CODING PRACTICES

Life with R

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1. Quality of Life Improvements
   - Coding in R
   - Documenting Your Work
2. Code Structure
3. Sharing Work
   - Reproducibility
   - Functions & Sourcing
4. User-Friendliness
   - Progress Bar
   - Estimators
   - Parallel Processing

Objects

Assign **recognizable**, **concise** names to your objects!

Let's start with the object `MyData` - this can be anything. Let's assume it is a raster of NDVI values during the year 1982. How do we come up with a better name?

Specificity in your naming helps you keep track of your data in your code:

- `NDVI1982`

Classes of objects determine how they get handled. Add them as a suffix:

- `NDVI1982_ras`

The same goes for **loop indicators**! Avoid single-letter indicators and instead use something like `Iter_Years` - an indicator *iterating* (`Iter`) over years.

Also, always use `<-` for assigning objects!

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Quality of Life Improvements

Use **spaces** to improve readability of your code:

```r
c(1,2,rep(3,5)) # bad
c(1, 2, rep(3, 5)) # good
```

Insert **line breaks** to improve workflow. I like to break multiple lines of one function call into logical blocks. For example, in `ggplot2`, the first line holds data, the second contains aesthetics, the third adds a layer, and so on.

To avoid side-scrolling, use the automatic **soft-wrap** function in `RStudio`.

Be **consistent** in your coding style. Found a `tidyverse` solution to your problem online but don't use `tidyverse` syntax in the rest of your document? Adapt the solution to be in the same style as the rest of your coding!

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Comments

Don't be overly proud of your coding skills. Comment everything!

Bad comments:

- ambiguous
- sparse

```
# Data Manipulation
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Good comments:

- specify (what is the code doing)
- justify (why is it being done)

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# Z-Score calculation for comparability
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RMarkdown

Using `Rmarkdown` for your research comes with a multitude of advantages:

1. Entire **workflow in one program** (`RStudio`)
2. Great capabilities to **present code**
3. **Research** and reports **reproducible** at the click of **one button**
4. **Combines** `R` functionality and LaTeX formatting (if desired)
5. **Consistent formatting**
6. **Clear presentation of code**
7. **Dynamic documents** (you can generate various output document types)
8. Applicable for **almost all document types** you may desire as an output (e.g. manuscripts, presentations, posters, etc.)

Header

The **Head** is used as an information statement at the top of your code document that informs the user of the contents, author, and (sometimes) date of the last edit on said document:

```
# ############################################## #
# PROJECT: Project Title
# CONTENTS: What the code in your file is used for
# AUTHOR: Who worked on it
# EDIT: When the last edit was made
# ############################################## #
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Personally, I don't use the edit argument in my heads. Instead, I rely on *version control*.

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Preamble

The **Preamble** is where you set up the most important parameters/guidelines for your coding script. Personally, I *highly* recommend to make your first line in the preamble read `rm(list=ls())`.
This is also where you load **packages**. I recommend doing so as follows:

```
install.load.package <- function(x) {
    if (!require(x, character.only = TRUE))
        install.packages(x, repos = "http://cran.us.r-project.org")
    require(x, character.only = TRUE)
}
```

This functions *checks* whether the package is already installed. If it is, it will be *loaded*. If it is not, it will be *installed* from `CRAN` and subsequently loaded.
You use it for multiple packages like this:

```
package_vec <- c("ggplot2", "foreach", "doParallel")
sapply(package_vec, install.load.package)
```

Sections

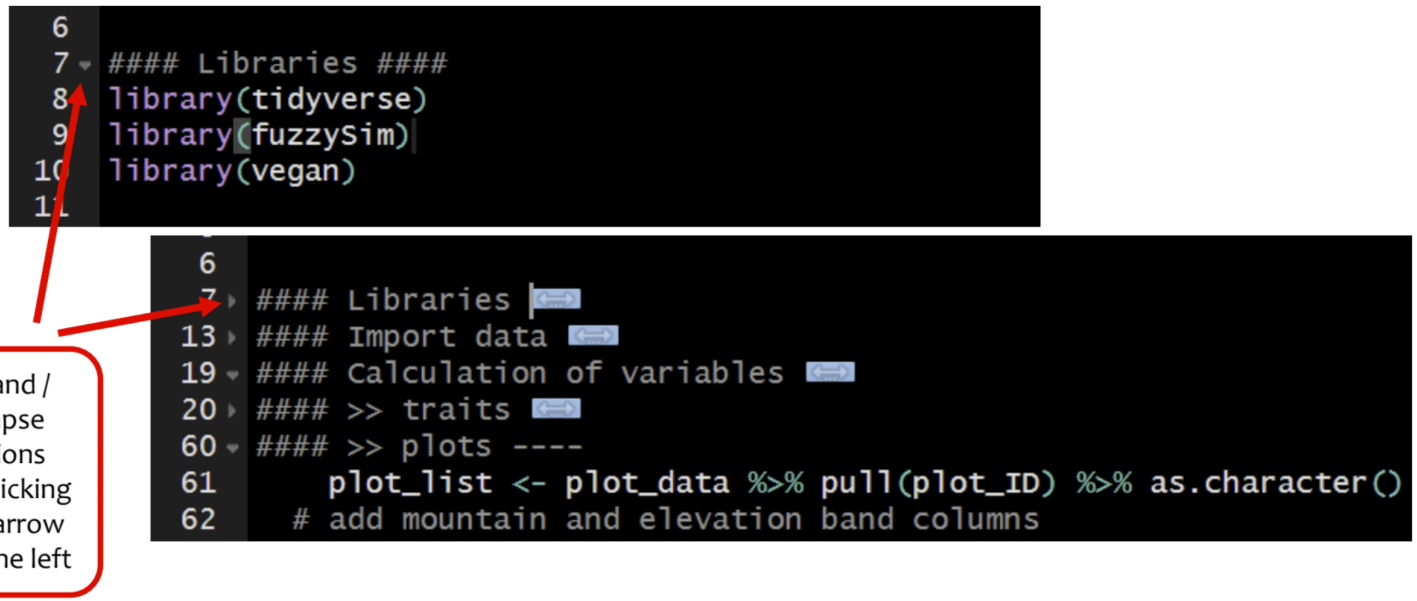
Sections are a powerful tool in `RStudio`!

They keep your code:

- *structured*
- *clear*
- *easy-to-use*

They do so by:

- *collapsing* code
- adding a *table of contents*



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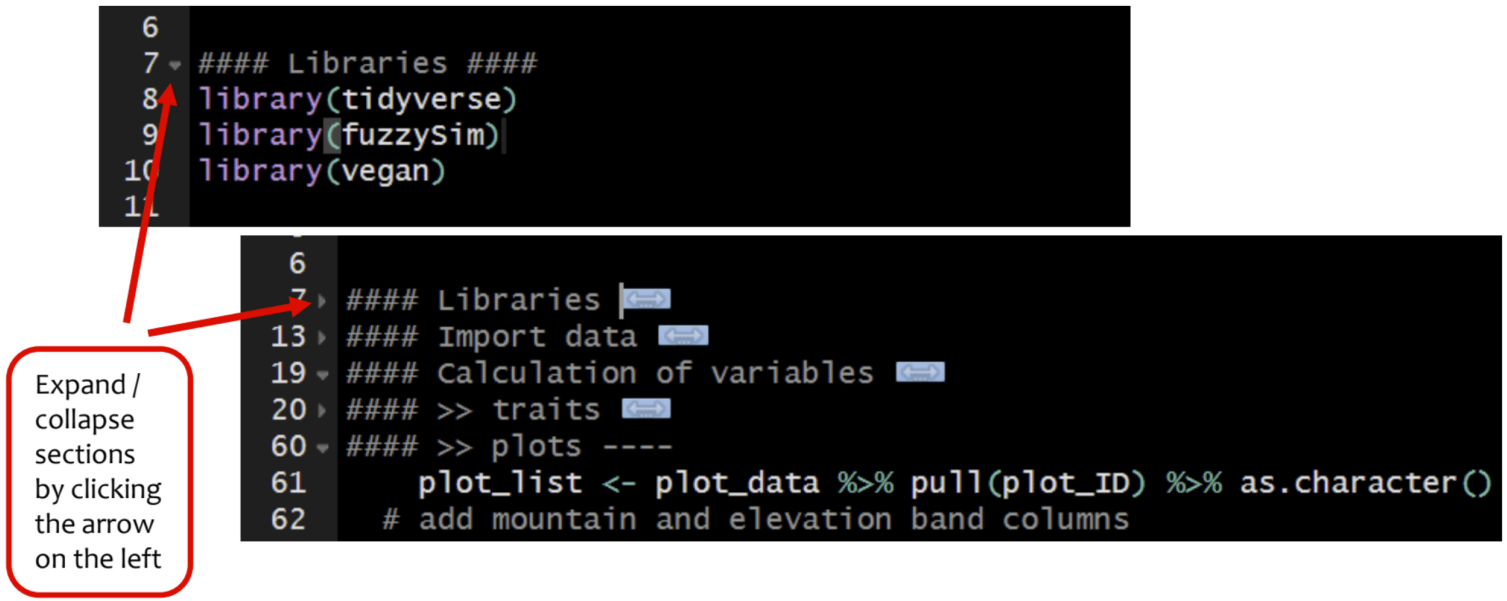

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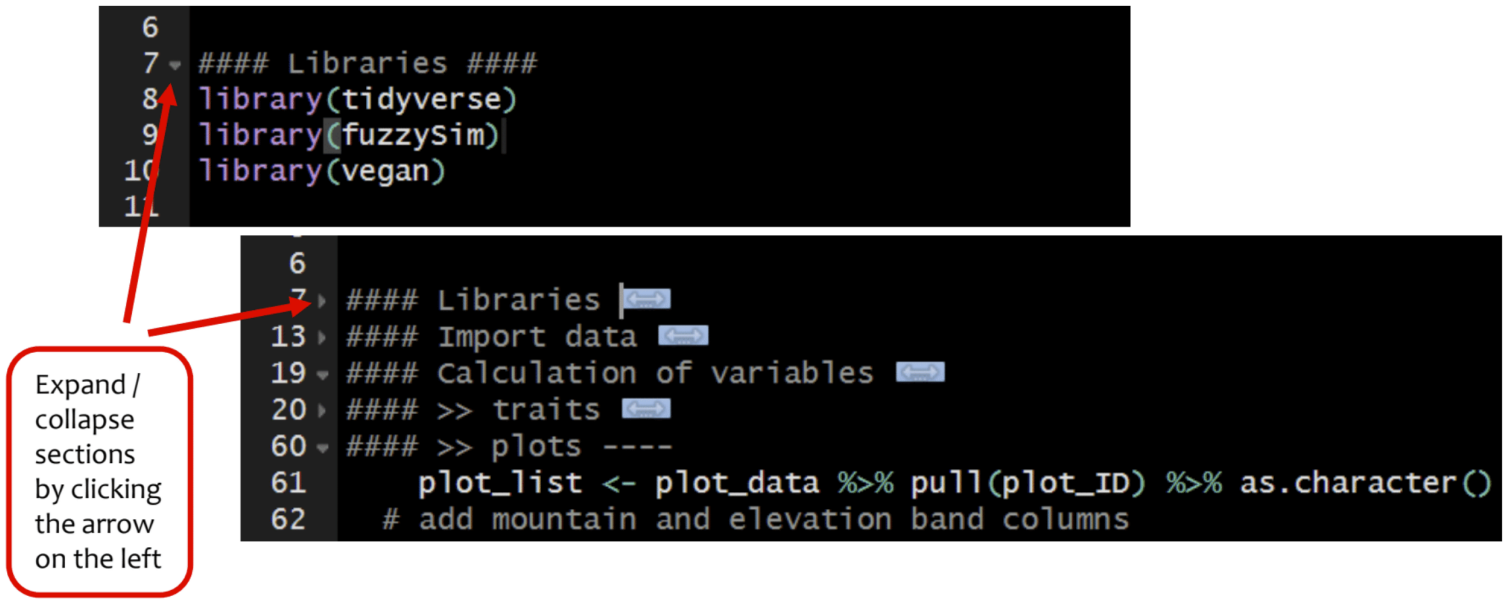

Reproducibility

Reproducibility is **paramount** in science.

Working directories

It is common to set a base directory at the beginning of your code and refer to sub-directories from there. We can *do better*:

- `getwd()` in a `project` will yield the directory of the `project` file
- the package `here` offers more functions to never have to set a directory path by hand

Randomness

Random processes (e.g. `sample()`, `rnorm()`, etc.) in `R` are always *pseudo-random* (their calculation is based on your computer time). We can make sure the result of a random process is always the same between researchers by using:

- `set.seed()`

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Functions & Sourcing

Big projects lend themselves well to a **multi-document workflow**:

Functions

User-defined functions are a great way of *soft-coding* your analyses to repeat them for different input parameters and I highly recommend doing so all the time. Make sure your functions are:

- internally *consistent*
- *well-documented*
- easy to *understand*

Sourcing

Splitting your code into multiple documents is a great idea to ensure your project remains *structured* and *easy to handle*. You can use the `source()` function to combine those documents. Keep in mind that you should:

- use *sensible file names*
- *sourced* functions still need to be *called*

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Progress Bar

A **progress bar** is a great way of keeping you updated on how your code is progressing so far. It is especially useful when your code involves *loops*:

```
Data_vec <- 1:100 # a vector on integers from 1 to 100
# creating progress bar
ProgBar <- txtProgressBar(min = 0, max = length(Data_vec),
                          style = 3)
# looping over contents of Data_vec
for(Iter_ProgBar in 1:length(Data_vec)){
  setTxtProgressBar(ProgBar, Iter_ProgBar) # updating ProgBar
} # end of Data_vec loop
```

Estimators

Estimators are a great way to know when to come back to your computer or server and check up on your data, code, and results. They are most useful in *loop* based approaches as they need a baseline for the estimation:

```
Data_vec <- 1:100 # a vector on integers from 1 to 100
T_Begin <- Sys.time() # record time
# looping over contents of Data_vec
for(Iter_Est in 1:length(Data_vec)){
  Sys.sleep(.1) # pause for .1 seconds
  # estimator produced on first iteration
  if(Iter_Est == 1){
    T_End <- Sys.time() # record time
    Duration <- as.numeric(T_End)-as.numeric(T_Begin) # time difference
    print(paste("Estimated time to finish:",
                as.POSIXlt(T_Begin + Duration*length(Data_vec),
                           tz = Sys.timezone(location=FALSE))
                ))
  } # end of estimator check
} # end of Data_vec loop
```

```
## [1] "Estimated time to finish: 2020-03-25 00:33:50"
```

Yes, I did work on this presentation past midnight.

Parallel Processing

Got a big data approach where you carry out the same kind of analysis for many different species or data sets? It's taking forever to complete? **Parallel processing** has your back! By default, R only uses one of the cores in your computer or server for processing code. Use this, to make use of all the computational power:

```
library(doParallel) # for registering clusters
library(foreach) # for parallel processing
Cores <- detectCores() # identify the number of cores in your machine
cl <- makeCluster(Cores) # create virtual cluster
registerDoParallel(cl) # register cluster of cores
# parallel processing
foreach(Iter_Par = 1:length(Data_vec)) %dopar% {
  # your function here
} # end of parallel processing
stopCluster(cl) # stop cluster
```