Ann & Robert H. Lurie Children's Hospital of Chicago®

INTRODUCTION TO R PROGRAMMING

Day 1: R Basics

October 24, 2023







Orientation to the workshop





Who is this workshop for?

Those with little or no experience with R

- Those who would like an R refresher
- Those with a need or interest for using R in their work
- Who are your instructors?



Joy Nyaanga, PhD Senior Bioinformatician Day 1 & 3



Stella Karuri, PhD Statistician Day 2



Workshop breakdown

Session 1: Lecture	11:00 a.m. – noon
Break	
Session 2: Interactive	2:00 p.m. – 4:00 p.m.

Course website: <u>https://stanley-manne-childrens-research.github.io/introR/</u>



The data analysis pipeline





Day 1: The Basics of R





Learning objectives

- Understand basic coding principles
- Use R as a calculator
- Be able to load in data
- Basic operations on data
- Be able to make a plot
- Know how to get help





Why use something other than Excel?

Excel can change your data and rename genes

Scientists rename human genes to stop Microsoft Excel from misreading them as dates / Sometimes it's easier to rewrite genetics than update Excel



By James Vincent, a senior reporter who has covered Al, robotics, and more for eight years at The Verge.

Aug 6, 2020, 7:44 AM CDT | D O. Comments / 0 New



Human Gene Nomenclature Committee

Symbols that affect data handling and retrieval. For

example, all symbols that autoconverted to dates in Microsoft Excel have been changed (for example, SEPT1 is now SEPTIN1; MARCH1 is now MARCHF1); tRNA synthetase symbols that were also common words have been changed (for example, WARS is now WARS1; CARS is now CARS1).



Why use something other than Excel?

Excel can change your data and rename genes

Cut and paste errors are easy to do and can have bad consequences

Excel snafu costs firm \$24m

Some cleric, some error

Prew Cullen

A simple spreadsheet error cost a firm a whopping US\$24m.

"... a cut-and-paste error in an Excel spreadsheet that we did not detect when we did our final sorting and ranking bids prior to submission" – chief executive Steve Snyder

The mistake led to TransAlta, a big Canadian power generator, buying more US power transmission hedging contracts in May at higher prices than it should have.



Why use something other than Excel?

- Excel can change your data and rename genes
- Cut and paste errors are easy to do and can have bad consequences
- Excel has a relatively low (for some researchers) ceiling on number of

available rows

Analysis

Covid: how Excel may have caused loss of 16,000 test results in England *Alex Hern UK technology editor*

Public Health England data error blamed on limitations of Microsoft spreadsheet

- Coronavirus latest updates
- See all our coronavirus coverage



Point-and-click is not reproducible



What is R?

- A programming language
 - A successor of the S language
 - Created in 1991 by 2 statisticians to teach introductory statistics
 - In 1995 the source code for the R system was made accessible to the public
 - In 2000 R version 1.0.0 was officially released!
- Focus on statistical modeling and data analysis
- Interfaces with other languages (i.e. python, bash, etc.)











R

Early developers ran R via the command line console

What is RStudio?

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An integrated development environment (IDE)

Allows you to write, save, and open R code

"RStudio gives you a way to talk to your computer. **R** gives you a language to speak in"

RStudio anatomy



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Coding in the console

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- Type code in the console
 - Press return to execute code
 - Output shown below
 - Coding in the console is not advisable for most situations!
 - Only recommended for short pieces of code that you don't need to save



Coding in a script



Scripts allow you to...

- Execute code in blocks
- Save your work
- Easily share your work



Coding basics





Using R as a calculator

> 10^2
[1] 100
> 6/9
[1] 0.6666667
> 9-43
[1] -34

R follows the rules for order of operations and ignores spaces between numbers

> log(10)

[1] 2.302585



Functions

\$ log() is an example of a function





Functions

- \$ log() is an example of a function
- Functions have "arguments"





Variables

Everything is stored as a variable





Variables

- Everything is stored as a variable
- ✤ Variables are assigned using <-</p>





Math with variables

Math using variables with just one value

> x <- 5 > x		
[1] 5		

> x + 3		
[1] 8		

Math using variables with *multiple* values

> a <- 3:6 > a
[1] 3 4 5 6
> a+2; a*3
[1] 5 6 7 8
[1] 9 12 15 18



Variable types

- * numeric 110, 55.2, 123
- ☆ integer 1L, 55L, 100L (where "L" declares this as an integer)
- character "hello", "R is fun", "5" (sometimes called strings)
- ✤ logical TRUE or FALSE
- * missing NA

We can use the class() function to check the data type of a variable

class(2023)

class("example")



Object types



Object types

Vector: One-dimensional data set of *one* data type

Vector



c(1, 2, 3)

c("one", "two", "three")

c(TRUE, FALSE, FALSE)



Data frame: Twodimensional data set of *any* data type

> Data Frame (Table)



	month	day	year
1	Мау	1	2023
2	June	12	2023
3	July	10	2023



Getting data into RStudio



Importing data using the environment window



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Importing **excel** data using the environment window



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Importing data using code

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Code Preview:

      library(readxl)

      chicago_temps <- read_excel("datasets/chicago_temps</td>

      .xlsx")

      View(chicago_temps)
```

* readxl is an R package

- R packages are a collection of data, code, and functions developed by the R user community
- Packages are stored under a directory called "library"

Library of packages

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Working with data



Basic operations on data: Selecting a column



Basic operations on data: Selecting a column

A data frame named 2021_temp:

1 2 3	month January January January	day 1 2 3	year 2021 2021 2021	temp_F 23 14 18
 363 364 365	December December December	29 30 31	2021 2021 2021	34 36 32



To single out the **month** column



Basic operations on data: Selecting a column

A data frame named 2021_temp:

1 2 3	month January January January	day 1 2 3	year 2021 2021 2021	temp_F 23 14 18
 363 364 365	December December December	29 30 31	2021 2021 2021	34 36 32



To single out the **month** column



Basic operations on data: Selecting multiple columns

A data frame named 2021_temp:

1 2 3	month January January January	day 1 2 3	year 2021 2021 2021	temp_F 23 14 18
 363 364 365	December December December	29 30 31	2021 2021 2021	34 36 32



To single out **month**, **day**, and **temp_F**

2021_temp[, c(1, 2, 4)]

2021_temp[, c(month, day, temp_F)]

1 2 3	month January January January	day 1 2 3	temp_F 23 14 18
363	December	29	34
364	December	30	36
365	December	31	32

Basic operations on data: Creating a new column

A data frame named 2021_temp:

1 2 3	month January January January	day 1 2 3	year 2021 2021 2021	temp_F 23 14 18
 363 364 365	December December December	29 30 31	2021 2021 2021	34 36 32



To create a new column: temp_C

2021_temp<mark>\$temp_C</mark> <-(2021_temp\$temp_F - 32)*(5/9)

1 2 3	month January January January	day 1 2 3	year 2021 2021 2021	temp_F 23 14 18	temp_C -5 -10 -8
 363 364 365	December December December	29 30 31	2021 2021 2021	34 36 32	1 2 0

Basic operations on data: Subsetting data

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A data frame named 2021_temp:

1 2 3	month January January January	day 1 2 3	year 2021 2021 2021	temp_F 23 14 18
 363 364 365	December December December	29 30 31	2021 2021 2021	34 36 32

To select rows where $temp_F < 20$

20	2021_temp[2021_temp\$temp_F < 20,]										
			r	ow	column						
		month	day	year	temp_F						
	1	January	2	2021	14						
	2	January	3	2021	18						
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Visualizing data



Basic plots: Histogram



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Basic plots: Boxplot



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Endless plotting possibilities



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Popularity of American names in the previous 30 years





The more you know...





How to get help

> ?boxplot

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Reproducible reports with Rmarkdown





Rmarkdown reports

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Workflow method

Our workflow relies on the nf-core ATAC-seq pipeline v1.2.2.

Briefly, reads were mapped to the reference genome using bwa and peaks were called for each sample independently using MACS2. Sample-specific peaks were combined into a consensus peak-set with bedtools. featurecounts was used to count the number of reads relative to the consensus peak-set across all samples. The resulting raw count matrix served as input to DESeq2 for differential accessibility analysis. Downstream analyses, including plotting and GSEA, were performed in R.

A detailed results description can be found under pipeline_info/results_description.html. A full list of software versions can be found at pipeline_info/software_versions.csv

Output files

The workflow generates a directory of files: atacseq-results.

Interactive reports with Rmarkdown

Workflow method Output files

Summarv

Visualizations

Gene set enrichment analysis

ATAC-seq Report

Generated by Lurie Bioinformatics 2023-06-02

Workflow method

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Output files

The workflow generates a directory of files: atacseq-results.

```
atacseq-results

peakannotatedresults.xlsx

bigwig

...

sample>.mLb.clN.bigWig

DiffAnalysis

consensus_peaks.mRp.clN.annotatePeaks.txt
```

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Questions?

