Introduction to Bioinformatics

Introduction to Basic Programming with R

Today's Outline

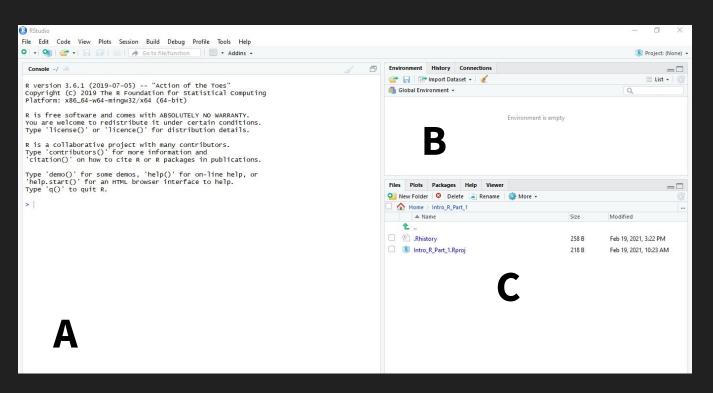
- Quick Overview of RStudio
- 2) Programming Fundamentals in R:
 - a) R Data Types
 - b) R Operations
- 3) Data Frames and Factors
- 4) Data Manipulation

A Quick Glimpse

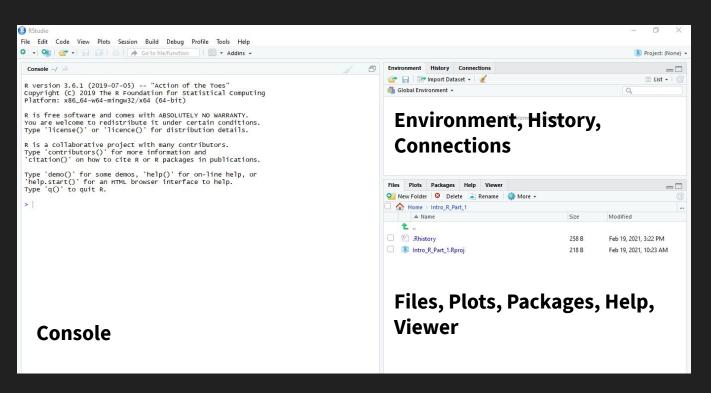
NGS (Bisulfite Sequencing)



Quick Introduction to R Studio



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Quick Introduction to RStudio

A typical RStudio layout contains the following:

- **Console**: to type our code and see the output directly

- **Environment**: Provide detailed list of every functions or variables that are defined
- **History**: Provide list of the history of the used commands

- **Files**: Store all the files that are currently available to user
- **Plots**: Where the charts and plots will appear
- **Packages**: List information about the packages installed
- **Help**: Allow to search the help directly from RStudio

Creating Objects/Variables in R

Objects stores the value of your choice so you can reuse it over and over again

To create an object you need:

- 1) a name (e.g. 'number_of_genes')
- 2) a value (e.g. '25')
- 3) the assignment operator ('<-')
- > number_of_genes <- 25
- > number_of_genes

[1] 25

Naming Objects/Variables in R

Objects stores the value of your choice so you can reuse it over and over again

1) Avoid spaces and special characters

- > number_of_genes <- 25 🗸
- > number of genes <- 25 X
- > n@mber_of_g#n#s <- 25 🗙

Naming Objects/Variables in R

Objects stores the value of your choice so you can reuse it over and over again

- 1) Avoid spaces and special characters
- 2) Use short, easy-to-understand names
- 3) Avoid commonly used names
- > number_of_genes <- 25 🔽
- > number of genes <- 25 X
- > n@mber_of_g#n#s <- 25 🗙
- > mean <- 25 X

Data Types in R

Similar to other programming languages R has the following data types

Basic Data Types

- LOGICAL : TRUE/ FALSE
- **NUMERIC: 4.0, 5, 1018**
- CHARACTER: 'ACGTGAC', 'TP53', 'This is a text'

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We can perform mathematical operations in R

>1+1	Addition
[1] 2	
> 190 - 18	Subtraction
[1] 172 > 5 * 3	Multiplication
[1] 15	Multiplication
> 8 / 4	Division
[1] 2	

We can perform mathematical operations in R

	Addition	> 5 ^ 2 [1] 25	Exponent
> 190 - 18 [1] 172	Subtraction	> 20 %% 2 [1] 0	Modulus (Remainder of division)
> 5 * 3 [1] 15	Multiplication	> 7 %/% 5 [1] 1	Integer Division
> 8 / 4	Division		

We can perform logical operations too in R

> 1 == 1	Exactly equal
[1] TRUE	
> 190 < 18	Less than
[1] FALSE	
> 5 > 3	Greater than
[1] TRUE	
> 8 != 4	Not equal to
[1] TRUE	

We can perform logical operations too in R

	Exactly equal	> 1 <= 1 [1] TRUE	Less than equal
> 190 < 18	Less than	> 190 >= 18	Greater than
[1] FALSE		[1] TRUE	
> 5 > 3	Greater than	> (5 > 3) (3 > 5)	OR
		[1] TRUE	
> 8 != 4	Not equal to	> (2 > 1) & (4 < 3)	AND
		[1] FALSE	

Data Types in R

Similar to other programming languages R has the following data types

More Data Types

- VECTORS
- LISTS
- MATRICES
- ARRAYS
- FACTORS
- DATA FRAMES

Data Types in R - VECTORS

Vector is one of the simplest data types in R, everything that is not defined as other data type is vector

- > c('Apple', 'Orange', 'Mango')
- > c(1, 2, 3, 4, 5, 6, 7, 8, 9)

Data Types in R - LISTS

List can contain many different types of elements inside it

- > list(c(2,5,3),21.3,sin)
- > list(1, 'apple', 2.9099090)

Data Types in R - MATRICES

A matrix is a two-dimensional rectangular data set. It can be created using a vector input to the matrix function.

```
> matrix( c('a','a','b','c','b','a'), nrow = 2, ncol = 3, byrow = TRUE)

[,1] [,2] [,3]

[1,] "a" "a" "b"

[2,] "c" "b" "a"
```

Data Types in R - FACTORS

When matrix can only take two dimensions, arrays can be any number of dimension.

> factor(c('green','green','yellow','red','red','green'))

[1] green green yellow red red green Levels: green red yellow

Data Types in R - DATA FRAMES

Data frames are tabular data objects. It's different from matrix in a way that each column can contain different modes of data.

```
> data.frame(
    gender = c("Male", "Male", "Female"),
                                                gender height weight Age
    height = c(152, 171.5, 165),
                                                Male
                                                         152.0
                                                                 81
                                                                        42
    weight = c(81,93,78),
                                                Male
                                                        171.5
                                                                 93
                                                                        38
    Age = c(42,38,26)
                                            3
                                                                        26
                                                Female 165.0
                                                                 78
```

Data frames:

- are tabular data objects
- can contain different types of data inside it
- contain vector of equal length

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```
> data.frame(
                                                          height weight
                                                 gender
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                                                                          Age
                                                 Male
                                                          152.0
                                                                   81
                                                                          42
    height = c(152, 171.5, 165),
                                                  Male
                                                          171.5
                                                                   93
                                                                          38
    weight = c(81,93,78),
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Reading data from your table is as simple as the following data_frame_variable <- read.csv("directory/filename")

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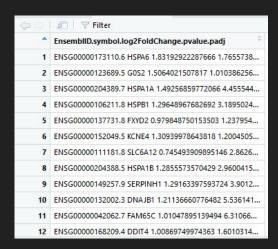
For example to read the shared data we can perform the following: parkinson_df <- readcsv("parkinson_de_data.tsv")

If the import is successful, we can see the variable listed in the environment

Clicking twice we can see our imported data frame

But this isn't what we wanted :(





read.csv can take multiple arguments, the most common ones are:

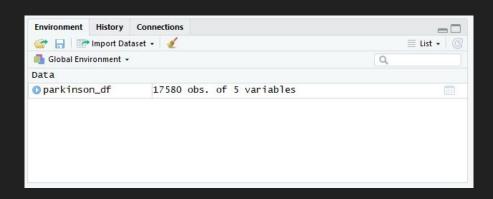
- **header**: whether to use the first line as the header or not
- **sep**: what character is being used to separate the columns in the data
- **dec**: what character is being used as the decimal point
- **nrows**: maximum number of rows to read

read.csv can take multiple arguments, the most common ones are:

- header: whether to use the first line as the header or not
- **sep** : what character is being used to separate the columns in the data
- **dec**: what character is being used as the decimal point
- **nrows**: maximum number of rows to read

More information regarding the function can be accessed like usual, just put question mark in front of the function name in RStudio (?read.csv)

If we read the previous data correctly, the following should appear in our screen:



If we read the previous data correctly, the following should appear in our screen:



Clicking the variable twice

EnsemblID ÷	symbol	log2FoldChange *	pvalue [‡]	padj ‡
ENSG00000173110.6	HSPA6	1.8319292	1.765574e-14	3.103879e-10
ENSG00000123689.5	G0S2	1.5064022	1.010386e-11	8.881295e-08
ENSG00000204389.7	HSPA1A	1.4925686	4.455545e-11	2.610949e-07
ENSG00000106211.8	HSPB1	1.2964897	3.189502e-10	1.401786e-06
ENSG00000137731.8	FXYD2	0.9798488	1,237955e-09	3.627207e-06
ENSG00000152049.5	KCNE4	1.3093998	1.200451e-09	3.627207e-06
ENSG00000111181.8	SLC6A12	0.7454939	2.862677e-09	6.504691e-06
ENSG00000204388.5	HSPA1B	1.2855574	2.960042e-09	6.504691e-06
ENSG00000149257.9	SERPINH1	1.2916340	3.901282e-09	7.620505e-06
ENSG00000132002.3	DNAJB1	1.2113666	5.536142e-09	9.732537e-06
ENSG00000042062.7	FAM65C	1.0104790	6.310661e-09	1.008558e-05
ENSG00000168209.4	DDIT4	1.0086975	1.601031e-08	2.345511e-05

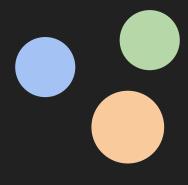
We can examine our data frames using the following functions:

- dim(): shows the dimensions of the data frame by row and column
- str(): shows the structure of the data frame
- summary(): provides summary statistics on the columns of the data frame
- colnames(): shows the name of each column in the data frame
- head(): shows the first 6 rows of the data frame
- tail(): shows the last 6 rows of the data frame
- View(): shows a spreadsheet-like display of the entire data frame

Factors

Factors:

- are usually used to store categorical variables
- are very important when doing statistical modelling
- very efficient when storing character data





Age is continuous

Subsetting Data Frames

Previously we already talked on how we can perform subsetting in 1 dimensional data (vector) but how do we do it in dataframe?

[Move to practice]

More Function for Data Frames

There are also tremendous amounts of data frame function that we haven't explored, here are the followings:

- Aggregate functions [max(), min(), avg(), sum()]
- Ordering functions [order()]
- Rename columns

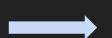
Saving data frames:

write.csv(variable, file=filename)

DPLYR

dplyr is a grammar of data manipulation, providing a consistent set of verbs that help you solve the most common data manipulation challenges

Previous subsets []



- select()
- filter()
- group_by()
- summarize()
- mutate()

Installing and using DPLYR (and other packages)

installing is simple, you just have to type the following
install.packages("name_of_the_packages")

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if (!requireNamespace('BiocManager', quietly = TRUE))
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To load the installed library we can use **library("package_name")**

DPLYR

Common functions in DPLYR

- select(): select our intended column
- filter(): filter the data by some conditions
- group_by(): group the data by column
- summarize(): summarize the results of grouping
- mutate(): mutate a column, create new column with new logic