Coding Milestones 2

2024-08-02

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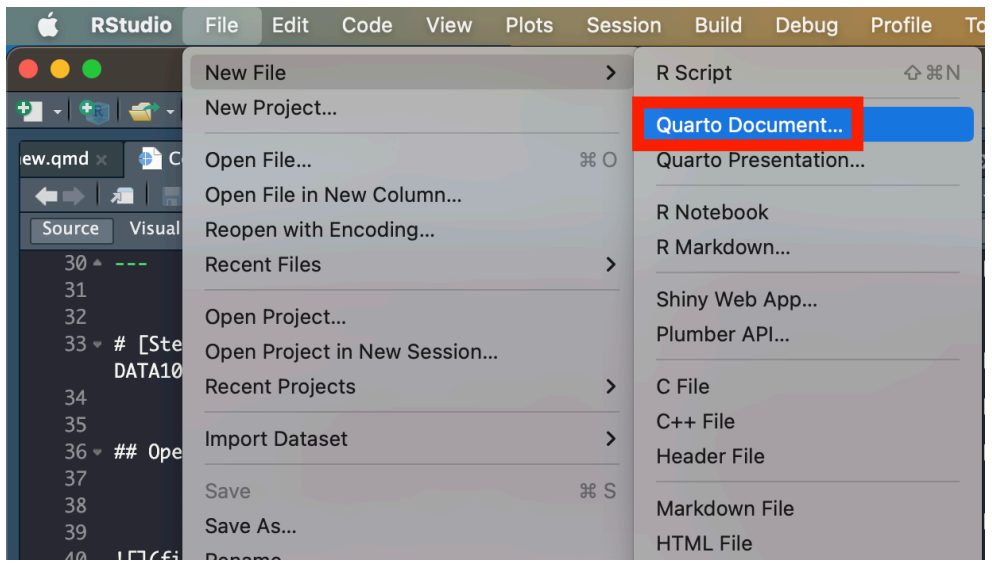
- Open RStudio, create a .qmd file & store it in your DATA1001 folder
  - Create a .qmd in RStudio
  - Store in your DATA1001 folder
- Clean the .qmd file, by keeping the YAML and removing the other lines.
  - Clean the .qmd, keeping the YAML
  - Create a code chunk
- Perform IDA on the iris data, using `str()`, `head()` and `tail()`
  - IDA on iris using `str()`, `head()` and `tail()`
- Create a `ggplot` of the iris data, from a blank canvas to a full plot with title
  - Example 1: Making a `ggplot` simple boxplot
  - Example 2: Making a `ggplot` sliced histogram with title
- Edit & knit your .qmd file to produce an .html file
  - Render your .qmd to create a .html

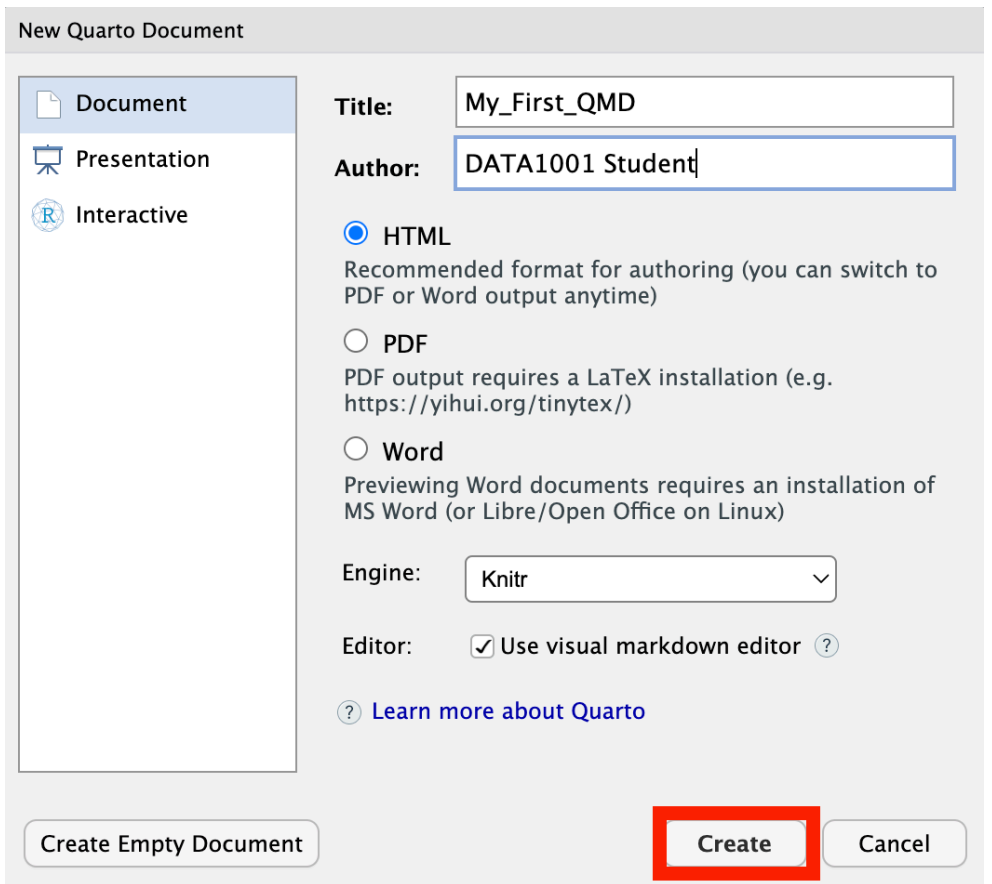
Open RStudio, create a .qmd file & store it in your DATA1001 folder

Create a .qmd in RStudio

Open a Quarto Document (.qmd) in RStudio.

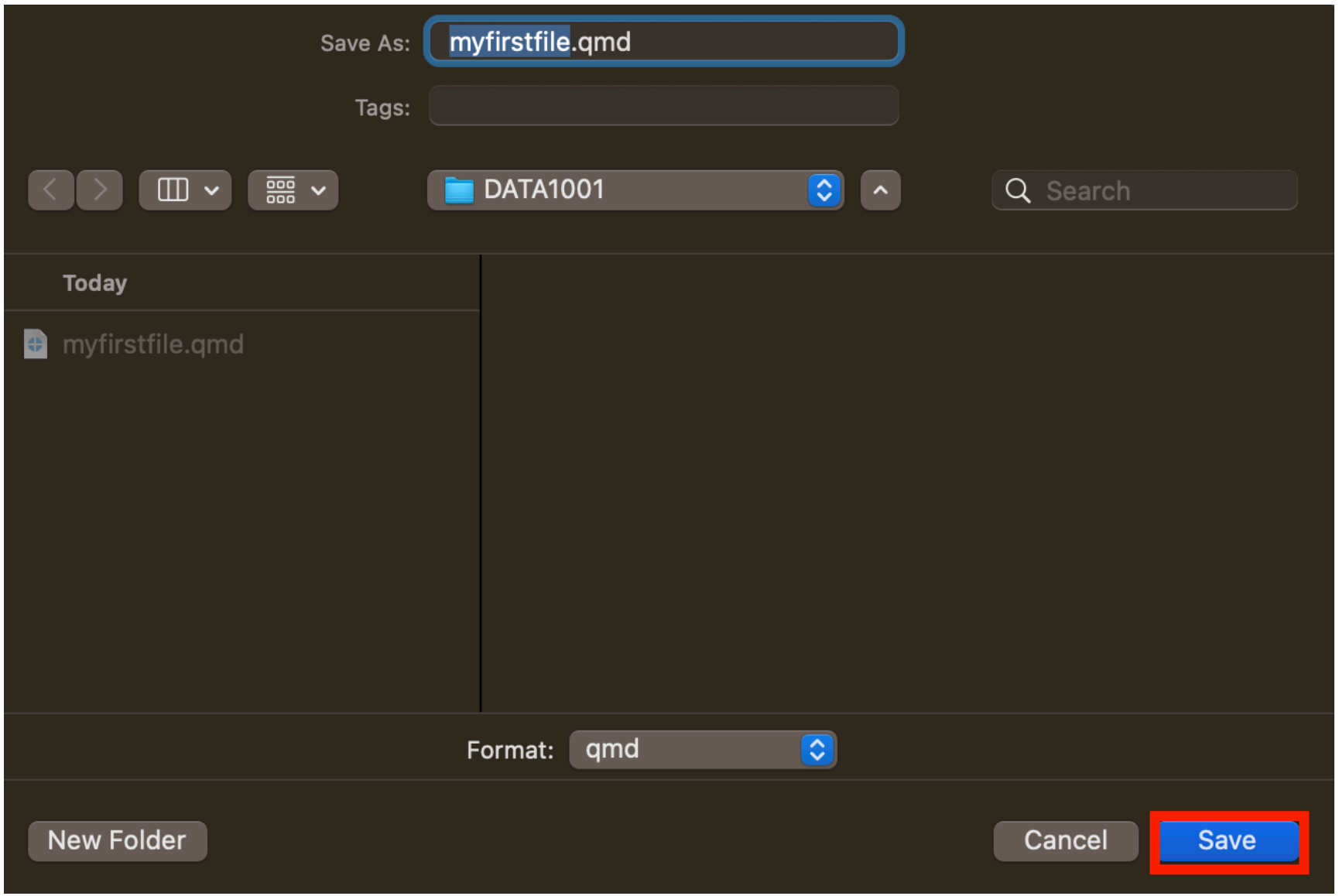


Give your .qmd a title and author, then click create.



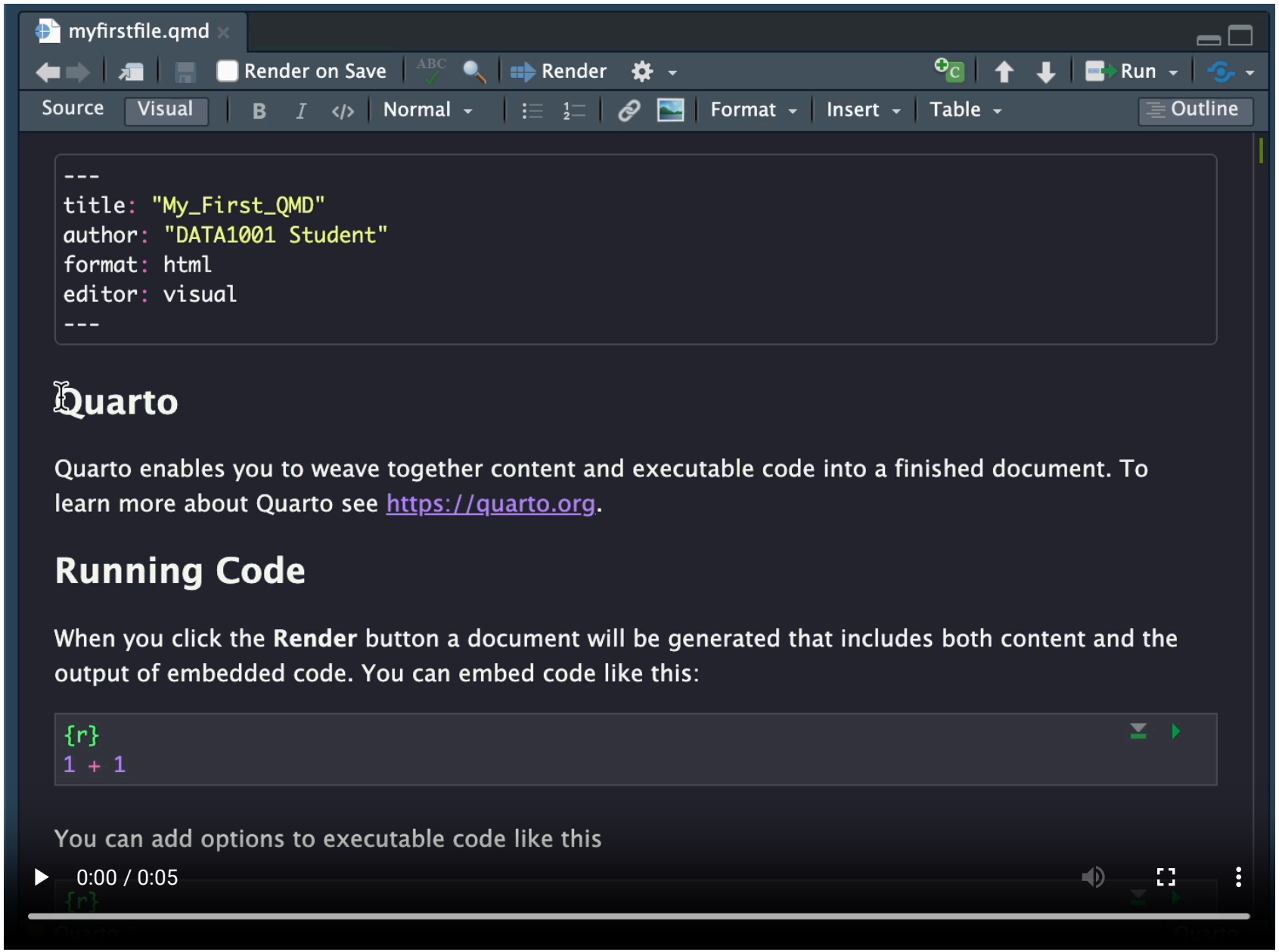
Store in your DATA1001 folder

Name your file and save it in your DATA1001 folder.



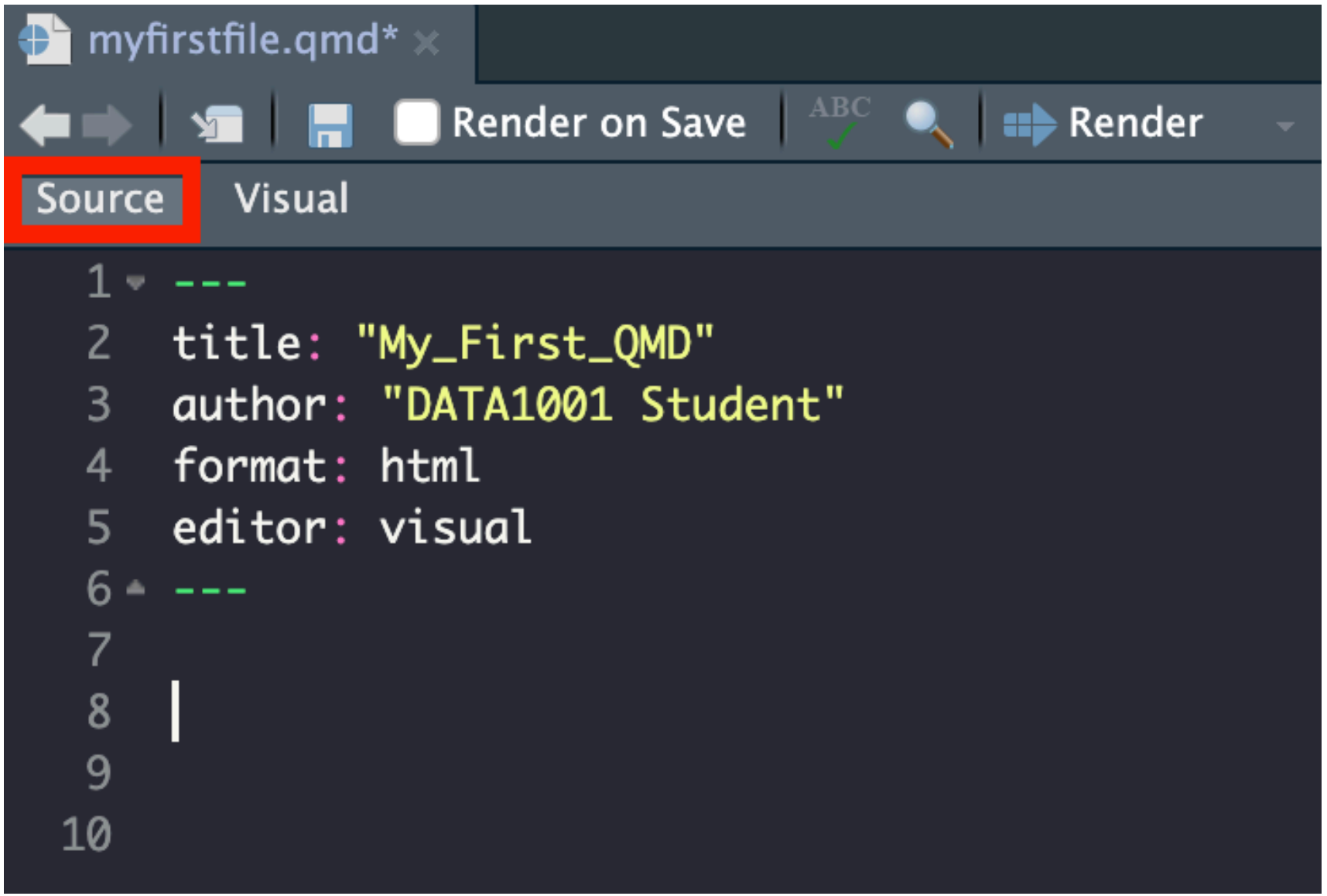
Clean the .qmd file, by keeping the YAML and removing the other lines.

Clean the .qmd, keeping the YAML



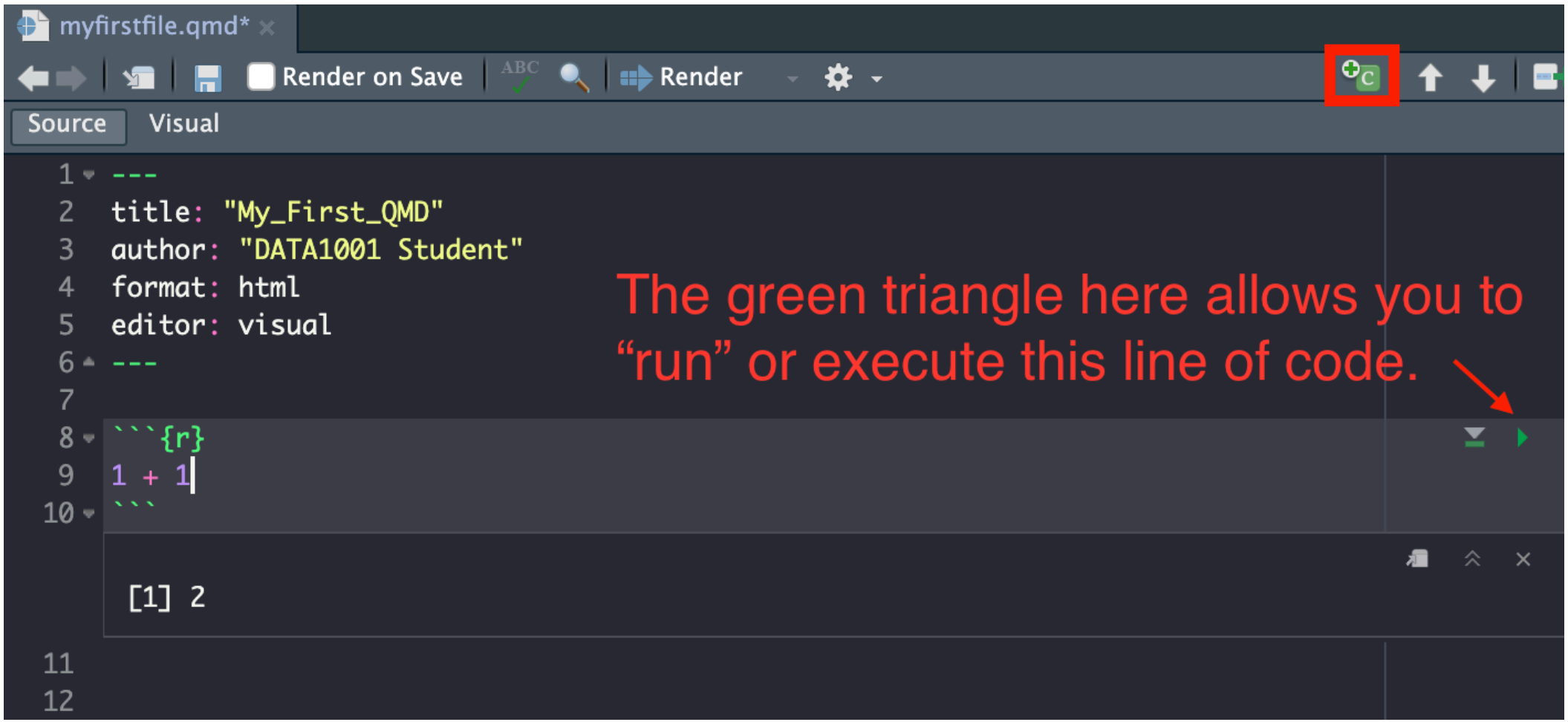
Create a code chunk

Switch over to “Source”.



Create a code chunk

Click the green “C” button to create a code chunk, where you will write your code!



Perform IDA on the iris data, using `str()`, `head()` and `tail()`

IDA on iris using `str()`, `head()` and `tail()`

```
str(iris)
```

```
'data.frame':   150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1
...
```

```
head(iris)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

```r
tail(iris)
```

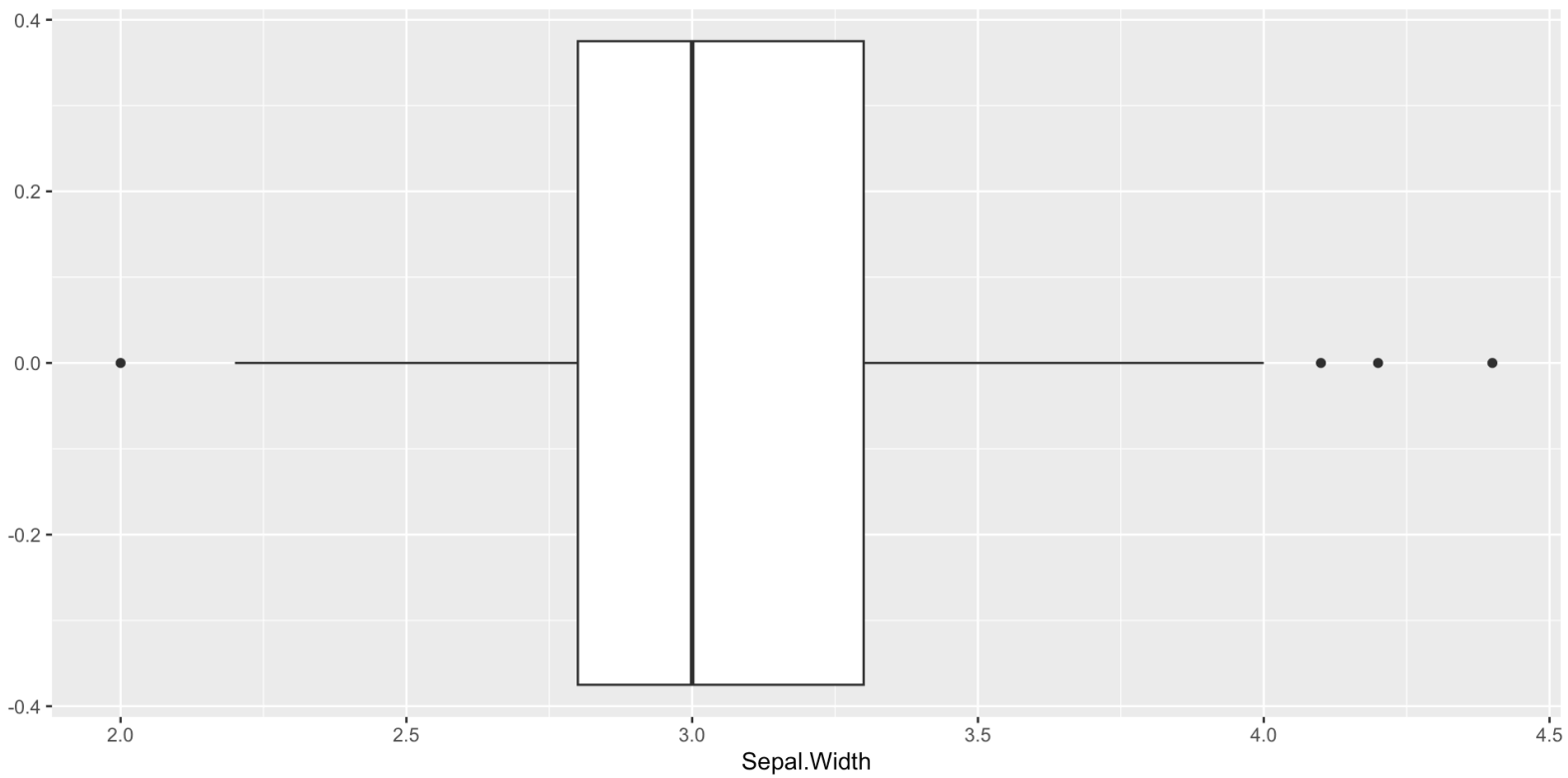
```
    Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
145          6.7         3.3          5.7         2.5 virginica
146          6.7         3.0          5.2         2.3 virginica
147          6.3         2.5          5.0         1.9 virginica
148          6.5         3.0          5.2         2.0 virginica
149          6.2         3.4          5.4         2.3 virginica
150          5.9         3.0          5.1         1.8 virginica
```

Create a `ggplot` of the iris data, from a blank canvas to a full plot with title

Example 1: Making a `ggplot` simple boxplot

Let's say we want to see a simple boxplot of **Sepal Width**. This means we will use 1 quantitative variable.

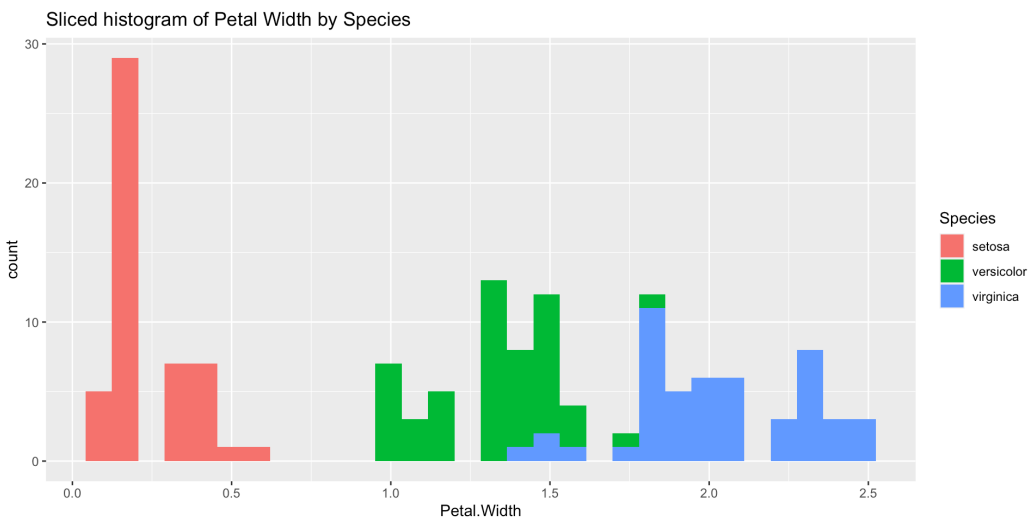
```
library(tidyverse) # Load the required library

ggplot(iris, aes(x = Sepal.Width)) +
  geom_boxplot() # Making a boxplot
```



Example 2: Making a `ggplot` sliced histogram with title

Let's say we want to see a sliced histogram with the variables **Petal Width** (quantitative) and **Species** (qualitative).

```
ggplot(iris, aes(x = Petal.Width, fill = Species)) +
  geom_histogram() + # Making a histogram
  labs(title = "Sliced histogram of Petal Width by Species") # Adding a title
```

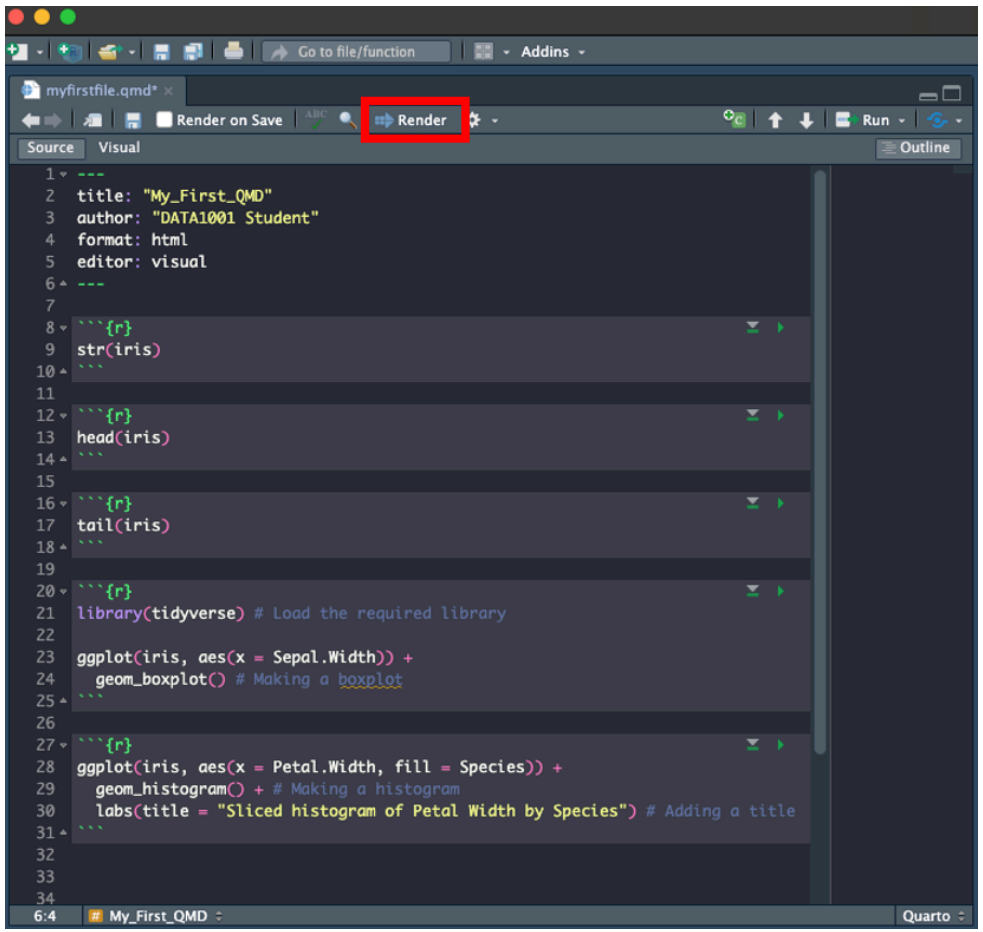


Now it's your turn! Try making another graph using any of the variables you found from `str()`. Try it on another dataset too!

Edit & knit your .qmd file to produce an .html file

Render your .qmd to create a .html

Render your .qmd file to produce .html output.



Now navigate to your DATA1001 folder and you will have a .html file!