

Exercise sheet: Day 1

***Vangelis Theodorakis, Fatemeh Behjati, Julien Gagneur,
Marcel Schulz***

09 April, 2021

Contents

1	Vectors	2
2	Factors	2
3	Data tables	2
3.1	Basic operations	2
3.2	More exciting operations	3
4	Looping	3
5	Functions.	3
6	R Markdown.	3

1 Vectors

First, create three named numeric vectors of size 10, 11 and 12 respectively in the following manner:

- 1) One vector with the “colon” approach: `from:to`
- 2) One vector with the `seq()` function: `seq(from, to)`
- 3) And one vector with the `seq()` function and the `by` argument: `seq(from, to, by)`

For easier naming you can use the vector `letters` or `LETTERS` which contain the latin alphabet in small and capital, respectively. In order to select specific letters just use e.g. `letters[1:4]` to get the first four letters. Check their types. What is the outcome? Where do you think the difference comes from?

2 Factors

- 1) Create a character vector consisting of three annotations *Mutant-1*, *Mutant-2*, *Control*.
- 2) Using this annotation vector, create a factor where each annotation is repeated 4 times in a sequential manner (*Mutant-1*, *Mutant-2*, *Control*, *Mutant-1*, *Mutant-2*, *Control*, ...). In addition, the levels are the sorted annotation values.
- 3) Print the results.

3 Data tables

The purpose of this exercise is to get familiarized with `data.table` and try out some of its useful features.

3.1 Basic operations

Please follow the steps listed below:

- 1) load the library called *dslabs*
- 2) Access the database called *brexit_polls*. You can take a look at the the *help* documentation of this database (*?brexit_polls*) to learn about its content.

For example:

column name	Description
<code>pollster</code>	Pollster conducting the poll.
<code>poll_type</code>	Online or telephone poll.
<code>samplesize</code>	Sample size of poll.
<code>remain</code>	Proportion voting Remain.
<code>leave</code>	Proportion voting Leave.

- 3) Inspect this data by checking properties such as the class type, the number of rows and columns, its column names, the unique values in the *poll_type* column.
- 4) Create a new variable called *brexit_DT* and assign the `data.table` converted version of *brexit_polls*.

3.2 More exciting operations

Continue from the previous part and perform the following actions:

- 5) From *brexit_DT* get the counts of Online and Telephone polls
- 6) What are the mean and median values of the *samplesize*
- 7) Add a new column *remain_polls* to *brexit_DT* that holds the multiplication of *samplesize* to *remain*
- 8) What is the range of values in this newly created column?
- 9) How do the mean values of *undecided* look like when grouped by *pollster*? How do they look like when grouped by *poll_type*?
- 10) Remove the column *remain_polls* created in step 7.

4 Looping

- 1) Initialize a variable called *counter* by 0.
- 2) Using a for loop that iterates 10 times,
 - create a random number drawn from a uniform distribution with *min=0* and *max=5*.
 - whenever this random number is bigger than or equal to 1, increment *counter* by 1.
- 3) Print the final value in *counter*.

5 Functions

- 1) Write a function named *get_counts* that takes a GTEx data table as input and outputs the total counts of rows that the sample tissue type (*SMTS*) is *Heart* and the sample analysis freeze (*SMAFRZE*) is *RNASEQ*.
- 2) How about if you try the same but for *Blood*.
 - If this task was too easy, can you modify your function such that instead of taking only one argument, it takes two additional ones, one for the *SMTS* and another for *SMAFRZE*. Iterate over all possible values of *SMTS* (**Hint:** `unique(data$SMTS)`) and call your function by providing the sample tissue type.

6 R Markdown

Downloaded and stored the *sample_annotation.tsv* file from Google drive. Then, create an Rmarkdown file and perform the following tasks: 1) Read the *sample_annotation.tsv* file. 2) Create a new variable containing the counts of each *tissue* existing in the data. 3) Use the *barplot* function to plot the number of tissue types in the GTEx data. 4) Try to sort the bars according to the tissue counts (optional).