Introduction to RStudio Server

The CCDL

The following two analysis examples are both microarray differential expression analyses.

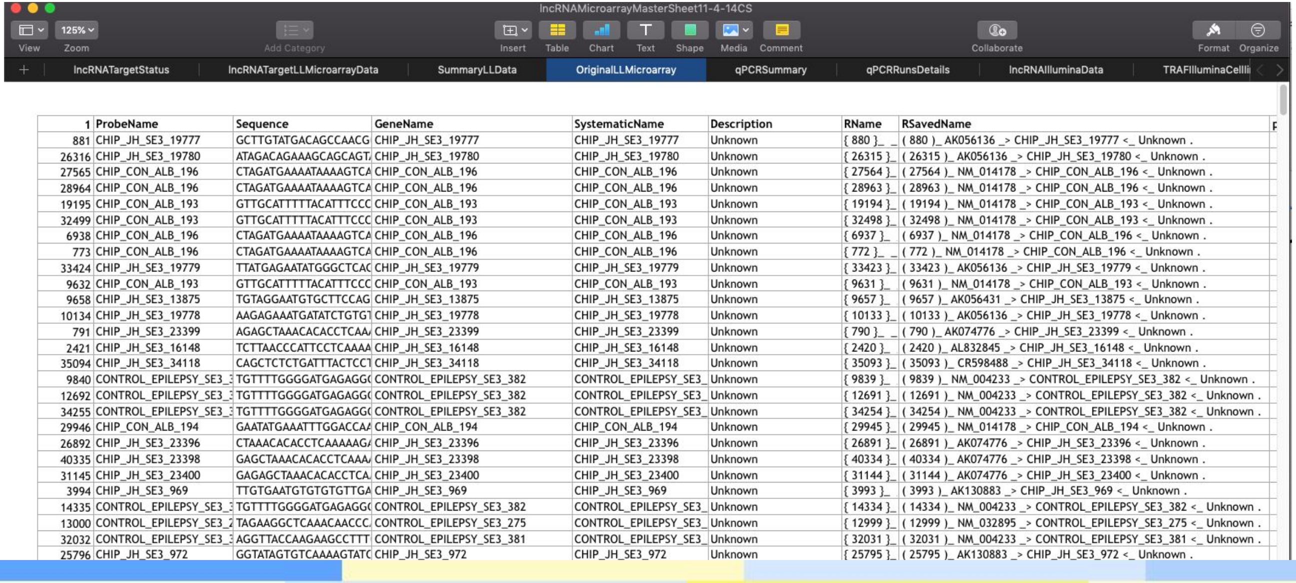
Differential Analysis Example 1: “100% Up to Date Analysis”

Methods Documentation: ~200 words describe the general methods in a publication. The step-by-step recount of how these data came to be were handwritten, with one copy located in a lab closet.

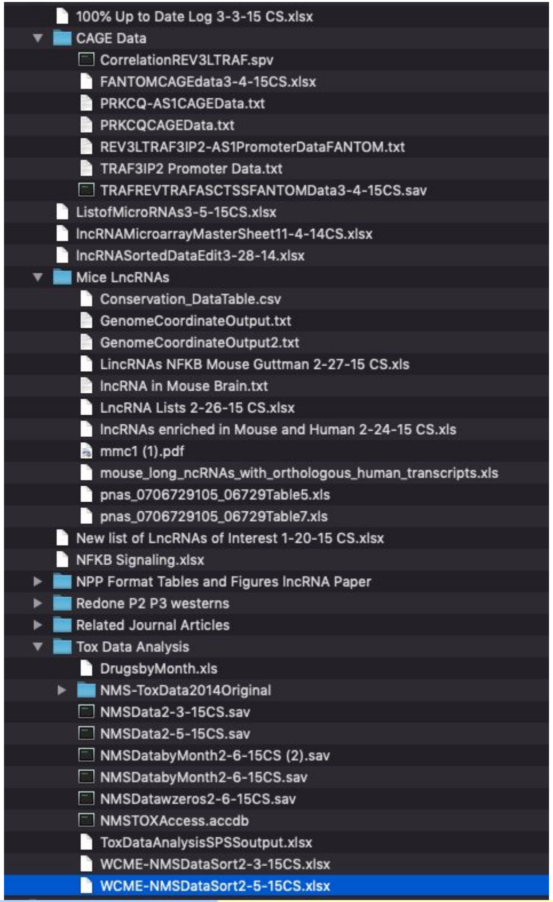
Data availability: The original data are on a flashdrive, in a desk drawer, in a lab. The already processed version is on GEO.

Project organization: Many files with various nebulous terms like “MasterSheet” and “Sorted” and “Edit” and “100% Up to Date”.

Software versions: No idea what software package(s), regardless of version.



1	ProbeName	Sequence	GeneName	SystematicName	Description	RName	RSavedName
881	CHIP_JH_SE3_19777	GCTTGTATGACAGCCAACG	CHIP_JH_SE3_19777	CHIP_JH_SE3_19777	Unknown	{ 880 }_ _	(880)_ AK056136 _> CHIP_JH_SE3_19777 <_ Unknown .
26316	CHIP_JH_SE3_19780	ATAGACAGAAAGCAGCAGT	CHIP_JH_SE3_19780	CHIP_JH_SE3_19780	Unknown	{ 26315 }_	(26315)_ AK056136 _> CHIP_JH_SE3_19780 <_ Unknown .
27565	CHIP_CON_ALB_196	CTAGATGAAAATAAAAGTCA	CHIP_CON_ALB_196	CHIP_CON_ALB_196	Unknown	{ 27564 }_	(27564)_ NM_014178 _> CHIP_CON_ALB_196 <_ Unknown .
28964	CHIP_CON_ALB_196	CTAGATGAAAATAAAAGTCA	CHIP_CON_ALB_196	CHIP_CON_ALB_196	Unknown	{ 28963 }_	(28963)_ NM_014178 _> CHIP_CON_ALB_196 <_ Unknown .
19195	CHIP_CON_ALB_193	GTTGCATTTTTACATTTCCC	CHIP_CON_ALB_193	CHIP_CON_ALB_193	Unknown	{ 19194 }_	(19194)_ NM_014178 _> CHIP_CON_ALB_193 <_ Unknown .
32499	CHIP_CON_ALB_193	GTTGCATTTTTACATTTCCC	CHIP_CON_ALB_193	CHIP_CON_ALB_193	Unknown	{ 32498 }_	(32498)_ NM_014178 _> CHIP_CON_ALB_193 <_ Unknown .
6938	CHIP_CON_ALB_196	CTAGATGAAAATAAAAGTCA	CHIP_CON_ALB_196	CHIP_CON_ALB_196	Unknown	{ 6937 }_	(6937)_ NM_014178 _> CHIP_CON_ALB_196 <_ Unknown .
773	CHIP_CON_ALB_196	CTAGATGAAAATAAAAGTCA	CHIP_CON_ALB_196	CHIP_CON_ALB_196	Unknown	{ 772 }_ _	(772)_ NM_014178 _> CHIP_CON_ALB_196 <_ Unknown .
33424	CHIP_JH_SE3_19779	TTATGAGAATATGGGCTCAC	CHIP_JH_SE3_19779	CHIP_JH_SE3_19779	Unknown	{ 33423 }_	(33423)_ AK056136 _> CHIP_JH_SE3_19779 <_ Unknown .
9632	CHIP_CON_ALB_193	GTTGCATTTTTACATTTCCC	CHIP_CON_ALB_193	CHIP_CON_ALB_193	Unknown	{ 9631 }_	(9631)_ NM_014178 _> CHIP_CON_ALB_193 <_ Unknown .
9658	CHIP_JH_SE3_13875	TGTAGGAATGTGCTTCCAG	CHIP_JH_SE3_13875	CHIP_JH_SE3_13875	Unknown	{ 9657 }_	(9657)_ AK056431 _> CHIP_JH_SE3_13875 <_ Unknown .
10134	CHIP_JH_SE3_19778	AAGAGAAATGATATCTGTGT	CHIP_JH_SE3_19778	CHIP_JH_SE3_19778	Unknown	{ 10133 }_	(10133)_ AK056136 _> CHIP_JH_SE3_19778 <_ Unknown .
791	CHIP_JH_SE3_23399	AGAGCTAAACACACCTCAA	CHIP_JH_SE3_23399	CHIP_JH_SE3_23399	Unknown	{ 790 }_ _	(790)_ AK074776 _> CHIP_JH_SE3_23399 <_ Unknown .
2421	CHIP_JH_SE3_16148	TCTTAACCCATTCCTCAAAA	CHIP_JH_SE3_16148	CHIP_JH_SE3_16148	Unknown	{ 2420 }_	(2420)_ AL832845 _> CHIP_JH_SE3_16148 <_ Unknown .
35094	CHIP_JH_SE3_34118	CAGCTCTCTGATTTACTCCT	CHIP_JH_SE3_34118	CHIP_JH_SE3_34118	Unknown	{ 35093 }_	(35093)_ CR598488 _> CHIP_JH_SE3_34118 <_ Unknown .
9840	CONTROL_EPILEPSY_SE3_3	TGTTTTGGGGATGAGAGG	CONTROL_EPILEPSY_SE3_382	CONTROL_EPILEPSY_SE3_	Unknown	{ 9839 }_	(9839)_ NM_004233 _> CONTROL_EPILEPSY_SE3_382 <_ Unknown .
12692	CONTROL_EPILEPSY_SE3_3	TGTTTTGGGGATGAGAGG	CONTROL_EPILEPSY_SE3_382	CONTROL_EPILEPSY_SE3_	Unknown	{ 12691 }_	(12691)_ NM_004233 _> CONTROL_EPILEPSY_SE3_382 <_ Unknown .
34255	CONTROL_EPILEPSY_SE3_3	TGTTTTGGGGATGAGAGG	CONTROL_EPILEPSY_SE3_382	CONTROL_EPILEPSY_SE3_	Unknown	{ 34254 }_	(34254)_ NM_004233 _> CONTROL_EPILEPSY_SE3_382 <_ Unknown .
29946	CHIP_CON_ALB_194	GAATATGAAATTTGGACCAA	CHIP_CON_ALB_194	CHIP_CON_ALB_194	Unknown	{ 29945 }_	(29945)_ NM_014178 _> CHIP_CON_ALB_194 <_ Unknown .
26892	CHIP_JH_SE3_23396	CTAAACACACCTCAAAAAGA	CHIP_JH_SE3_23396	CHIP_JH_SE3_23396	Unknown	{ 26891 }_	(26891)_ AK074776 _> CHIP_JH_SE3_23396 <_ Unknown .
40335	CHIP_JH_SE3_23398	GAGCTAAACACACCTCAAA	CHIP_JH_SE3_23398	CHIP_JH_SE3_23398	Unknown	{ 40334 }_	(40334)_ AK074776 _> CHIP_JH_SE3_23398 <_ Unknown .
31145	CHIP_JH_SE3_23400	GAGAGCTAAACACACCTCA	CHIP_JH_SE3_23400	CHIP_JH_SE3_23400	Unknown	{ 31144 }_	(31144)_ AK074776 _> CHIP_JH_SE3_23400 <_ Unknown .
3994	CHIP_JH_SE3_969	TTGTGAATGTGTGTGTTGA	CHIP_JH_SE3_969	CHIP_JH_SE3_969	Unknown	{ 3993 }_	(3993)_ AK130883 _> CHIP_JH_SE3_969 <_ Unknown .
14335	CONTROL_EPILEPSY_SE3_3	TGTTTTGGGGATGAGAGG	CONTROL_EPILEPSY_SE3_382	CONTROL_EPILEPSY_SE3_	Unknown	{ 14334 }_	(14334)_ NM_004233 _> CONTROL_EPILEPSY_SE3_382 <_ Unknown .
13000	CONTROL_EPILEPSY_SE3_2	TAGAAGGCTCAAACAACCC	CONTROL_EPILEPSY_SE3_275	CONTROL_EPILEPSY_SE3_	Unknown	{ 12999 }_	(12999)_ NM_032895 _> CONTROL_EPILEPSY_SE3_275 <_ Unknown .
32032	CONTROL_EPILEPSY_SE3_3	AGGTTACCAAGAAGCCTTT	CONTROL_EPILEPSY_SE3_381	CONTROL_EPILEPSY_SE3_	Unknown	{ 32031 }_	(32031)_ NM_004233 _> CONTROL_EPILEPSY_SE3_381 <_ Unknown .
25796	CHIP_JH_SE3_972	GGTATAGTGTCAAAAGTATC	CHIP_JH_SE3_972	CHIP_JH_SE3_972	Unknown	{ 25795 }_	(25795)_ AK130883 _> CHIP_JH_SE3_972 <_ Unknown .



- 100% Up to Date Log 3-3-15 CS.xlsx
- CAGE Data
  - CorrelationREV3LTRAF.spv
  - FANTOMCAGEdata3-4-15CS.xlsx
  - PRKCQ-AS1CAGEData.txt
  - PRKCQCAGEData.txt
  - REV3LTRAF3IP2-AS1PromoterDataFANTOM.txt
  - TRAF3IP2 Promoter Data.txt
  - TRAFREVTRAFASCTSSFANTOMData3-4-15CS.sav
- ListofMicroRNAs3-5-15CS.xlsx
- lncRNAMicroarrayMasterSheet11-4-14CS.xlsx
- lncRNASortedDataEdit3-28-14.xlsx
- Mice LncRNAs
  - Conservation_DataTable.csv
  - GenomeCoordinateOutput.txt
  - GenomeCoordinateOutput2.txt
  - LincRNAs NFKB Mouse Guttman 2-27-15 CS.xls
  - lncRNA in Mouse Brain.txt
  - LncRNA Lists 2-26-15 CS.xlsx
  - lncRNAs enriched in Mouse and Human 2-24-15 CS.xls
  - mmc1 (1).pdf
  - mouse_long_ncRNAs_with_orthologous_human_transcripts.xls
  - pnas_0706729105_06729Table5.xls
  - pnas_0706729105_06729Table7.xls
- New list of LncRNAs of Interest 1-20-15 CS.xlsx
- NFKB Signaling.xlsx
- NPP Format Tables and Figures lncRNA Paper
- Redone P2 P3 westerns
- Related Journal Articles
- Tox Data Analysis
  - DrugsbyMonth.xls
  - NMS-ToxData2014Original
  - NMSData2-3-15CS.sav
  - NMSData2-5-15CS.sav
  - NMSDatabyMonth2-6-15CS (2).sav
  - NMSDatabyMonth2-6-15CS.sav
  - NMSDatawzeros2-6-15CS.sav
  - NMSTOXAccess.accdb
  - ToxDataAnalysisSPSSoutput.xlsx
  - WCME-NMSDataSort2-3-15CS.xlsx
  - WCME-NMSDataSort2-5-15CS.xlsx

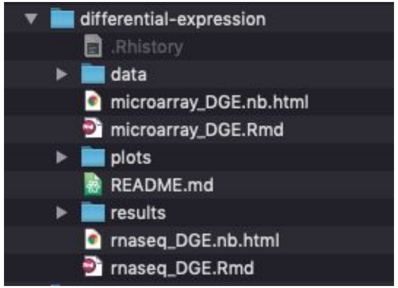
Data Analysis Example 2: “GitHubbed Analysis”

Methods Documentation: Publicly available, online notebooks show step-by-step process that can be re-run.

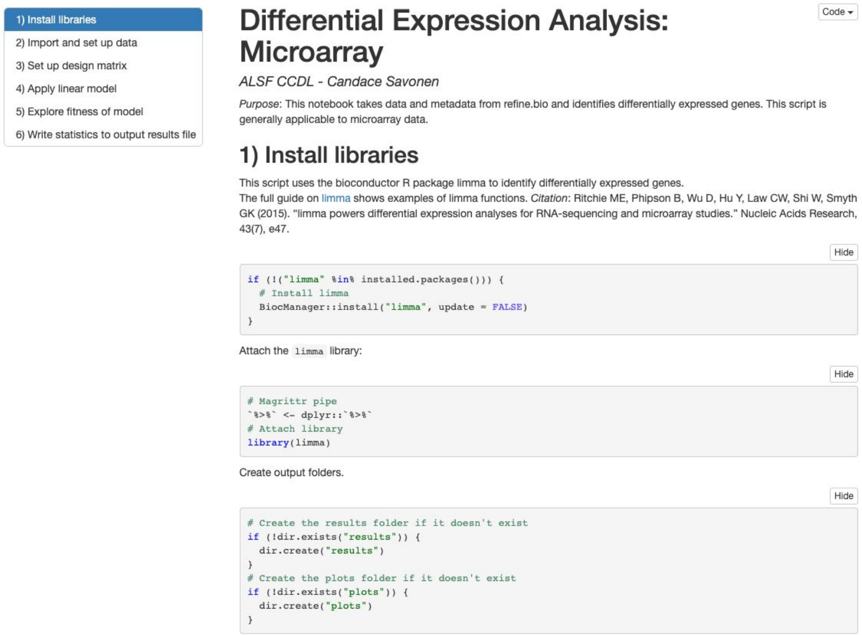
Data availability: Data that was originally used is available for download online.

Project organization: Folders labeled, most recent is present, with prior versions tracked on GitHub.

Software versions: Specific requirements and version numbers shown in notebook and README.



```
▼ differential-expression
    .Rhistory
  ▶ data
    microarray_DGE.nb.html
    microarray_DGE.Rmd
  ▶ plots
    README.md
  ▶ results
    rnaseq_DGE.nb.html
    rnaseq_DGE.Rmd
```



Differential Expression Analysis: Microarray

ALSF CCDL - Candace Savonen

Purpose: This notebook takes data and metadata from refine.bio and identifies differentially expressed genes. This script is generally applicable to microarray data.

1) Install libraries

This script uses the bioconductor R package limma to identify differentially expressed genes.
The full guide on limma shows examples of limma functions. *Citation*: Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK (2015). “limma powers differential expression analyses for RNA-sequencing and microarray studies.” Nucleic Acids Research, 43(7), e47.

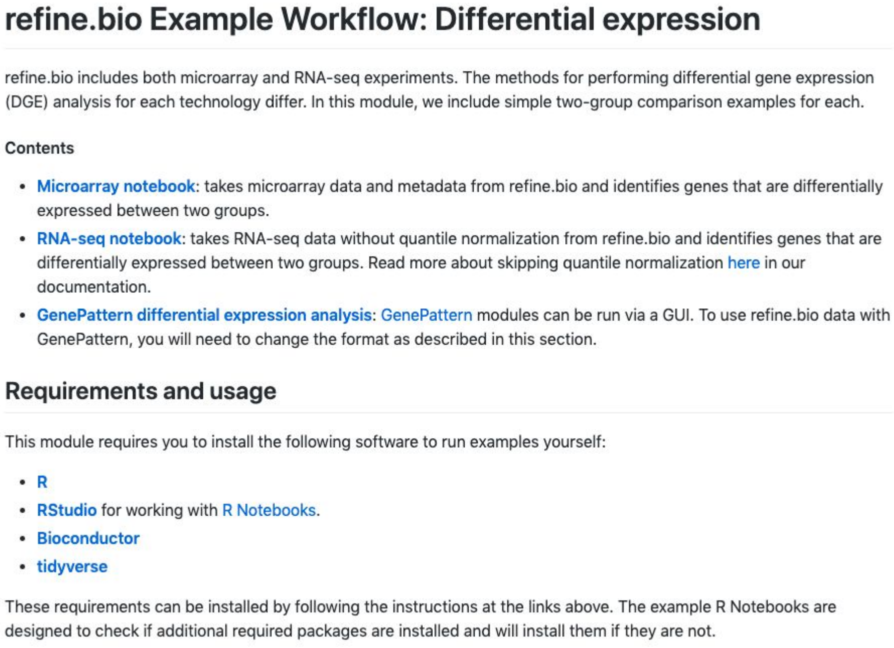
```
if (!("limma" %in% installed.packages())) {
  # Install limma
  BiocManager::install("limma", update = FALSE)
}
```

Attach the `limma` library:

```
# Magrittr pipe
`%>%` <- dplyr::`%>%`
# Attach library
library(limma)
```

Create output folders.

```
# Create the results folder if it doesn't exist
if (!dir.exists("results")) {
  dir.create("results")
}
# Create the plots folder if it doesn't exist
if (!dir.exists("plots")) {
  dir.create("plots")
}
```



refine.bio Example Workflow: Differential expression

refine.bio includes both microarray and RNA-seq experiments. The methods for performing differential gene expression (DGE) analysis for each technology differ. In this module, we include simple two-group comparison examples for each.

Contents

- **Microarray notebook**: takes microarray data and metadata from refine.bio and identifies genes that are differentially expressed between two groups.
- **RNA-seq notebook**: takes RNA-seq data without quantile normalization from refine.bio and identifies genes that are differentially expressed between two groups. Read more about skipping quantile normalization here in our documentation.
- **GenePattern differential expression analysis**: GenePattern modules can be run via a GUI. To use refine.bio data with GenePattern, you will need to change the format as described in this section.

Requirements and usage

This module requires you to install the following software to run examples yourself:

- **R**
- **RStudio** for working with R Notebooks.
- **Bioconductor**
- **tidyverse**

These requirements can be installed by following the instructions at the links above. The example R Notebooks are designed to check if additional required packages are installed and will install them if they are not.

“100% Up to Date Analysis” OR “GitHubbed Analysis”

Which analysis would you...

...be more inclined to borrow the methods from?

...trust the methods of more?

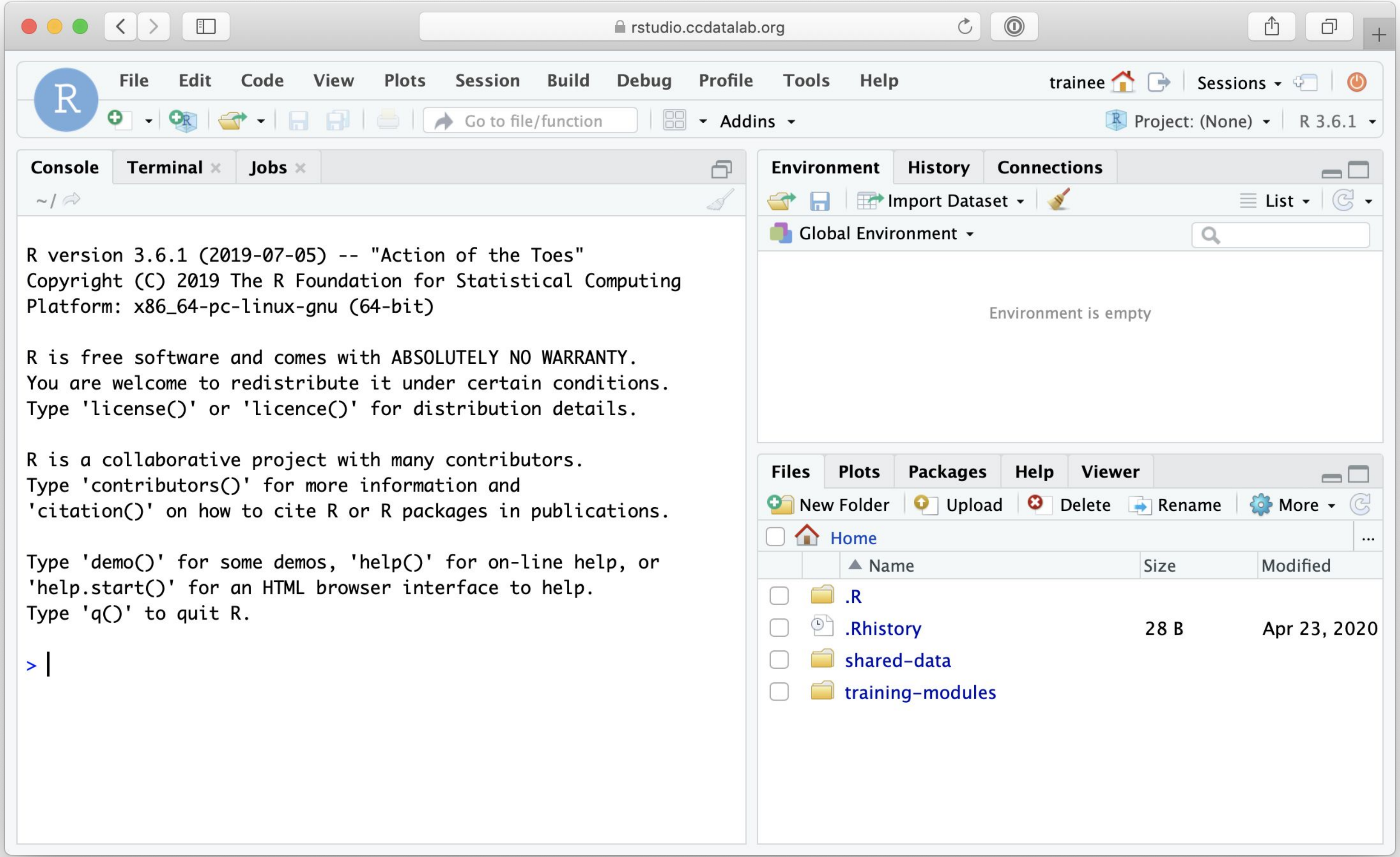
...feel would be *easier to reproduce*?

Command line vs GUI (graphics user interface)

- An interface is how you interact with a program

- GUI’s have buttons you can *click* to do things,
- Command-line interfaces have you *type* out things to do them

RStudio Server: A basic guide



```
R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

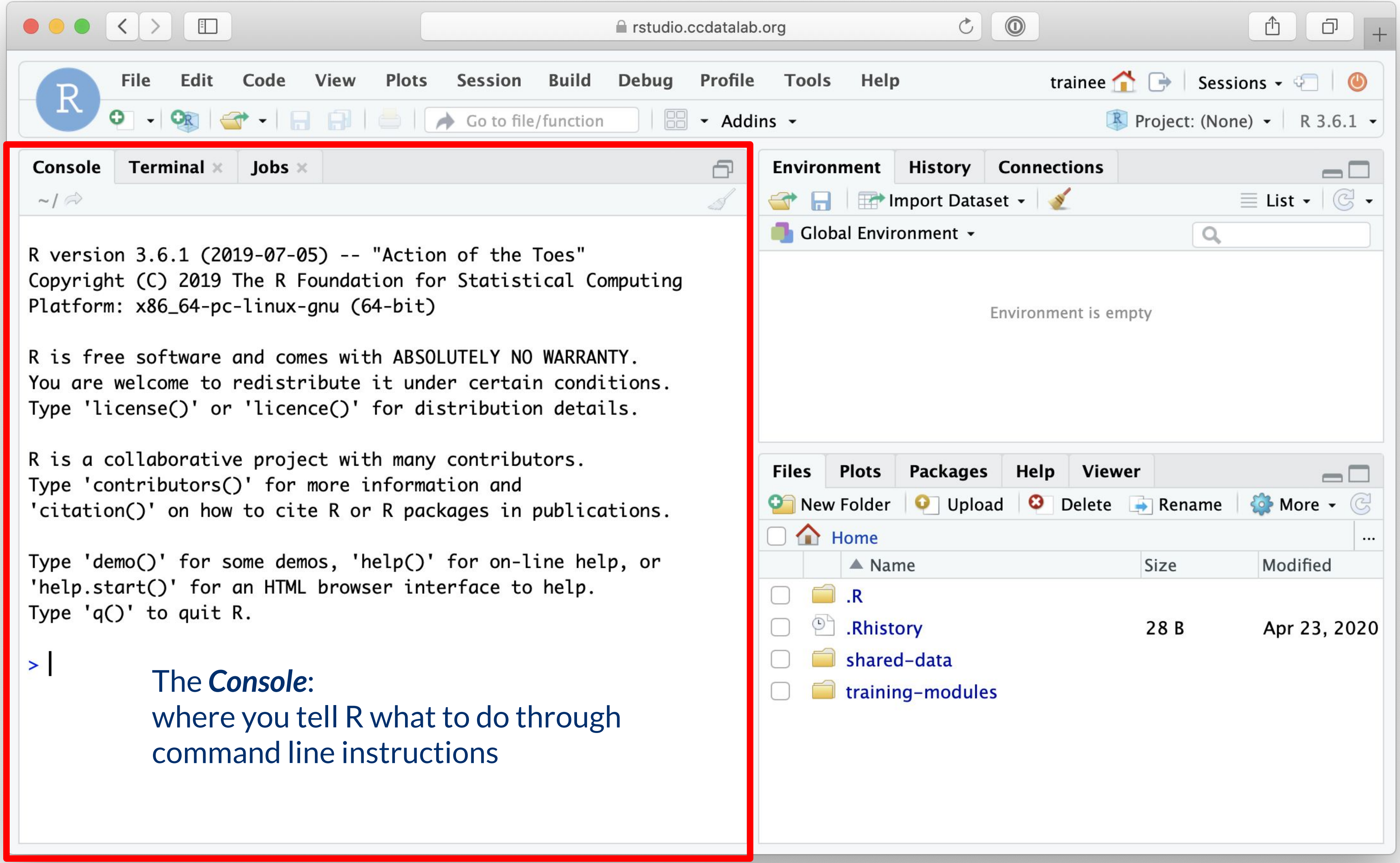
R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 
```

☐	Name	Size	Modified
☐	.R		
☐	.Rhistory	28 B	Apr 23, 2020
☐	shared-data		
☐	training-modules		



```
R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

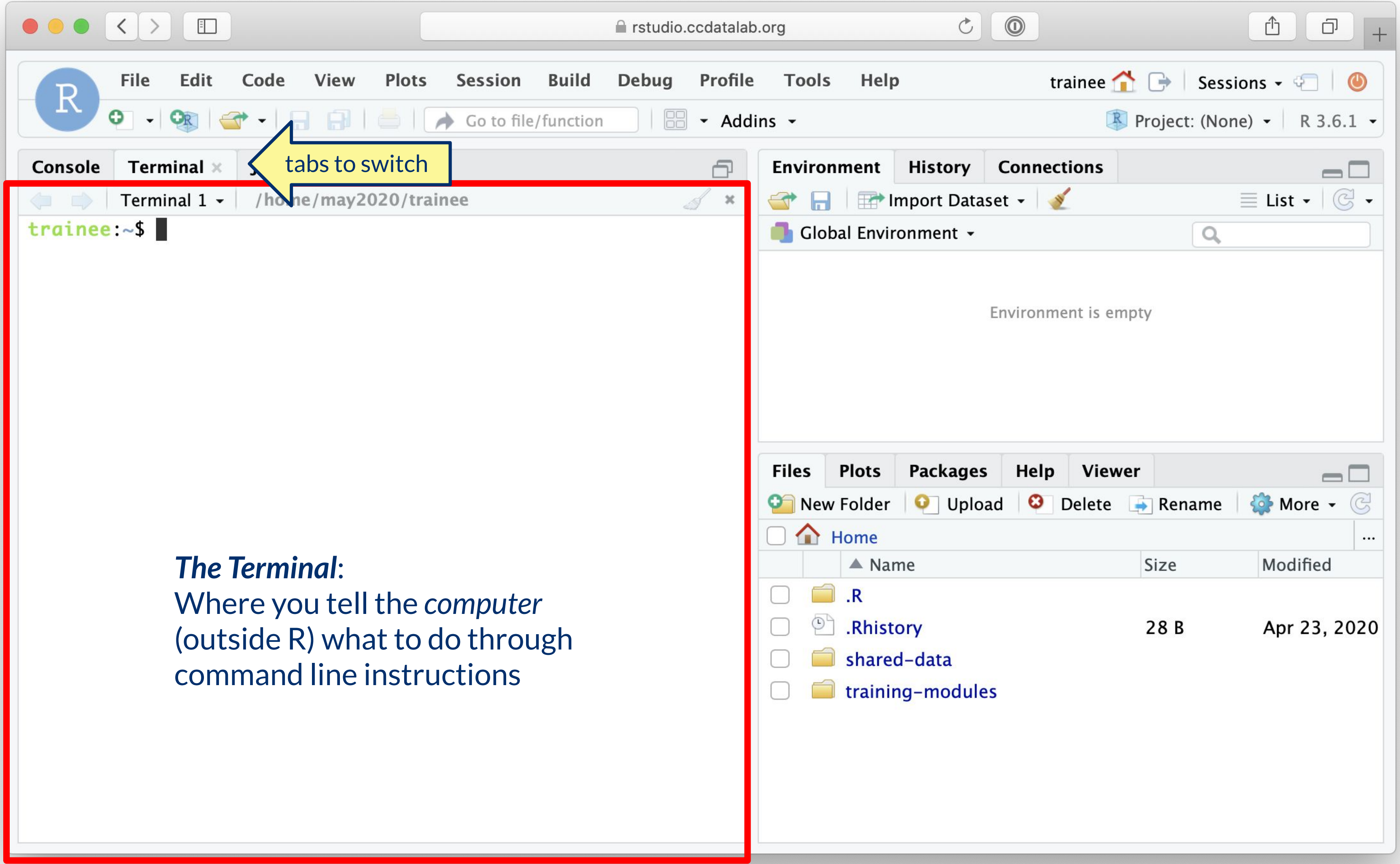
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> |
```

Name	Size	Modified
.R		
.Rhistory	28 B	Apr 23, 2020
shared-data		
training-modules		

The ***Console***:
where you tell R what to do through command line instructions

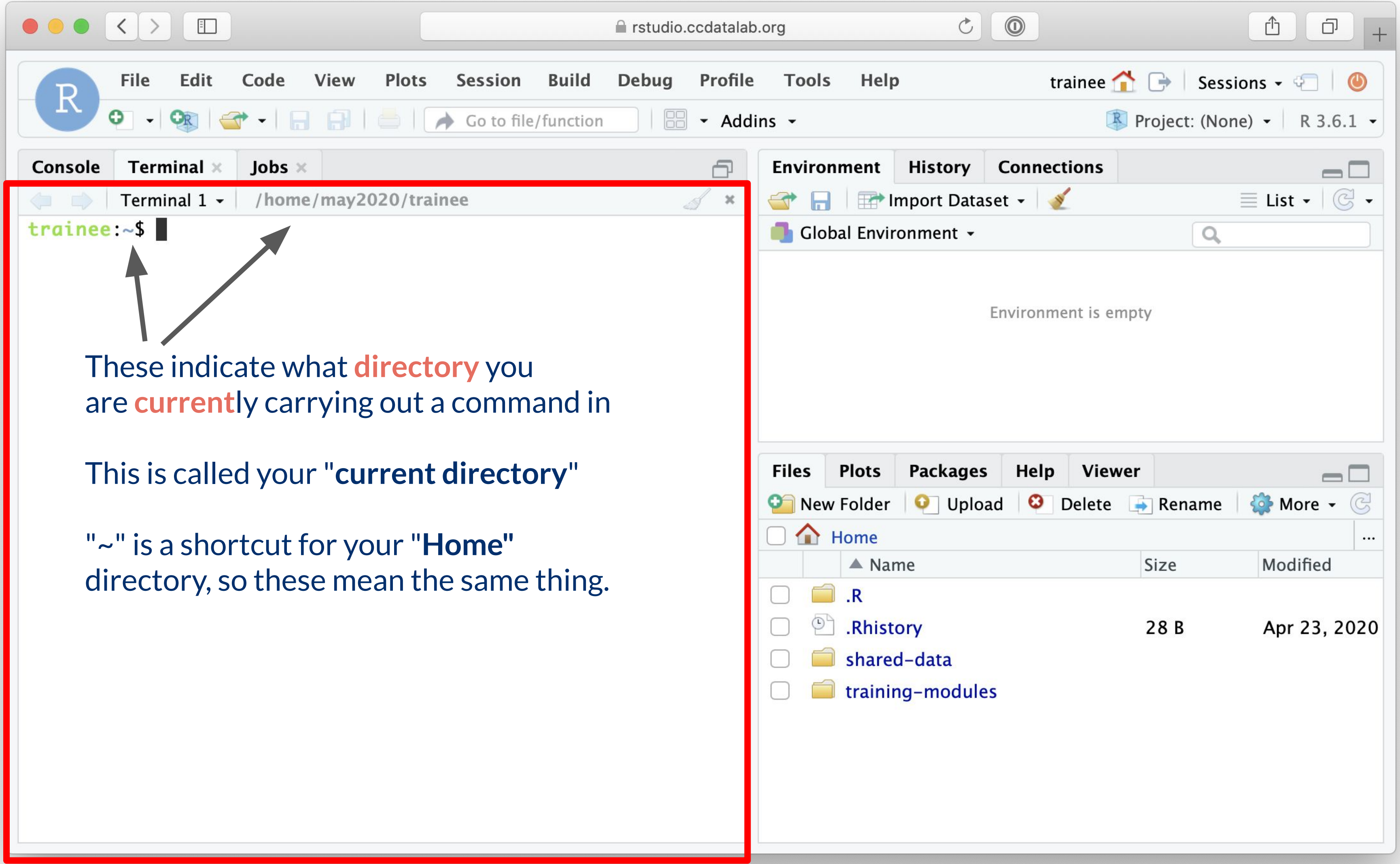


tabs to switch

```
trainee:~$ █
```

☐	Name	Size	Modified
☐	.R		
☐	.Rhistory	28 B	Apr 23, 2020
☐	shared-data		
☐	training-modules		

The Terminal:
Where you tell the *computer* (outside R) what to do through command line instructions



```
/home/may2020/trainee
trainee:~$
```

Environment is empty

These indicate what directory you are currently carrying out a command in

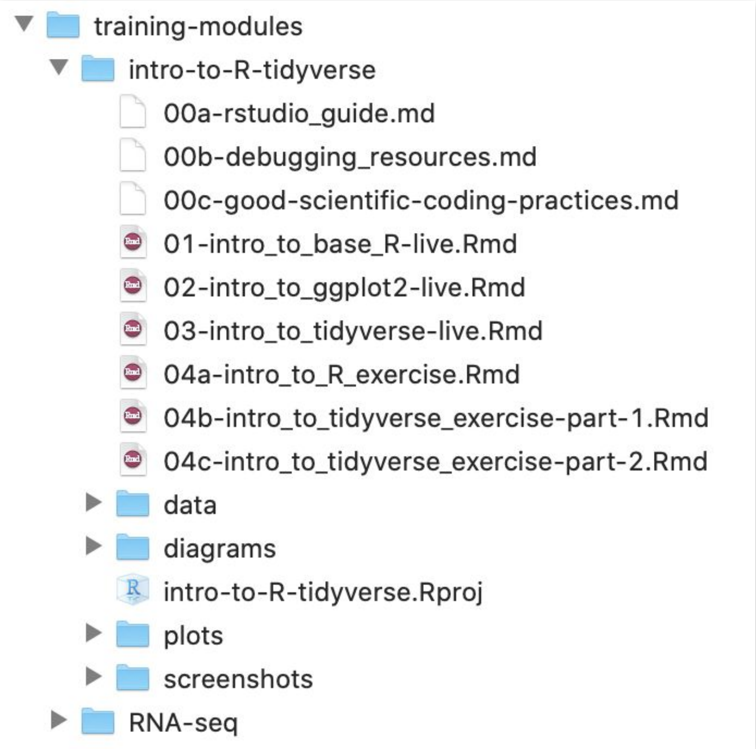
This is called your "**current directory**"

"~" is a shortcut for your "**Home**" directory, so these mean the same thing.

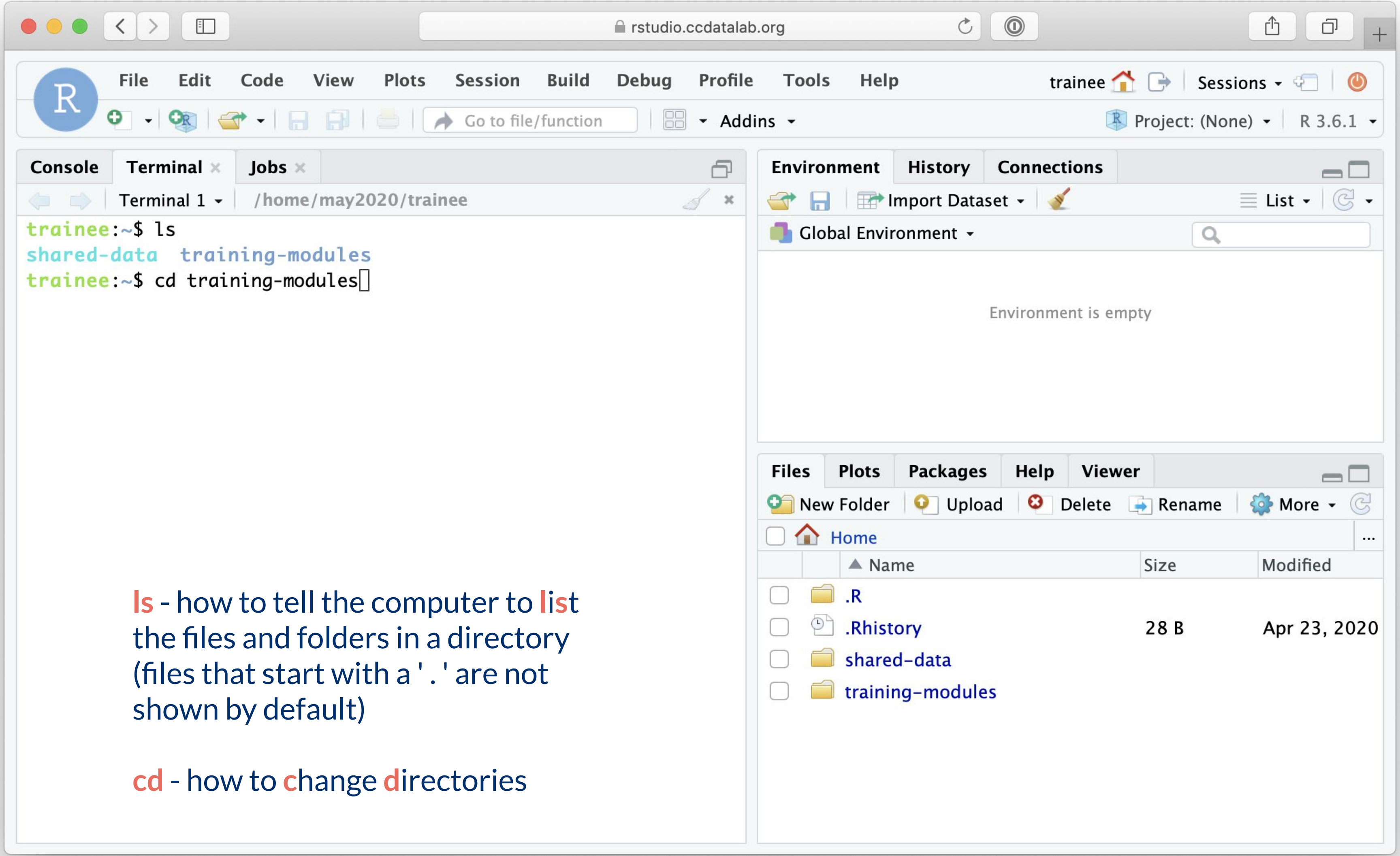
Name	Size	Modified
.R		
.Rhistory	28 B	Apr 23, 2020
shared-data		
training-modules		

Directories = Folders

When we are working on the command line, we have to keep track of where the files we are using are being kept.



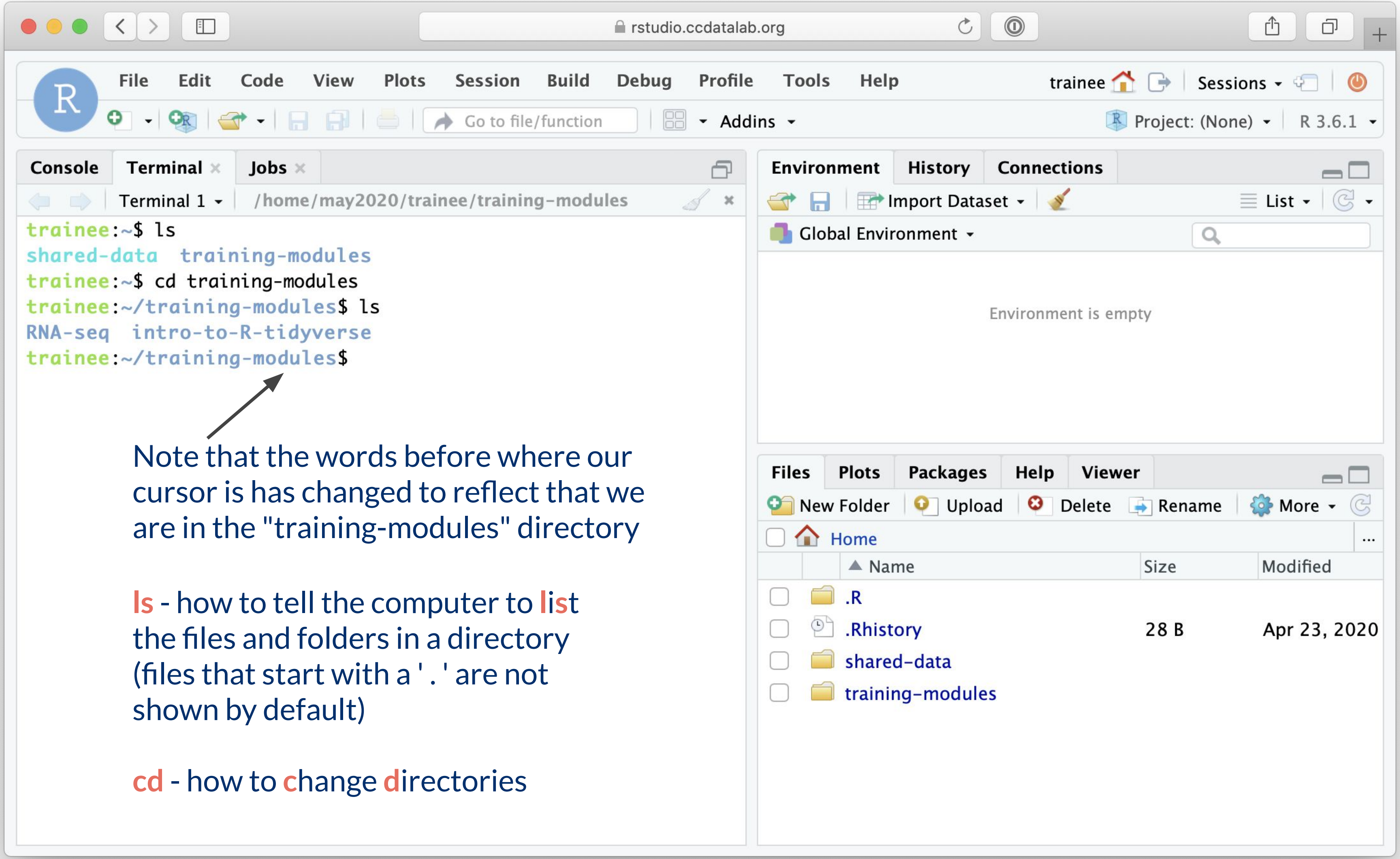
- training-modules
  - intro-to-R-tidyverse
    - 00a-rstudio_guide.md
    - 00b-debugging_resources.md
    - 00c-good-scientific-coding-practices.md
    - 01-intro_to_base_R-live.Rmd
    - 02-intro_to_ggplot2-live.Rmd
    - 03-intro_to_tidyverse-live.Rmd
    - 04a-intro_to_R_exercise.Rmd
    - 04b-intro_to_tidyverse_exercise-part-1.Rmd
    - 04c-intro_to_tidyverse_exercise-part-2.Rmd
    - data
    - diagrams
    - intro-to-R-tidyverse.Rproj
    - plots
    - screenshots
  - RNA-seq



```
trainee:~$ ls
shared-data  training-modules
trainee:~$ cd training-modules
```

ls - how to tell the computer to list the files and folders in a directory (files that start with a ' . ' are not shown by default)

cd - how to change directories



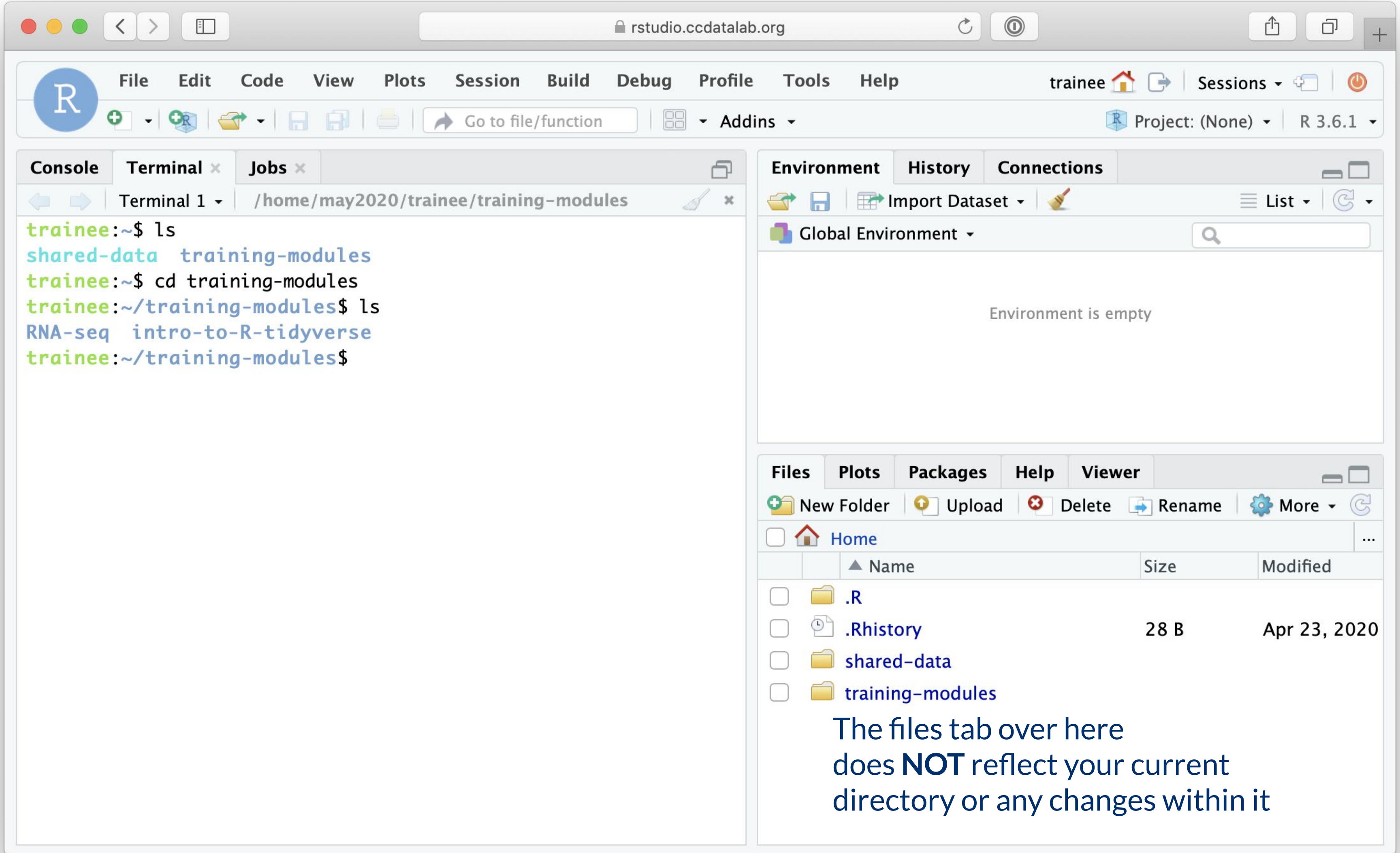
```
trainee:~$ ls
shared-data  training-modules
trainee:~$ cd training-modules
trainee:~/training-modules$ ls
RNA-seq  intro-to-R-tidyverse
trainee:~/training-modules$
```

	Name	Size	Modified
☐	.R		
☐	.Rhistory	28 B	Apr 23, 2020
☐	shared-data		
☐	training-modules		

Note that the words before where our cursor is has changed to reflect that we are in the "training-modules" directory

ls - how to tell the computer to list the files and folders in a directory (files that start with a ' . ' are not shown by default)

cd - how to change directories



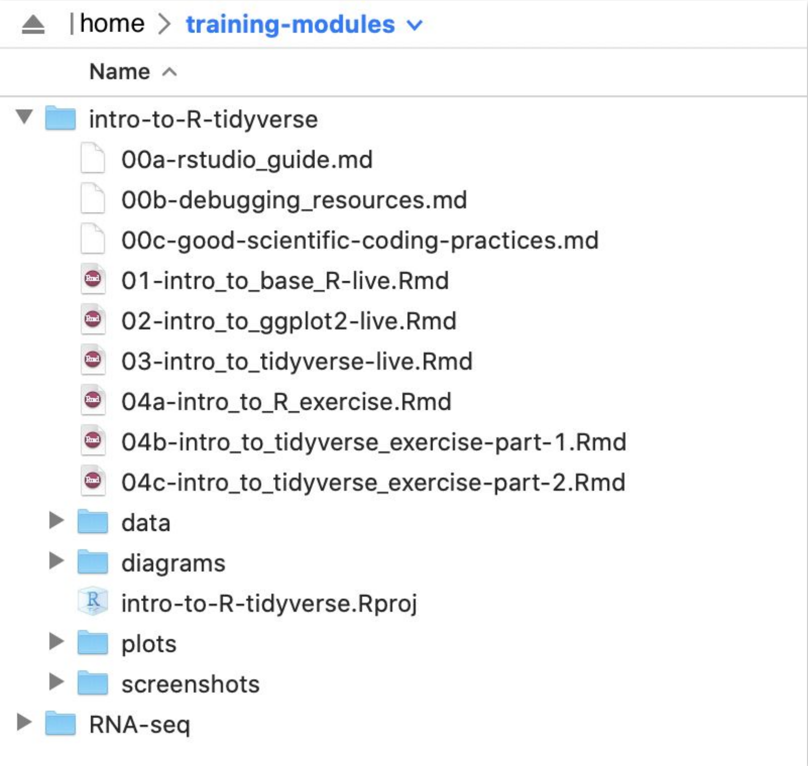
```
trainee:~$ ls
shared-data  training-modules
trainee:~$ cd training-modules
trainee:~/training-modules$ ls
RNA-seq  intro-to-R-tidyverse
trainee:~/training-modules$
```

Name	Size	Modified
☐ .R		
☐ .Rhistory	28 B	Apr 23, 2020
☐ shared-data		
☐ training-modules		

The files tab over here
does **NOT** reflect your current
directory or any changes within it

File paths: Directions to a file or folder

Let's say we want access to "01-intro_to_base_R-live.Rmd"



| home > training-modules

Name

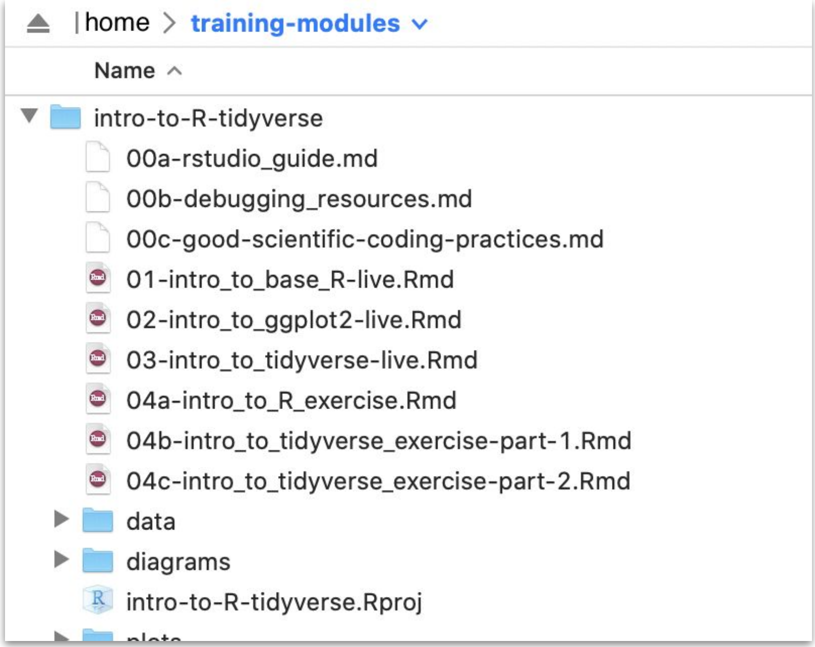
- intro-to-R-tidyverse
  - 00a-rstudio_guide.md
  - 00b-debugging_resources.md
  - 00c-good-scientific-coding-practices.md
  - 01-intro_to_base_R-live.Rmd
  - 02-intro_to_ggplot2-live.Rmd
  - 03-intro_to_tidyverse-live.Rmd
  - 04a-intro_to_R_exercise.Rmd
  - 04b-intro_to_tidyverse_exercise-part-1.Rmd
  - 04c-intro_to_tidyverse_exercise-part-2.Rmd
  - data
  - diagrams
  - intro-to-R-tidyverse.Rproj
  - plots
  - screenshots
- RNA-seq

Current directory = "training-modules"

File path = "intro-to-R-tidyverse/01-intro_to_base_R-live.Rmd"

File Paths can be *relative*

Let's say we want access to "01-intro_to_base_R-live.Rmd"



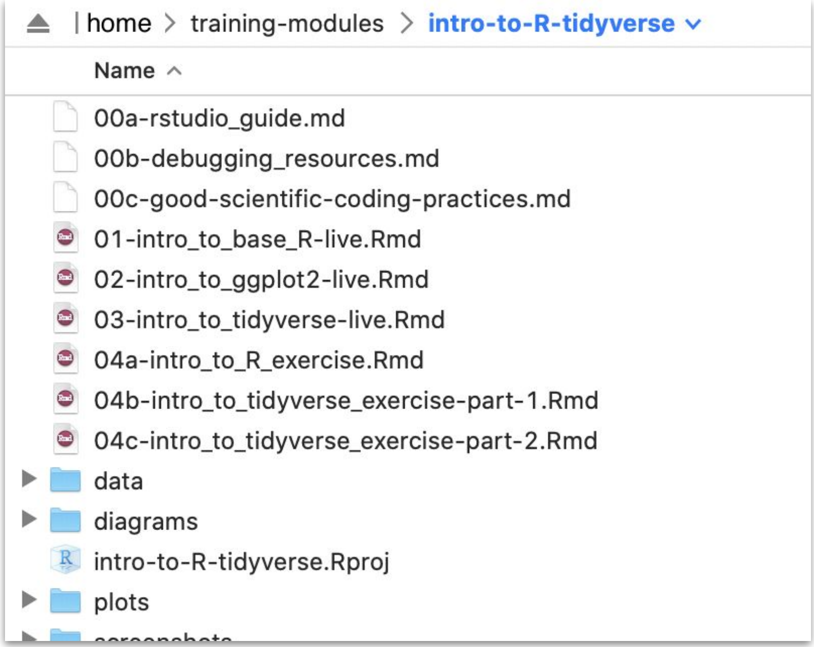
home > **training-modules**

Name

intro-to-R-tidyverse
  00a-rstudio_guide.md
  00b-debugging_resources.md
  00c-good-scientific-coding-practices.md
  01-intro_to_base_R-live.Rmd
  02-intro_to_ggplot2-live.Rmd
  03-intro_to_tidyverse-live.Rmd
  04a-intro_to_R_exercise.Rmd
  04b-intro_to_tidyverse_exercise-part-1.Rmd
  04c-intro_to_tidyverse_exercise-part-2.Rmd
  data
  diagrams
  intro-to-R-tidyverse.Rproj
  plots

Current directory = "training-modules"

Relative file path =
"intro-to-R-tidyverse/01-intro_to_base_R-live.Rmd"



home > training-modules > **intro-to-R-tidyverse**

Name

00a-rstudio_guide.md
00b-debugging_resources.md
00c-good-scientific-coding-practices.md
01-intro_to_base_R-live.Rmd
02-intro_to_ggplot2-live.Rmd
03-intro_to_tidyverse-live.Rmd
04a-intro_to_R_exercise.Rmd
04b-intro_to_tidyverse_exercise-part-1.Rmd
04c-intro_to_tidyverse_exercise-part-2.Rmd
data
diagrams
intro-to-R-tidyverse.Rproj
plots
screenshots

Current directory = "training-modules/intro-to-R-tidyverse"

Relative file path = "01-intro_to_base_R-live.Rmd"

Introduction to R

The CCDL

R programming

Programming: making executable scripts for accomplishing a task
(in this case, data analysis is our task)

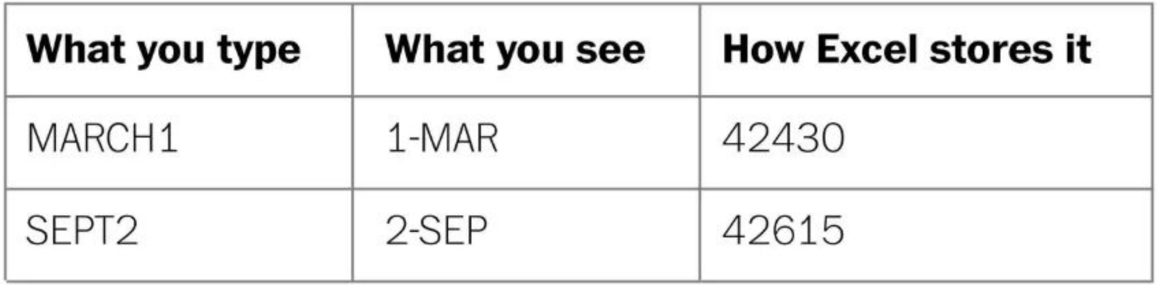
Scripts allow others to see, step-by-step, what you did.

Why we use R:

- It's free
- People make cool packages that do stuff for us
- Many researchers in genomics use it (as well as Python)

One in five genetics papers contains errors thanks to Microsoft Excel

By **Jessica Boddy** | Aug. 29, 2016 , 1:45 PM

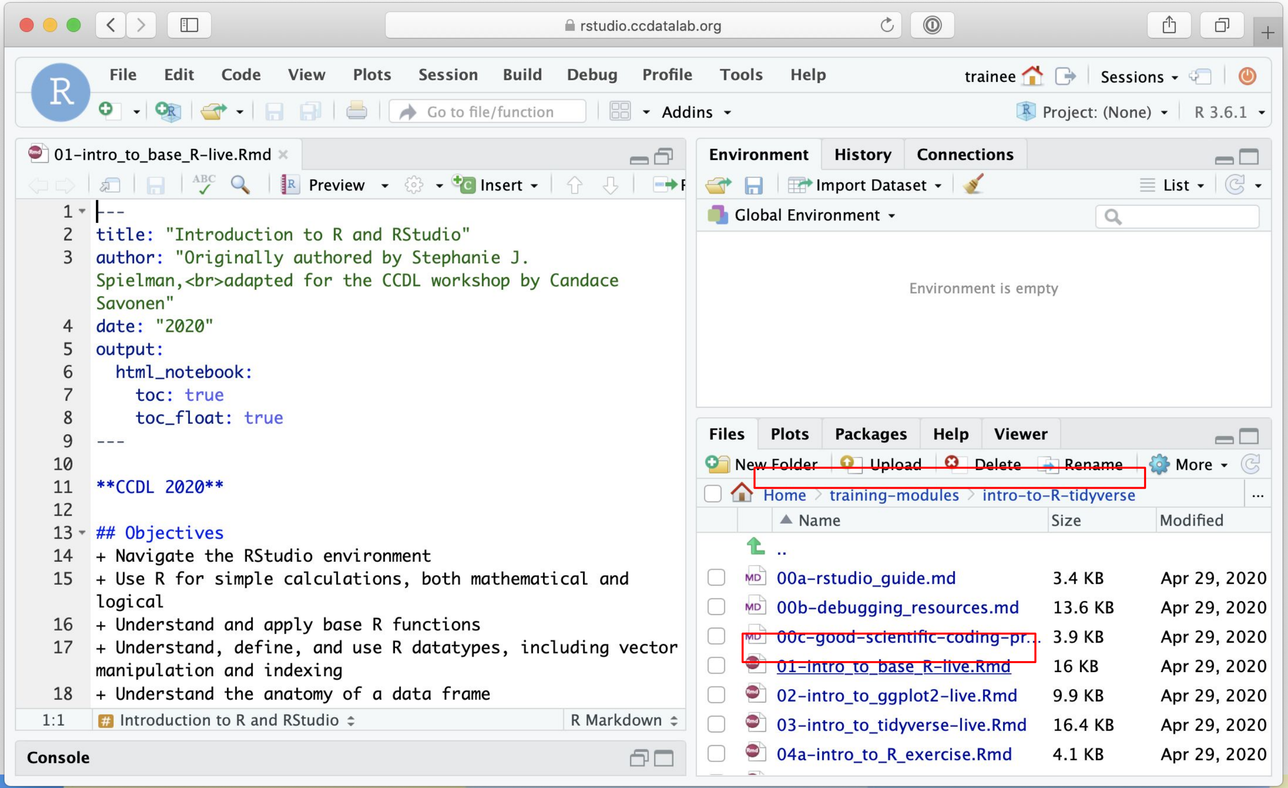


What you type	What you see	How Excel stores it
MARCH1	1-MAR	42430
SEPT2	2-SEP	42615

https://www.sciencemag.org/news/2016/08/one-five-genetics-papers-contains-errors-thanks-microsoft-excel
Ziemann et al. Genome Biology (2016) 17:177 DOI 10.1186/s13059-016-1044-7

R Notebooks

Use the "**Files**" tab to open: training-modules/intro-to-R-tidyverse/01-intro_to_base_R-live.Rmd



```
---
title: "Introduction to R and RStudio"
author: "Originally authored by Stephanie J. Spielman,<br>adapted for the CCDL workshop by Candace Savonen"
date: "2020"
output:
  html_notebook:
    toc: true
    toc_float: true
---

**CCDL 2020**

## Objectives
+ Navigate the RStudio environment
+ Use R for simple calculations, both mathematical and logical
+ Understand and apply base R functions
+ Understand, define, and use R datatypes, including vector manipulation and indexing
+ Understand the anatomy of a data frame
```

Name	Size	Modified
..		
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
00b-debugging_resources.md	13.6 KB	Apr 29, 2020
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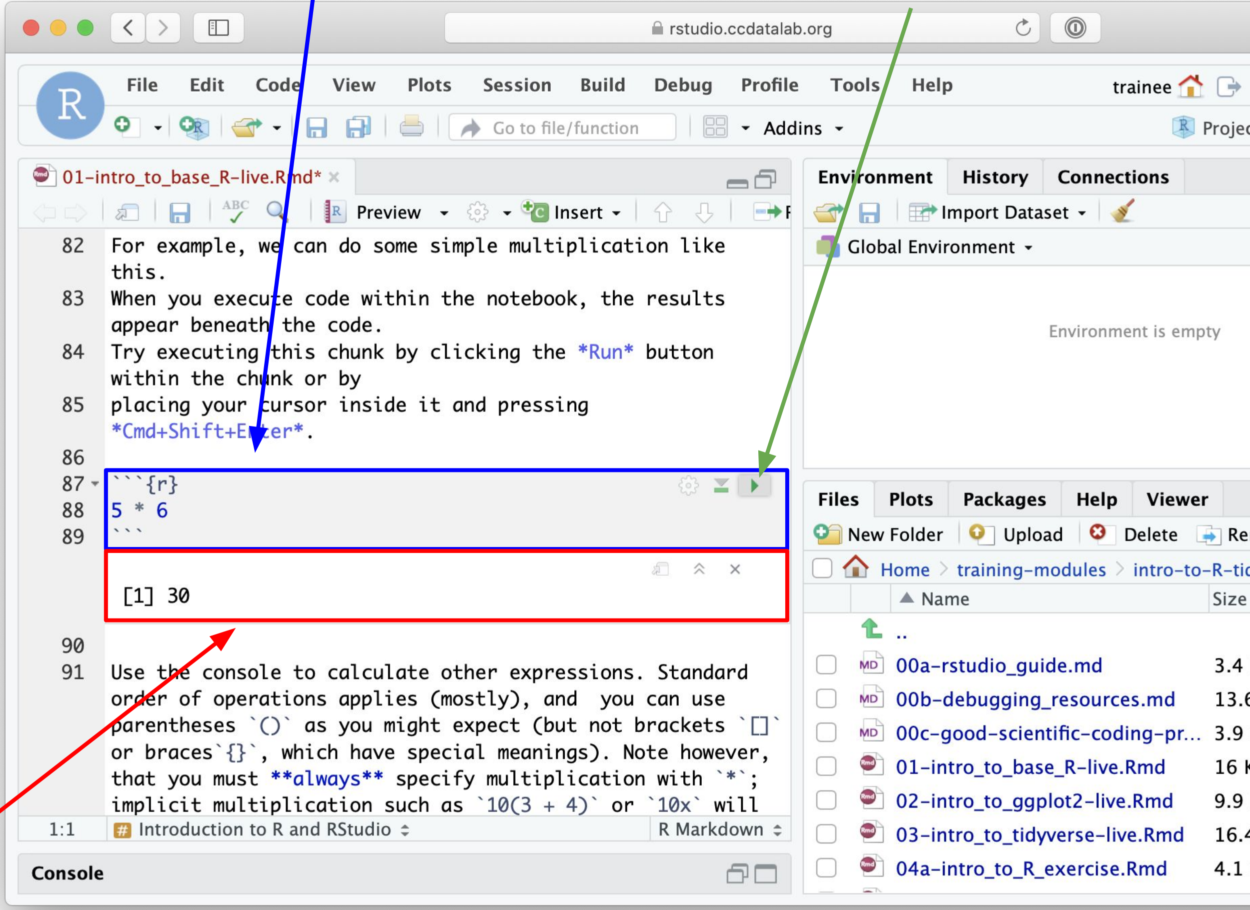
04a-intro_to_R_exercise.Rmd	4.1 KB	Apr 29, 2020

R Notebooks

- R Notebooks allow you to have files that show both your code and results

Executable code chunk

Can click here to run a code chunk



~~~
For example, we can do some simple multiplication like this.
When you execute code within the notebook, the results appear beneath the code.
Try executing this chunk by clicking the *Run* button within the chunk or by
placing your cursor inside it and pressing *Cmd+Shift+Enter*.

```{r}
5 * 6
```
~~~

```
[1] 30
```

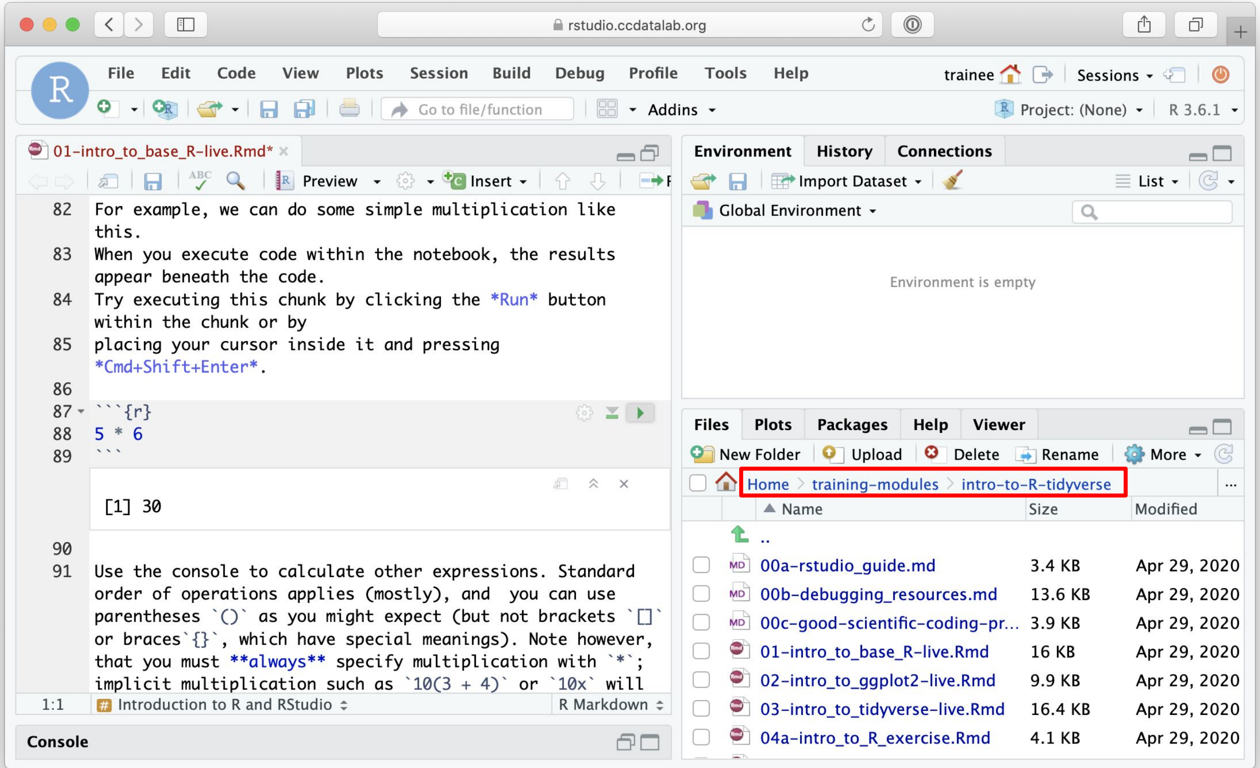
```

Use the console to calculate other expressions. Standard order of operations applies (mostly), and  you can use parentheses `()` as you might expect (but not brackets `[]` or braces`{}`, which have special meanings). Note however, that you must **always** specify multiplication with `*`; implicit multiplication such as `10(3 + 4)` or `10x` will
```

Output from above code chunk

R Notebooks

- Code that runs in R Notebooks uses wherever the file is saved as its *current directory*



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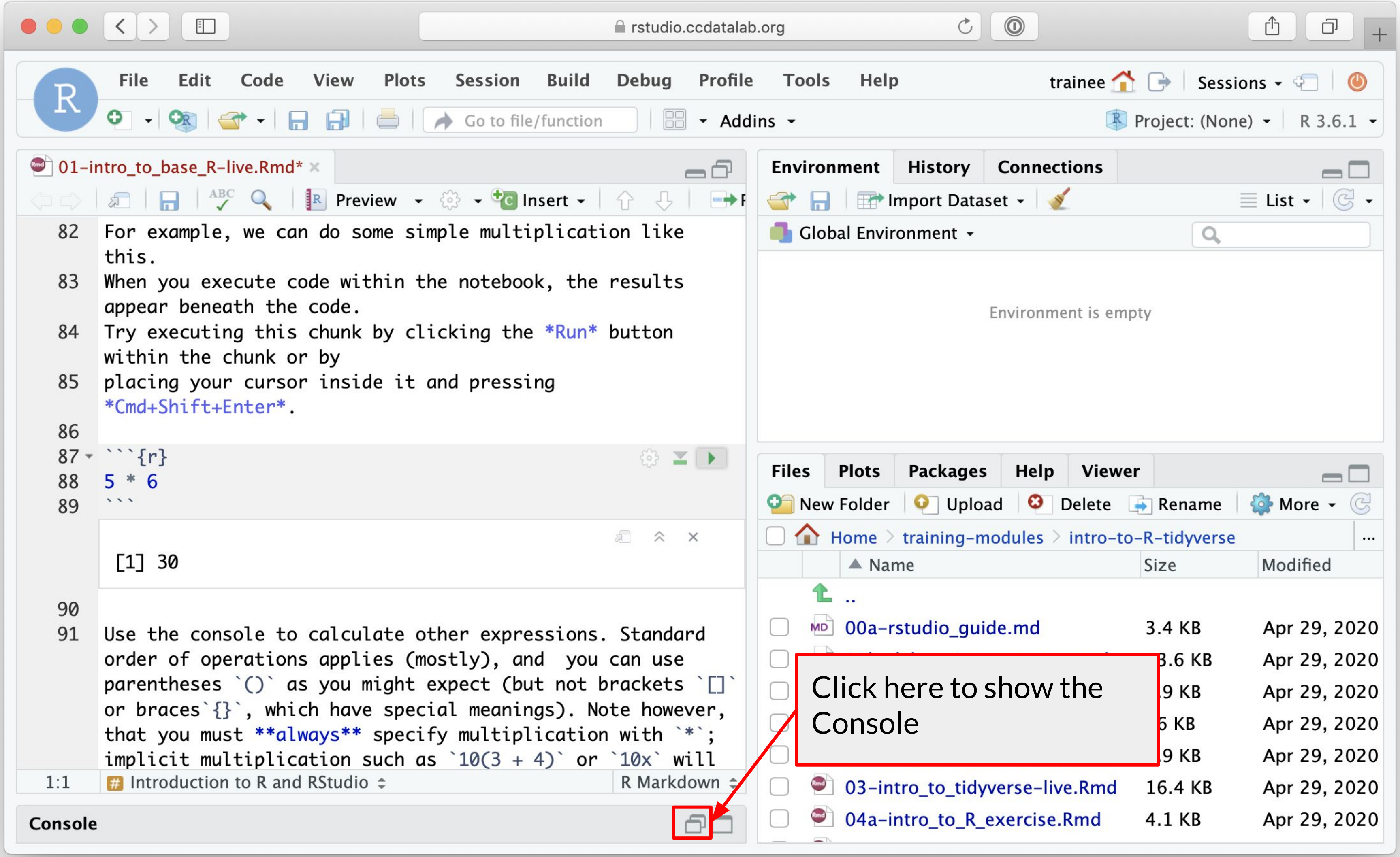

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```
[1] 30
```

```

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```

Environment is empty

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☐		9 KB	Apr 29, 2020
☐		6 KB	Apr 29, 2020
☐		9 KB	Apr 29, 2020
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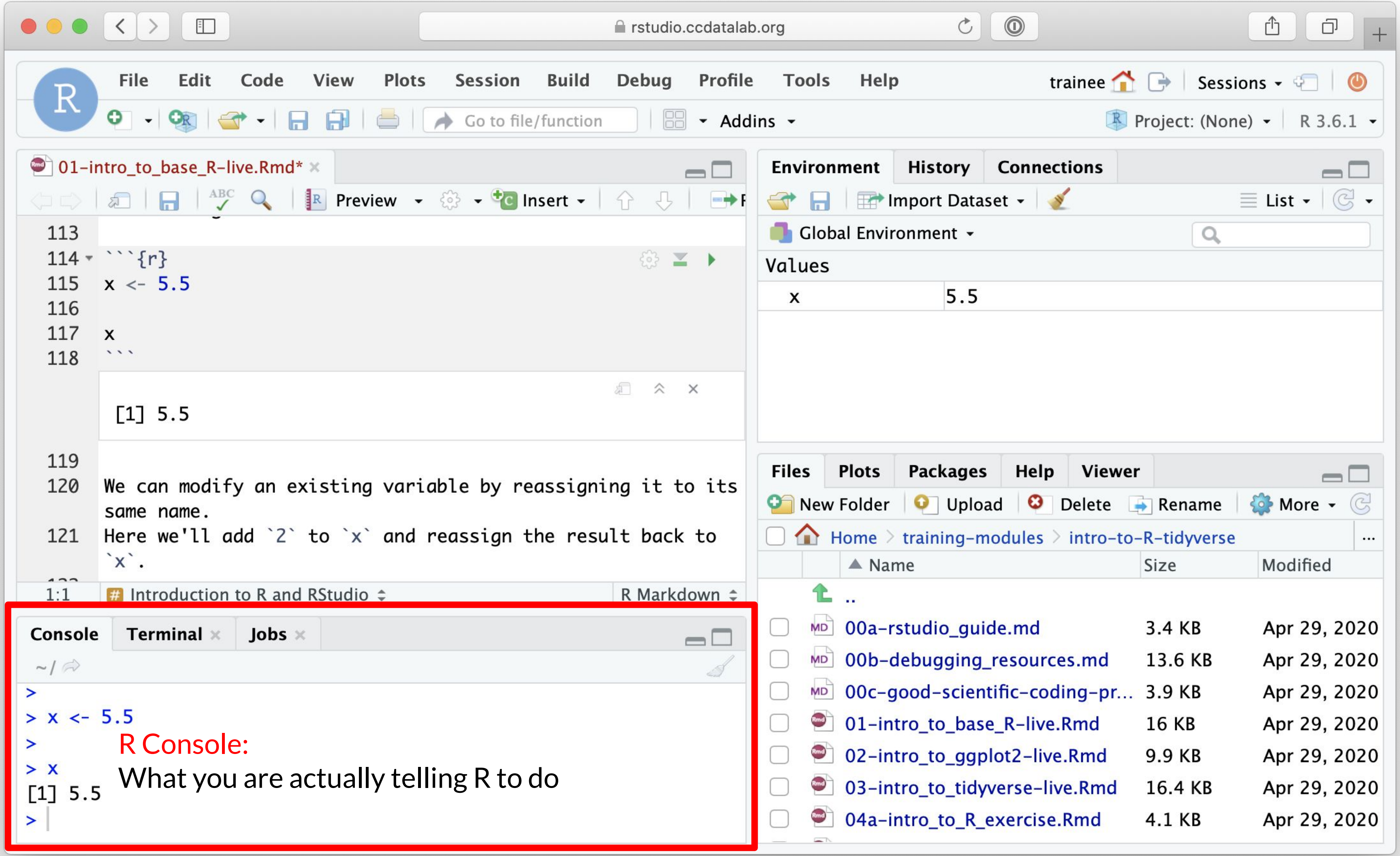
Click here to show the Console



~~~
```{r}
x <- 5.5

x
```
~~~

```
[1] 5.5
```

We can modify an existing variable by reassigning it to its same name.
Here we'll add `2` to `x` and reassign the result back to `x`.

1:1 Introduction to R and RStudio — R Markdown

Values

x	5.5

Home > training-modules > intro-to-R-tidyverse

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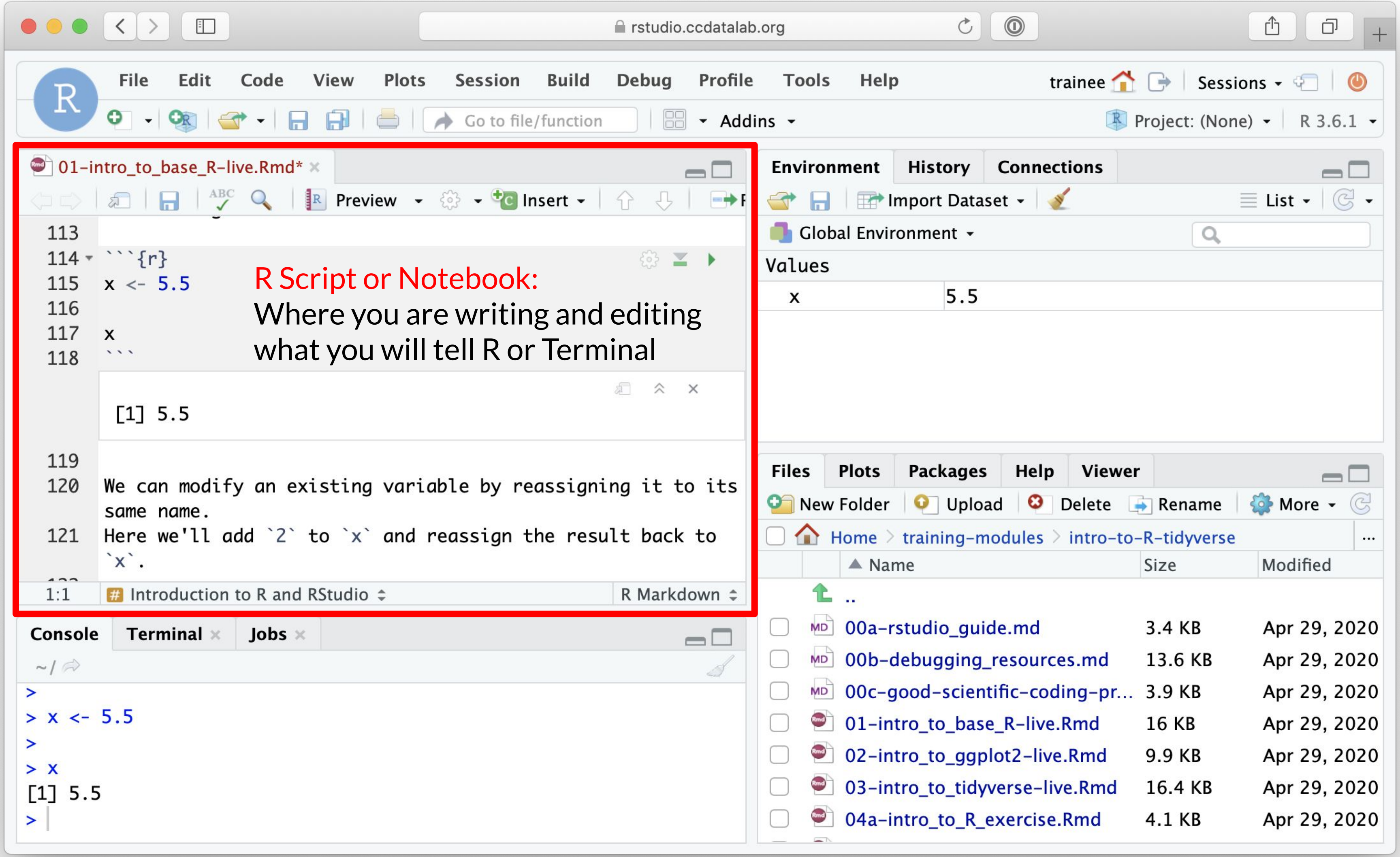
```
>
> x <- 5.5
>
> x
[1] 5.5
>
```

R Console:
What you are actually telling R to do



R Script or Notebook:
Where you are writing and editing what you will tell R or Terminal

~~~
```{r}
x <- 5.5

x
```
~~~

```
[1] 5.5
```

We can modify an existing variable by reassigning it to its same name.
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```
>
> x <- 5.5
>
> x
[1] 5.5
>
```

Values

x	5.5

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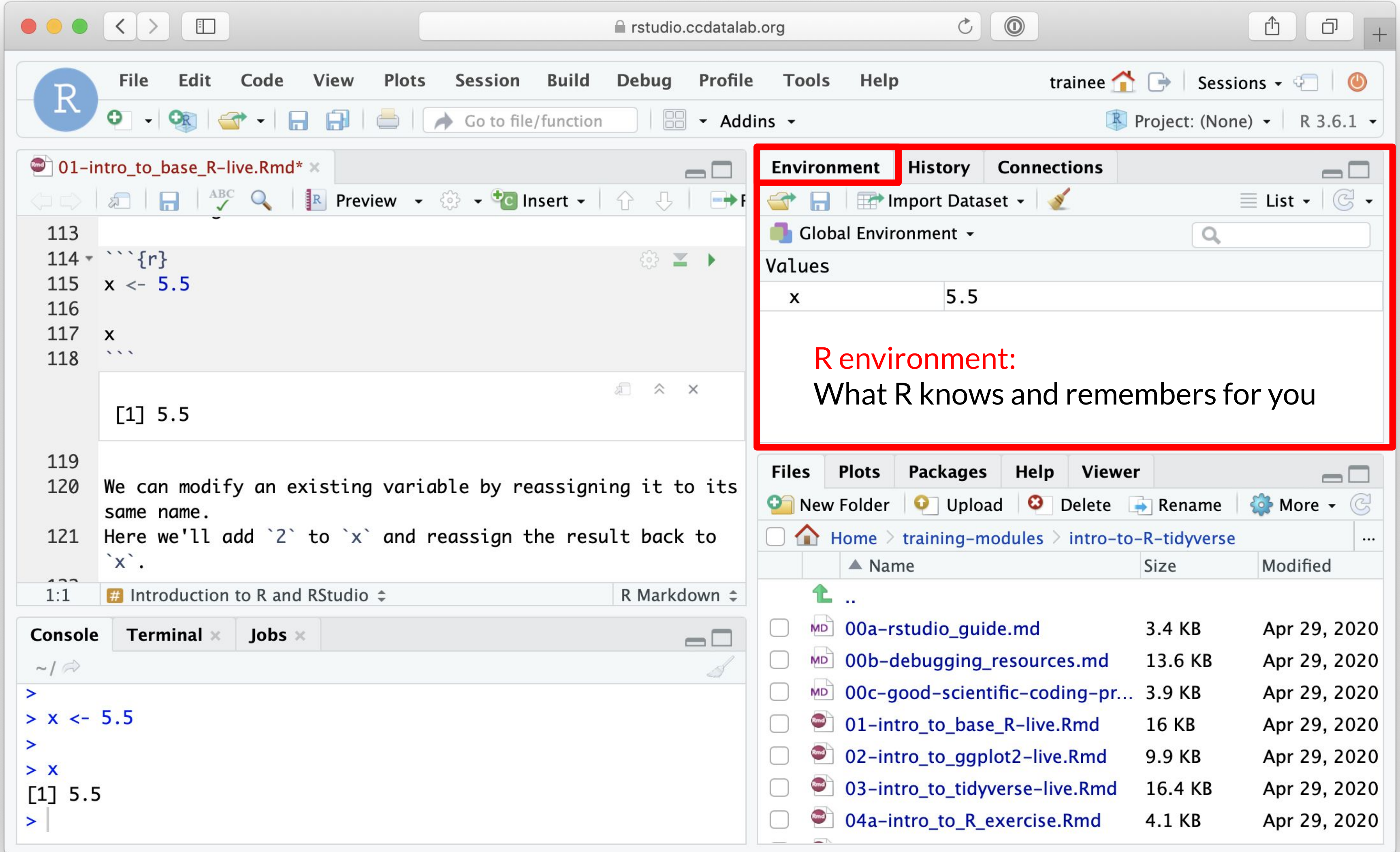

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x <- 5.5

x
```
~~~

```
[1] 5.5
```

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```
>
> x <- 5.5
>
> x
[1] 5.5
>
```

Values

x 5.5

R environment:
What R knows and remembers for you

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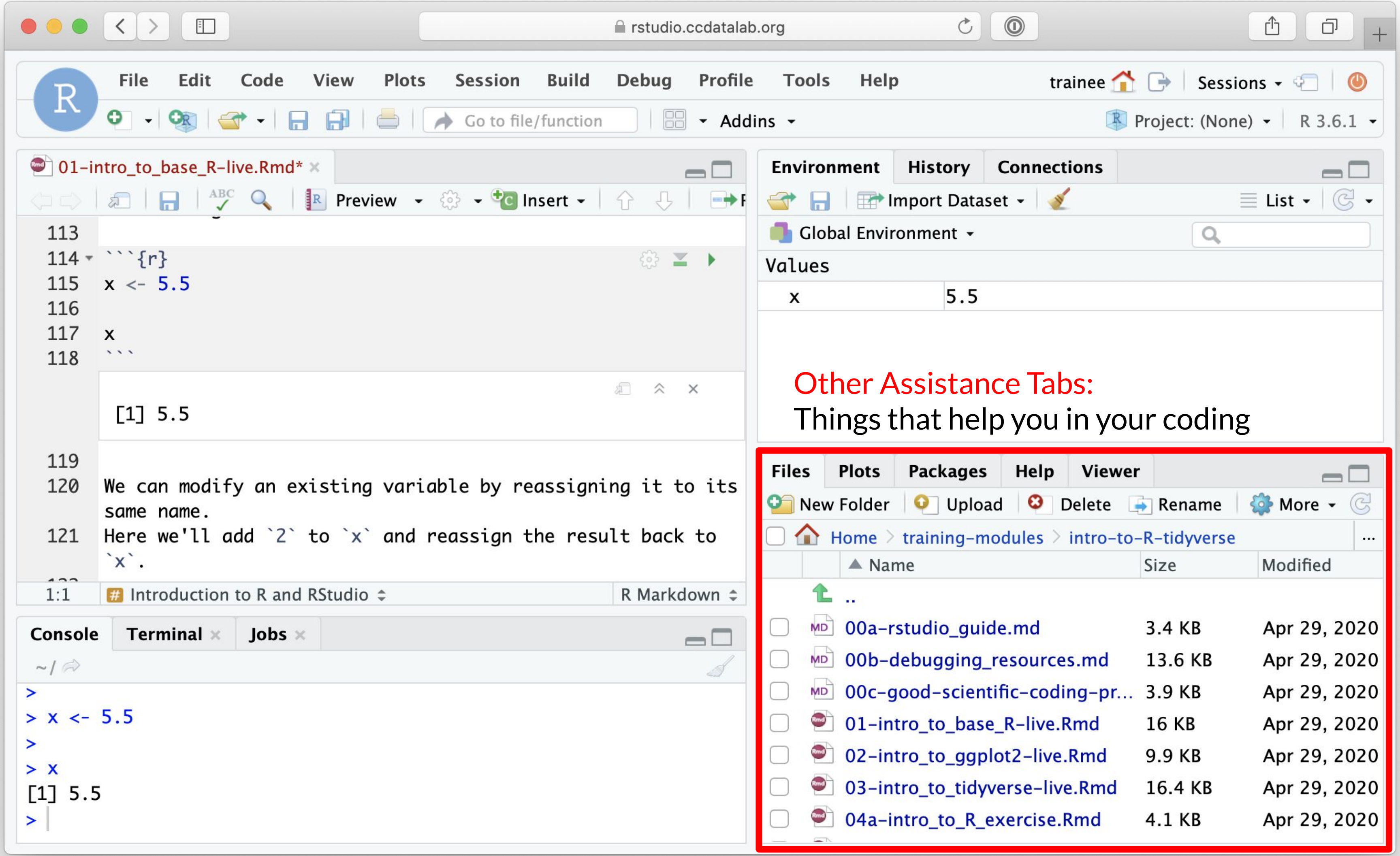

Other Assistance Tabs:
Things that help you in your coding

~~~
```{r}
x <- 5.5

x
```
~~~

```
[1] 5.5
```

We can modify an existing variable by reassigning it to its same name.
Here we'll add `2` to `x` and reassign the result back to `x`.

Values

x	5.5

```
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```

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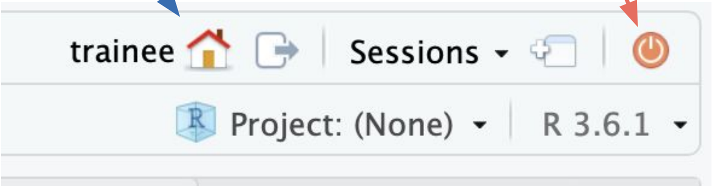
RStudio Sessions

- On the server, R is running many times at once
  - Each user has their own "**Session**" running, with its own memory and processes
  - It is possible for a user to have more than one session at a time

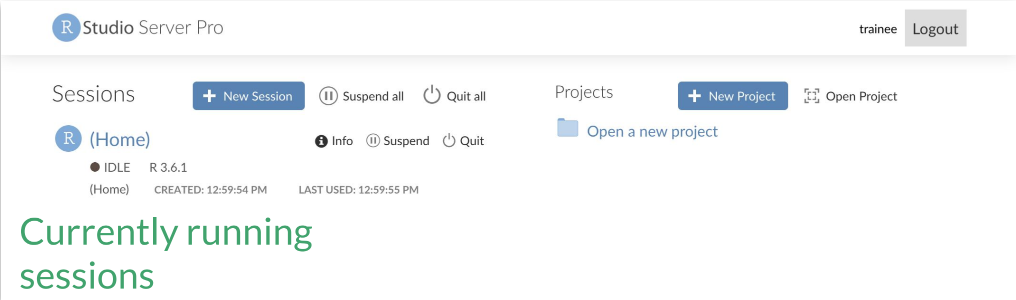
- We will usually want to start new sessions between notebooks to keep the environment clean

Go to the sessions page

End the current session



Session Page



IDLE R 3.6.1

(Home) CREATED: 12:59:54 PM LAST USED: 12:59:55 PM

Currently running sessions