Day 3, Session 1: R and RStudio basics

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Learning objectives

By the end of this session, you should be able to

- **organize** your files for a data analysis
- **download** data from the internet
- **load** data into an R workspace
- **explore** your data (subset, index, plot, summarize)
- **load** R packages

Goals

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This module is meant to give you a space to engage with R and RStudio prior to diving into coursework. **All R functions required for your courses will be introduced in the specific course**.

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This workspace is a **folder** on your computer that:

- is easy for you to find **now**
- will be easy for you to find in the **future**
- will hold **all relevant files** for your analysis (e.g., the data file, R code, plots, results)

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2. set up a new folder for the project
    - under *Courses* if it relates to a course, e.g., `Courses/BIOST511`
    - under *the name of the project* if not, e.g., `Projects/HPTN063` refers to a clinical trial I have worked on

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   - under *the name of the project* if not, e.g., `Projects/HPTN063` refers to a clinical trial I have worked on
3. store all documents, data, code, and output in this folder (with subfolders for each of these)

Downloading data

The datasets for your coursework will typically be found either

- on **Canvas**, the UW's file-hosting site for courses, or
- on your professor's webpage, or
- on the webpage for a textbook

Your instructor will tell you **exactly where** to find the datasets necessary for your coursework.

Once you have set up a folder (workspace) for your project, download the data into this folder.

Exercise: downloading data

Create a new folder titled `fev_analysis` in the folder you are using for the files for this workshop.

Next, go to the Canvas webpage for this workshop and download the file `fev.txt`, located in the `Data` folder under the `Files` tab. Download these data into the `fev_analysis` folder.

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RStudio is a program that makes it easier to interact with R to perform your analysis.

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Once you have set up a workspace on your computer for your new project, and downloaded your data, it's time to use R!

R is a statistical programming language, and does all of the computing for your analysis (e.g., plots, summaries).

RStudio is a program that makes it easier to interact with R to perform your analysis.

I suggest that you **only interact with R through RStudio** – this is all you need for your Biostatistics coursework.

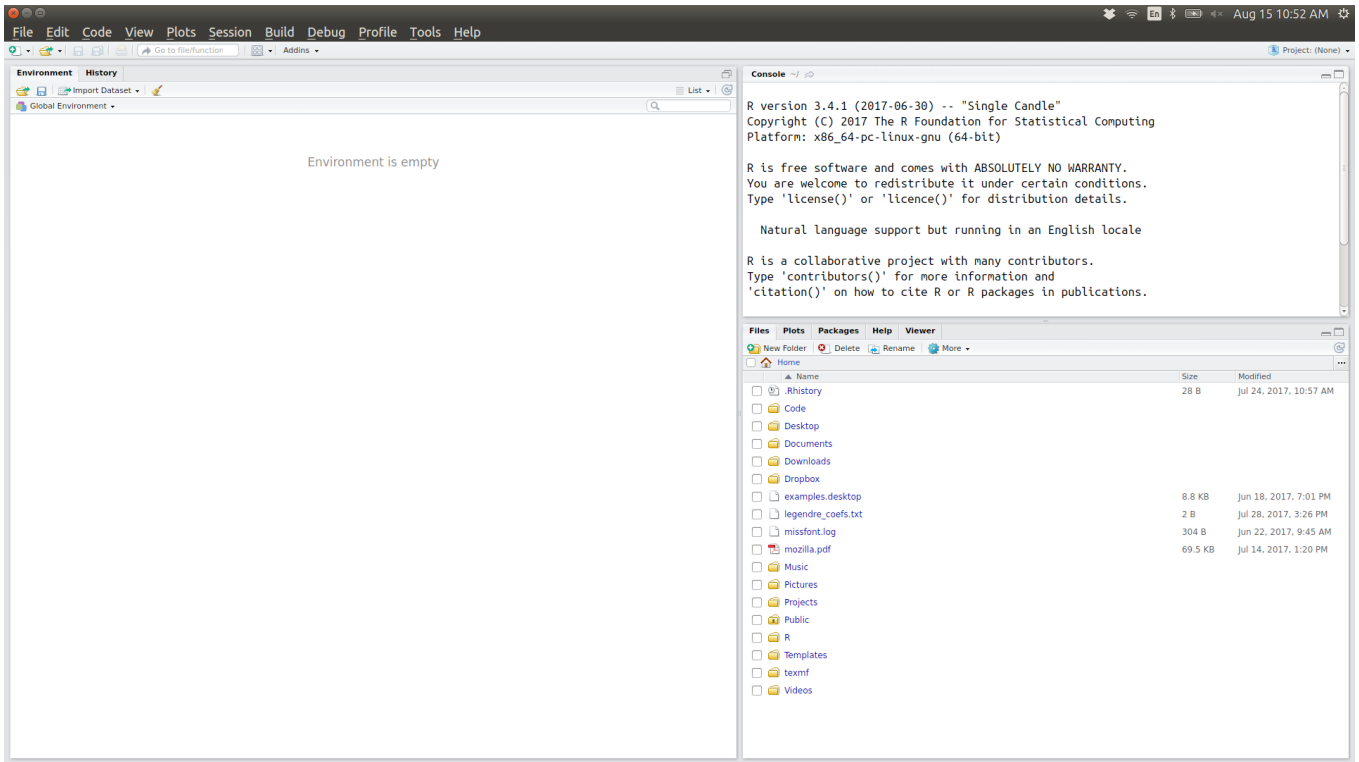
Using R and RStudio: the interface

We interact with both R and RStudio using an interface. For R, this is the command line. For RStudio, this is the graphical user interface.

Both of these concepts deserve a bit of introduction, since familiarity with the interface makes using R and RStudio much easier!

Using R and RStudio: RStudio

When you first open RStudio, you are met with a blank set of four panes:



Using R and RStudio: RStudio

You can edit pane layout under `Tools > Global Options > Pane Layout`. My preference is to have the source in the upper left, console in the upper right, environment in the lower left, and viewer in the lower right.

You'll notice that on the previous slide, there were only three panes visible: since we haven't opened or created any files to edit, the source pane is not currently open.

RStudio: the console

The console is our interface to the R command line.

Any commands that we wish to enter go through the console, and any results that are output by these commands will appear in the console.

Example: the console

Typing `47` at the > symbol (from now on, called the execution line) and hitting `Enter` on the keyboard yields the following:

```
> 47
[1] 47
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Since R is a functional programming language, typing `47` and hitting `Enter` is the same thing as using the `print()` function:

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Since R is a functional programming language, typing `47` and hitting `Enter` is the same thing as using the `print()` function:

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[1] 47
```

The output is displayed as a vector, one of the fundamental data structures in R. The `[1]` helps to tell which element of the vector we are looking at (which is most useful if the vector spans multiple lines in the console).

Exercise: the console

Use the RStudio console to perform the following computations. Write down your answers and your process for arriving at your answers.

1. Multiply 55 and 389
2. Divide 500 by 15
3. Add 1525 and 3225

Exercise: the console

You just used your first R functions!

The *, + and −, and / symbols on your keyboard operate (unsurprisingly) as R functions to multiply, add and subtract, and divide.

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For more complicated analyses, this can lead to a lot of confusion. Also, typing only in the console can lead you to forget what steps you took to get a certain figure or table.

Organizing commands into scripts allows you to save exactly what you did during a given data analysis, which makes reproducible research easy. This helps both your future self and your collaborators, so that you can share what you did!

RStudio: the text editor ("Source")

The text editor (which RStudio calls the source) is the second most powerful part of the IDE. This allows us to edit and save files, and to run commands directly from the text file into the console.

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To create a new R script, either type `Ctrl+Shift+N` or go to `File > New > R script`. There are many other options here (most notably R markdown, which we won't cover but is incredibly useful). This brings up the source pane.

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At the top of the source pane are a set of buttons (with associated keyboard shortcuts) that will save the current file, run sections of code, or run the entire document.

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```
##############################################################################
##
## FILE: <insert file name here>.R
##
## CREATED: <insert date here> by <your name here>
##
## PURPOSE: <Give a brief description of what the code in this file is supposed to do>
##
## INPUTS: <What inputs? Where does the data come from?>
##
## OUTPUTS: <What outputs? Plot/table names and locations>
##
## UPDATES:
## DDMMYY INIT COMMENTS
## ------ ---- --------
## <date> <inits> <What did you change?>
##############################################################################
```

Running commands from R scripts

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- hitting the green `Run` button, or
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Similarly, you run multiple lines by highlighting all desired lines and doing one of the two options described above.

Example: heights and weights

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Save this R script as `ht_wt_analysis.R`. This is a start to analyzing these data! The script now looks like this:

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```
################################################################################
##
## FILE: ht_wt_analysis.R
##
## CREATED: 24 September 2018 by Brian Williamson
##
## PURPOSE: Learn some R basics using height and weight data on 5 imaginary individuals
##
## INPUTS: None
##
## OUTPUTS: None
##
## UPDATES:
## DDMMYY INIT COMMENTS
## ------ ---- --------
################################################################################

ht <- c(72,65,84,73,68)
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The `Global Environment` is where commands that are executed in the console typically live — intermediate objects created within functions (but not returned) live within function-specific environments.

The full command history for a given session is accessed in the `History` tab; this can be cycled through in the console using the up/down arrow keys.

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Execute the commands in `ht_wt_analysis.R` using one of the two options we described earlier (`Run` button or `Ctrl/Cmd+Enter`).

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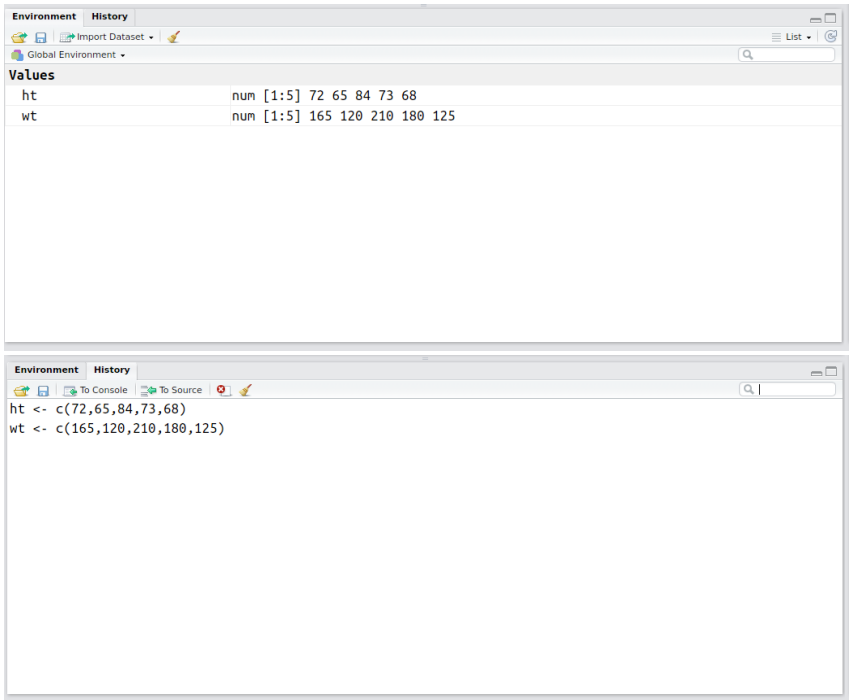
The environment pane then shows that `ht` and `wt` are `Values` (not data sets since they are vectors), and the history pane shows that we have input these two lines into the console.



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We will cover packages and help files later on.

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You have a file called `ht_wt_analysis.R`, located in the `Epi-Biost-Workshop` directory, which is a subdirectory of `UW`, which is a subdirectory of `Documents`, which is part of your home directory. If you double-click `ht_wt_analysis.R`, which opens RStudio to edit the document, your current working directory is `<your home>/Documents/UW/Epi-Biost-Workshop`.

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  3. Click `Set as working directory`
- Using code:
  1. Find the path to the folder where your data resides (e.g., `/home/brian/Documents/UW/Epi-Biost-Workshop`)

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  3. Click `Set as working directory`
- Using code:
  1. Find the path to the folder where your data resides (e.g., `/home/brian/Documents/UW/Epi-Biost-Workshop`)
  2. Place the code `setwd("<path to your data>")` in your R script, or enter it at the command line

Introduction to R programming

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We have already seen some examples of R programming: in the heights and weights example, we learned about the special <- command, which assigns a value to an object; and we learned about the `c()` command, which creates a vector.

These commands relate functions to objects – both of these are fundamental concepts in R programming.

Functions

R functions take in arguments and return values. A function is accessed by typing its name, followed by an open and closed set of parentheses: e.g., `quantile()`, a function to compute desired sample quantiles (e.g., minimum, median, maximum).

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Arguments to functions go between the parentheses, and are separated by columns. You specify which object corresponds to which argument using =, e.g., `quantile(x = ht, probs = 0.5)` returns the median value of the `ht` object.

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Values are returned by functions, and are generally either a combination of objects, plots, and printout. The value of the result of entering `quantile(x = ht, probs = 0.5)` into the console is a vector containing the number 72.

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Both `ht` and `wt` are objects; we created them by manipulating raw numbers using the `c()` function.

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The menus and buttons ultimately call a function; each data storage type (e.g., `.txt`, `.csv`, `.sas7bdat`, `.dta`) has its own function (and some functions come from special packages).

Regardless of how you load the data, once done it will show up in your environment. It can then be manipulated to display summary statistics, make plots, or do more complex analyses.

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6. Click `Import`

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Loading data: buttons

1. In the `Environment` pane, click `Import Dataset`
2. Select the type of data from the menu (e.g., `From CSV`)
3. Browse to the directory or website where the data are stored
4. Specify any input options
5. Edit the `Code Preview` section to rename the object, if necessary
6. Click `Import`

Loading data: menus and buttons

Regardless of whether you use a menu or button to import data, there was a step where you had to look at the `Code Preview` box. When you click the `Import` button, this code is executed in the console, and the dataset shows up in your environment.

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This means that, under the hood, both methods use R code to import data!

Also, both of these methods are hard to reproduce: each time you want to analyze a dataset (which may be multiple times on a problem set or during the course of a project/paper), you have to click through these buttons.

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Also, both of these methods are hard to reproduce: each time you want to analyze a dataset (which may be multiple times on a problem set or during the course of a project/paper), you have to click through these buttons.

To make your code fully reproducible, embed the code to load the data directly in your R script! While this involves finding the correct functions, at the end of the day you have more control over how your data are handled.

Loading data: functions

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4. Run this line to load the data

Loading data: common functions and packages

File extension	Package	Function
.txt	utils (always loaded)	read.table()
		read.delim()
	readr	read_table()
		read_delim()
.csv	utils	read.csv()
	readr	read_csv()
.dta	haven	read_stata()
.sas7bdat	haven	read_sas()
.xlsx	readxl	read_excel()
.Rdata	base (always loaded)	load()
.Rds	base	readRDS()

Exercise: Reading in data

Load the height and weight data by placing the following code in your R script `ht_wt_analysis.R` (replace `<path to here>` with the path to your folder):

```
dat <- read.table("<path to here>/Epi-Biost-Workshop/
                  day_3_session_1/data/ht_wt_data.txt",
                   header = TRUE)
```

Look at the data by typing `View(dat)` on a new line in your R script, and executing the line in R.

What do you notice about this new dataset? How does it relate to the two vectors `ht` and `wt` that we created earlier?

Exercise: reading data

Now read in the FEV data, again using the function `read.table`. *Hint: you may copy the code from the height and weight example, but you will have to change the path to the data*.

Again, use the `View()` function to take a look at the data, and answer the following questions:

1. How many columns do the data have?
2. Write down what you think the meaning of at least 3 of the variables is, based on the column names.

Manipulating data

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By manipulating the columns of a data frame we create new variables or change existing ones; and by manipulating the rows of our data we restrict our attention to different subsets of the observations.

Manipulating data: accessing values in vectors

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To access a continuous range of elements *i* through *l*, use square brackets with a colon; `vec[i:l]` accomplishes this. For example, `ht[1:4]` returns the first four elements of `ht`.

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To access a set of elements (*i*, *k*, *n*), use square brackets with `c()`; `vec[c(i, k, n)]` accomplishes this. For example, `ht[c(1, 3, 5)]` returns the first, third, and fifth elements of `ht`.

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For example, in the heights and weights data, `dat[1, 2]` returns the weight of the first individual.

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For example, in the heights and weights data, `dat[1, 2]` returns the weight of the first individual.

We can use the same rules as those for vectors to select groups of rows and/or columns.

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- the column number; `dat[, 2]` returns the variable `y` from `dat`
- the column name; `dat[, "y"]` returns the variable `y` from `dat`

The methods using the square brackets introduce a new concept: we are selecting all rows from `dat` (since there is nothing between the first bracket and the comma), and are selecting certain columns from `dat`.

Manipulating data: subsetting data frames

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The common logical operations are:

Operation	Meaning	Result
|	or	`TRUE` if any argument is `TRUE`
&	and	`TRUE` only if all arguments are `TRUE`
!	negation	`FALSE` if argument returns `TRUE`, `TRUE` else
==	equals	`TRUE` if the two arguments are equal

We can also make comparisons, using $<$, $>$, $<=$, $>=$.

Example: heights and weights

The following code loads the data as a data frame, and then: prints out the height column, and displays the data from participants whose weight is below 160 lbs (replace <path to here> with your own path):

```
## load using read.table
dat <- read.table("<path to here>/Epi-Biost-Workshop/
                  day_3_session_1/data/ht_wt_data.txt", header = TRUE)
## print out the height column multiple ways
dat$height
dat[, "height"]
dat[, 2]

## print out the observations with weight under 160
dat[dat$weight < 160, ]
```

Exercise: manipulating data

These questions all pertain to the `fev` data.

1. The logical expression `fev$age <= 8` returns `TRUE` for those individuals who are less than or equal to 8 years old, and `FALSE` for those who are older than 8 years old. Create a new dataset called `sub_less_equal_8` that contains the data for all participants with age less than or equal to 8 years old.
2. What does `fev$sex == 1` return?
3. The `$` allows you to both access variables and create new variables within a dataset. Create a new variable called `fev$female` that takes value 0 if the participant is male and 1 if the participant is female, using the command `fev$female <- ifelse(fev$sex == 1, 0, 1)`. What is the sex of the participant with `fev$subjid == 451`?

Summarizing data

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Two powerful ways of summarizing the data are:

- summary statistics (e.g., mean, median)
- graphical summaries (e.g., boxplots, scatterplots)

Computing summary statistics

Quick summary statistics are available in R using the `summary()` function. This function automatically computes the minimum, mean, maximum, and 25th, 50th (median) and 75th percentile values of each variable in your data.

Example: heights and weights

```
summary(dat)
```

Plotting data

Quick plots are also powerful ways to convey information and get a glimpse at trends in the data.

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The two main arguments, `x` and `y`, tell R the data to plot on the x- and y-axis, respectively. Other arguments help to make the plot understandable by adding informative labels and titles.

Example: heights and weights

```
# plot of height (on x-axis) vs weight
plot(dat$height, dat$weight)
```

Exercise: summarizing data

All of these questions involve either the full `fev` data, or the subset of participants with age less than or equal to eight years old `sub_less_equal_8`.

1. What is the average age of participants in the `fev` data?
2. What is the proportion of subjects that are female? That are male?
3. What is the average FEV measurement in the full data?
4. What is the average FEV measurement in those who are less than or equal to eight years old?
5. If your answers to 3 and 4 are different, why do you think that is?
6. Plot FEV on the y-axis versus age on the x-axis for the full data. What do you notice about the trend between age and FEV? Does that help you answer 5?

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However, some packages are always loaded each time you open R. These are `stats`, `graphics`, `grDevices`, `utils`, `datasets`, `methods`, and `base`.

Finding new R packages

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You can install packages from CRAN using `install.packages()`; from Bioconductor by first running `source("https://bioconductor.org/biocLite.R")` and then using `biocLite()`; and from GitHub using the function `install_github()` from the `devtools` package.

Example: heights and weights

The following code reads in the height and weight data using the `read_table()` function from `readr`:

```
## install if necessary
# install.packages("readr")
## load the package; do this each time you re-open R!
library("readr")
## read in the data
dat <- read_table("<path to here>/Epi-Biost-Workshop/
                  day_3_session_1/ht_wt_data.txt", header = TRUE)
```