

# ds4biomed

## Pre-Workshop Exercise

### Pre-Workshop Exercise

#### Exercise 1

#### Exercise 2

#### Exercise 3

#### Summative


Start Over

Please write the code for the following pipeline steps:

1. Load the `tidyverse` and `readxl` libraries.
2. Read in the Excel file located in:  
"data/medicaldata\_tumorgrowth.xlsx" into a variable `tumor`.
3. Select the all the columns except `Grp`, and filter the rows such that `Day` is `0` or `20`. Save this data subset into a variable `tumor_subset`.
4. We want to compare baseline tumor sizes (Day 0) with tumor sizes at Day 20 between each of the groups.
  - Using `tumor_subset`, calculate the average `tumor Size` for each `Grp` and `Day`.
5. Save `tumor_subset` into a CSV file located in "data/tumorsubset.csv".

R Code

 Start Over

 Run Code

```
1  
2  
3
```

Next Topic