Exercise & solution sheet: Day 1

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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?

```
# Answer :

# A. Create vectors
vector.1 <- 1:10
names(vector.1) <- letters[vector.1]

vector.2 <- seq(1, 11)
names(vector.2) <- letters[vector.2]

vector.3 <- seq(1, 12, by = 1)
names(vector.3) <- letters[vector.3]

typeof(vector.1)
## [1] "integer"
typeof(vector.2)
## [1] "integer"
typeof(vector.3)
## [1] "double"
```

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.

```
# Answer :
#1)
annotation <- c("Mutant-1", "Mutant-2", "Control")
#2)
test.factor <- factor(rep(annotation, 4), levels = sort(annotation))
#3)
print(test.factor)
##  [1] Mutant-1 Mutant-2 Control  Mutant-1 Mutant-2 Control  Mutant-1 Mutant-2
##  [9] Control  Mutant-1 Mutant-2 Control
## Levels: Control Mutant-1 Mutant-2
```

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

```
# Answer :
library(data.table)
data <- fread("~/GTEx_v7_Annotations_SampleAttributesDS.txt")

print("class of data is")
## [1] "class of data is"
class(data)
## [1] "data.table" "data.frame"

print("dim of data is")
## [1] "dim of data is"
dim(data)
## [1] 15598    63

print("column names of data are")
## [1] "column names of data are"
colnames(data)
##  [1] "SAMPID"     "SMATSSCR"   "SMCENTER"   "SMPTHNTS"   "SMRIN"      "SMTS"
##  [7] "SMTSD"      "SMUBRID"    "SMTSISCH"   "SMTSPAX"    "SMNABTCH"   "SMNABTCHT"
## [13] "SMNABTCHD"  "SMGEBTCH"   "SMGEBTCHD"  "SMGEBTCHT"  "SMAFRZE"    "SMGTC"
## [19] "SME2MPRT"   "SMCHMPRS"   "SMNTRART"   "SMNUMGPS"   "SMMAPRT"    "SMEXNCRT"
## [25] "SM550NRM"   "SMGNSDTC"   "SMUNMPRT"   "SM350NRM"   "SMRDLGTH"   "SMMNCPB"
## [31] "SME1MMRT"   "SMSFLGTH"   "SMESTLBS"   "SMMPPD"     "SMNTERRT"   "SMRRNANM"
## [37] "SMRDTTL"    "SMVQCFL"    "SMMNCV"     "SMTRSCPT"   "SMMPPDPR"   "SMCGLGTH"
## [43] "SMGAPPCT"   "SMUNPDRD"   "SMNTRNRT"   "SMMPUNRT"   "SMEXPEFF"   "SMMPPDUN"
## [49] "SME2MMRT"   "SME2ANTI"   "SMALTALG"   "SME2SNSE"   "SMMFLGTH"   "SME1ANTI"
## [55] "SMSPLTRD"   "SMBSMMRT"   "SME1SNSE"   "SME1PCTS"   "SMRRNART"   "SME1MPRT"
## [61] "SMNUM5CD"   "SMDPMPRT"   "SME2PCTS"

print("a small subset of data looks like")
## [1] "a small subset of data looks like"
data[1:3, 1:5]
##                      SAMPID SMATSSCR SMCENTER SMPTHNTS SMRIN
## 1: GTEX-1117F-0003-SM-58Q7G       NA       B1             NA
## 2: GTEX-1117F-0003-SM-5DWSB       NA       B1             NA
## 3: GTEX-1117F-0003-SM-6WBT7       NA       B1             NA

print("tissue types in data:")
## [1] "tissue types in data:"
unique(data$SMTS)
##  [1] "Blood"           "Adipose Tissue"  "Muscle"          "Blood Vessel"
##  [5] "Heart"           "Ovary"           "Uterus"          "Vagina"
##  [9] "Breast"          "Skin"            "Salivary Gland"  "Brain"
## [13] "Adrenal Gland"   "Thyroid"         "Lung"            "Spleen"
## [17] "Pancreas"        "Esophagus"       "Stomach"         "Colon"
## [21] "Small Intestine" "Prostate"        "Testis"          "Nerve"
## [25] "Pituitary"       "Liver"           "Kidney"          "Fallopian Tube"
## [29] "Bladder"         "Cervix Uteri"    "Bone Marrow"
```

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.

```
# Answer :
#3
data_Brain <- data[data$SMTS == "Brain", ]

#4
print("class of data_Brain is")
## [1] "class of data_Brain is"
class(data_Brain)
## [1] "data.table" "data.frame"
```

```
print("dim of data_Brain is")
## [1] "dim of data_Brain is"
dim(data_Brain)
## [1] 2076   63

print("column names of data_Brain are")
## [1] "column names of data_Brain are"
colnames(data_Brain)
##  [1] "SAMPID"    "SMATSSCR"  "SMCENTER"  "SMPTHNTS"  "SMRIN"     "SMTS"
##  [7] "SMTSD"     "SMUBRID"   "SMTSISCH"  "SMTSPAX"   "SMNABTCH"  "SMNABTCHT"
## [13] "SMNABTCHD" "SMGEBTCH"  "SMGEBTCHD" "SMGEBTCHT" "SMAFRZE"   "SMGTC"
## [19] "SME2MPRT"  "SMCHMPRS"  "SMNTRART"  "SMNUMGPS"  "SMMAPRT"   "SMEXNCRT"
## [25] "SM550NRM"  "SMGNSDTC"  "SMUNMPRT"  "SM350NRM"  "SMRDLGTH"  "SMMNCPB"
## [31] "SME1MMRT"  "SMSFLGTH"  "SMESTLBS"  "SMMPPD"    "SMNTERRT"  "SMRRNANM"
## [37] "SMRDTTL"   "SMVQCFL"   "SMMNCV"    "SMTRSCPT"  "SMMPPDPR"  "SMCGLGTH"
## [43] "SMGAPPCT"  "SMUNPDRD"  "SMNTRNRT"  "SMMPUNRT"  "SMEXPEFF"  "SMMPPDUN"
## [49] "SME2MMRT"  "SME2ANTI"  "SMALTALG"  "SME2SNSE"  "SMMFLGTH"  "SME1ANTI"
## [55] "SMSPLTRD"  "SMBSMMRT"  "SME1SNSE"  "SME1PCTS"  "SMRRNART"  "SME1MPRT"
## [61] "SMNUM5CD"  "SMDPMPRT"  "SME2PCTS"

print("a small subset of data_Brain looks like")
## [1] "a small subset of data_Brain looks like"
data_Brain[1:3, 1:5]
##                      SAMPID SMATSSCR SMCENTER SMPTHNTS SMRIN
## 1: GTEX-1117F-3226-SM-5N9CT        1       B1 2 pieces   6.2
## 2: GTEX-111FC-3126-SM-5GZZ2        1       B1 2 pieces   6.1
## 3: GTEX-111FC-3326-SM-5GZYV        2       B1 2 pieces   7.1

print("tissue types in data_Brain:e")
## [1] "tissue types in data_Brain:e"
unique(data_Brain$SMTS)
## [1] "Brain"

#5
print("range of values in data_Brain$SMEXPEFF (Expression Profiling Efficiency):")
## [1] "range of values in data_Brain$SMEXPEFF (Expression Profiling Efficiency):"
range(data_Brain$SMEXPEFF)
## [1] NA NA

print("range of values in data_Brain$SMEXPEFF when NA's are removed:")
## [1] "range of values in data_Brain$SMEXPEFF when NA's are removed:"
range(data_Brain$SMEXPEFF, na.rm= T)
## [1] 0.07202903 0.92567736
#6
mean(data_Brain$SMEXPEFF)
## [1] NA
mean(data_Brain$SMEXPEFF, na.rm= T)
## [1] 0.7674499

min(data_Brain$SME1MPRT)
```

```
## [1] NA
min(data_Brain$SME1MPRT, na.rm= T)
## [1] 0.08879356
#7
cor(data_Brain$SME1MPRT, data_Brain$SMEXPEFF)
## [1] NA
#8
data_Brain <- data_Brain[!is.na(data_Brain$SMEXPEFF) | !is.na(data_Brain$SME1MPRT), ]
cor(data_Brain$SME1MPRT, data_Brain$SMEXPEFF)
## [1] 0.8865701
```

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*.

```
#Answer :

# Looping
counter <- 0
for(i in seq(10)){
  r <- runif(1, 0, 5)
  if(r >= 1){
    print(r)
    counter <- counter + 1
  }
}
## [1] 3.229196
## [1] 2.186006
## [1] 2.755855
## [1] 4.973864
## [1] 2.008321
## [1] 3.87833
## [1] 1.362431
## [1] 1.808443
print(counter)
## [1] 8
```

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*.

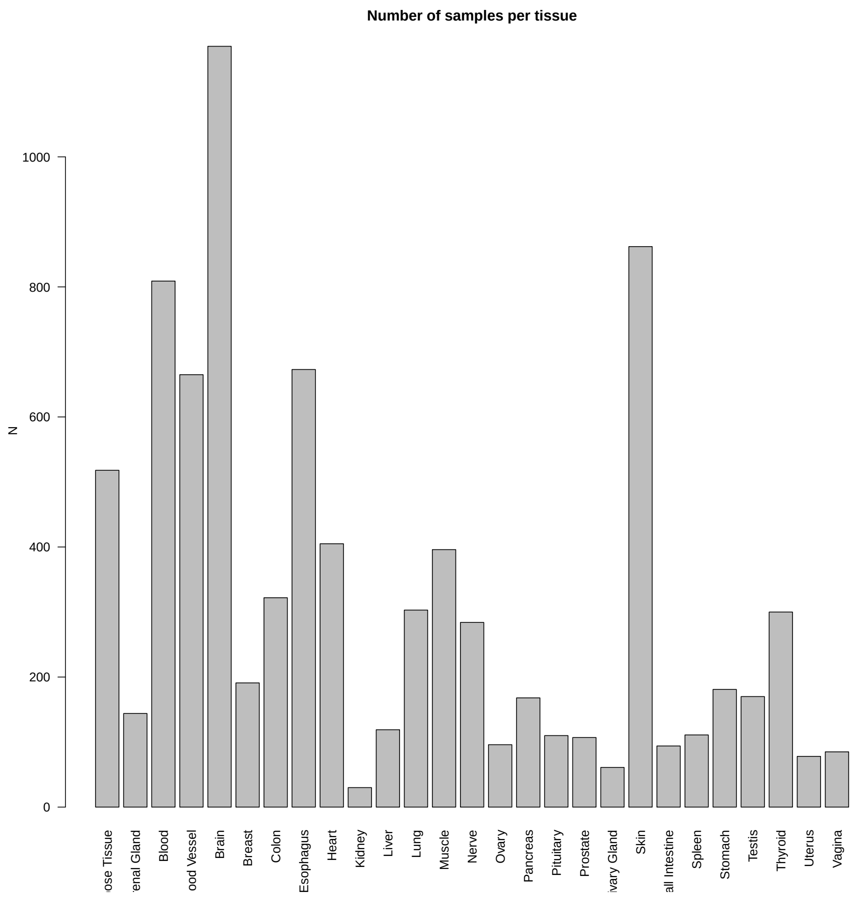
- If this task was too easy, can you modify your function such that instead of taking only one argument, it takes two additional ones, one for the *SMTS* and another for *SMAFRZE*. Iterate over all possible values of *SMTS* (**Hint:** *unique(data$SMTS)*) and call your function by providing the sample tissue type.

```
#Answer :
get_counts <- function(gtex){
  counter <- 0
  for(i in seq(nrow(gtex)))
    if(gtex$SMTS[i] == "Heart" & gtex$SMAFRZE[i] == "RNASEQ"){
      counter <- counter + 1
    }
  return(counter)
}

fun_res <- get_counts(data)
print(fun_res)
## [1] 600

#modified version
get_counts2 <- function(gtex, var1, var2){
  counter <- 0
  for(i in seq(nrow(gtex)))
    if(gtex$SMTS[i] == var1 & gtex$SMAFRZE[i] == var2){
      counter <- counter + 1
    }
  return(counter)
}

all_tissues <- unique(data$SMTS)
for(ts in all_tissues){
  fun_res <- get_counts2(data, ts, "RNASEQ")
  print(paste("Number of RNASEQ cases for", ts, ":", fun_res))
}
## [1] "Number of RNASEQ cases for Blood : 537"
## [1] "Number of RNASEQ cases for Adipose Tissue : 797"
## [1] "Number of RNASEQ cases for Muscle : 564"
## [1] "Number of RNASEQ cases for Blood Vessel : 913"
## [1] "Number of RNASEQ cases for Heart : 600"
## [1] "Number of RNASEQ cases for Ovary : 133"
## [1] "Number of RNASEQ cases for Uterus : 111"
## [1] "Number of RNASEQ cases for Vagina : 115"
## [1] "Number of RNASEQ cases for Breast : 290"
## [1] "Number of RNASEQ cases for Skin : 1203"
## [1] "Number of RNASEQ cases for Salivary Gland : 97"
## [1] "Number of RNASEQ cases for Brain : 1671"
## [1] "Number of RNASEQ cases for Adrenal Gland : 190"
## [1] "Number of RNASEQ cases for Thyroid : 446"
## [1] "Number of RNASEQ cases for Lung : 427"
## [1] "Number of RNASEQ cases for Spleen : 162"
## [1] "Number of RNASEQ cases for Pancreas : 248"
## [1] "Number of RNASEQ cases for Esophagus : 1021"
## [1] "Number of RNASEQ cases for Stomach : 262"
## [1] "Number of RNASEQ cases for Colon : 507"
## [1] "Number of RNASEQ cases for Small Intestine : 137"
## [1] "Number of RNASEQ cases for Prostate : 152"
## [1] "Number of RNASEQ cases for Testis : 259"
## [1] "Number of RNASEQ cases for Nerve : 414"
## [1] "Number of RNASEQ cases for Pituitary : 183"
## [1] "Number of RNASEQ cases for Liver : 175"
## [1] "Number of RNASEQ cases for Kidney : 45"
## [1] "Number of RNASEQ cases for Fallopian Tube : 7"
## [1] "Number of RNASEQ cases for Bladder : 11"
## [1] "Number of RNASEQ cases for Cervix Uteri : 11"
## [1] "Number of RNASEQ cases for Bone Marrow : 0"
```

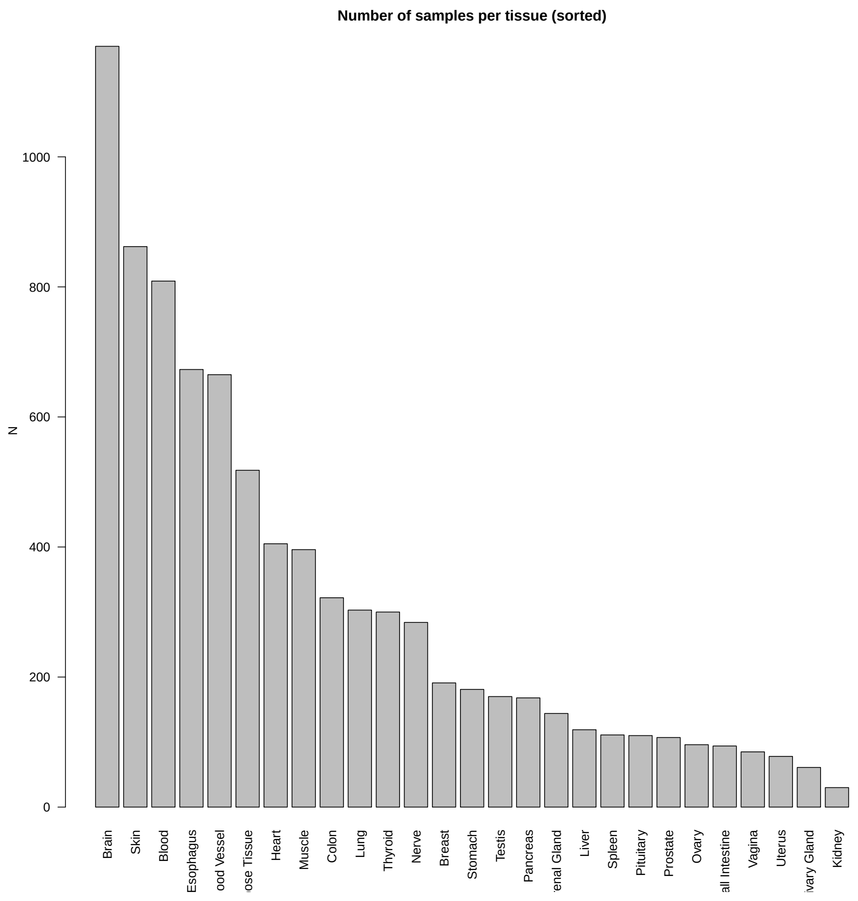
6 R Markdown

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).

```
gtex.annotation <- fread("../../extdata/sample_annotation.tsv")
samples.per.tissue <- gtex.annotation[, .N, by = "tissue"]
barplot(N~tissue, samples.per.tissue, las = 2, xlab = "",
        main= "Number of samples per tissue")
```



```r
samples.per.tissue.ordered <- samples.per.tissue[order(-N)]
samples.per.tissue.ordered$tissue <- factor(samples.per.tissue.ordered$tissue,
                                            levels = samples.per.tissue.ordered$tissue)
barplot(N~tissue, samples.per.tissue.ordered, las = 2, xlab = "",
        main= "Number of samples per tissue (sorted)")
```


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