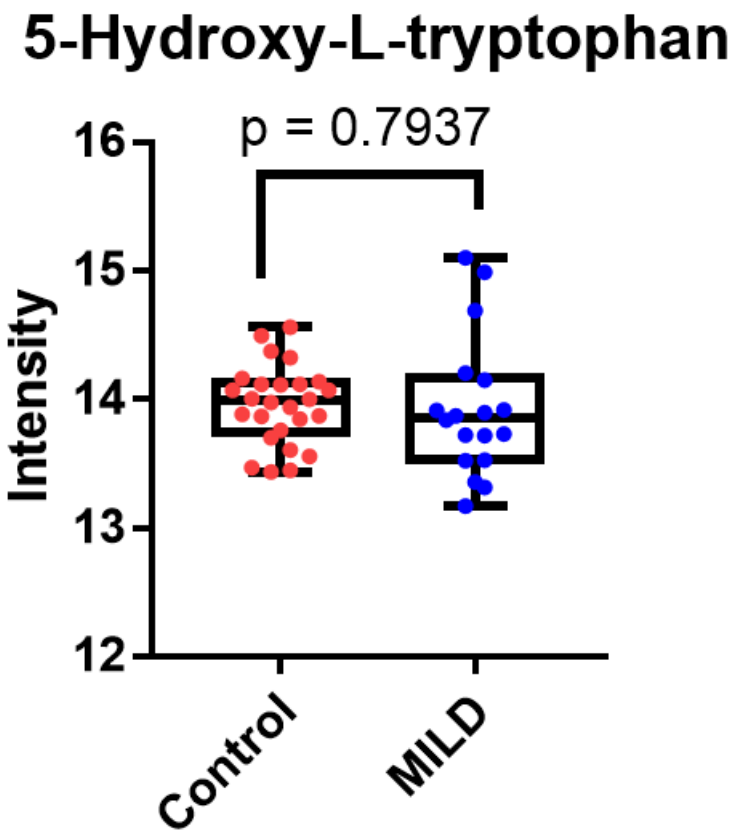



The Spearman correlation is less sensitive than the Pearson correlation to strong outliers

# Practice: correlation matrix



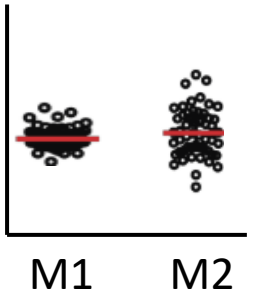
# Practice: using t-test to compare two groups



## Advice: when to plot SEM vs. SD

- **SD**: standard deviation, quantifies how much the values vary from one another
- **SEM**: standard error of the mean, represents the accuracy of the true mean for the population. SEM = SD/(square root of sample size)

- **SD**: If you want to show the variation of your data. For example, if you want to present that one metabolite is much more stable than another one by stimulus.
- **SEM**: If you want to show how precisely you determine the true mean. For example, you want to present that one metabolite is up regulated after infection.



# Practice: using anova to compare multiple groups

**We want to see if selected metabolite significantly changed after infected.**

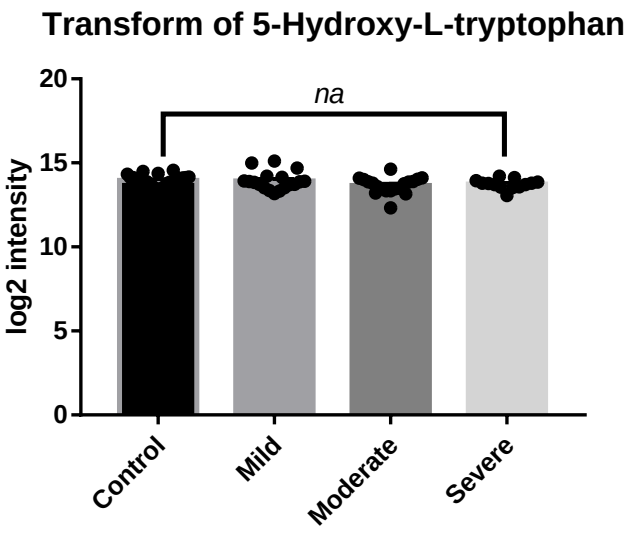
**One-way anova** (you can simply think it as a multiple t-test):

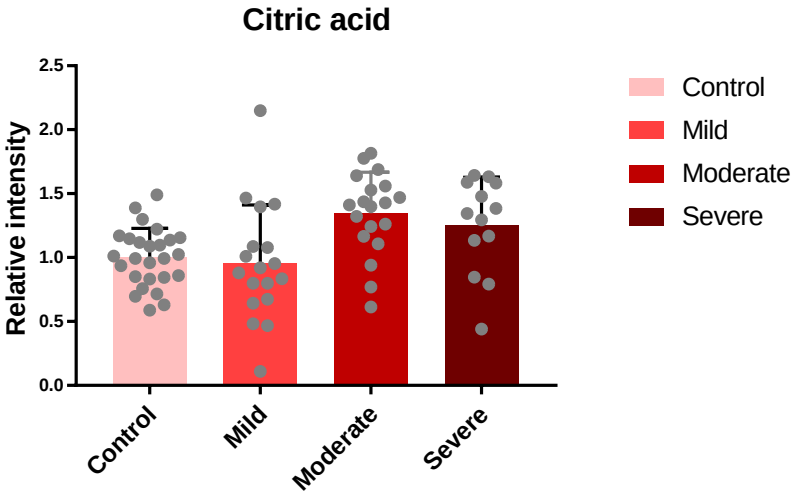
determine whether there are any statistically significant differences between the means of two or more independent (unrelated)

Null and Alternative hypotheses

H0: *μ(control) == μ (mild) == μ(moderate) == μ(severe)*

H1: not all *μ* are equal

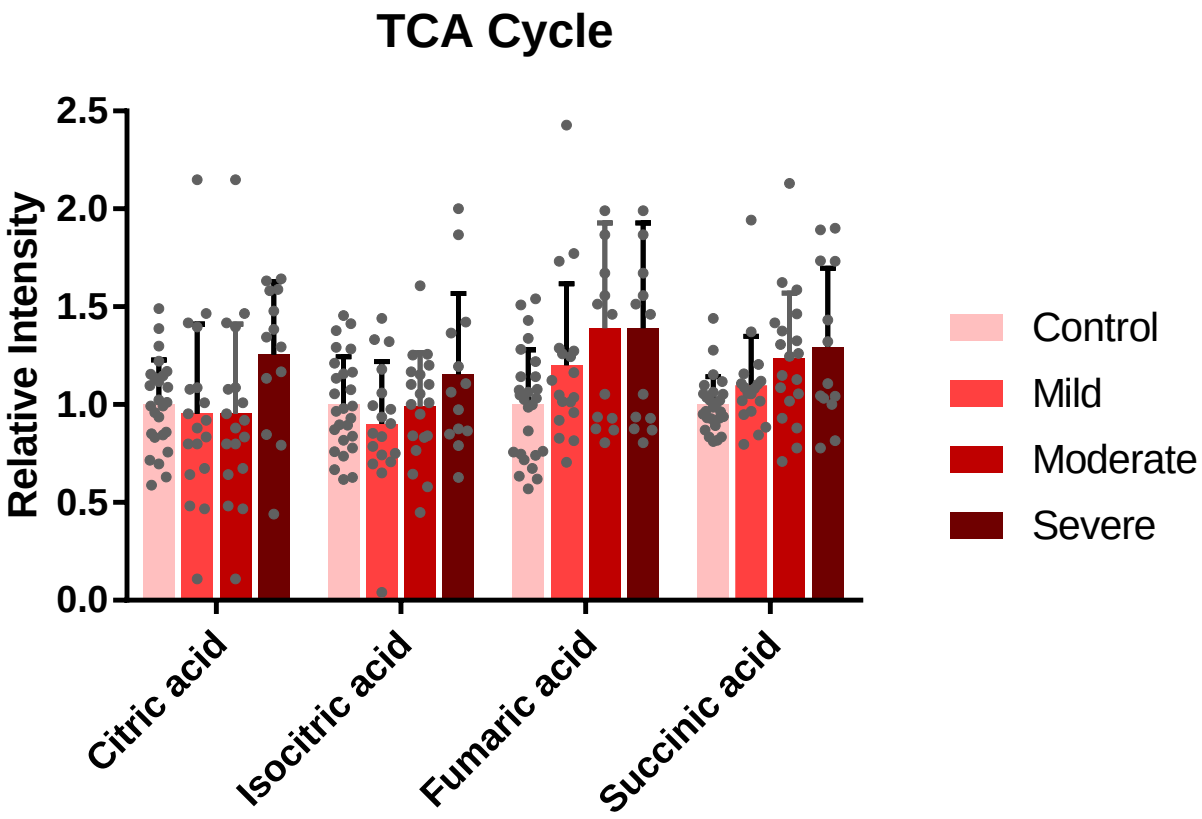



**We want to see the relative intensities to control group.**

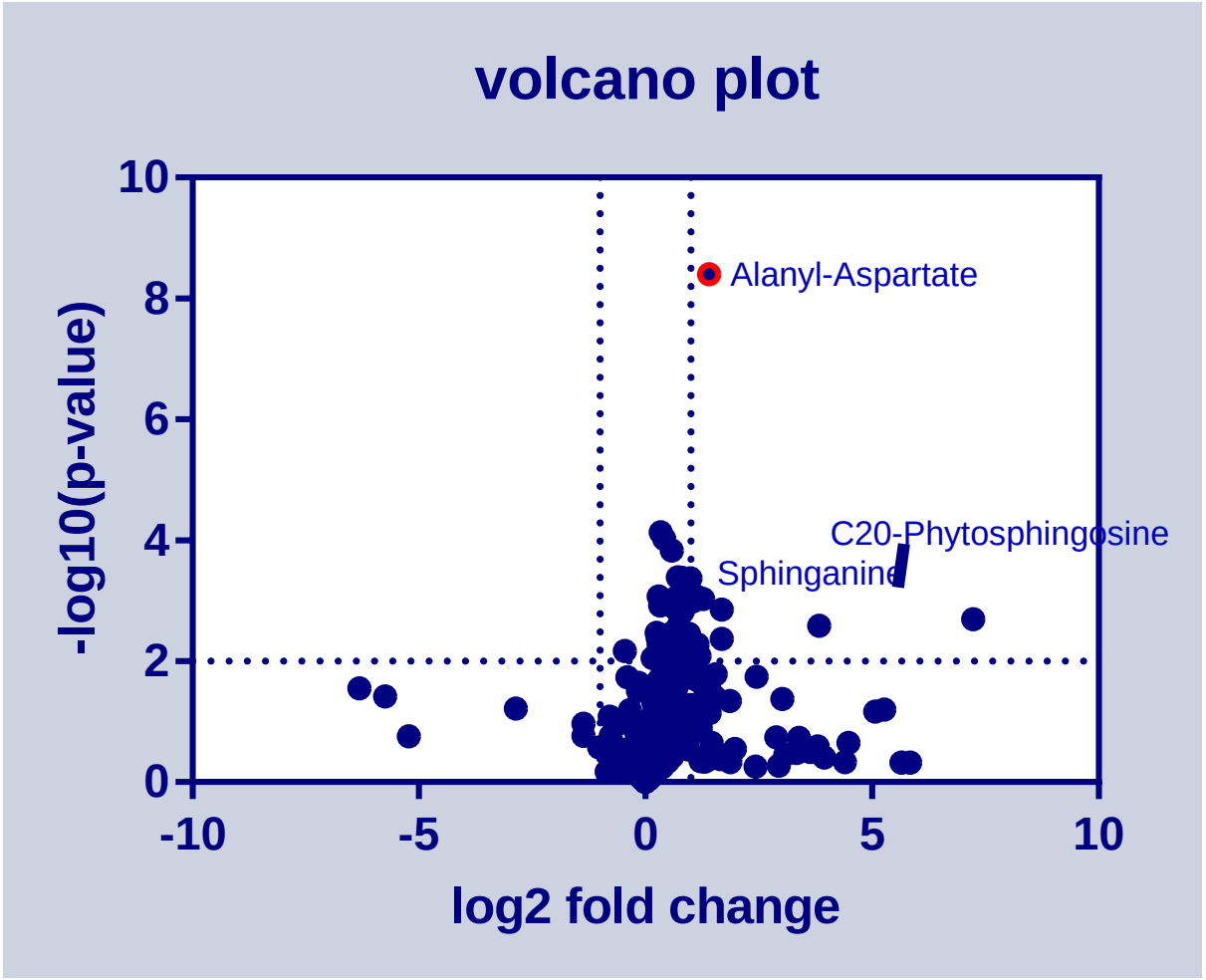
# Practice: Group Bar Graph

**We want to see the relative intensities of all metabolites in TCA cycle**



# Practice: volcano plot

**Volcano plot: significance vs magnitude of changes in metabliltes**



## More information

- ❑ Prism user guide
- ❑ Prism statistics guide
- ❑ Prism Tips

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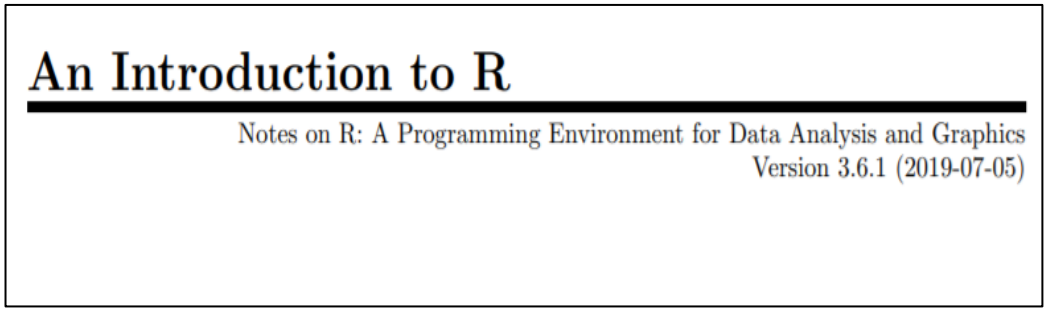
## Next lecture




**https://cran.r-project.org/doc/manuals/r-release/R-intro.pdf**

https://github.com/zhengtaoxiao/NCSU_R