# Lab: Learning R

Genomic Technologies Workshop 2024 (PLPTH885)

Sanzhen Liu

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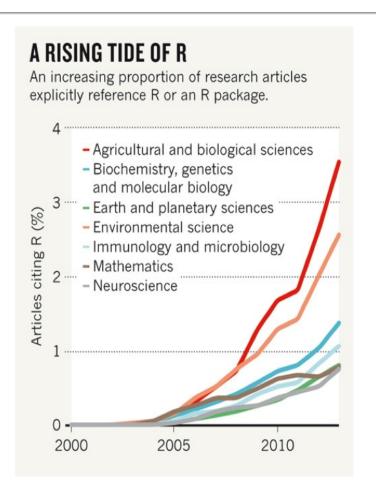
#### **Outlines**

- Introduction of R programming
- Introduction of RStudio's IDE
- Running basic R
  - Data structure (vector and data frame)
  - Data importing and exporting
  - Plotting
  - String operations

#### Why R?

- R is a free software
- R is great at statistical computing and graphics
- R has great community supports (CRAN repository, Bioconductor, GitHub)

r-project.org



# R example 1 (R for statistics)

#### Chi-square test

```
d <- c(12, 36, 24, 70)
dm <- matrix(d, nrow=2, byrow=T)
dm

[,1] [,2]
[1,] 12 36
[2,] 24 70

chisq.test(dm)</pre>
```

Pearson's Chi-squared test with Yates' continuity correction data: dm

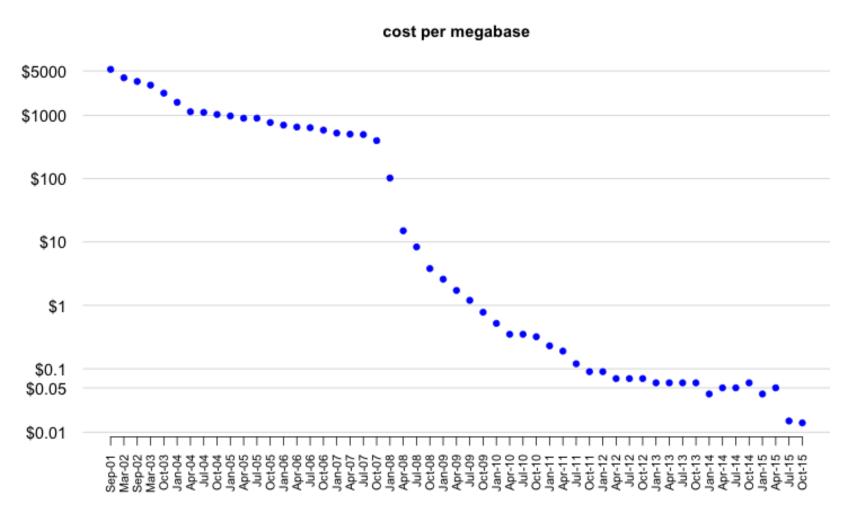
X-squared = 7.8894e-31, df = 1, p-value = 1

# R example 2 (R for graphs)

ts="https://raw.githubusercontent.com/liu3zhenlab/teaching/master/RN/
source(ts)

# R example 3 (R for graphs)

cs="https://raw.githubusercontent.com/liu3zhenlab/teaching/master/RN/
source(cs)



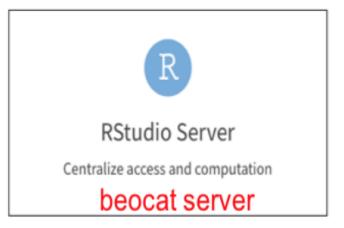
#### How to run R?

Rstudio is an open source integrated development environment (IDE) for R.

https://www.rstudio.com/products/rstudio/

There are two versions of RStudio:





#### **Install RStudio**

- On your own machine (Rstudio Desktop)
  - Download and install R
  - Download and install Rstudio

#### Slides and codes



https://github.com/liu3zhenlab/teaching/tree/master/RNA-Seq-Workshop/2024/forYOU

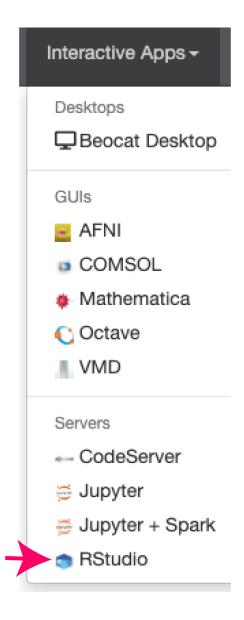
#### OnDemand at Beocat

ondemand https://ondemand.beocat.ksu.edu

login with eID



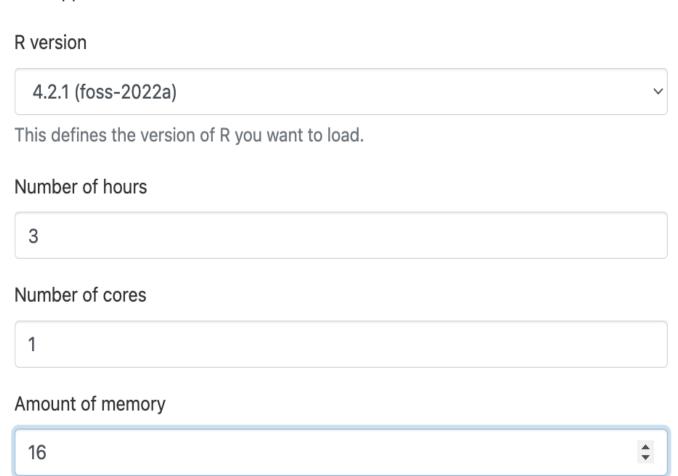
#### Select RStudio



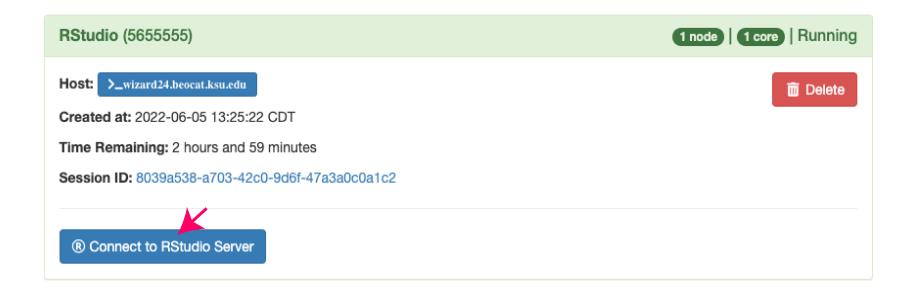
#### Request resources

#### **RStudio**

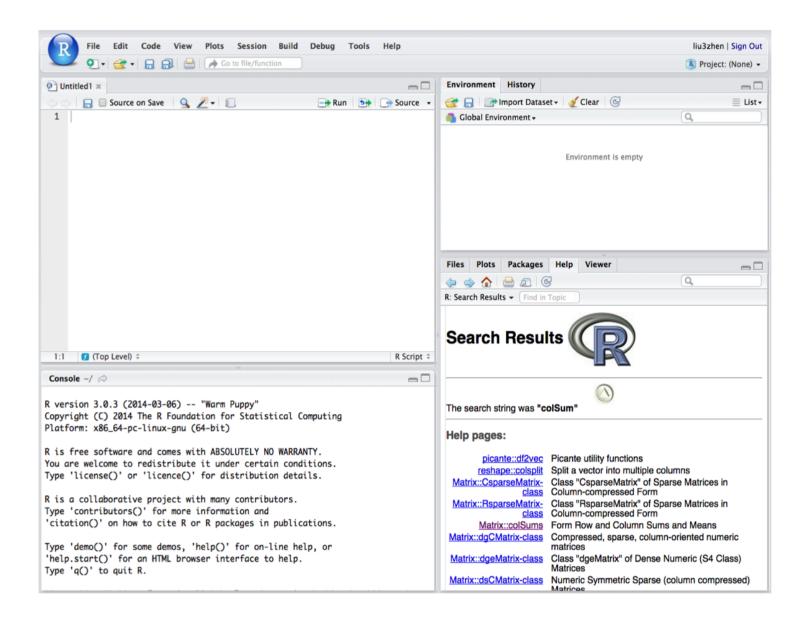
This app will launch RStudio Server an IDE for R.



#### Connect to RStudio

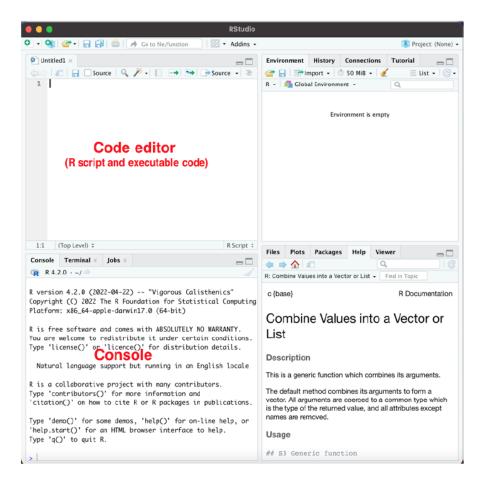


#### Rstudio interface



#### RStudio Interface

#### RStudio IDE cheatsheet



- Executing commands for the code editor
  - PC window: control + return (enter)
  - Apple MAC: command + return (enter)

# Setup working directory

Working directory is the default folder for input and output data.

setwd("/Users/liu3zhen/Downloads")

# Getting started, R commands

**Expression**: evaluated, printed, and the value lost

```
2 + 4
[1] 6
68 * 0.15
```

[1] 10.2

#### **Assignment**

assign values to a variable the value passed to a variable but NOT printed

assignment operator: <- or =</pre>

```
y <- 2
y = 2
y
```

[1] 2

```
info <- "hello world"
cat(info)</pre>
```

hello world

#### Notes

• Comments (#): Notes to scripts, starting with a hashtag ('#'), everything to the end of the line is a comment.

```
y <- 2 + 4 # an example of the assignment
```

• Variable names are case senstive

```
y <- 2
Y <- 3
y
```

[1] 2

Υ

[1] 3

#### vector: multiple elements

A vector is a single entity consisting of an ordered collection of numbers, characters, logical quantities, etc.

concatenate command: c()

• Numeric vector c(10.4, 5.6, 3.1, 6.4, 21.7)

# vector manipulation (I)

```
# Numeric vector
x \leftarrow c(10.4, 5.6, 3.1, 6.4, 21.7)
sum(x)
[1] 47.2
2*x
[1] 20.8 11.2 6.2 12.8 43.4
### extract 2nd elements
x[2]
[1] 5.6
```

# vector manipulation (II)

# Logical vector

```
lv <- c(TRUE, FALSE, TRUE, TRUE)
!lv

## [1] FALSE TRUE FALSE

lv == FALSE

## [1] FALSE TRUE FALSE FALSE</pre>
```

## vector manipulation (III)

```
# Character vector
cv <- c("a", "b", "c")
cv2 <- paste(cv, 1:3, sep="")
cv2

[1] "a1" "b2" "c3"

# Missing value (NA, not available)
mvv <- c("a", "b", "c", NA)
is.na(mvv)</pre>
```

[1] FALSE FALSE TRUE

# vector manipulation (IV)

[1] 0 1 2 3 4 5 6 7 8 9

Vectors must have their values with the same mode, either numeric, character, logical, or other types. **conversion to other modes** 

```
z < -0:9
is.numeric(z)
[1] TRUE
Z
[1] 0 1 2 3 4 5 6 7 8 9
digits <- as.character(z) # convert to character</pre>
digits
 [1] "0" "1" "2" "3" "4" "5" "6" "7" "8" "9"
d <- as.numeric(digits) # convert to numeric</pre>
d
```

# vector manipulation (V)

• Select a subset of a vector

```
x <- c(4, 5, 7, 3, 9)
x[c(2, 3)]

[1] 5 7

x[x>6]

[1] 7 9

x[-c(1, 5)]
```

[1] 5 7 3

• Modify a vector

```
x[3] <- 23.1
c(x, 10.9)
```

[1] 4.0 5.0 23.1 3.0 9.0 10.9

## Question

Can a vector contain different types of elements?

```
c(1, "a")
c(1, TRUE)
c(TRUE, "a")
c(1, "a", TRUE)
```

#### Data frame

A data frame may be regarded as a matrix (table) with columns possibly of differing modes

• Making data frames

```
df <- data.frame(name=c("Josh", "rose"), age=c(23, 35))
df

name age
1 Josh 23
2 rose 35</pre>
```

# Working with a data frame

```
name age
1 Josh 23
2 rose 35
```

#### Trying these commands:

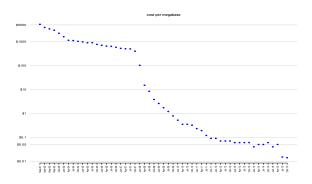
```
head(df, 1)
tail(df, 1)
str(df)
df[2, 1]
df[2, 2]
df[2]
df[, 2]
```

#### Importing data

read.table(): to read a data frame (table)
read.delim, read.csv

```
cpm="https://raw.githubusercontent.com/liu3zhenlab/teaching/master/RN
d <- read.delim(cpm)
head(d, 3)</pre>
```

```
Date Cost.per.Mb Cost.per.Genome
1 Sep-01 5292.39 95263072
2 Mar-02 3898.64 70175437
3 Sep-02 3413.80 61448422
```



cpm="https://raw.githubusercontent.com/liu3zhenlab/teaching/master/RNA-Seq-Workshop/2024/lab\_DE/data/cs.txt"

#### **Exporting data**

#### write.table() or write.csv()

To write a tab-delimited file

```
x <- data.frame(a = "pi", b = pi)
write.table(x, file="foo.txt", sep="\t", row.names=FALSE)</pre>
```

- file="foo.txt": foo.txt is the ouput file name
- sep="\t": separated by a tab (\t)
- row.names=FALSE: row names are not included in the output

#### Practice by your own

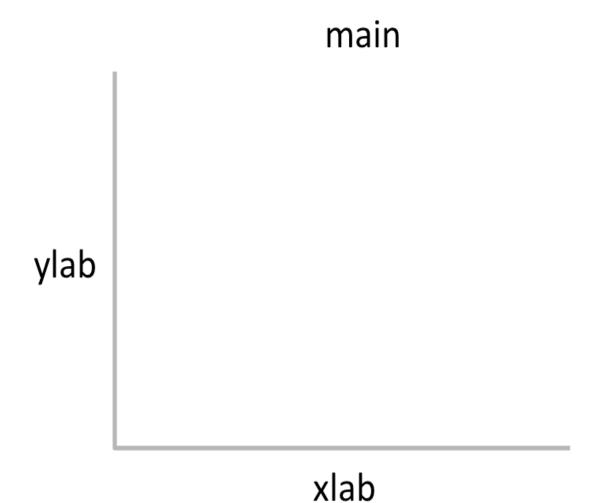
• Create a data frame

three columns: 1. Name 2. Major 3. Gender three rows (entries): your neighbors and you

- Write the data frame to an output file
- Read the file to R and add one more column (e.g., favorite color)

# Plotting: plot()

```
High-level plot: create a new plot plot(x, y, xlab, ylab, main, ...)
```

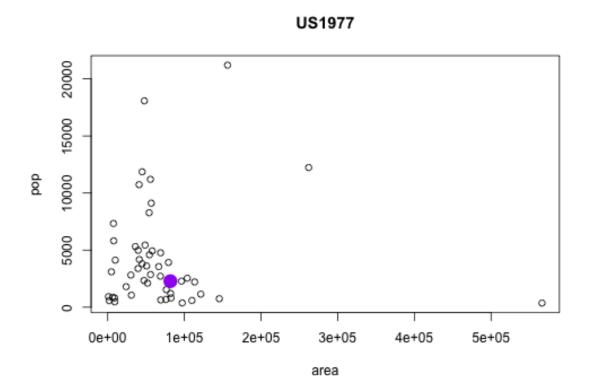


# Adding contents to a plot

Low-level plot: add to an existing plot

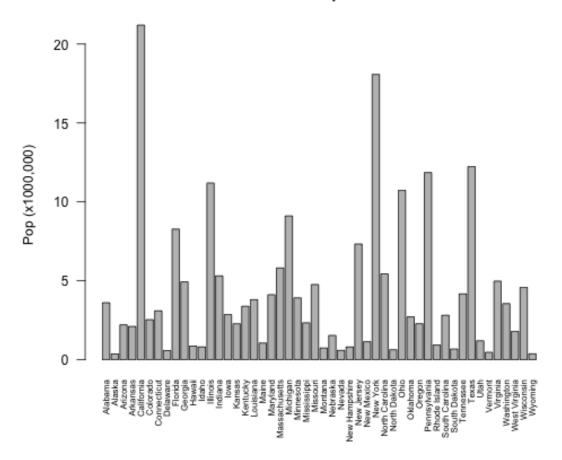
- add points points()
- add lines lines()
- add text or legend text() legend()

## Scatter plot



## **Boxplot**

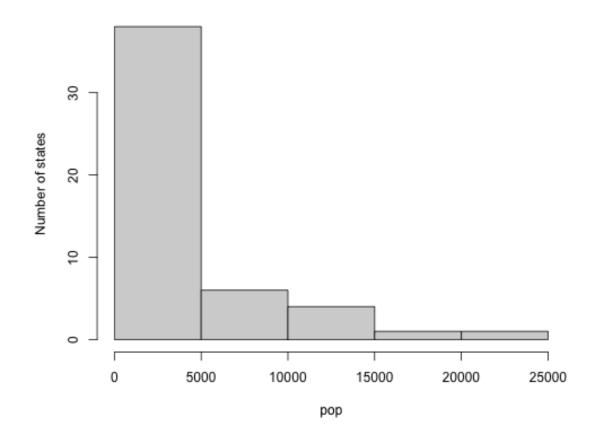




# Histogram

hist(pop, ylab="Number of states", main="US 1977 Population")





## String operations - nchar

**nchar()** nchar the sizes of the corresponding elements of a vector.

```
cvec <- c("google", "hello", "the", "world")
nchar(cvec)</pre>
```

[1] 6 5 3 5

#### String operations - grep

**grep()** grep searches for matches to argument pattern within each element of a character vector

```
cvec
[1] "google" "hello" "the" "world"
grep("o", cvec)
[1] 1 2 4
```

# String operations – sub and gsub

**sub()** and **gsub()** sub and gsub perform replacement of the first and all matches respectively.

```
cvec
[1] "google" "hello" "the" "world"

sub("o", "O", cvec)

[1] "gOogle" "hello" "the" "wOrld"

gsub("o", "O", cvec)

[1] "gOOgle" "hello" "the" "wOrld"
```

# Getting help

#### Usage of commands

- help(nchar)
- ?nchar
- ??colsum

#### R Reference Card

- stack overflow
- google

Learning R at swirlstats

education.rstudio.com