Organizing and Visualizing Data in R Workshop

By Gabriel Kamener
FCE Information Manager, Florida International University

Today’s workshop

- Workshop will focus on:
  - RStudio projects
  - Organizing and visualizing data in R[1]
  - Organizing and documenting code[2]
- After this workshop, you will be able to:
  - Organize data projects
  - Manipulate and visualize data in R
  - Organize, document, and review code

1. With content adapted from Seok et al. 2023
2. With content adapted from Ivimey-Cook et al. 2023

Today’s workshop

- Workshop files: https://github.com/FCE-LTER/organizing_and_visualizing_data_in_r_spring_2024_workshop

Schedule

Time	Topic	Content
4:00 – 4:10	Introduction and setup	Why organize data? Why organize and document code?
4:10 – 4:15	Best practices in using RStudio projects	What are RStudio projects, and how can we utilize them?
4:15 – 4:35	Manipulating imported data	Manipulate, analyze, and export data with tidyverse.
4:35 – 4:50	Visualizing data	Plot and customize visualizations with ggplot.
4:50 – 5:20	Code organization and commenting	The 4Rs of code review, organizing code, reviewing code
5:20 – 6:00	Personal project and code development	Work on improving project and code

Introduction

- Why organize data projects?
- Why organize and document code?

My initial R experience

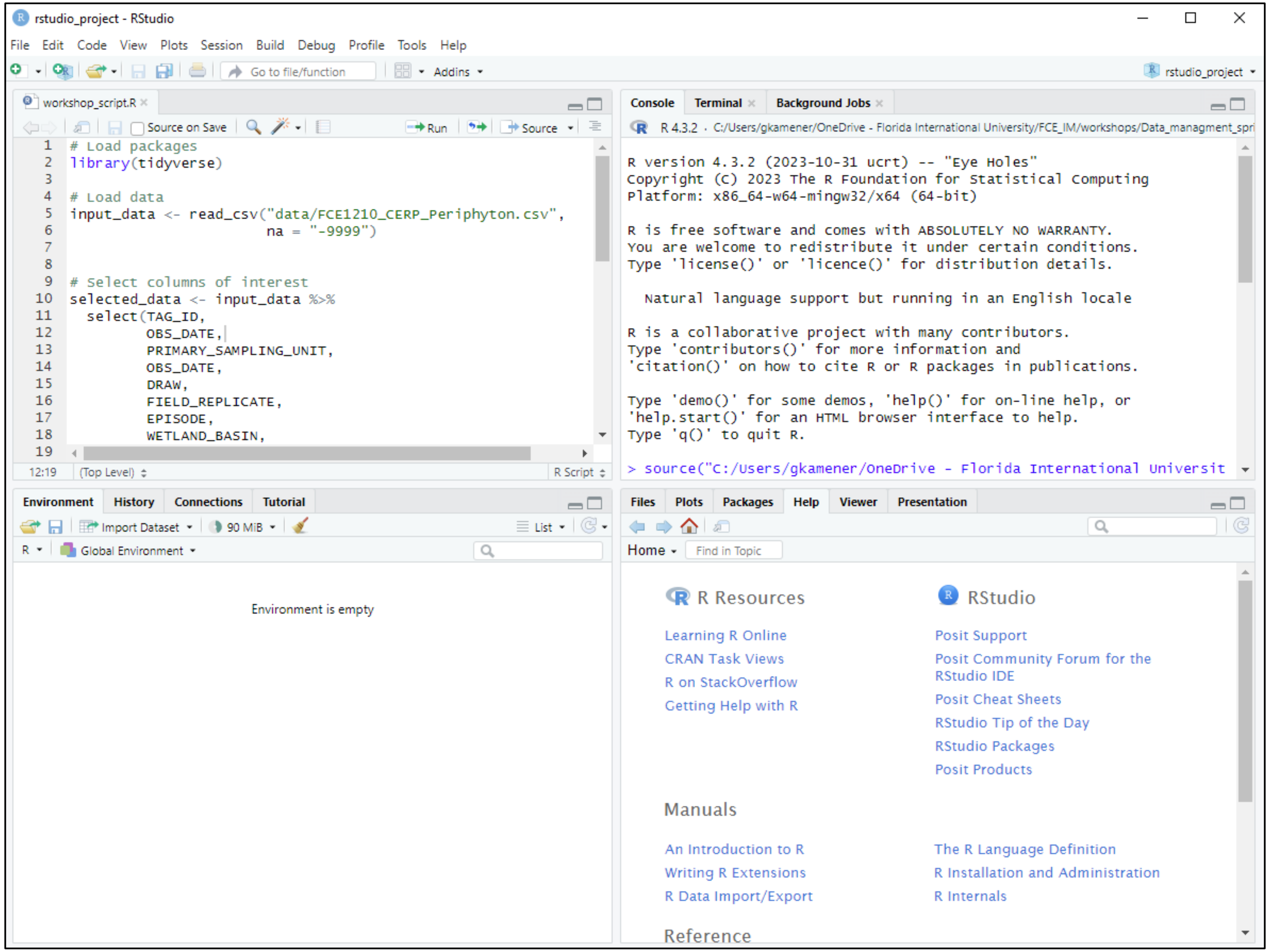
Artwork by @allison_horst (CC BY 4.0)

After some organization

bless this workflow
TOOLS
REPORT
FILES
CODE
@allison_horst

Artwork by @allison_horst (CC BY 4.0)

RStudio



```r
# Load packages
library(tidyverse)

# Load data
input_data <- read_csv("data/FCE1210_CERP_Periphyton.csv",
                       na = "-9999")


# Select columns of interest
selected_data <- input_data %>%
  select(TAG_ID,
         OBS_DATE,
         PRIMARY_SAMPLING_UNIT,
         OBS_DATE,
         DRAW,
         FIELD_REPLICATE,
         EPISODE,
         WETLAND_BASIN,
```

```
R version 4.3.2 (2023-10-31 ucrt) -- "Eye Holes"
Copyright (C) 2023 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (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.

  Natural language support but running in an English locale

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.

> source("C:/Users/gkamener/OneDrive - Florida International Universit
```

Environment is empty

RStudio Projects

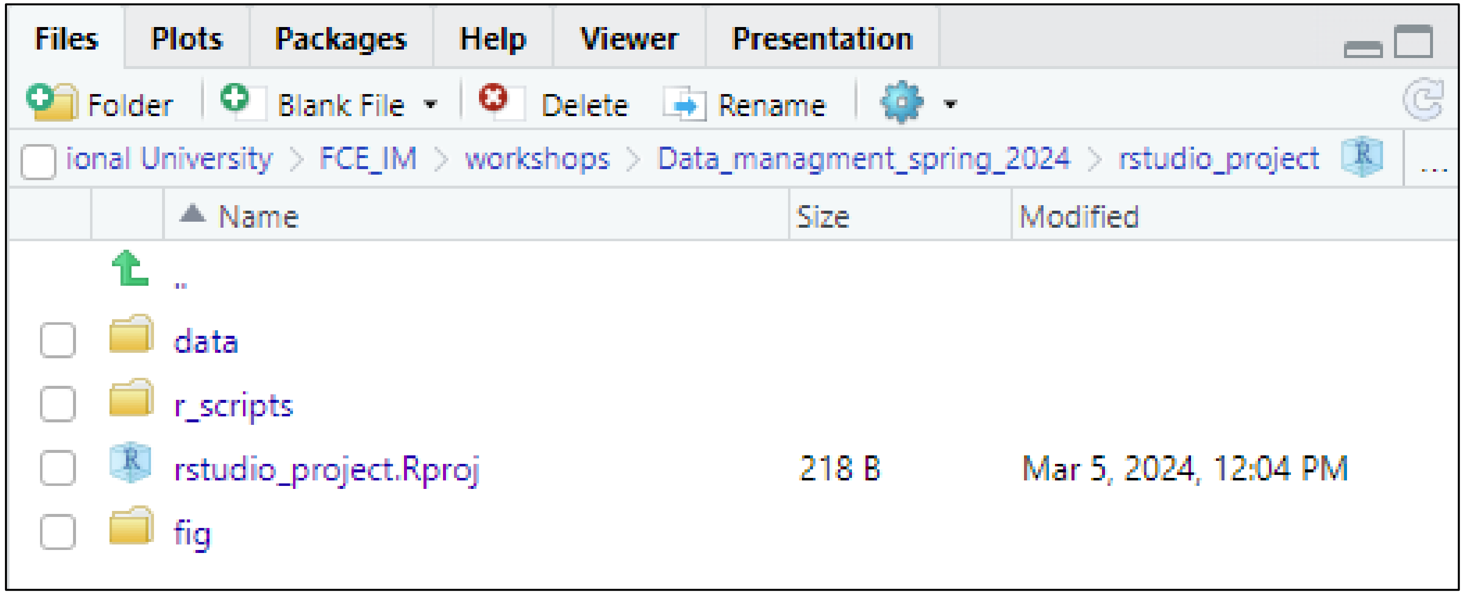
Advantages of RStudio Projects:

- Automatically set working directory
- Portable
- Share friendly
- Can integrate with Git/GitHub
- Can aid reproducibility with renv package

Setup an RStudio Project

1. Start RStudio.
2. Under the File menu, click on New Project. Choose New Directory, then New Project.
3. Enter a name for this new folder (or “directory”), and choose a convenient location for it. This will be your working directory for the rest of the day (e.g., ~/fce_data_workshop).
4. Click on Create Project.
5. Create folders for data (with “raw”, “intermediate”, and “final” subfolders), r scripts, and figures in your working directory.
6. Download code handout + data files and place into folders.
7. (Optional) Set Preferences to ‘Never’ save workspace in RStudio.

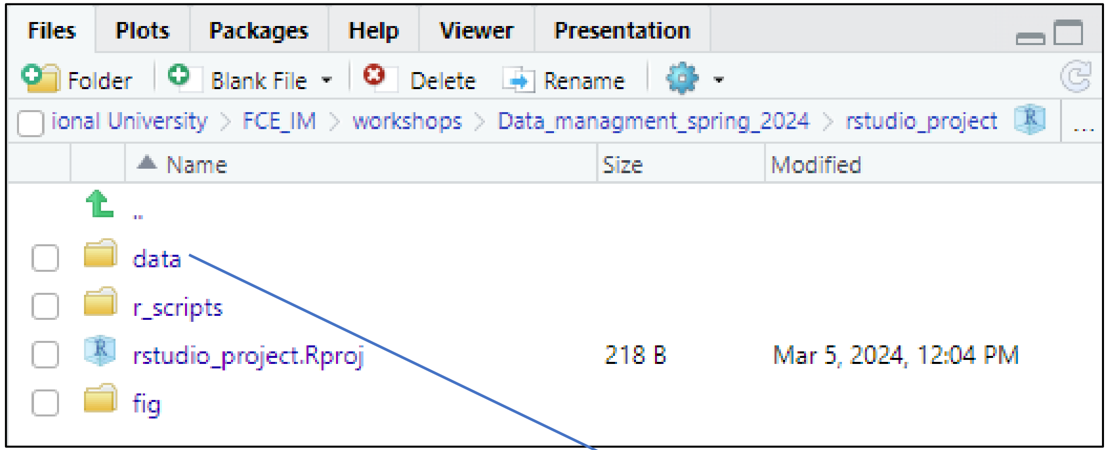
Organizing your working directory



ional University > FCE_IM > workshops > Data_managment_spring_2024 > rstudio_project

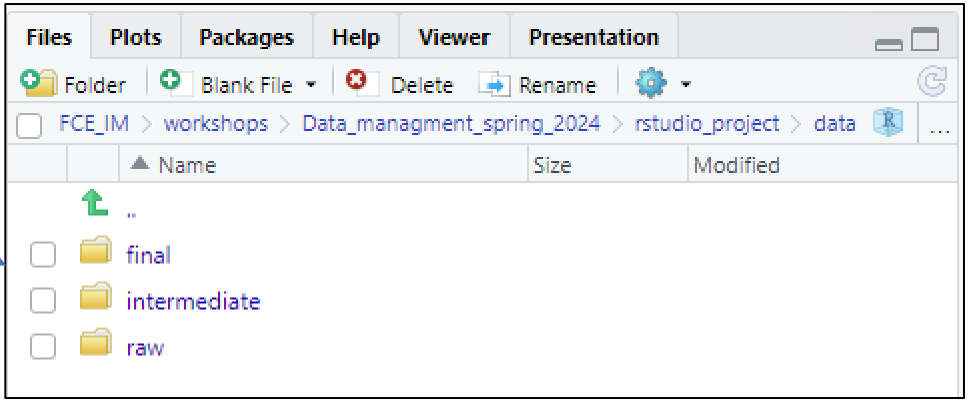
	Name	Size	Modified
	..		
□	data		
□	r_scripts		
□	rstudio_project.Rproj	218 B	Mar 5, 2024, 12:04 PM
□	fig		

Organizing your working directory



ional University > FCE_IM > workshops > Data_managment_spring_2024 > rstudio_project

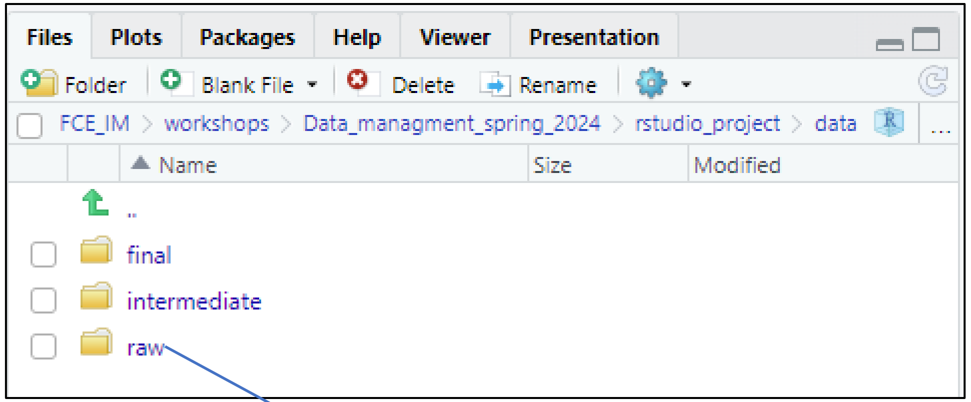
Name	Size	Modified
..		
data		
r_scripts		
rstudio_project.Rproj	218 B	Mar 5, 2024, 12:04 PM
fig		



FCE_IM > workshops > Data_managment_spring_2024 > rstudio_project > data

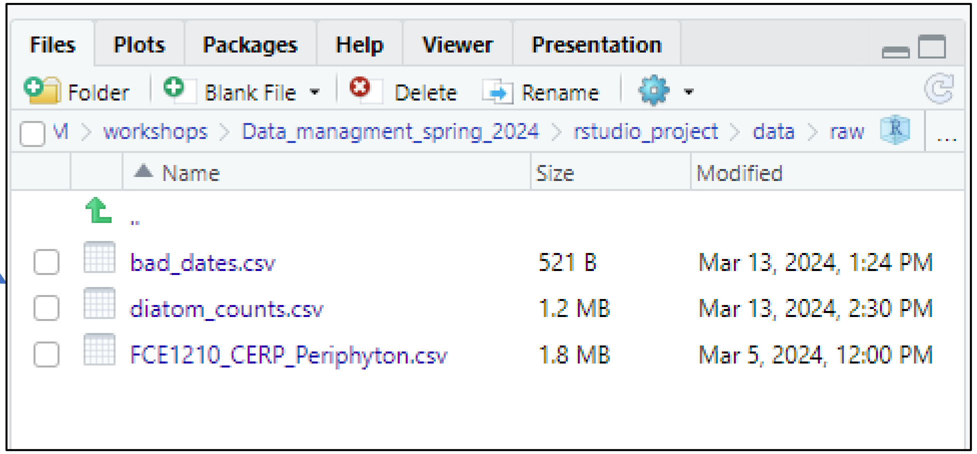
Name	Size	Modified
..		
final		
intermediate		
raw		

Organizing your working directory



FCE_IM > workshops > Data_managment_spring_2024 > rstudio_project > data

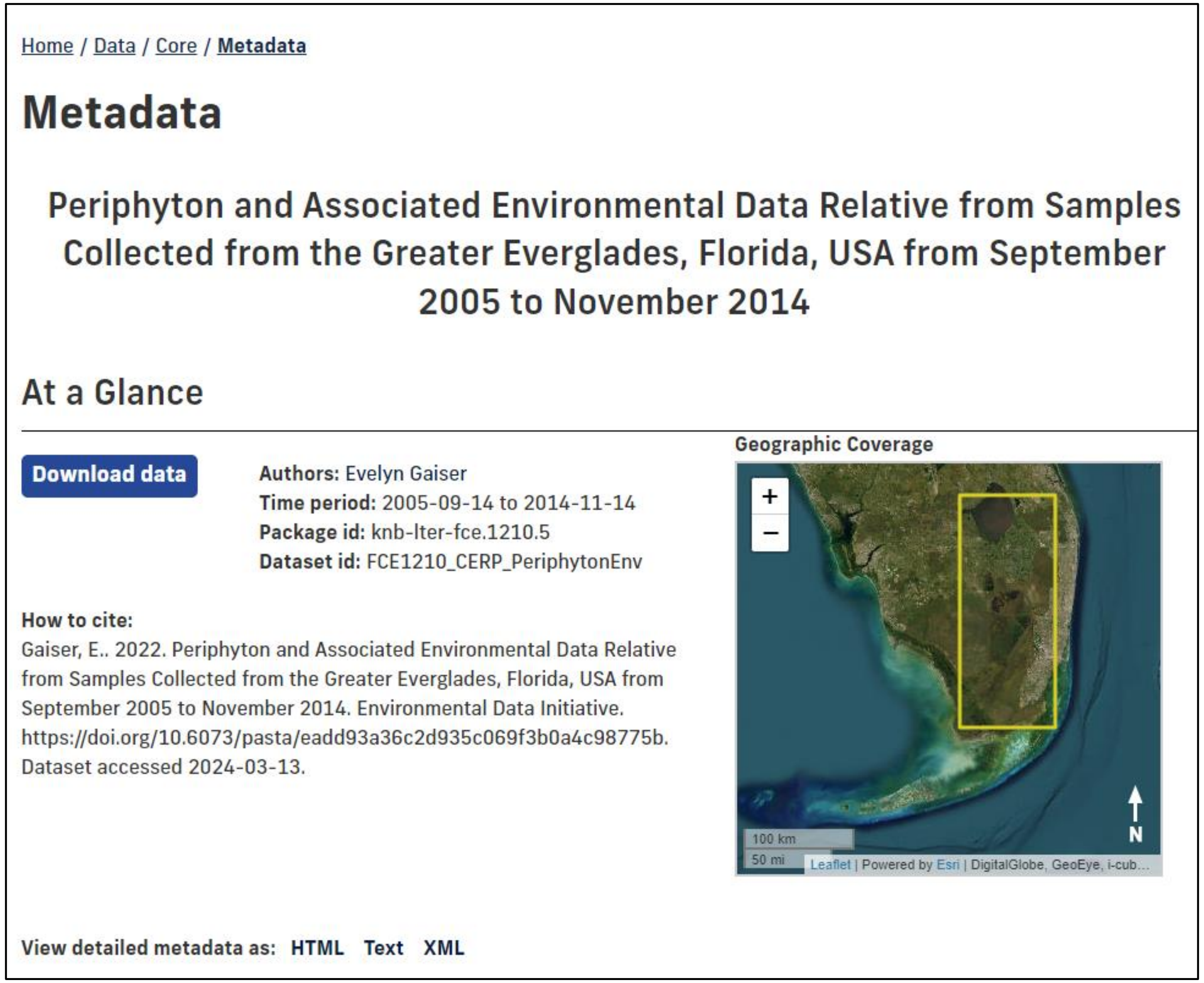
	Name	Size	Modified
	..		
□	final		
□	intermediate		
□	raw		



M > workshops > Data_managment_spring_2024 > rstudio_project > data > raw

	Name	Size	Modified
	..		
□	bad_dates.csv	521 B	Mar 13, 2024, 1:24 PM
□	diatom_counts.csv	1.2 MB	Mar 13, 2024, 2:30 PM
□	FCE1210_CERP_Periphyton.csv	1.8 MB	Mar 5, 2024, 12:00 PM

The data we are using today



Home / Data / Core / **Metadata**

Metadata

Periphyton and Associated Environmental Data Relative from Samples Collected from the Greater Everglades, Florida, USA from September 2005 to November 2014

At a Glance

Download data

Authors: Evelyn Gaiser
Time period: 2005-09-14 to 2014-11-14
Package id: knb-lter-fce.1210.5
Dataset id: FCE1210_CERP_PeriphytonEnv

How to cite:
Gaiser, E.. 2022. Periphyton and Associated Environmental Data Relative from Samples Collected from the Greater Everglades, Florida, USA from September 2005 to November 2014. Environmental Data Initiative. https://doi.org/10.6073/pasta/eadd93a36c2d935c069f3b0a4c98775b. Dataset accessed 2024-03-13.

Geographic Coverage

View detailed metadata as: **HTML** **Text** **XML**

https://fce-lter.fiu.edu/data/core/metadata/?packageid=knb-lter-fce.1210.5

Starting with data

- Open code handout file
- library(tidyverse)

```
peri_df <- read_csv("data/raw/FCE1210_CERP_Periphyton.csv",
                    na = "-9999")

diatoms_df <- read_csv("data/raw/diatom_counts.csv",
                       na = "NA")

bad_dates_df <- read_csv("data/raw/bad_dates.csv",
                         na = "-9999")
```

Indexing and subsetting data frames

- Indexed by row, column
- Can subset as data_frame[row_index, column_index]
- Subset data frame
  - peri_df[1, 1]
  - peri_df[1,]
  - peri_df[, 1]

Indexing and subsetting data frames

- Subset multiple rows/columns
  - peri_df[c(1, 2, 3), c(5, 6)]
  - peri_df[1:3, 5:6]
- Return vector instead with “[[ ]]”
  - peri_df[[1, 1]]

Indexing and subsetting data frames

- Subset by column name
  - peri_df[1, "WATER_DEPTH_CM"]

- Heads and tails
  - first_ten_rows <- head(peri_df, 10)
  - first_ten_rows
  - last_ten_rows <- tail(peri_df, 10)
  - view(last_ten_rows)

Factors

- Useful for categorical variables
  - peri_df$FLOATING_SP1 <- factor(peri_df$FLOATING_SP1)
  - nlevels(peri_df$FLOATING_SP1)
  - levels(peri_df$FLOATING_SP1)

Formatting dates

- my_date <- ymd("2015-01-01")
- str(my_date)

- my_date <- ymd(paste("2015", "1", "1", sep = "-"))
- str(my_date)

Formatting dates

- paste(bad_dates_df$YEAR, bad_dates_df$MONTH, bad_dates_df$DAY, sep = "-")

- ymd(paste(bad_dates_df$YEAR, bad_dates_df$MONTH, bad_dates_df$DAY, sep = "-"))

Formatting dates

- bad_dates_df$DATE <- ymd(paste(bad_dates_df$YEAR, bad_dates_df$MONTH, bad_dates_df$DAY, sep = "-"))

- str(bad_dates_df)

- summary(bad_dates_df$DATE)

- missing_dates <- bad_dates_df[is.na(bad_dates_df$DATE), c("YEAR", "MONTH", "DAY")]

- head(missing_dates)

Manipulating data

- Select
- Filter
- Mutate
- Pivot wider and longer
- Group and summarize
- Count
- Exporting data

Select

```
selected_peri <- peri_df %>%
  dplyr::select(TAG_ID,
                OBS_DATE,
                PRIMARY_SAMPLING_UNIT,
                FIELD_REPLICATE,
                EPISODE,
                WETLAND_BASIN,
                WATER_DEPTH_CM,
                FLOATING_SP1,
                PERI_AFDM_G_PER_M2,
                PERI_TP_UG_PER_G_DRY_MASS,
                PERI_PROP_ORGANIC
  )
```

Filter

```
filtered_peri <- selected_peri %>%
        filter(month(OBS_DATE) > 8)

filter_missing_peri_tp <- selected_peri %>%
        filter(!is.na(PERI_TP_UG_PER_G_DRY_MASS))
```

Mutate

```
mutated_peri <- filtered_peri %>%  mutate(peri_percent_organic = PERI_PROP_ORGANIC*100)
```

```
mutated_peri %>%
        select(PERI_PROP_ORGANIC,
                 peri_percent_organic)
```

Pivot wider and longer

```
diatoms_counts_long <- diatoms_df %>%
        pivot_longer(-c(TAG_ID:LSU_NAME),
                     values_to = "SPECIMENS_COUNTED",
                     names_to = "TAXON_CODE")

diatom_counts_wide <- diatoms_counts_long %>%
        pivot_wider(names_from = "TAXON_CODE",
                    values_from = "SPECIMENS_COUNTED",
                    names_sort = TRUE,
                    values_fill = 0)
```

Group and summarize

```
summarized_water_depths <- filtered_peri %>%
      group_by(WETLAND_BASIN,
                YEAR = year(OBS_DATE)) %>%
      summarize(mean_water_depth_cm = mean(WATER_DEPTH_CM))

summarized_water_depths

summarized_water_depths_wide <- summarized_water_depths %>%
      pivot_wider(names_from = WETLAND_BASIN,
                 values_from = mean_water_depth_cm)

summarized_water_depths_wide
```

Group and summarize

```
diatoms_counts_filtered <- diatoms_counts_long %>%
        filter(!is.na(SPECIMENS_COUNTED)
              & SPECIMENS_COUNTED != 0)

total_diatoms <- diatoms_counts_long %>%
        group_by(TAG_ID) %>%
        summarize(TOTAL_COUNT = sum(SPECIMENS_COUNTED))

total_diatoms
```

Group and summarize

```
rel_abund <- diatoms_counts_filtered %>%
        # Using dplyr's left_join function to join with the total_diatoms data frame
        left_join(., total_diatoms, by = "TAG_ID") %>%
        mutate(RELATIVE_PCT_ABUND = SPECIMENS_COUNTED/TOTAL_COUNT*100) %>%
        select(TAG_ID,
              OBS_DATE,
              PRIMARY_SAMPLING_UNIT,
             WETLAND_BASIN,
             TAXON_CODE,
             RELATIVE_PCT_ABUND
)

rel_abund
```

Count

```
filtered_peri %>%
        count(FLOATING_SP1, sort = TRUE)

diatoms_counts_filtered %>%
        count(TAXON_CODE, sort = TRUE)
```

Exporting data

write_csv(filtered_peri, "data/**intermediate**/filtered_peri.csv")

write_csv(summarized_water_depths_wide,
"data/**final**/summarized_water_depths_wide.csv")

Activity: make your own variable

- Organize your data
- Mutate a new variable
- Share that variable
  (including how you made it)
  with your neighbor

Visualizing data with ggplot

```
#ggplot(data = <DATA>, mapping = aes(<MAPPINGS>)) +  <GEOM_FUNCTION>()

ggplot(data = filtered_peri)

ggplot(data = filtered_peri, mapping = aes(x = WATER_DEPTH_CM, y =
PERI_AFDM_G_PER_M2))
```

Scatter plots

```
ggplot(data = filtered_peri, mapping = aes(x = WATER_DEPTH_CM, y = PERI_AFDM_G_PER_M2)) +
        geom_point()
```

Boxplots

```
ggplot(data = filtered_peri, mapping = aes(x = WETLAND_BASIN, y =
WATER_DEPTH_CM)) +
        geom_boxplot()
```

Trend lines

```
ggplot(data = filtered_peri, mapping = aes(x = year(OBS_DATE), y =
WATER_DEPTH_CM)) +
        geom_line()
```

```
ggplot(data = summarized_water_depths, mapping = aes(x = YEAR, y =
mean_water_depth_cm, color = WETLAND_BASIN)) +
        geom_line() +
        scale_x_continuous(breaks = c(2005:2014))
```

Stacked bar

```
rel_abund_2014_W3B <- rel_abund %>%
        filter(year(OBS_DATE) == 2014
              & WETLAND_BASIN == "W3B")

ggplot(rel_abund_2014_W3B,
        aes(fill = TAXON_CODE,
             y = RELATIVE_PCT_ABUND,
             x = PRIMARY_SAMPLING_UNIT)) +
        geom_bar(position="stack", stat="identity")
```

Customizing plots

```
ggplot(rel_abund_2014_W3B,
          aes(fill = TAXON_CODE,
          y = RELATIVE_PCT_ABUND,
          x = PRIMARY_SAMPLING_UNIT)) +
          geom_bar(position="stack", stat="identity") +
          labs(title = "Relative % abundance at W3B sites in 2014",
                x = "Primary Sampling Unit",
                y = "Relative Percent Abundance",
                fill = "Diatom taxon code") +
        theme(axis.title.x = element_text(size = 11),
                axis.title.y = element_text(size = 15))
```

Customizing plots

```
rel_abund_2014_w3b_cut <- rel_abund %>%
        filter(year(OBS_DATE) == 2014
        & WETLAND_BASIN == "W3B") %>%
        mutate(TAXON_CODE = if_else(RELATIVE_PCT_ABUND < 2,
                                    "OTHER",
                                     TAXON_CODE)) %>%
        group_by(PRIMARY_SAMPLING_UNIT,
                 TAXON_CODE) %>%
        summarize(RELATIVE_PCT_ABUND = sum(RELATIVE_PCT_ABUND))
```

Customizing plots

```
plot_2014_w3b_cut <- ggplot(rel_abund_2014_w3b_cut,
                            aes(fill = TAXON_CODE,
                                y = RELATIVE_PCT_ABUND,
                                x = PRIMARY_SAMPLING_UNIT)) +
  geom_bar(position="stack", stat="identity") +
  labs(title = "Relative % abundance at W3B sites in 2014",
       x = "Primary Sampling Unit",
       y = "Relative Percent Abundance",
       fill = "Diatom taxon code") +
  theme(plot.title = element_text(size = 15),
        axis.title.x = element_text(size = 12),
        axis.title.y = element_text(size = 12))
```

Customizing plots

plot_2014_w3b_cut

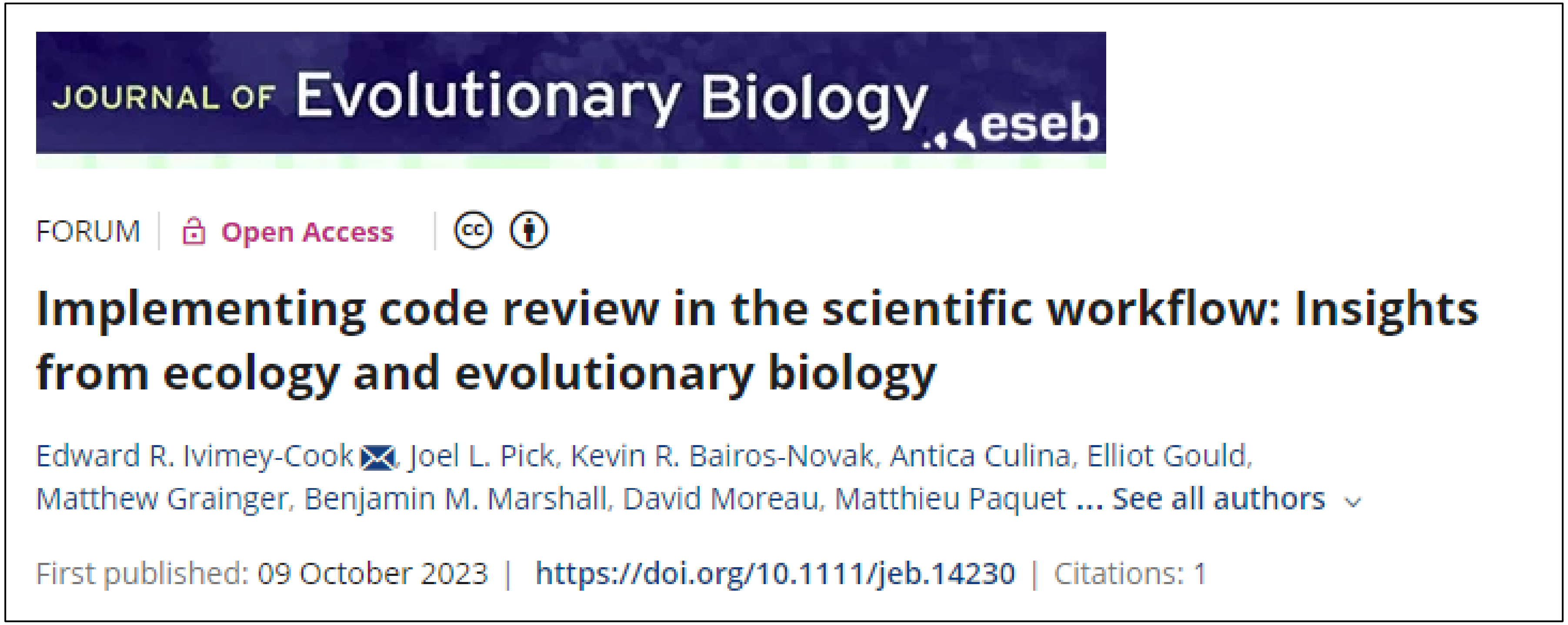
Saving plots

```
ggsave("fig/W3B_2014_relative_abundance.png",
          plot = plot_2014_w3b_cut)

ggsave("fig/W3B_2014_relative_abundance_custom_size.png",
          plot = plot_2014_w3b_cut,
          width = 46,
          height = 26,
          units = "cm",
          limitsize = FALSE)
```

Make your own plot

- Make your own plot
- Share it with your neighbor (including how you made it)

Code organization and review



FORUM | Open Access | 🅭 🅯

Implementing code review in the scientific workflow: Insights from ecology and evolutionary biology

Edward R. Ivimey-Cook, Joel L. Pick, Kevin R. Bairos-Novak, Antica Culina, Elliot Gould, Matthew Grainger, Benjamin M. Marshall, David Moreau, Matthieu Paquet ... See all authors

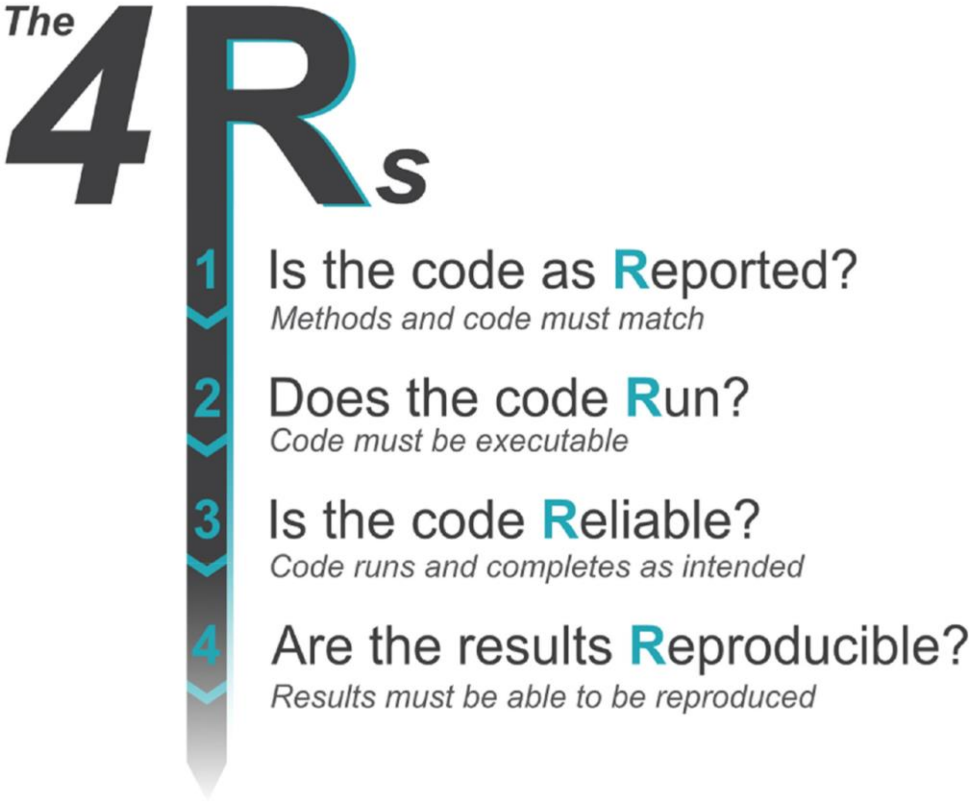
First published: 09 October 2023 | https://doi.org/10.1111/jeb.14230 | Citations: 1

https://doi.org/10.1111/jeb.14230

Potential code issues

- Reading in data files with paths outside project
- Order of workflow is unclear
- Comments say “go right” but code goes left
- Code fails to run on another computer
- Code fails or outputs change after updating R or packages
- Results not reproducible for manuscript reviewer

The four ‘Rs’ of code review



1 Is the code as **R**eported?
Methods and code must match

2 Does the code **R**un?
Code must be executable

3 Is the code **R**eliable?
Code runs and completes as intended

4 Are the results **R**eproducible?
Results must be able to be reproduced

J of Evolutionary Biology, Volume: 36, Issue: 10, Pages: 1347-1356, First published: 09 October 2023, DOI: (10.1111/jeb.14230)

Is the code as Reported?

- Are analyses as described in manuscript?
- Are relevant packages (with version numbers) documented in manuscript?

Does the code Run?

- library(tidyverse)
  Error in library(tidyverse): there is no package called ‘tidyverse’.
- install.packages("tRophicPosition")
  Warning in install.packages :
  package ‘tRophicPosition’ is not available for this version of R
- Misspelled code

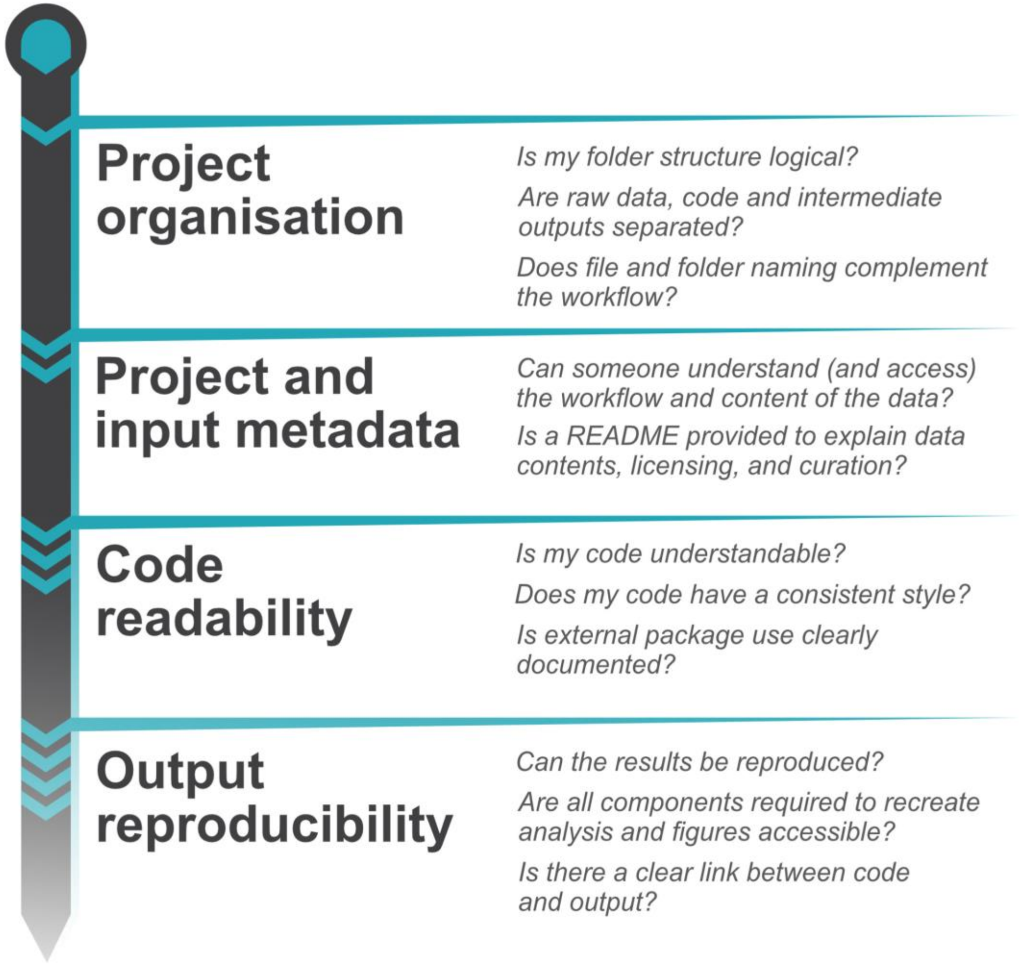
Is the code Reliable?

-
  ```
  #remove MC28 duplicate empty stomach
  stomachs.raw <- stomachs.raw[-c(4),]
  ```
  - May run but removes different row than described

Are the results Reproducible?

- Do reproduced results match those reported?
- If they differ, by how much?
- Is an observed difference reasonable to expect?

Where code fits into the workflow



Project organisation

Is my folder structure logical?

Are raw data, code and intermediate outputs separated?

Does file and folder naming complement the workflow?

Project and input metadata

Can someone understand (and access) the workflow and content of the data?

Is a README provided to explain data contents, licensing, and curation?

Code readability

Is my code understandable?

Does my code have a consistent style?

Is external package use clearly documented?

Output reproducibility

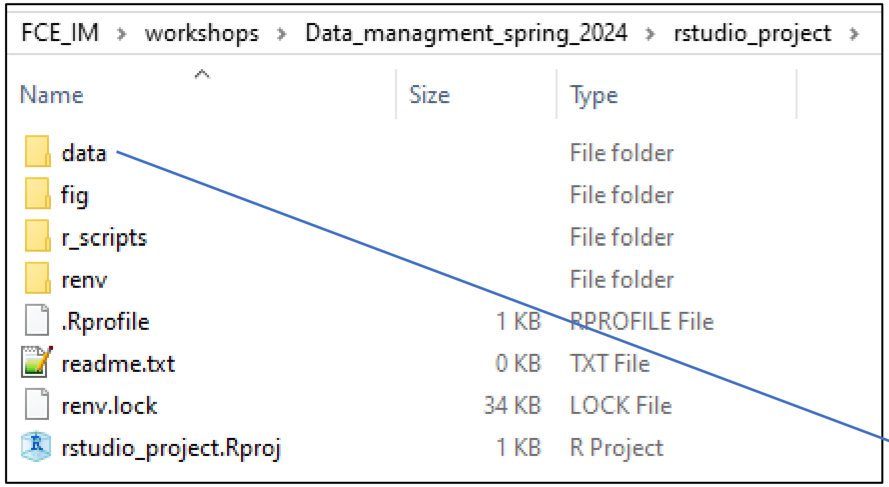
Can the results be reproduced?

Are all components required to recreate analysis and figures accessible?

Is there a clear link between code and output?

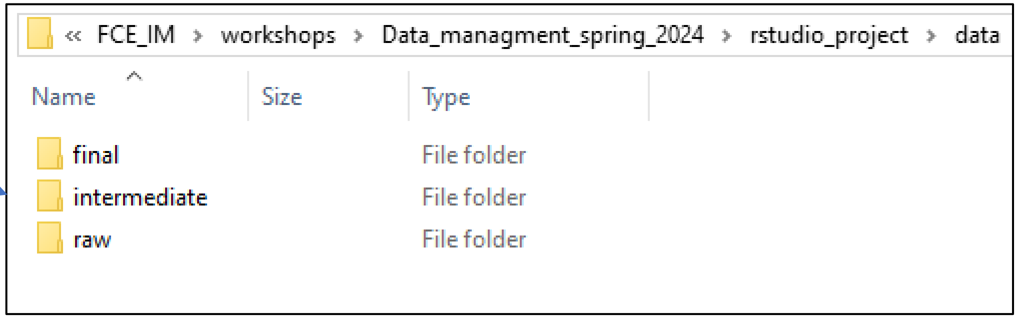
J of Evolutionary Biology, Volume: 36, Issue: 10, Pages: 1347-1356, First published: 09 October 2023, DOI: (10.1111/jeb.14230)

Project organization: data



FCE_IM › workshops › Data_managment_spring_2024 › rstudio_project ›

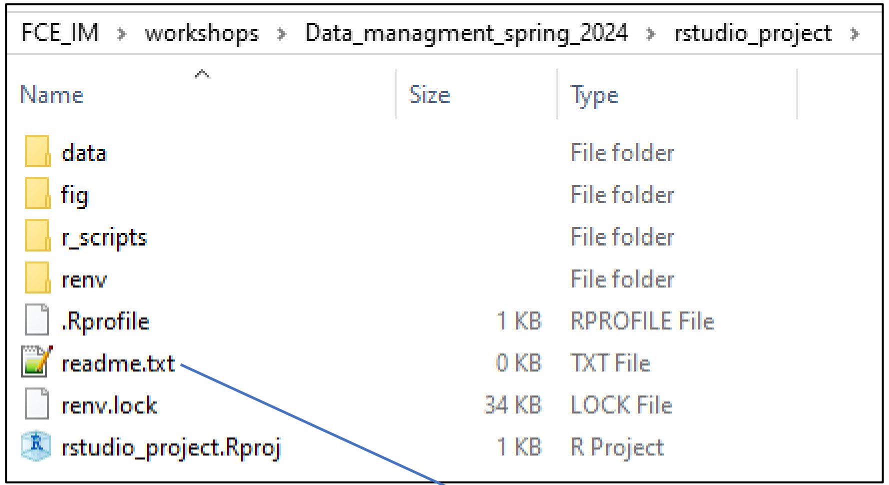
Name	Size	Type
data		File folder
fig		File folder
r_scripts		File folder
renv		File folder
.Rprofile	1 KB	RPROFILE File
readme.txt	0 KB	TXT File
renv.lock	34 KB	LOCK File
rstudio_project.Rproj	1 KB	R Project



« FCE_IM › workshops › Data_managment_spring_2024 › rstudio_project › data

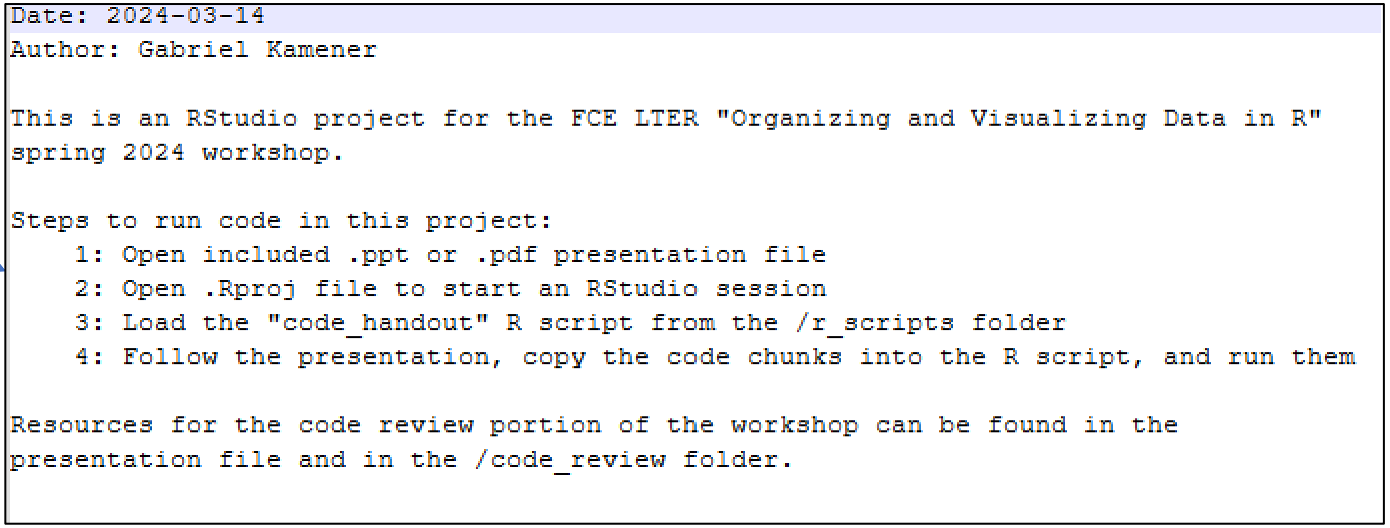
Name	Size	Type
final		File folder
intermediate		File folder
raw		File folder

Project and input metadata: README



FCE_IM › workshops › Data_managment_spring_2024 › rstudio_project ›

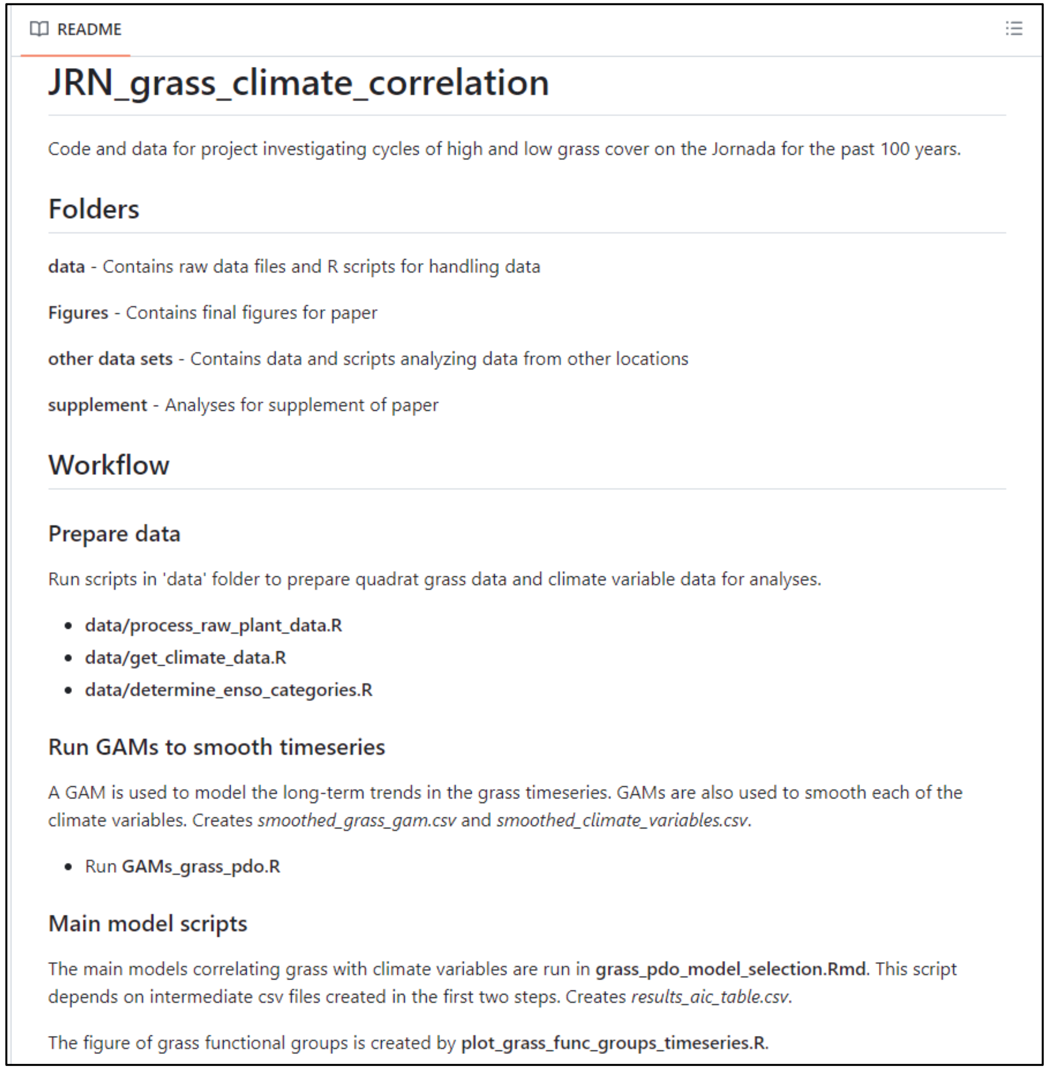
Name	Size	Type
data		File folder
fig		File folder
r_scripts		File folder
renv		File folder
.Rprofile	1 KB	RPROFILE File
readme.txt	0 KB	TXT File
renv.lock	34 KB	LOCK File
rstudio_project.Rproj	1 KB	R Project



```
Date: 2024-03-14
Author: Gabriel Kamener

This is an RStudio project for the FCE LTER "Organizing and Visualizing Data in R"
spring 2024 workshop.

Steps to run code in this project:
    1: Open included .ppt or .pdf presentation file
    2: Open .Rproj file to start an RStudio session
    3: Load the "code_handout" R script from the /r_scripts folder
    4: Follow the presentation, copy the code chunks into the R script, and run them

Resources for the code review portion of the workshop can be found in the
presentation file and in the /code_review folder.
```

Project and input metadata: README

- Can scale in complexity



JRN_grass_climate_correlation

Code and data for project investigating cycles of high and low grass cover on the Jornada for the past 100 years.

Folders

data - Contains raw data files and R scripts for handling data

Figures - Contains final figures for paper

other data sets - Contains data and scripts analyzing data from other locations

supplement - Analyses for supplement of paper

Workflow

Prepare data

Run scripts in 'data' folder to prepare quadrat grass data and climate variable data for analyses.

- **data/process_raw_plant_data.R**
- **data/get_climate_data.R**
- **data/determine_enso_categories.R**

Run GAMs to smooth timeseries

A GAM is used to model the long-term trends in the grass timeseries. GAMs are also used to smooth each of the climate variables. Creates *smoothed_grass_gam.csv* and *smoothed_climate_variables.csv*.

- Run **GAMs_grass_pdo.R**

Main model scripts

The main models correlating grass with climate variables are run in **grass_pdo_model_selection.Rmd**. This script depends on intermediate csv files created in the first two steps. Creates *results_aic_table.csv*.

The figure of grass functional groups is created by **plot_grass_func_groups_timeseries.R**.

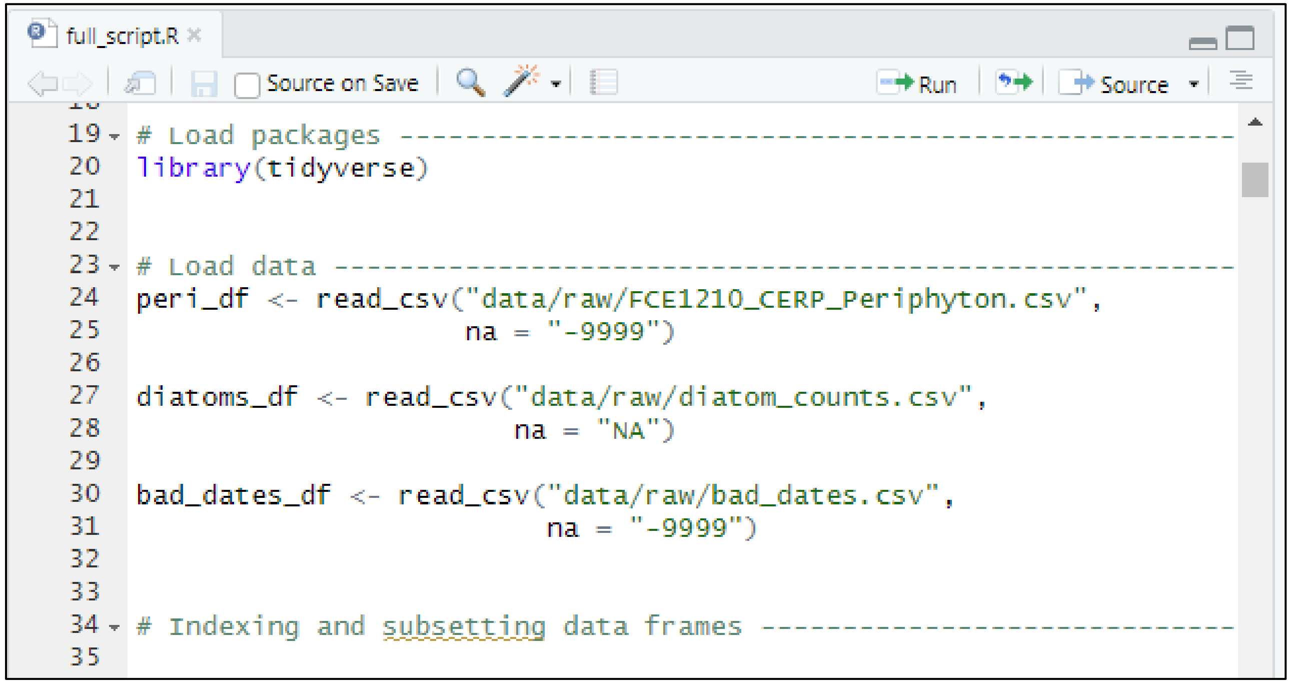
Christensen, E. 2023. https://github.com/emchristensen/JRN_grass_climate_correlation

Code readability

1. Explicitly calling package namespace (e.g. dplyr::select())
2. Using relative file paths
3. Removing redundant packages
4. Writing code with
    a) Clear subheadings
    b) Intuitive comments
    c) Easy-to-understand object names

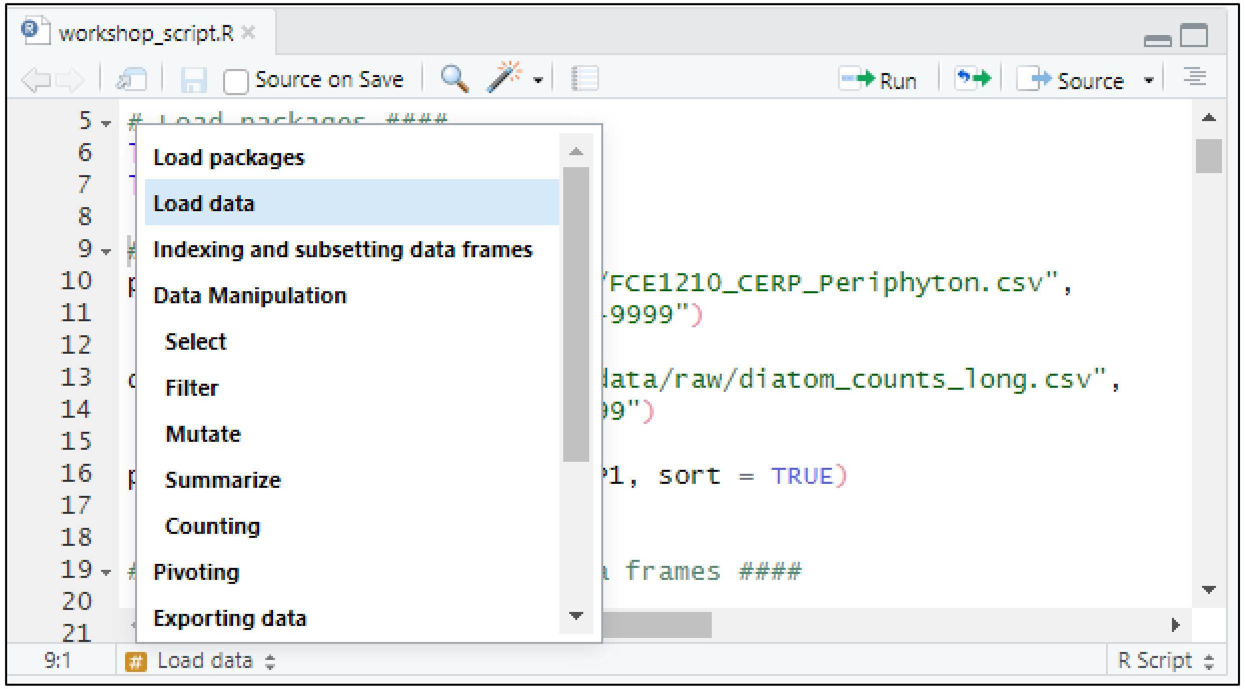
Code readability: code sections

- Break code down by region
- Comment line with at least 4 trailing “-”, “=“, or “#”
- Code -> Insert Section
- Crtl+Shift+R



```
# Load packages ---------------------------------------------------
library(tidyverse)


# Load data -------------------------------------------------------
peri_df <- read_csv("data/raw/FCE1210_CERP_Periphyton.csv",
                    na = "-9999")

diatoms_df <- read_csv("data/raw/diatom_counts.csv",
                       na = "NA")

bad_dates_df <- read_csv("data/raw/bad_dates.csv",
                         na = "-9999")


# Indexing and subsetting data frames -----------------------------

```

Code readability: navigating sections



```
# Load packages ####
'FCE1210_CERP_Periphyton.csv",
-9999")
data/raw/diatom_counts_long.csv",
99")
1, sort = TRUE)
 frames ####
```

Output reproducibility

- Link between code sections and published outputs should be clear
- Use set.seed() before running simulations
- Increase reproducibility of environment with renv package

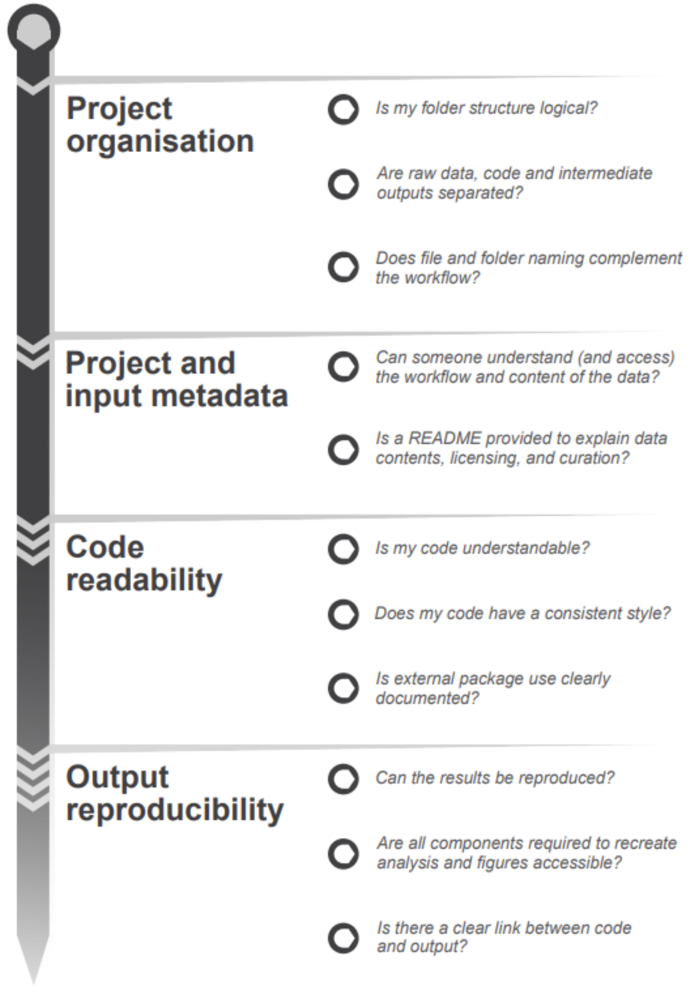
Generating citations

- R version citation: citation()
- Package version: citation("dplyr")
- RStudio.Version()

Other suggestions

- Keep primary R scripts for yourself
  - Include all analyses and comments
- Distill down code for manuscript submission
  - Only relevant analyses and comments
- Use version control (e.g. Git/GitHub) to track changes
- Code sections to cover each dependent variable
- Form code review group in your lab or with other students

Project code checklist



Project organisation

- ○ *Is my folder structure logical?*
- ○ *Are raw data, code and intermediate outputs separated?*
- ○ *Does file and folder naming complement the workflow?*

Project and input metadata

- ○ *Can someone understand (and access) the workflow and content of the data?*
- ○ *Is a README provided to explain data contents, licensing, and curation?*

Code readability

- ○ *Is my code understandable?*
- ○ *Does my code have a consistent style?*
- ○ *Is external package use clearly documented?*

Output reproducibility

- ○ *Can the results be reproduced?*
- ○ *Are all components required to recreate analysis and figures accessible?*
- ○ *Is there a clear link between code and output?*

Figure S1. A printable checklist for code review. Figure design by B.M.M.

J of Evolutionary Biology, Volume: 36, Issue: 10, Pages: 1347-1356, First published: 09 October 2023, DOI: (10.1111/jeb.14230)

Activity: Project and Code Development

- Use the checklist to review your own project and code
- Work with your neighbor to review each other’s code or the provided example code

Constructive feedback

- How much of this did you know?
- How much did you not know?
- What would you like us to include or exclude in the future?

References and resources

- Christensen, E. 2023. “Emchristensen/JRN_Grass_Climate_Correlation: ARIMA Models.” Zenodo. https://doi.org/10.5281/zenodo.7787243.
- Ivimey-Cook, E. R., Pick, J. L., Bairos-Novak, K. R., Culina, A., Gould, E., Grainger, M., ... & Windecker, S. M. (2023). Implementing code review in the scientific workflow: Insights from ecology and evolutionary biology. *Journal of evolutionary biology*, *36*(10), 1347-1356. https://doi.org/10.1111/jeb.14230
- Brian Seok, François Michonneau, Tobias Busch, Katrin Leinweber, Maneesha Sane, njlyon0, Ed Bennett, Hugo Tavares, Mike Mahoney, Paula Nieto, Susan Washko, Terry Loecke, Wasila Dahdul, xli677, Abhijna Parigi, Aleksander Jankowski, Allison Shay Theobold, Analytics Enlightened LLC, Anna K. Moeller, … vmzhang. (2023). datacarpentry/R-ecology-lesson: Data Carpentry: Data Analysis and Visualization in R for Ecologists 2023-05 (2023.05). Zenodo. https://doi.org/10.5281/zenodo.7892261

References and resources

- Data Analysis and Visualization in R for Ecologists workshop website
  - https://datacarpentry.org/R-ecology-lesson/
- R cheatsheets (also findable as PDFs from Rstudio “help” tab)
  - https://rstudio.github.io/cheatsheets/
- Code Folding and Sections in the RStudio IDE
  - https://support.posit.co/hc/en-us/articles/200484568-Code-Folding-and-Sections-in-the-RStudio-IDE
- How to Cite R and R Packages
  - https://ropensci.org/blog/2021/11/16/how-to-cite-r-and-r-packages/
- Introduction to renv to help create reproducible environments for R projects
  - https://rstudio.github.io/renv/articles/renv.html