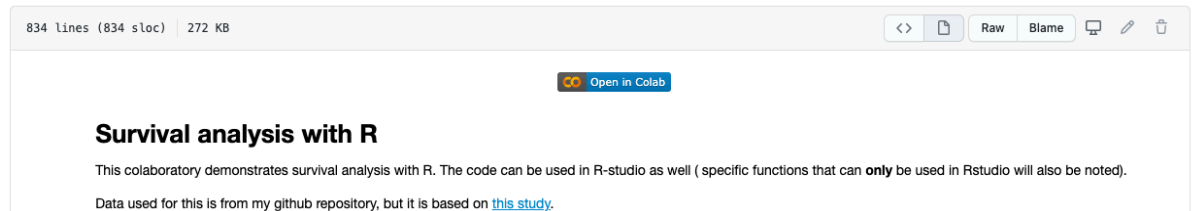
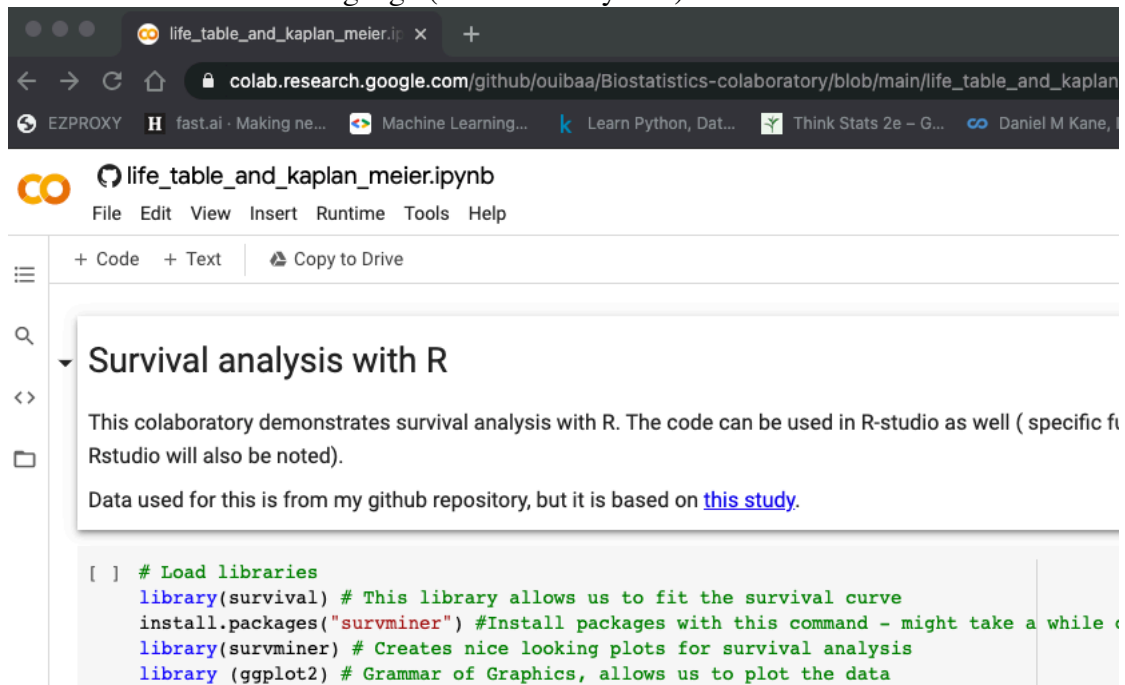


How to run a colaboratory link from Github

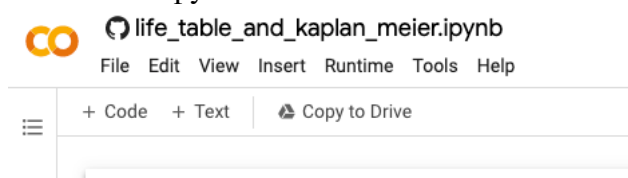
1. Access the github repository and open the jupyter notebook (https://github.com/ouibaa/Biostatistics-colaboratory/blob/main/life_table_and_kaplan_meier.ipynb)
2. Click the 'Open in Colab' link



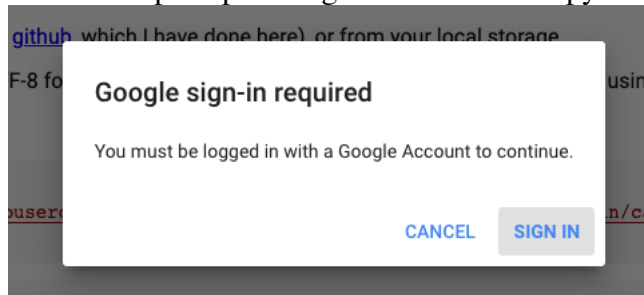
3. The jupyter notebook will open automatically in Google Colaboratory. This notebook has been built in the R language (rather than Python).



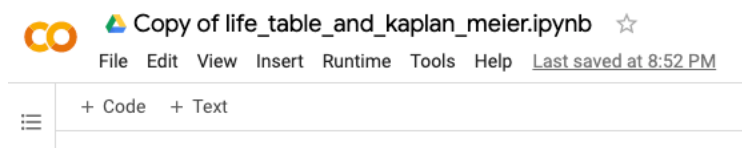
4. You **should** copy the notebook to your own drive so you have your own copy saved – click the 'Copy to drive' button



5. Follow the prompts to sign in and save a copy of the notebook

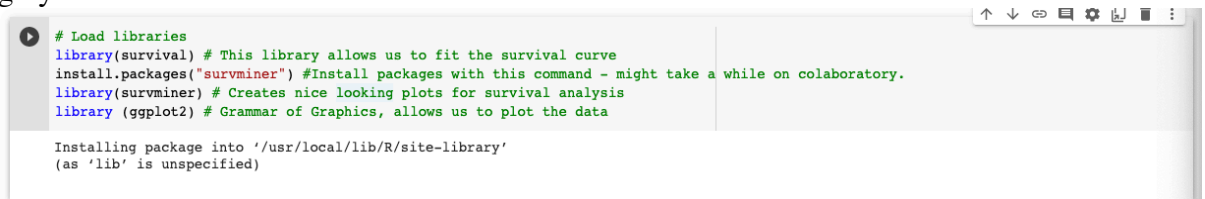


6. Click 'Copy to drive' again – this will reload the page and the new set of code will run from your own google drive. Once it has been copied, you **should see** that the symbol next to the title of the notebook now has a google drive logo



How to run code from colaboratory notebooks

1. Colaboratory notebooks use a virtual computer on Google's servers to run. Whilst you can explicitly start up an instance and get the code running, you can alternatively just start running the code and it will automatically connect
2. To run a piece of code, click on a code block – they are usually highlighted in a light grey



```
# Load libraries
library(survival) # This library allows us to fit the survival curve
install.packages("survminer") # Install packages with this command - might take a while on colaboratory.
library(survminer) # Creates nice looking plots for survival analysis
library(ggplot2) # Grammar of Graphics, allows us to plot the data

Installing package into '/usr/local/lib/R/site-library'
(as 'lib' is unspecified)
```

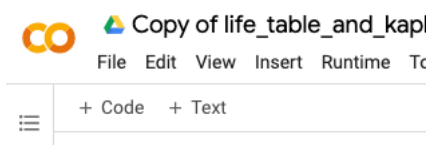
3. When running the code block, you have to run everything at once. The way this notebook has been written, running whole blocks of code at once is not an issue.
 - a. To run code, you can press the **play button** on the left side of the code
 - b. Alternatively, you can run the code like you do in R-studio: by pressing ctrl + enter (Windows) or cmd + enter (Mac)
4. Once the code has been run, a number should pop up in the square brackets where the play button once was – the number tells you the order in which the code was run

```
[2] # Load data
data = read.csv("https:
```

5. Like in R-studio, if you load data to memory when running code, this data is carried through the whole notebook, so all other code blocks can access stored memory. For example, if we run read.csv() and store the csv data into a variable called 'data' (as seen above), the 'data' variable can be accessed through all other code blocks from here on out.

How to write your own code in the colaboratory notebooks

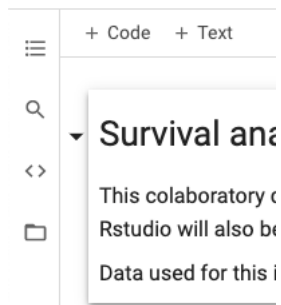
1. To make changes to the code in the notebook, you can just write over the existing code (or write up your own code blocks).
2. Alternatively, as some of the functions are only available on R-Studio (e.g. ggsvrplot() and View()), you can just copy and paste the code (in the correct order!) into your own R-studio script.
3. You can also create a new block of code by clicking “+ Code” in the top left corner



How to load your own data into the colaboratory notebooks

Say you want to load your own data and use these functions out of the notebooks from your local storage (i.e. from your laptop).

1. First, prepare your dataset. The colaboratory has functions for both reading .csv files and .xlsx files under Step 1
2. Next, click the folder button on the side panel – this should open up a directory of files which you can access from your colaboratory notebook



3. Drag your dataset into the directory – it can now be accessed from the colaboratory notebook, just as if you had dragged the file into the working directory of your R-studio command line.

Alternatively, if your data is stored in the web (e.g. in a github repository) and you can hot-load the .csv data, you can just directly copy the link as a string argument into the read.csv() function, as is done in the colaboratory.

```
# Load data
data = read.csv("https://raw.githubusercontent.com/ouibaa/Biostatistics-colaboratory/main/cancerdata.csv")
```