

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.

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<table border="1"><thead><tr><th>1</th><th>ProbeName</th><th>Sequence</th><th>GeneName</th><th>SystematicName</th><th>Description</th><th>RName</th><th>RSavedName</th><th>F</th></tr></thead><tbody><tr><td>881</td><td>CHIP_JH_SE3_19777</td><td>GCTTGTATGACGCCAAGC CHIP_JH_SE3_19777</td><td></td><td>CHIP_JH_SE3_19777</td><td>Unknown</td><td>{ 880 }</td><td>{ 880 }_AK056136_> CHIP_JH_SE3_19777 < Unknown .</td><td></td></tr><tr><td>26316</td><td>CHIP_JH_SE3_19780</td><td>CTAGACAGAAACAGCACT CHIP_JH_SE3_19780</td><td></td><td>CHIP_JH_SE3_19780</td><td>Unknown</td><td>{ 26315 }</td><td>{ 26315 }_AK056136_> CHIP_JH_SE3_19780 < Unknown .</td><td></td></tr><tr><td>27565</td><td>CHIP_CON_ALB_196</td><td>CTAGATGAAAATAAAAGTC CHIP_CON_ALB_196</td><td></td><td>CHIP_CON_ALB_196</td><td>Unknown</td><td>{ 27564 }</td><td>{ 27564 }_NM_014178_> CHIP_CON_ALB_196 < Unknown .</td><td></td></tr><tr><td>28964</td><td>CHIP_CON_ALB_196</td><td>CTAGATGAAAATAAAAGTC 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CHIP_JH_SE3_23398		CHIP_JH_SE3_23398	Unknown	{ 40334 }	{ 40334 }_NM_014178_> CHIP_JH_SE3_23398 < Unknown .		31145	CHIP_JH_SE3_23400	GAGACGACTACACACTCA CHIP_JH_SE3_23400		CHIP_JH_SE3_23400	Unknown	{ 31144 }	{ 31144 }_NM_014178_> CHIP_JH_SE3_23400 < Unknown .		3994	CHIP_JH_SE3_969	TTGTGAATGTTGTGTTGA CHIP_JH_SE3_969		CHIP_JH_SE3_969	Unknown	{ 3993 }	{ 3993 }_NM_014178_> CHIP_JH_SE3_969 < Unknown .		14335	CONTROL_EPILEPSY_SE3_3	TGTTTTGGGGATGGAGGG CONTROL_EPILEPSY_SE3_382		CONTROL_EPILEPSY_SE3_3	Unknown	{ 14334 }	{ 14334 }_NM_004233_> CONTROL_EPILEPSY_SE3_382 < Unknown .		13000	CONTROL_EPILEPSY_SE3_2	TAGAAGCTAACACAAACCC CONTROL_EPILEPSY_SE3_275		CONTROL_EPILEPSY_SE3_2	Unknown	{ 12999 }	{ 12999 }_NM_032895_> CONTROL_EPILEPSY_SE3_275 < Unknown .		32032	CONTROL_EPILEPSY_SE3_3	AGGTAGTACCAAGGACCTT CONTROL_EPILEPSY_SE3_381		CONTROL_EPILEPSY_SE3_3	Unknown	{ 32031 }	{ 32031 }_NM_004233_> CONTROL_EPILEPSY_SE3_381 < Unknown .		25796	CHIP_JH_SE3_972	GGTAGATGTTCAAAGTATC 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26892	CHIP_JH_SE3_23396	CTAACACACACAAAGC CHIP_JH_SE3_23396		CHIP_JH_SE3_23396	Unknown	{ 26891 }	{ 26891 }_NM_014178_> CHIP_JH_SE3_23396 < Unknown .																																																																																																																																																																																																																																																					
40335	CHIP_JH_SE3_23398	GAGCTAACACACCAAA CHIP_JH_SE3_23398		CHIP_JH_SE3_23398	Unknown	{ 40334 }	{ 40334 }_NM_014178_> CHIP_JH_SE3_23398 < Unknown .																																																																																																																																																																																																																																																					
31145	CHIP_JH_SE3_23400	GAGACGACTACACACTCA CHIP_JH_SE3_23400		CHIP_JH_SE3_23400	Unknown	{ 31144 }	{ 31144 }_NM_014178_> CHIP_JH_SE3_23400 < Unknown .																																																																																																																																																																																																																																																					
3994	CHIP_JH_SE3_969	TTGTGAATGTTGTGTTGA CHIP_JH_SE3_969		CHIP_JH_SE3_969	Unknown	{ 3993 }	{ 3993 }_NM_014178_> CHIP_JH_SE3_969 < Unknown .																																																																																																																																																																																																																																																					
14335	CONTROL_EPILEPSY_SE3_3	TGTTTTGGGGATGGAGGG CONTROL_EPILEPSY_SE3_382		CONTROL_EPILEPSY_SE3_3	Unknown	{ 14334 }	{ 14334 }_NM_004233_> CONTROL_EPILEPSY_SE3_382 < Unknown .																																																																																																																																																																																																																																																					
13000	CONTROL_EPILEPSY_SE3_2	TAGAAGCTAACACAAACCC CONTROL_EPILEPSY_SE3_275		CONTROL_EPILEPSY_SE3_2	Unknown	{ 12999 }	{ 12999 }_NM_032895_> CONTROL_EPILEPSY_SE3_275 < Unknown .																																																																																																																																																																																																																																																					
32032	CONTROL_EPILEPSY_SE3_3	AGGTAGTACCAAGGACCTT CONTROL_EPILEPSY_SE3_381		CONTROL_EPILEPSY_SE3_3	Unknown	{ 32031 }	{ 32031 }_NM_004233_> CONTROL_EPILEPSY_SE3_381 < Unknown .																																																																																																																																																																																																																																																					
25796	CHIP_JH_SE3_972	GGTAGATGTTCAAAGTATC CHIP_JH_SE3_972		CHIP_JH_SE3_972	Unknown	{ 25795 }	{ 25795 }_NM_014178_> 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
TRAf3IP2 Promoter Data.txt
ListofMicroRNAs3-5-15CS.xlsx
IncRNAMicroarrayMasterSheet11-4-14CS.xlsx
IncRNASortedDataEdit3-28-14.xlsx
Mice LncRNAs
Conservation_DataTable.csv
GenomeCoordinateOutput.txt
GenomeCoordinateOutput2.txt
LncRNAs_NFKB Mouse Gutman 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
mmcl1 (1).pdf
mouse_long_lncRNAs_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 IncRNA 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
NMSDatazeros2-6-15CS.sav
NMSTOAccess.accdb
ToxDataAnalysisSPSSoutput.xlsx
WCME-NMSDataSort2-3-15CS.xlsx
WCME-NMSDataSort2-5-15CS.xlsx

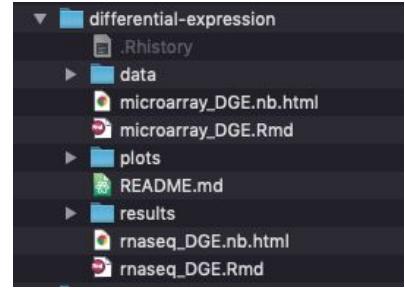
Data Analysis Example 2: “GitHubbed Analysis”

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](#).



- 1) Install libraries
- 2) Import and set up data
- 3) Set up design matrix
- 4) Apply linear model
- 5) Explore fitness of model
- 6) Write statistics to output results file

Differential Expression Analysis: Microarray

ALSF CCDEL - 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?

“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?

“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

The screenshot shows the RStudio Server interface running in a web browser. The top navigation bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help, and Sessions. The user is identified as "trainee". The Project dropdown shows "(None)" and the R version is 3.6.1.

Console Tab:

```
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.
```

Environment Tab:

Global Environment

Environment is empty

Files Tab:

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

Terminal Tab:

```
> |
```

The screenshot shows the RStudio interface running on a Mac OS X system. The title bar indicates the session is named "trainee" and the version is "R 3.6.1".

Console Pane: This pane is highlighted with a red border. It displays the standard R startup message, including the version number (3.6.1), copyright information, and license details. It also shows the R environment as empty.

```
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.
```

Environment Pane: This pane shows the Global Environment, which is currently empty.

Files Pane: This pane shows the directory structure under "Home".

	Name	Size	Modified
<input type="checkbox"/>	.R	28 B	Apr 23, 2020
<input type="checkbox"/>	.Rhistory		
<input type="checkbox"/>	shared-data		
<input type="checkbox"/>	training-modules		

The screenshot shows the RStudio interface with several panes open:

- Top Bar:** File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help, trainee, Sessions, Project: (None), R 3.6.1.
- Toolbar:** Includes tabs for R, Addins, Go to file/function, and a search bar.
- Console Tab:** Shows "trainee:~\$".
- Terminal Tab:** Shows "Terminal 1 /home/may2020/trainee". A yellow box highlights the tabs with the text "tabs to switch".
- Environment Tab:** Shows "Global Environment" with "Environment is empty".
- Files Tab:** Shows a file tree with the following contents:

	Name	Size	Modified
<input type="checkbox"/>	.R		
<input type="checkbox"/>	.Rhistory	28 B	Apr 23, 2020
<input type="checkbox"/>	shared-data		
<input type="checkbox"/>	training-modules		

The Terminal:

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

The screenshot shows the RStudio interface with a red box highlighting the Terminal and Environment panes.

Terminal Pane:

- Shows the command `trainee:~$`.
- Two arrows point from the text "These indicate what **directory** you are **currently** carrying out a command in" to the tilde (~) and the dollar sign (\$).
- The path `/home/may2020/trainee` is displayed above the prompt.

Environment Pane:

- Shows the "Global Environment" tab.
- Text: "Environment is empty".

Files Pane:

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

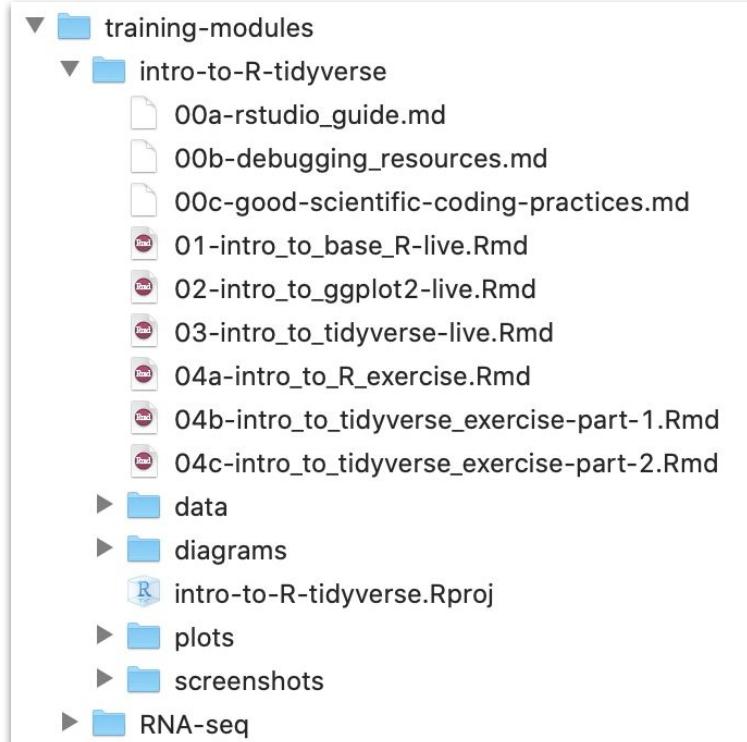
These indicate what **directory** you
are **currently** carrying out a command in

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

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

Directories = Folders

When we are doing things through command line, we have to look at where the files we are using are being kept.



The screenshot shows the RStudio interface running on a Mac OS X system. The top bar includes standard OS X window controls, a lock icon, and a URL field showing "rstudio.ccdatalab.org". The main menu bar has options: File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help, and Addins. The status bar indicates "trainee" as the user, "Project: (None)", and "R 3.6.1".

Console pane: Shows a terminal session. The user runs "ls" to list files in the current directory, which contains "shared-data" and "training-modules". Then, "cd training-modules" is run to change the directory.

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

Environment pane: Shows the Global Environment. It displays a message: "Environment is empty".

Files pane: Shows the contents of the "Home" directory. It lists four items: ".R", ".Rhistory", "shared-data", and "training-modules". The "shared-data" folder is 28 B in size and was modified on Apr 23, 2020.

	Name	Size	Modified
<input type="checkbox"/>	.R		
<input type="checkbox"/>	.Rhistory	28 B	Apr 23, 2020
<input type="checkbox"/>	shared-data		
<input type="checkbox"/>	training-modules		

Plots pane: This pane is currently empty.

The screenshot shows the RStudio interface. The top bar includes the title 'rstudio.ccdatalab.org', a refresh button, and a session name 'trainee'. The menu bar has options like File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help, and Addins. The bottom navigation bar shows 'Console', 'Terminal x', and 'Jobs x'. The 'Terminal' tab is active, displaying a command-line session:

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

Console

Terminal x

Jobs x

Terminal 1

/home/may2020/trainee/training-modules

trainee:~\$ ls

shared-data training-modules

trainee:~\$ cd training-modules

trainee:~/training-modules\$ ls

RNA-seq intro-to-R-tidyverse

trainee:~/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

Environment

History

Connections



Environment is empty

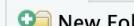
Files

Plots

Packages

Help

Viewer



New Folder



Upload



Delete



Rename



More



Home

	Name	Size	Modified
<input type="checkbox"/>	.R		
<input type="checkbox"/>	.Rhistory	28 B	Apr 23, 2020
<input type="checkbox"/>	shared-data		
<input type="checkbox"/>	training-modules		

The screenshot shows the RStudio interface on a Mac OS X system. The top menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help, and a user-specific section for 'trainee'. The top right corner shows session details ('trainee' at home), a refresh icon, and a plus sign for new sessions.

The main workspace is divided into several panes:

- Console:** Displays a terminal session:

```
trainee:~$ ls
shared-data training-modules
trainee:~$ cd training-modules
trainee:~/training-modules$ ls
RNA-seq intro-to-R-tidyverse
trainee:~/training-modules$
```
- Environment:** Shows the global environment, which is currently empty.
- Files:** Shows the current directory structure:

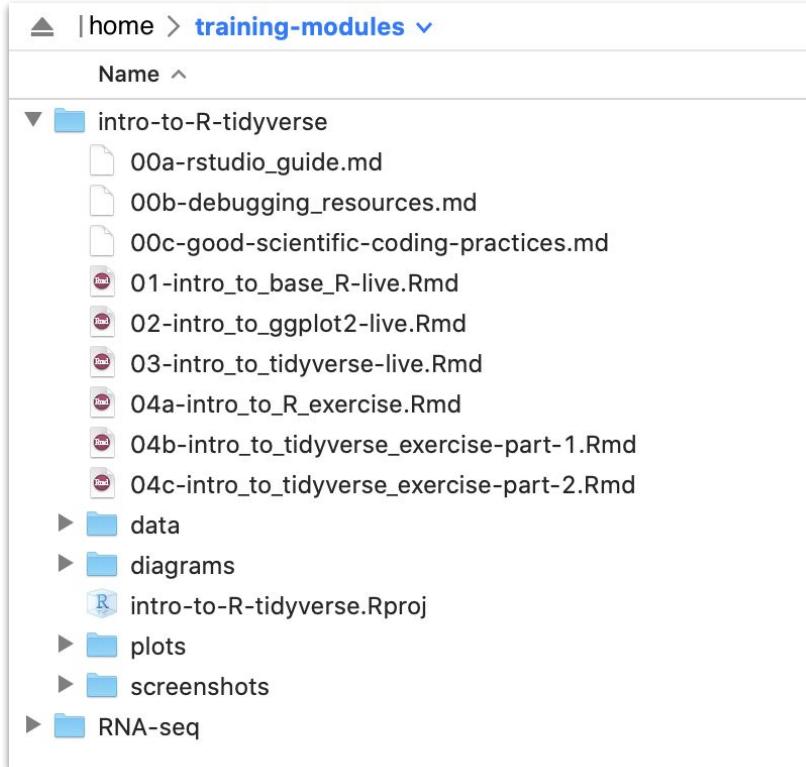
	Name	Size	Modified
<input type="checkbox"/>	.R		
<input type="checkbox"/>	.Rhistory	28 B	Apr 23, 2020
<input type="checkbox"/>	shared-data		
<input type="checkbox"/>	training-modules		

A large blue text overlay in the bottom right corner reads:

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**”

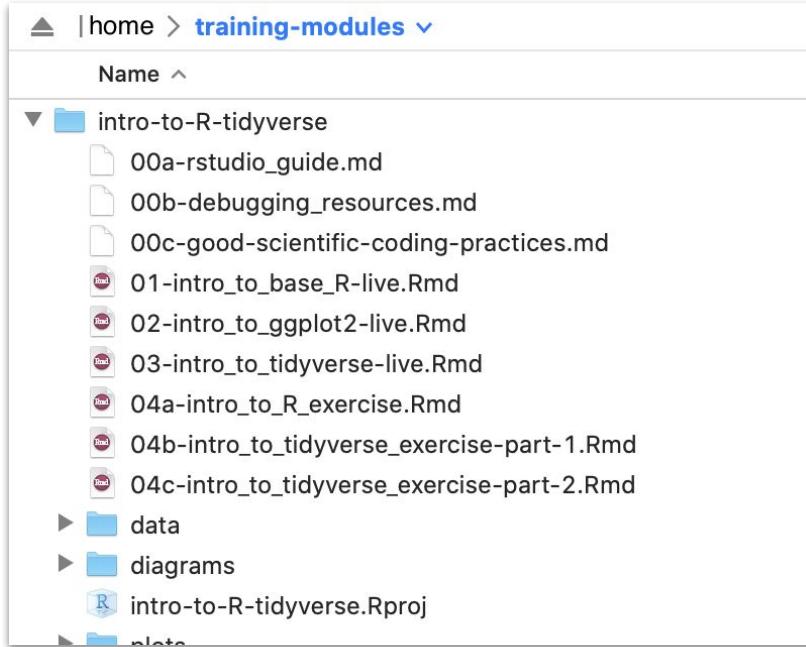


Current directory = “**training-modules**”

File path = “**intro-to-R-tidyverse/01-intro_to_base_R-live.Rmd**”

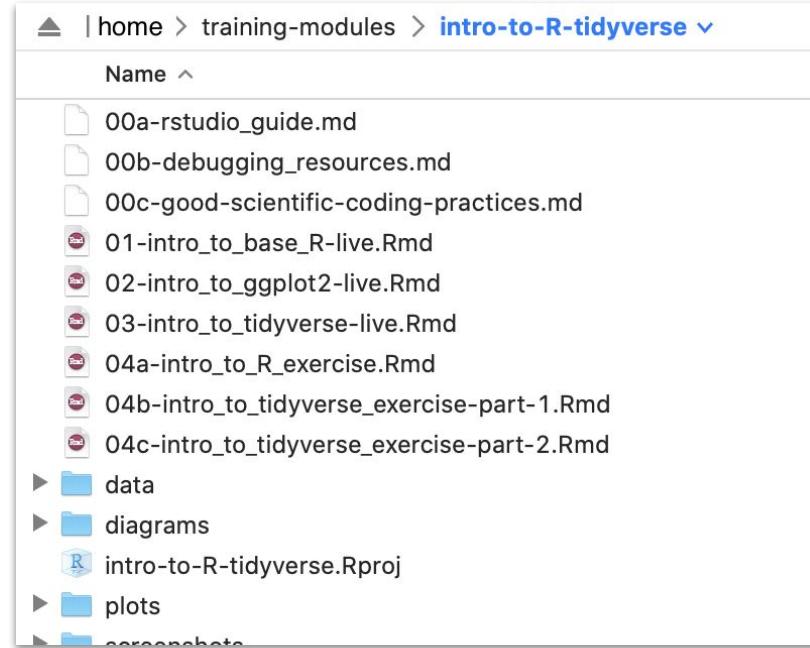
File Paths can be *relative*

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



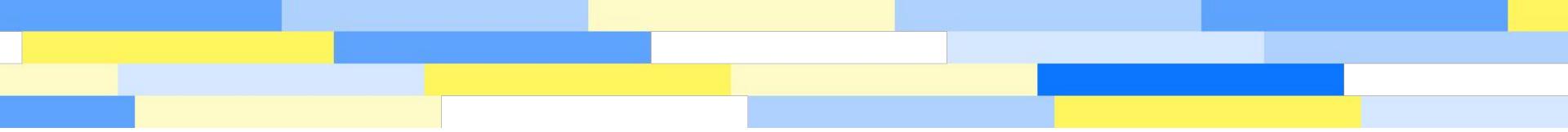
Current directory = “**training-modules**”

Relative file path =
“**intro-to-R-tidyverse/01-intro_to_base_R-live.Rmd**”



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](#)

The screenshot shows the RStudio interface with the following details:

- Editor Tab:** The main window displays the content of the file `01-intro_to_base_R-live.Rmd`. The code includes metadata like title, author, date, and output type, followed by sections for objectives and a list of topics.
- Environment Tab:** Shows the Global Environment, which is currently empty.
- Files Tab:** The "Files" tab is active, showing a list of files in the current directory:

Name	Size	Modified
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
00b-debugging_resources.md	13.6 KB	Apr 29, 2020
00c-good-scientific-coding-pr...	3.9 KB	Apr 29, 2020
01-intro_to_base_R-live.Rmd	16 KB	Apr 29, 2020
02-intro_to_ggplot2-live.Rmd	9.9 KB	Apr 29, 2020
03-intro_to_tidyverse-live.Rmd	16.4 KB	Apr 29, 2020
04a-intro_to_R-exercise.Rmd	4.1 KB	Apr 29, 2020
- Console Tab:** The console tab is visible at the bottom left.

R Notebooks

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

Output from above code chunk

Executable code chunk

Can click here to run a code chunk

The screenshot shows the RStudio interface with an R Notebook open. The notebook contains the following text:

```
82 For example, we can do some simple multiplication like
83 When you execute code within the notebook, the results
84 appear beneath the code.
85 Try executing this chunk by clicking the *Run* button
86 within the chunk or by
87 placing your cursor inside it and pressing
88 *Cmd+Shift+Enter*.
89
90 ````{r}
91 5 * 6
92 ````
```

The code chunk at lines 87-92 is highlighted with a red rectangle. The output of the code, '[1] 30', is highlighted with a blue rectangle and has a green arrow pointing to the 'Run' button in the toolbar above the code chunk.

The RStudio environment pane shows the Global Environment is empty. The file browser pane shows a folder structure under 'Home > training-modules > intro-to-R-tic'. The bottom pane shows the 'Console' tab with the command '# Introduction to R and RStudio' entered.

R Notebooks

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

The screenshot shows the RStudio interface with an R Notebook open. The notebook file is titled "01-intro_to_base_R-live.Rmd". The code chunk at line 88 contains the expression `5 * 6`, which is executed and returns the result `[1] 30` in the console output window. The RStudio environment pane shows that the global environment is empty. The files pane displays a folder structure: Home > training-modules > intro-to-R-tidyverse. A red box highlights the path "Home > training-modules > intro-to-R-tidyverse" in the files list.

Name	Size	Modified
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
00b-debugging_resources.md	13.6 KB	Apr 29, 2020
00c-good-scientific-coding-pr...	3.9 KB	Apr 29, 2020
01-intro_to_base_R-live.Rmd	16 KB	Apr 29, 2020
02-intro_to_ggplot2-live.Rmd	9.9 KB	Apr 29, 2020
03-intro_to_tidyverse-live.Rmd	16.4 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	4.1 KB	Apr 29, 2020

File Edit Code View Plots Session Build Debug Profile Tools Help trainee Sessions Project: (None) R 3.6.1

01-intro_to_base_R-live.Rmd*

82 For example, we can do some simple multiplication like this.

83 When you execute code within the notebook, the results appear beneath the code.

84 Try executing this chunk by clicking the ***Run*** button within the chunk or by

85 placing your cursor inside it and pressing ***Cmd+Shift+Enter***.

86

87 ````{r}`

88 `5 * 6`

89 `````

[1] 30

90

91 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

1:1 # Introduction to R and RStudio ▾ R Markdown ▾

Console

Environment History Connections

Import Dataset

Global Environment

Environment is empty

Files Plots Packages Help Viewer

New Folder Upload Delete Rename More

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

Name	Size	Modified
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
03-intro_to_tidyverse-live.Rmd	16.4 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	4.1 KB	Apr 29, 2020
..		
3.6 KB		
9 KB		
6 KB		
9 KB		

Click here to show the Console

The screenshot shows the RStudio interface with the following components:

- Top Bar:** Contains the RStudio logo, a search bar with the URL "rstudio.ccdatalab.org", and various application icons.
- File Menu:** File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help.
- User Information:** trainee, Sessions, Project: (None), R 3.6.1.
- Left Panel:** Shows the code editor for "01-intro_to_base_R-live.Rmd". The code includes:

```
113
114 ``{r}
115 x <- 5.5
116
117 x
118``
```

[1] 5.5

119
120 We can modify an existing variable by reassigning it to its same name.
121 Here we'll add `2` to `x` and reassign the result back to `x`.

1:1 # Introduction to R and RStudio
- Environment Tab:** Shows the global environment with a value for "x":

x	5.5
---	-----
- Files Tab:** Shows the directory structure:

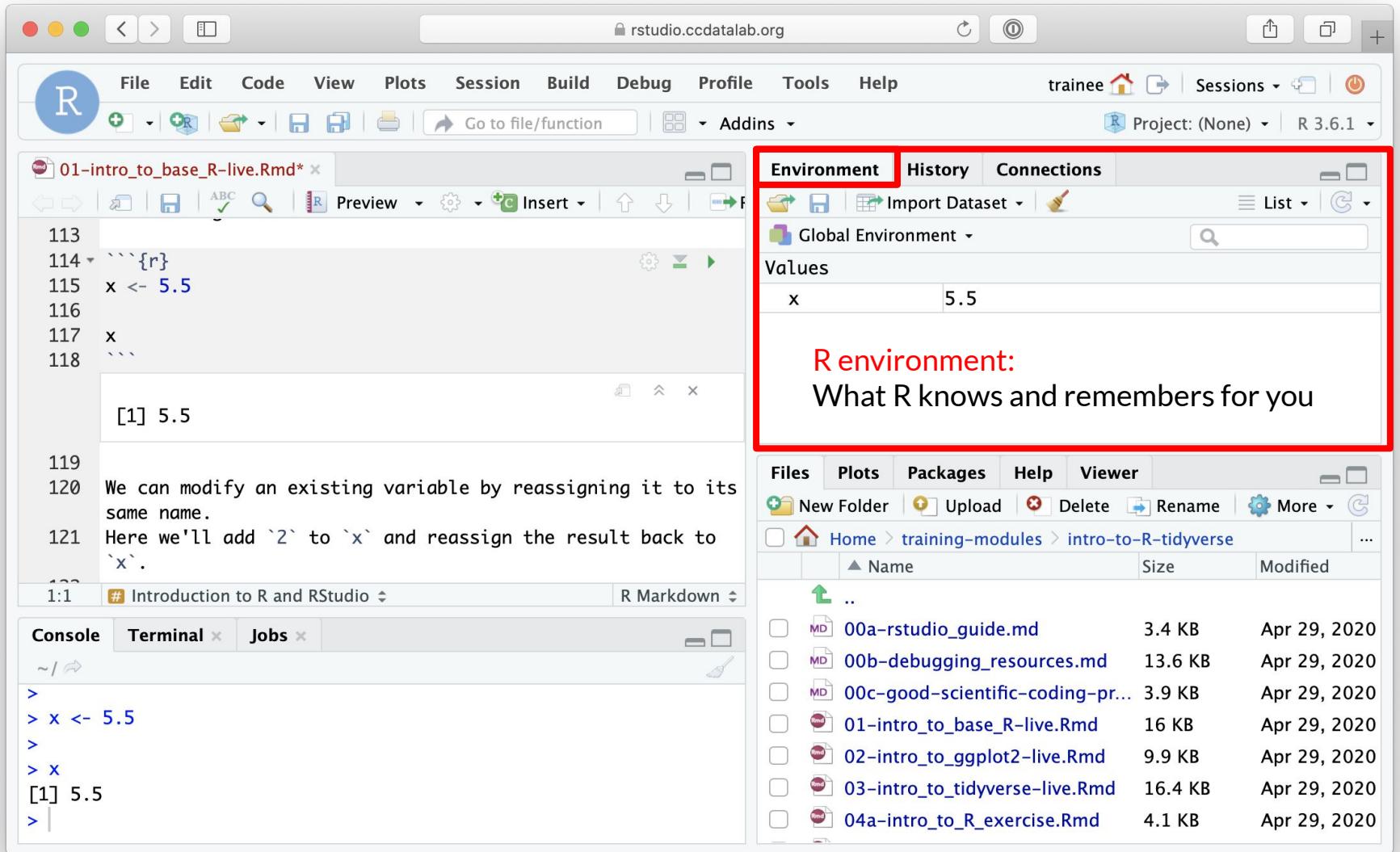
Name	Size	Modified
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
00b-debugging_resources.md	13.6 KB	Apr 29, 2020
00c-good-scientific-coding-pr... 01-intro_to_base_R-live.Rmd	3.9 KB	Apr 29, 2020
02-intro_to_ggplot2-live.Rmd	16 KB	Apr 29, 2020
03-intro_to_tidyverse-live.Rmd	9.9 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	16.4 KB	Apr 29, 2020
	4.1 KB	Apr 29, 2020
- Console Tab:** Shows the R console output:

```
>
> x <- 5.5
> R Console:
> x
[1] 5.5
What you are actually telling R to do
```

The screenshot shows the RStudio interface with several panes:

- Code/Script Editor:** The main editor pane displays an R Markdown script titled "01-intro_to_base_R-live.Rmd". The code includes a block of R code and a narrative text block. A red box highlights the entire editor area.
- Environment Pane:** Shows the current state of the R environment. It includes tabs for "Environment", "History", and "Connections". Under "Values", there is a single entry for "x" with the value "5.5".
- Files Pane:** Shows a file tree under "Home > training-modules > intro-to-R-tidyverse". The tree lists several R Markdown files: "00a-rstudio_guide.md", "00b-debugging_resources.md", "00c-good-scientific-coding-pr...". Below them are "01-intro_to_base_R-live.Rmd", "02-intro_to_ggplot2-live.Rmd", "03-intro_to_tidyverse-live.Rmd", and "04a-intro_to_R_exercise.Rmd". All files were modified on April 29, 2020.
- Console:** The bottom-left pane shows the R console history:

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



The screenshot shows the RStudio interface with the following components:

- Top Bar:** Contains the RStudio logo, menu items (File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help), session information (trainee), and project details (Project: (None) | R 3.6.1).
- Code Editor:** Displays the file `01-intro_to_base_R-live.Rmd*` containing R code and its output. The code includes:

```
113
114 ````{r}
115 x <- 5.5
116
117 x
118 ````
```

[1] 5.5

119
120 We can modify an existing variable by reassigning it to its same name.
121 Here we'll add `2` to `x` and reassign the result back to `x`.
- Environment Tab:** Shows the variable `x` with the value `5.5`.
- Files Tab:** A red box highlights this tab, which displays a list of files in the current directory:

Name	Size	Modified
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
00b-debugging_resources.md	13.6 KB	Apr 29, 2020
00c-good-scientific-coding-pr... 01-intro_to_base_R-live.Rmd	3.9 KB	Apr 29, 2020
02-intro_to_ggplot2-live.Rmd	16 KB	Apr 29, 2020
03-intro_to_tidyverse-live.Rmd	9.9 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	16.4 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	4.1 KB	Apr 29, 2020
- Console:** Shows the command `> x <- 5.5` and its output `[1] 5.5`.
- Terminal:** Shows the command `> x`.
- Jobs:** Shows the command `>`.

Other Assistance Tabs:

Things that help you in your coding

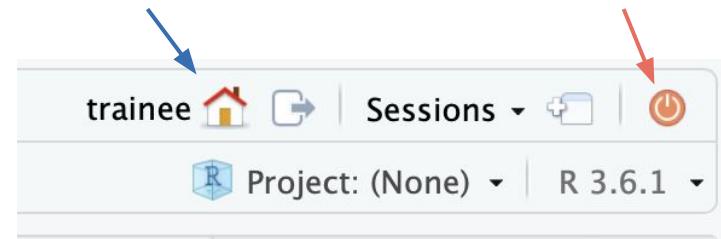
Files	Plots	Packages	Help	Viewer
New Folder	Upload	Delete	Rename	More
Home > training-modules > intro-to-R-tidyverse				

Name	Size	Modified
00a-rstudio_guide.md	3.4 KB	Apr 29, 2020
00b-debugging_resources.md	13.6 KB	Apr 29, 2020
00c-good-scientific-coding-pr... 01-intro_to_base_R-live.Rmd	3.9 KB	Apr 29, 2020
02-intro_to_ggplot2-live.Rmd	16 KB	Apr 29, 2020
03-intro_to_tidyverse-live.Rmd	9.9 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	16.4 KB	Apr 29, 2020
04a-intro_to_R_exercise.Rmd	4.1 KB	Apr 29, 2020

RStudio Sessions

- On the server, R run 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

The 'Session Page' interface for RStudio Server Pro. At the top, it says 'R Studio Server Pro' and shows 'trainee Logout'. Below that is a navigation bar with 'Sessions', '+ New Session', 'Suspend all', 'Quit all', 'Projects', '+ New Project', and 'Open Project'. Under the 'Sessions' section, there is a table with one row:

(Home)	IDLE	R 3.6.1
(Home)	CREATED: 12:59:54 PM	LAST USED: 12:59:55 PM

Below the table, the text 'Currently running sessions' is displayed in green.