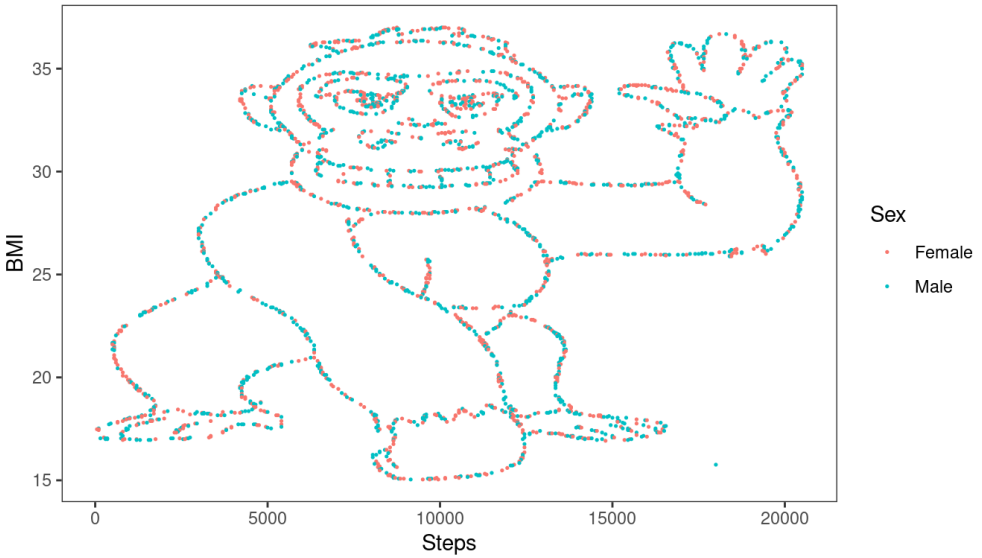
Introduction to R

Workshop on Data Visualization in R

Lokesh Mano • 17-Oct-2022
NBIS, SciLifeLab

Contents

Quick checkups



If you don't recognize the correlation you see in the figure above, I would highly recommend you to read the following paper ;)

Yanai, I., Lercher, M. A hypothesis is a liability. Genome Biol 21, 231 (2020).

- Coffe breaks (15 minutes is fine?)
- Webpage structure
- Plots from drop-down
- Times mentioned in schedule are **super** arbitrary

R

- Derived from a statistical programming language called **S**
- You can write your own functions
- Powerful and flexible.
- Available for all platforms

- `GUI` with **Rstudio**

- **RMarkdown**: Embedding codes and results together

Data Formats

- Wide format

	Sample_1	Sample_2	Sample_3	Sample_4
ENSG00000000003	321	303	204	492
ENSG00000000005	0	0	0	0
ENSG00000000419	696	660	472	951
ENSG00000000457	59	54	44	109
ENSG00000000460	399	405	236	445
ENSG00000000938	0	0	0	0

- familiarity
- conveniency
- you see more data

Data Formats

- Long format

Sample_ID	Gene	count
Sample_1	ENSG00000000003	321
Sample_1	ENSG00000000005	0
Sample_1	ENSG00000000419	696
Sample_1	ENSG00000000457	59
Sample_1	ENSG00000000460	399
Sample_1	ENSG00000000938	0

Sample_ID	Sample_Name	Time	Replicate	Cell	Gene	count
Sample_1	t0_A	t0	A	A431	ENSG00000000003	321
Sample_1	t0_A	t0	A	A431	ENSG00000000005	0
Sample_1	t0_A	t0	A	A431	ENSG00000000419	696
Sample_1	t0_A	t0	A	A431	ENSG00000000457	59
Sample_1	t0_A	t0	A	A431	ENSG00000000460	399

Data Formats

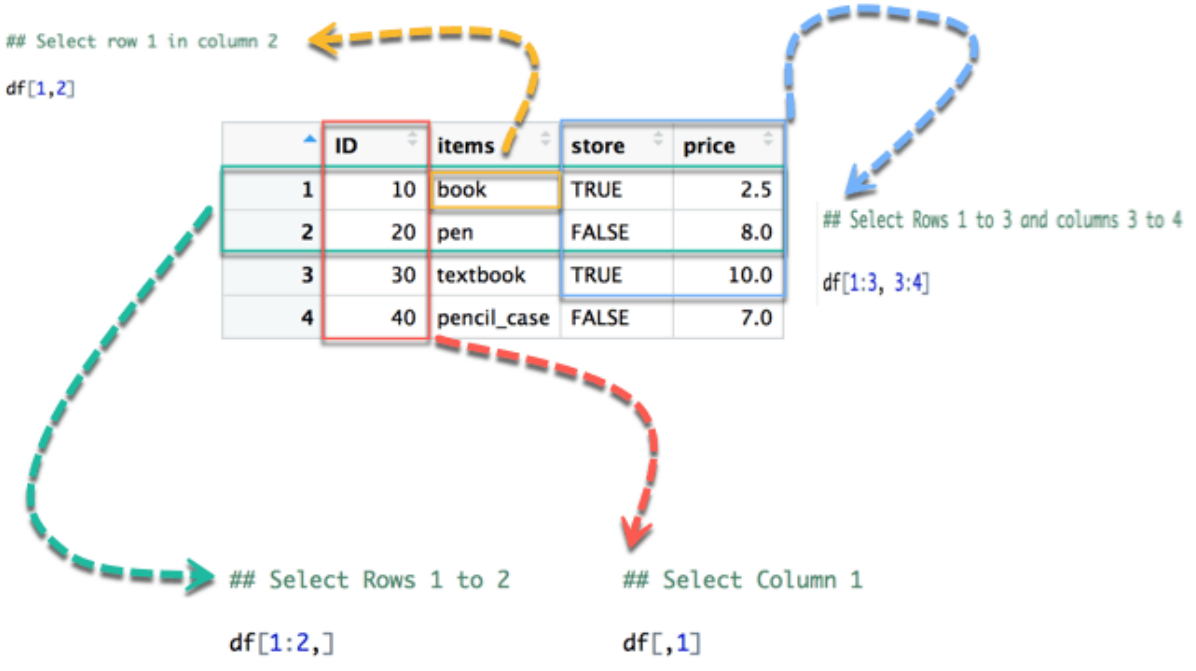
- Long format

Sample_ID	Sample_Name	Time	Replicate	Cell	Gene	count
Sample_1	t0_A	t0	A	A431	ENSG00000000003	321
Sample_1	t0_A	t0	A	A431	ENSG00000000005	0
Sample_1	t0_A	t0	A	A431	ENSG00000000419	696
Sample_1	t0_A	t0	A	A431	ENSG00000000457	59
Sample_1	t0_A	t0	A	A431	ENSG00000000460	399
Sample_1	t0_A	t0	A	A431	ENSG00000000938	0

- easier to add data to the existing
- Most databases store and maintain in long-formats due to its efficiency
- R tools **like ggplot** require data in long format.

Data Frames

- Let us take a quick look into `data.frame` in `R`:



- imported files re usually in `data.frame`
- Structured matrix with `row.names` and `colnames`
- Probably most used `data.type` in Biology!

Vectors

```
n <- c(2,3,4,2,1,2,4,5,10,11,8,9)
print(n)
```

```
##  [1]  2  3  4  2  1  2  4  5 10 11  8  9
```

```
z <- n +3
print(z)
```

```
##  [1]  5  6  7  5  4  5  7  8 13 14 11 12
```

```
z <- n +3
mean(z)
```

```
## [1] 8.083333
```

```
s <- c("I", "love", "Batman")
print(s)
```

```
## [1] "I"      "love"   "Batman"
```

Vector types

- `int` stands for *integers*
- `dbl` stands for *doubles* or real numbers
- `chr` stands for *character* vectors or strings
- `dttm` stands for *date and time*,
- `lgl` stands for *logical* with just TRUE or FALSE
- `fctr` stands for *factors* which R uses to state categorical variables.
- `date` stands for *dates*

You can find what kind of vectors you have or imported by using the function `class()`

Thank you. Questions?

R version 4.1.3 (2022-03-10)

Platform: x86_64-pc-linux-gnu (64-bit)

OS: Ubuntu 18.04.6 LTS

Built on : 17-Oct-2022 at 15:29:23

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