Exercise sheet: Day 1

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12 October, 2020

Contents

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) Download the GTEx data (annotation v7) from the Google drive:
2) Read the file downloaded above and store it in a variable named: *data*.
3) Inspect *data* by checking properties such as the class type, the number of rows and columns, its column names, the unique values in the *SMTS* column.

If the column names are unfamiliar to you, please take a look at the description list below for some of the relevant columns to this exercise:

column name	Description
SMTS	Tissue Type (area of retrieval)
SMAFRZE	Samples in GTEx Analysis Freeze
SME1MPRT	End 1 Mapping Rate
SMEXPEFF	Expression Profiling Efficiency

3.2 More exciting operations

Continue from the previous part and perform the following actions:

4) Subset the data based on the *Brain* cell type sample and store the result in a variable called: *data_Brain*.

5) Inspect the *data_Brain* similar to the point 3 above.

6) Examine the range of values in *SMEXPEFF* (Expression Profiling Efficiency) column of *data_Brain*. How can you make it more meaningful?

7) For *data_Brain*, compute the average of the values stored in the *SMEXPEFF* column. Also, compute the min of values stored in *SME1MPRT* (End 1 Mapping Rate).

8) Compute the correlation between the two columns mentioned above.

9) Remove the rows that are NA from *data_Brain*$SMEXPEFF*and*data_Brain$*SME1MPRT*. Retry the correlation on the NA-removed *data_Brain_noNA*.

Hint: Use the *is.na()* function to find the rows that are NA.

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*.

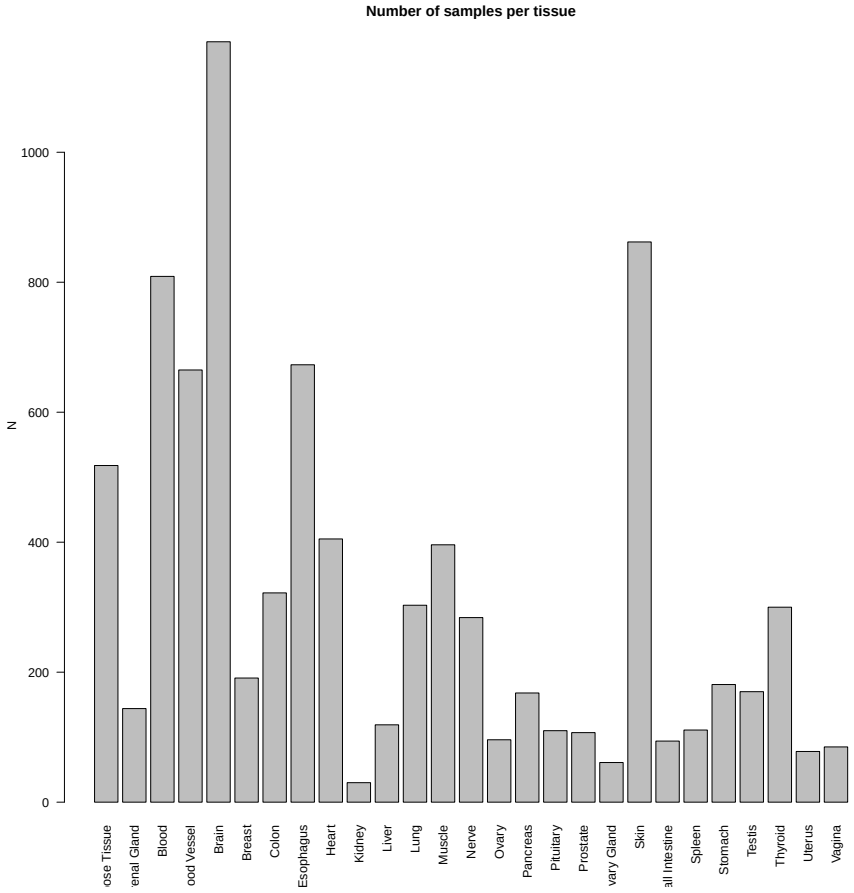
5 Functions

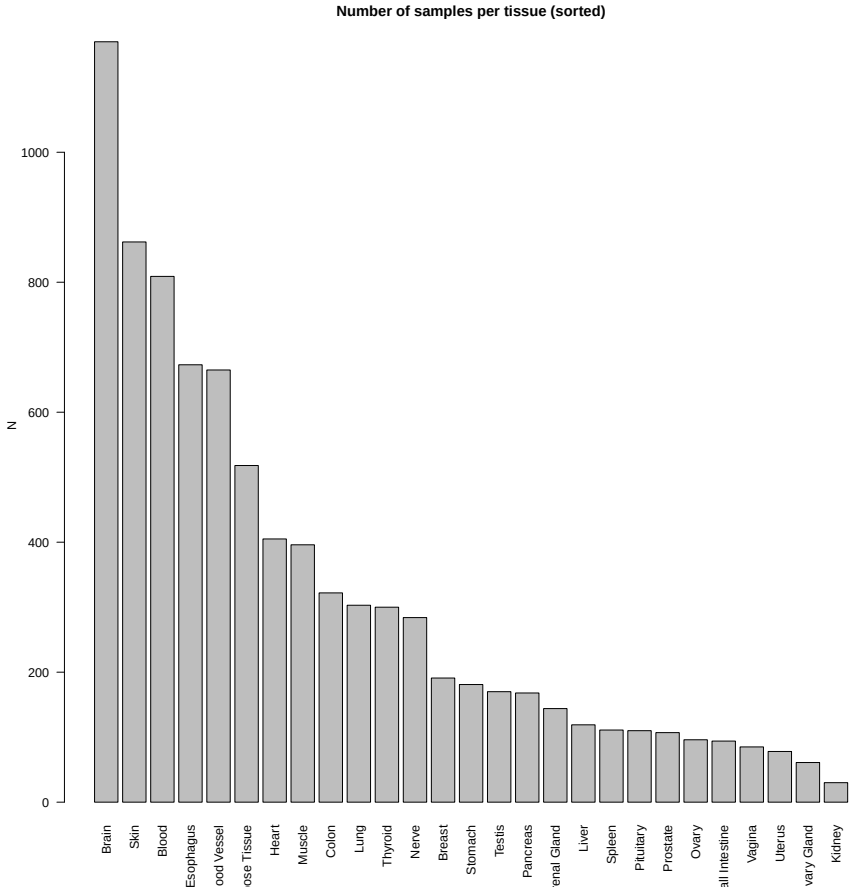
1) Write a function named *get_counts* that takes a GTEx data table as input and outputs the total counts of rows that the sample tissue type (*SMTS*) is *Heart* and the sample analysis freeze (*SMAFRZE*) is *RNASEQ*.
2) How about if you try the same but for *Blood*.

- 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).


Number of samples per tissue
N
0
200
400
600
800
1000
ose Tissue
enal Gland
Blood
ood Vessel
Brain
Breast
Colon
Esophagus
Heart
Kidney
Liver
Lung
Muscle
Nerve
Ovary
Pancreas
Pituitary
Prostate
vary Gland
Skin
all Intestine
Spleen
Stomach
Testis
Thyroid
Uterus
Vagina


Number of samples per tissue (sorted)
N
0
200
400
600
800
1000
Brain
Skin
Blood
Esophagus
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ose Tissue
Heart
Muscle
Colon
Lung
Thyroid
Nerve
Breast
Stomach
Testis
Pancreas
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Liver
Spleen
Pituitary
Prostate
Ovary
all Intestine
Vagina
Uterus
vary Gland
Kidney