Introduction to R

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Overview

- Intro
- Goals
- Lab
 - R Basics

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 - Next week (fingers crossed)

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- git
 - Best to wait for groups to be formed
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- I'll upload my finished document after class as a reference

Today's Goals

- Get familiarized with R basics
- Import your own data
- Visualize it
- Test something about it
- Produce a graph and save the code

Variables

- Notes and tips go here
- Descriptions of actions not meant to be typed

within these boxes will be typed into R
it will also have monospaced font
> it may also begin with a carat character,
which symbolizes the prompt
when it is italicized, it is output from R

<ロ > ← □

Variables

- Scalars, Vectors, Data Frames
- Access parts of each with brackets:

```
> a <- c(15,12,10,93)
> a[2]
12
```

Variables |

or multiple parts at once with a second vector

```
> a <- c(15,12,10,93)
> a[c(2,4)]
12 93
```

Variables

or with a TRUE/FALSE vector

```
> a <- c(15,12,10,93)
```

> a[c(FALSE,TRUE,TRUE,FALSE)]

12 93

Variables & Math

Scalar mathematical operations apply to an entire vector

```
> a * 5
75 60 50 465
```

Variables & Math

 Vector mathematical operations apply to each entry

```
> a + c(1,1,10,-50)
16 13 20 43
```

- This is useful because it allows you to manipulate entire sets of data at once
 - Take the absolute value of a column
 - Combine columns to create new measures
 - Plot the log(value) of a dataset instead of the raw value

Data Frames and Matrices

- Used to hold data
- Can keep track of large sets of data
- Like the data from the hypoxia example

Data Frames and Matrices

- Can also be accessed with brackets []
 - Brackets require 2 entries instead of 1
 - because the data has two dimensions
- dataframe[row,column]
- For example, access a column of the data with brackets:
- > hypoxiaTested[,1]
 [1] TIMM TIMM TIMM TIMM
 - (leaving either row or column blank returns the entire range)

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- How would you go about answering this question?

?read.table

R Documentation read.table (utils) Data Input Description Reads a file in table format and creates a data frame from it, with cases corresponding to lines and variables to fields in the file Usage read.table(file, header = FALSE, sep = "", quote = "\"'", dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"), row.names, col.names, as.is = IstringsAsFactors, na.strings = "NA", colClasses = NA, nrows = -1, skip = 0, check.names = TRUE, fill = !blank.lines.skip, strip, white = FALSE, blank, lines, skip = TRUE, comment.char = "#", allowEscapes = FALSE, flush = FALSE, stringsAsFactors = default.stringsAsFactors(), fileEncoding = "", encoding = "unknown", text, skipNul = FALSE) read.csv(file, header = TRUE, sep = ",", quote = "\"", dec = ".", fill = TRUE, comment.char = "", ...) read.csv2(file, header = TRUE, sep = ";", quote = "\"", dec = ".", fill = TRUE, comment.char = "", ...) read.delim(file, header = TRUE, sep = "\t", quote = "\"", dec = ".", fill = TRUE, comment.char = "", ...) read.delim2(file, header = TRUE, sep = "\t", quote = "\"", dec = ",", fill = TRUE, comment.char = "", ...) Arguments file the name of the file which the data are to be read from. Each row of the table appears as one line of the file. If it does not contain an absolute path, the file name is relative to the current working directory, getwd(). Tilde-expansion is performed Console ~/ @ > ?read.csv

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 - file name of file to bring in, can include location
 - "filename.txt" or "/Users/ryan/Documents/filename.txt"

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```
> read.table(''hsap_hypoxia_gene_exp_FORCLASS.diff'',
header = TRUE, dec = ''.'')
gene_family sample_1 sample_2...
1 TIMM hypo norm...
```

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> hypoxiaRAW <- read.table(''hsap_hypoxia_gene_exp_FORCLASS.diff'',
header = TRUE, dec = ''.'')</pre>
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```

Was there output from the command? Why or why not?

Data Frames & Matrices

- In addition to brackets to access parts of a data frame you can also use the \$ in combination with the column name:
- - Gives the same as using [,1] next to hypoxiaTested
 - However it has several advantages
 - Clearer in code, so you recognize it later
 - You can use the TAB key to pick a column name within R-Studio

Data Frames & Matrices

- Another useful way to use the \$ is to add new data to an existing data frame
- Simply generate data and define it as a new column name:

```
> hypoxiaTested$r_value <- ( hypoxiaTested$p_value +
hypoxiaTested$q_value ) / 2</pre>
```

- What variables did I manipulate?
- What is the new "r value" column I created?

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A Simple T-Test

 To conduct a simple T-Test I'm going to generate some random, normal data:

(pick your own values for the n and mean to fill out the class chart)

```
> meanzero <- rnorm(100,0,1)
> meanthree <- rnorm(100,3,1)</pre>
```

• How would I confirm that this data is normally distributed?

A Simple T-Test

 To conduct a simple T-Test use the t.test() function

```
> t.test(meanzero,meanthree,var.equal = T)
Two Sample t-test
data: meanzero and meanthree
t = -21.004, df = 198, p-value < 2.2e-16</pre>
```

Bring in your own Data

- Pick some data from the github
- Bring it into a session of R
- Make sure the column names are correct
- Make sure R interprets numbers correctly
 - What do I mean by this?
 - How does one do this?

Bring in your own Data

- Pick some data from the github
 - Biology Data:
 - hsap_hypoxia_gene_exp_FORCLASS.diff
 - Political Data:
 - 2008to2016PresElections.csv
 - Movie Data:
 - movie_metadata_genre_FORCLASS.csv
 - Sports Data:
 - NCAA_BBall_KenPom_summary17.csv
 - NFL_game_scores.csv, Game_Logs_Quarterback.csv, Career_Stats_Passing.csv
- or Choose your own!



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- Decide on a pair of variables to test with a T-Test

Test the Data

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- Add a plot to show the T-Test results

The End