

# R: installation, variables and data structure

Most examples are from

<https://www.youtube.com/watch?v= V8eKsto3Ug>

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R help documents

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<https://www.benjaminbell.co.uk/2018/03/quick-guide-to-annotating-plots-in-r.html>

# Why R?

- The most widely used one for Data Science, 50% more than Python
- Tools are free
- Many packages are developed

# Download and installation

- <https://www.r-project.org/>
- Rstudio

# Useful packages

- CRAN, Crantastic, or Github.com/trending/r
- 21938 available packages in CRAN
- Type `help("INSTALL")` or `help("install.packages")` in R for information on how to install packages from CRAN
- For example, in R type `install.packages("package name")` to install the specific package with the specified name.

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# CRAN package task view

[Https://mirror.las.iastate.edu  
/CRAN/](https://mirror.las.iastate.edu/CRAN/)

# An example of package installation

- `install.packages("pacman") #install`
- `library(pacman) #load`
- `pacman::p_load(dplyr,psych,ggplot2, rio) #rio for input/output from files`

# Variable types

- Type: numeric (integer, single, double), logical, character, complex, (raw)
- Structure: vector, matrix/array, data frame, list
- Vector, 1-d, the same type of data
- Matrix, 2-d, the same type of data, the same length, use the index number to work with the columns and rows.
- Array, similar to matrix,  $\geq 3$  dimensions
- Data frame, 2-d vectors of multiple types, the same length, analogue to spreadsheet
- List, 1-d, ordered collection of any type of elements including lists

# Variable names

- Variable names can be a combination of letters, digits, period, and underscore.
- Underscore and digits cannot be the first one while others can in a variable name.
- Period must be followed by letter.
- Case sensitive

# Variable type examples

- n1<-15
- typeof(n1)
- X<-TRUE, x<-F
- Y<-"this is a string or character"
- typeof(Y)
- v1<-c(1,2,3,4,5,6)
- is.vector(v1)
- M1<-matrix(v1, nrow=2, byrow=T)
- A1<-array(c(1:24), c(4,3,2))

list

- O1<-c(1,2,3)
- O2<-c(T, F,T, T, F)
- O3<-c(2,3,4,5)
- List1<-list(O1,O2, O3)
- List1
- List2<-c(O1,O2,O3, List1)
- List2

# Convert data types 1

- `vN<-c(1,2,3)`
- `vC<-c("a","b","c")`
- `vL<-c(T,F, T)`
- `Df1<-cbind(vN,vC,vL)`
- `Df1`
- `Df2<-as.data.frame(Df1)`
- `as.numeric`
- `as.character`

## Convert data types 2

- `x<-1:3`
- `y<-1:9`
- `df1<-cbind(x,y)`
- `typeof(df1)`
- `typeof(df1$x)`
- `df1<-cbind.data.frame(x,y)`
- `typeof(df1$x)`
- `str(df1)`
- `typeof(df1$x)`

## In-class question #3

Open an account at galaxy, (1) download a ChIP-seq dataset, (2) run trimmomatic to clean the downloaded dataset, (3). Map the clean paired reads to the reference genome with Bowtie2. Submit a picture showing your log history of the above three steps at galaxy through the webcourses. Due 6pm on January 30.