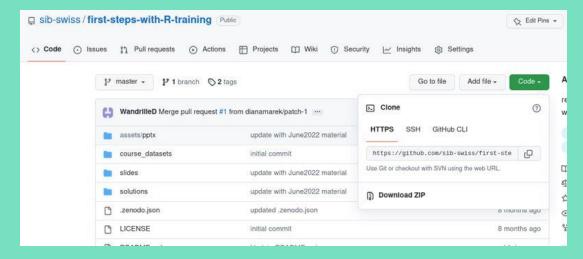
1. Outside Rstudio: prepare the course data for the exercises

Download the course material from:

https://github.com/sib-swiss/first-steps-with-R-training

Either use git clone OR click **Download ZIP**



and UNZIP and then move the folder where you want it

2. Inside Rstudio: project setup

In Rstudio, create a new project set in the folder of the course material you just recovered.

1. Prepare your first script

- 1. Open a script file and save it.
- 2. Type or paste the following code

```
# First steps with R, ex1 w <- 3
```

```
h<- 0.5
```

area <- w*h

area

- 2. **Look at the script** (before running it) can you understand each line? What do you expect it to print to the console?
- 3. Run the script and explore Rstudio's feature:

Run the script line-by-line or Run all lines at once by selecting them

Let's practice - 2bis

- Look at your project option (Tools > Project Options). If needed, modify them to save your workspace and history and to restore them at startup.
- 2. Check that it works:
 - Close Rstudio
 - 2. Double-click the .Rproj file
 - 3. Does the project open? Is your workspace empty?
- 3. Check other behaviours:
 - 1. Close your project
 - 2. Open your project again from Rstudio

Open a new script and save it

- 1. Assign the values 6.7 and 56.3 to variable **a** and **b**, respectively
- 2. Calculate (2*a)/b+(a*b) and assign the result to variable x. Display the content of
- Find out how to compute the square root of variables. Compute the square root of **a**, of **b**, and of **a/b**
- 4. Calculate:
- the logarithm of x
- the logarithm in base 2 of x

- Create two vectors:
 - vector_a, containing the values from -5 to 5
 - vector_b, from o to 1 by increment of o.1
- Calculate the (element-wise) sum, difference and product between the elements of vector_a
 and vector_b.
- 3. Calculate the sum of elements in vector_a.
- 4. Calculate the overall sum of elements in both **vector_a** and **vector_b**.
- 5. Identify the smallest and the largest value in **vector_a**
- 6. Identify the smallest and the largest value among both vector_a and vector_b.
- 7. Compute the overall mean of the values among both **vector_a** and **vector_b**.

Hint: Each task in exercises 1-7 can be performed in a single statement per vector (the minimum and maximum count as 2 separate tasks)

Open a new script and save it as "Ex5.R".

1. In your script, write and execute the commands

```
library(MASS) # loads the library MASS
data(bacteria) # loads the bacteria data set (from MASS)
Check: You should have a variable named "bacteria" in your Environment.
```

- 2. What are the names of the columns of the bacteria data.frame?
- 3. Use [] to select rows 100 to 119 of the column "ap".
- 4. Use \$ to get the column "week" and check how many 0 values it has.
- 5. Optional : using a comparison operator and [], select the rows which correspond to a "placebo" treatment (in the "trt" column).

Let's practice – 6a

A dataset from mouse experiments at 18 weeks is available in the file **mice_data.csv** in the **course_dataset** folder (courtesy of F. Schutz and F. Preitner). Let's explore the dataset to see what it contains.

- 1. Open a new script file in R studio, comment it and save it.
- 2. Have look at the csv file in R studio's file explorer. What do you need to check in order to be able to read in the file correctly?
- 3. Read the file into R, assign its content to object "mice_data". Examine the object.
- 4. How many observations and variables does the dataset have?
- 5. What is the structure of the dataset? What are the names and classes of the variables?

Let's practice – 6b

Continue from the mouse dataset used previously.

Use the following code if you do not have the dataframe already loaded

mice_data = read.csv("course_dataset/mice_data.csv")

- 1. Which variables appear to be categorical? Convert them to factors.
- 2. Get the summary statistics of "mice_data"
- 3. Use the function table() to compute the number of observations in different mouse groups.
 - How many mice are included of each genotype (WT, KO)?
 - 2. How many mice are included per diet (HFD, CHOW)?
 - 3. Make a 2x2 table by genotype and diet crossed.

Let's practice – 6c

Continue from the mouse dataset used previously.

Use the following code if you do not have the dataframe already loaded

```
mice_data = read.csv("course_dataset/mice_data.csv")
```

Subsets

- 1. Isolate the observations for the mice on high fat diet (HFD) using subset().
- 2. Compute the average weights of the subset.
- 3. Do the same for the mice on regular chow diet (CHOW).
- 4. Export the data of each subgroup to a csv file.
- 2. Look at the results from the two previous exercises. What does this initial exploration of the data suggest about mouse weights?
- 3. Optional: Compute the means and standard deviations for WT and KO mouse weights using tapply(). Then do the same for CHOW and HFD groups.