

# Coding Principles Exercises

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## Exercise 1: Object Classes and Assignment

### Part A: Set up

1. Open R Studio and navigate to your EVR628 project
2. Set up a code snippet for a header

```
#####  
# title  
#####  
#  
# Your Name Here  
# Your email here  
# date  
#  
# Description  
#  
#####
```

3. Create a new R script and save it as `objects_and_classes.R`
4. Use your new code snippet to add the header

### Part B: Create and Check Object Classes

In your R Script, create objects of different classes and check their types:

1. A character object called `my_name` with your name
2. A numeric object called `my_age` with your age (or any number, it doesn't have to be your age)
3. A logical object called `is_student` with TRUE or FALSE
4. Check the class of each object using `class()`

```
my_name <- "JC" # character object called `my_name` with your name  
my_age <- 32 # numeric object called `my_age` with your age  
is_student <- FALSE # logical object called `is_student` with TRUE or FALSE  
  
# Check the class of each object using `class()`  
class(my_name)
```

```
[1] "character"
```

```
class(my_age)
```

```
[1] "numeric"
```

```
class(is_student)
```

```
[1] "logical"
```

## Part C: Object Coercion

Let's see what happens when you try converting objects. In the R script, write and then execute code that will:

1. Convert your age to `character` using `as.character(my_age)`
2. Convert `TRUE` to numeric using `as.numeric()`
3. Try to convert `"hello"` to `numeric` - what happens?
4. Advanced: Use `|>` to build a code pipeline to:
  - a. Take your age
  - b. Convert it to character
  - c. Get it's class

```
# Note that I am overwriting the object. If I had only done `as.character(my_age)`,  
# then the coerced output would have been printed to the console.  
my_age <- as.character(my_age) # Convert your age to `character`  
# Check that it worked  
class(my_age)
```

```
[1] "character"
```

```
as.numeric(TRUE) # Convert `TRUE` to numeric using `as.numeric()`
```

```
[1] 1
```

```
as.numeric("hello") # Try to convert `"hello"` to `numeric` - what happens?
```

Warning: NAs introduced by coercion

```
[1] NA
```

```
# Build a pipeline  
my_age <- 32 # Start with my_age as numeric again  
# AND now build the pipeline  
my_age |>  
  as.character() |>  
  class()
```

```
[1] "character"
```

## Exercise 2: Vectors and Operations

### Part A: Create and Manipulate Vectors

1. Clean your environment (use the broom icon)
2. Create a numeric vector called `length_m` with values: 6, 4.1, 2.8, 5.5, 3.9, 5.8
3. Create a character vector called `shark_species` with: Great White Shark, Lemon Shark, Bull Shark, Hammerhead Shark, Mako Shark, and Great White Shark (yes, white shark again)
4. How many *variables* do you have in your environment?
5. How many length *observations* do we have? Find the length of both vectors using `length()`
6. How many unique *species* do we have? (Hint, use `|>` to build a pipeline)
7. Calculate the mean length of all sharks using `mean()`
8. Find the maximum length using `max()`

```
# Q2
length_m <- c(6, 4.1, 2.8, 5.5, 3.9, 5.8)
# Q3
shark_species <- c("Great White Shark", "Lemon Shark", "Bull Shark",
                  "Hammerhead Shark", "Mako Shark", "Great White Shark")
# Q5
length(length_m)
```

```
[1] 6
```

```
# Q6
shark_species |>
  unique() |>
  length()
```

```
[1] 5
```

```
# Q7
mean(x = length_m)
```

```
[1] 4.683333
```

```
# Q8
max(length_m)
```

```
[1] 6
```

#### ! Important

- When passing arguments to functions, use `=` not `<-`
- When creating objects, use `<-` not `=`

## Part B: Vector Operations and Indexing

1. Extract the first 3 shark species using indexing with `[]` and save them to an object called `first_3`
2. Extract shark species where maximum length is greater than 4 meters
3. Assuming the values in `length_m` and `sharks_species` are ordered so that they match each other, find the shark species that is the largest
4. Calculate the mean length for all great white sharks

```
# Q1
first_3 <- shark_species[1:3] # Extract values 1 through 3 and assign them
first_3 # See the values I assigned
```

```
[1] "Great White Shark" "Lemon Shark"      "Bull Shark"
```

```
# Q2
shark_species[length_m > 4] #Extract shark species where maximum length is greater than 4 m
```

```
[1] "Great White Shark" "Lemon Shark"      "Hammerhead Shark"
[4] "Great White Shark"
```

```
# Q3
shark_species[length_m == max(length_m)]
```

```
[1] "Great White Shark"
```

```
# Q4 (Option 1, no pipes)
# Read as : "Calculate the mean of lengths where shark species matches Great White Shark
mean(length_m[shark_species == "Great White Shark"])
```

```
[1] 5.9
```

```
# Q4 (Option 2, with pipe)
length_m[shark_species == "Great White Shark"] |> # Read as: Extract lengths where name mat
mean() # Calculate the mean
```

```
[1] 5.9
```

---

Likely pause here

---

## Exercise 3: Data Frames and Tibbles

### Part A: Estimate the effect of a Marine Protected Area on Biomass

1. Install and load an updated version of `EVR628tools`:

```
remotes::install_github("jcvdav/EVR628tools")
```

2. Start a new script called `MPA_analysis`, add a comment outline and then load the `EVR628tools` and `tidyverse` packages.
3. Load and inspect the new `?data_MPA`
  - a. What are the dimensions of the data?
  - b. What are the column names?
  - c. How many `unique()` sites are there?
  - d. How many `unique()` years?
  - e. Visualize the trends in biomass through time and across sites
4. Create four objects containing:
  - a. Mean biomass *inside* the MPA **before** it was protected
  - b. Mean biomass *inside* the MPA **after** it was protected
  - c. Mean biomass *outside* the MPA **before** the MPA was created
  - d. Mean biomass *outside* the MPA **after** the MPA was created

Hint: Use a combination of subsetting (`[ ]`), relational (`==`), and logical operators (`&`)

5. Then, calculate:
  - a. Change after vs before for the protected site
  - b. Change after vs before for the unprotected site
6. Finally, calculate the difference between these two values. This is called the *naive* difference-in-differences estimate. You are calculating the differences across treatments and across time. See Villasenor-Derbez et al. (2018) and Lynham and Villaseñor-Derbez (2024) for details.

```
# My code will be here
```

## Exercise 4: Code Style and Documentation

### Part A: Fix Code Style

Fix the style issues in this code:

```
mydataframe=data.frame(species=c("Great White","Tiger", "Bull"),  
length=c(4.5,3.2, NA))  
mean(mydataframe$length,na.rm=TRUE)
```

```
# My improved code will be here
```

Note: What's with `na.rm = TRUE`?

### Part B: Add Comments and Section Headers

1. Add meaningful comments to your R script

Lynham, John, and Juan Carlos Villaseñor-Derbez. 2024. "Evidence of Spillover Benefits from Large-Scale Marine Protected Areas to Purse Seine Fisheries." *Science* 386 (6727): 1276–81.

Villasenor-Derbez, Juan Carlos, Caio Faro, Melaina Wright, Jael Martinez, Sean Fitzgerald, Stuart Fulton, Maria del Mar Mancha-Cisneros, et al. 2018. "A User-Friendly Tool to Evaluate the Effectiveness of No-Take Marine Reserves." *PLoS One* 13 (1): e0191821.