welcome.html

workshop.R

Coding with ‘R’ {

[For Ecologists Workshop]

Learn data manipulation and visualization
with the Ecology and Zoology Course Union

}

R

Table Of ‘Contents’

welcome.html

workshop.R

Base R {

Base R refers to the functions built into R inherently. Using these functions, you tell R exactly what you want it to do, step by step

}

tidyverse {

tidyverse refers to a group of functions (e.g., dplyr, ggplot2, stringr) that you load into R. Using these, you describe what you want done using a verb-based style

}

R

Where to get help

‘RStudio has built in cheat sheets!’ %>%

these are great if you need quick reminders of all the functions available in a package

‘RStudio has built in help functions’ %>%

a single `?` will search for the help page of a given function
two `??` does a key word search in all the documentation bundled with R
`help(function)` also provides detealed documentation

welcome.html

workshop.R

A note on version control

version control is a helpful not only for yourself, but for anyone else who is looking at your code

in ecology and related fields, Git is commonly used for version control and for publishing repositories

we highly encourage that if you plan on using R for research that you spend some time learning how to use Git and GitHub

R

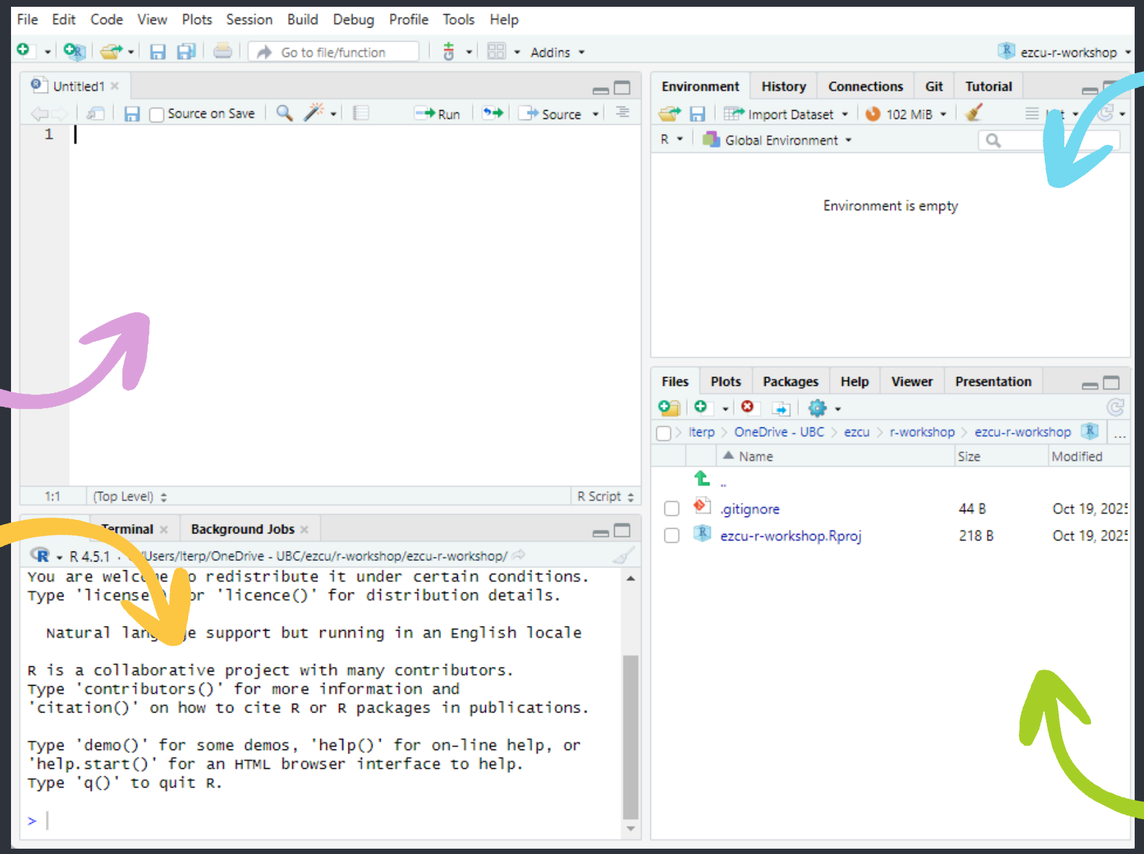
welcome.html

workshop.R

RStudio panes

Source

Console



Environment

Plots & Files

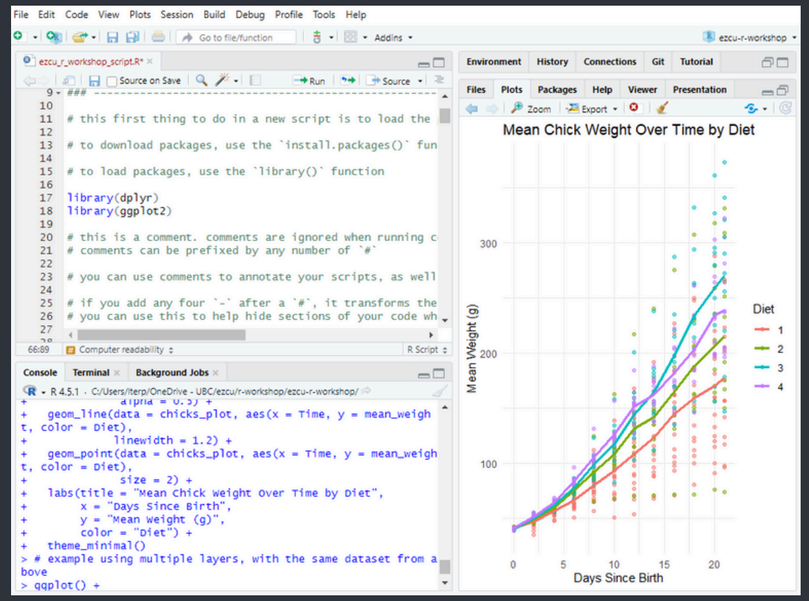
welcome.html

workshop.R

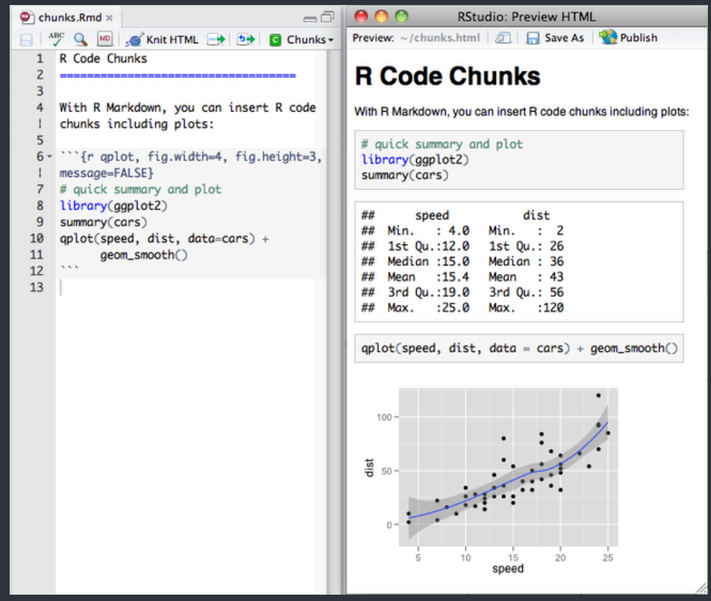
Getting started

FILE TYPES: The two most common file types used in RStudio are R scripts (.R) and R markdown files (.Rmd)

R Script



RMarkdown



https://rmarkdown.rstudio.com/authoring_quick_tour.html

Naming Conventions

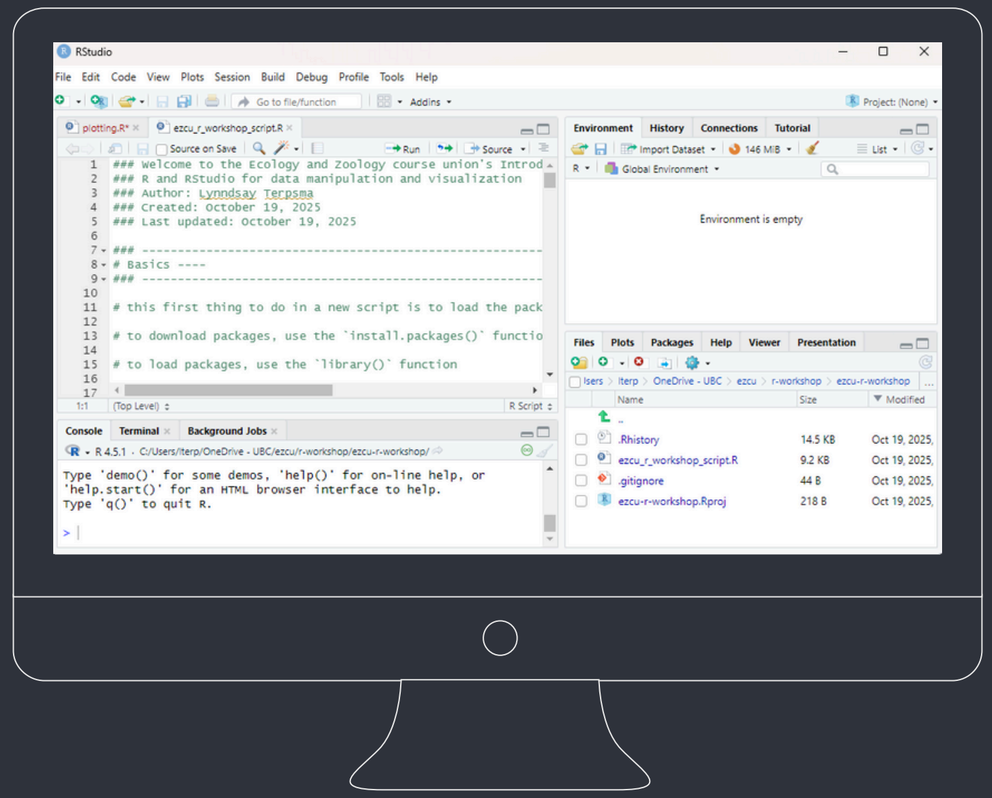
How to name files:

- **Step 01** use alphanumerical characters that are compatible with all computer systems
- **Step 02** have concise names that provide brief information. Names should be searchable and understandable
- **Step 03** start with an element that will order the files

Now that we've covered the basics, let's get coding!

Make sure:

1. R and RStudio are installed
2. You have downloaded the script provided on the EZCU canvas shell!

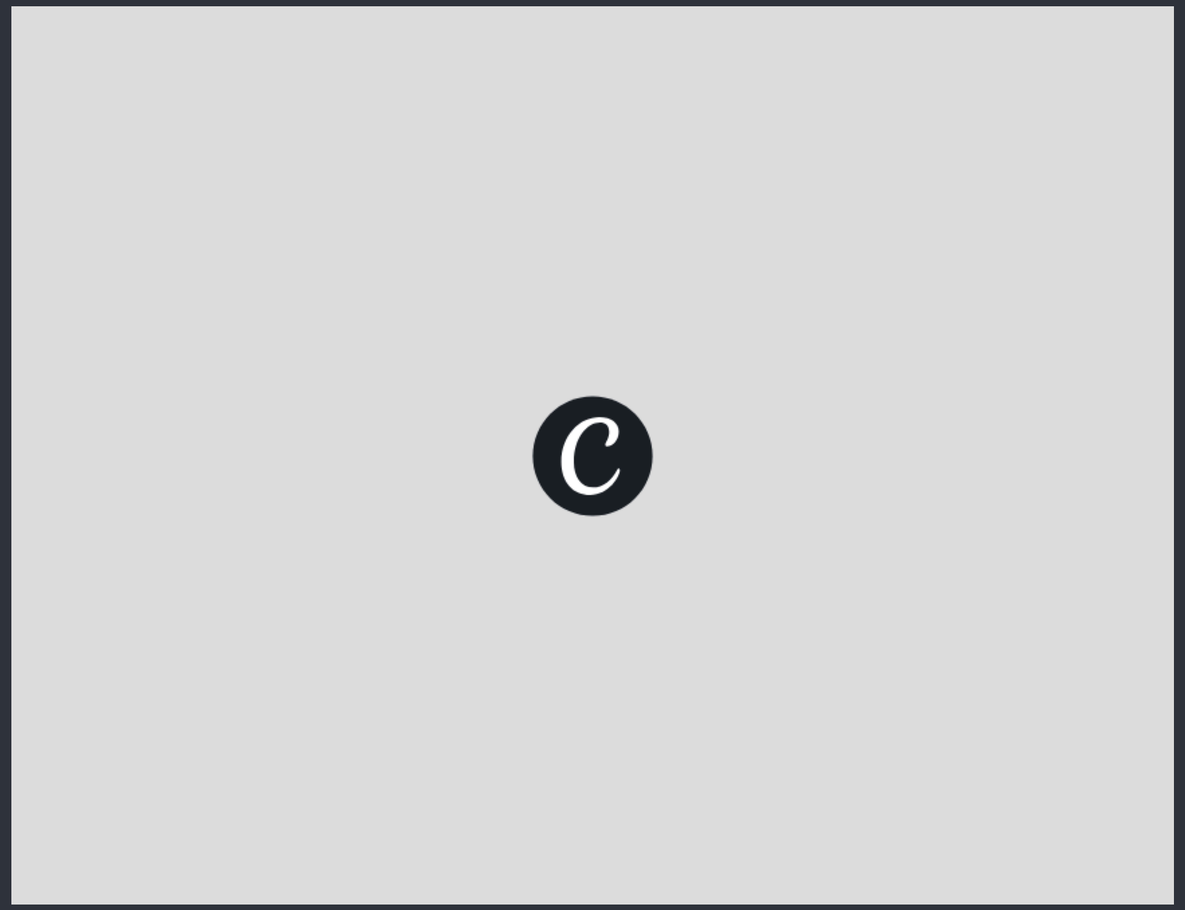


welcome.html

workshop.R

1
2
3
4
5
6
7
8
9
10
11
12
13
14

Data manipulation

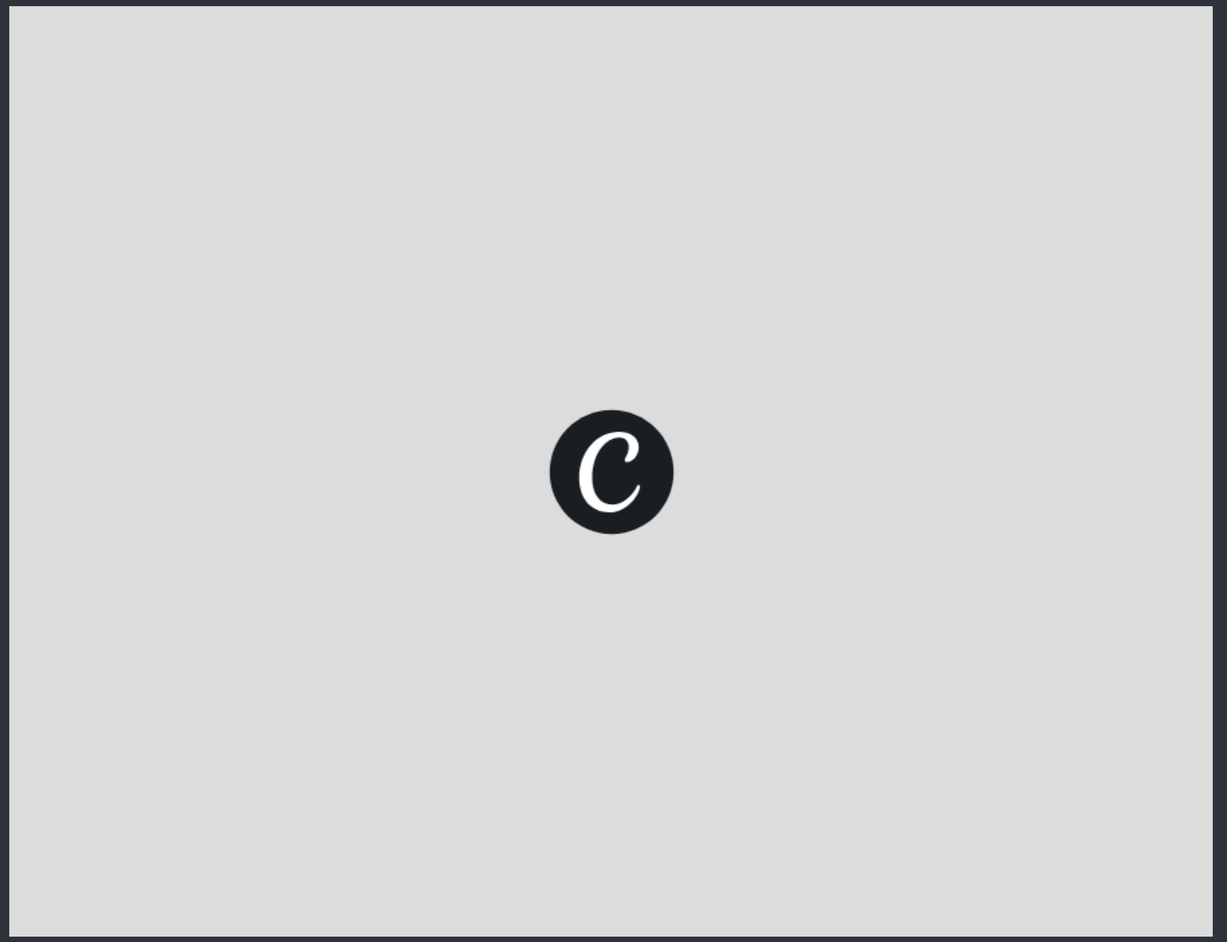


R

welcome.html

workshop.R

Data visualization



R

Thanks

Feel free to contact me with any questions you have!

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References:

- https://speciationgenomics.github.io/R_introduction/
- https://github.com/csc-ubc-okanagan/R-Fundamentals/tree/main
- https://drive.google.com/drive/u/0/folders/1clafk9L6OCyCccYSIErvUByNu9hn9gMs
- https://posit.co/resources/cheatsheets/
- https://ubc-library-rc.github.io/rdm/content/01_file_naming.html

Other resources to look at for R help (in no particular order)

- https://www.rforecology.com/post/
- https://csc-ubc-okanagan.github.io/R-Python-Blog/