

# Intro to R for Biologists

## Session 2

### **Data exploration**

Irina & Rao

21/04/2021

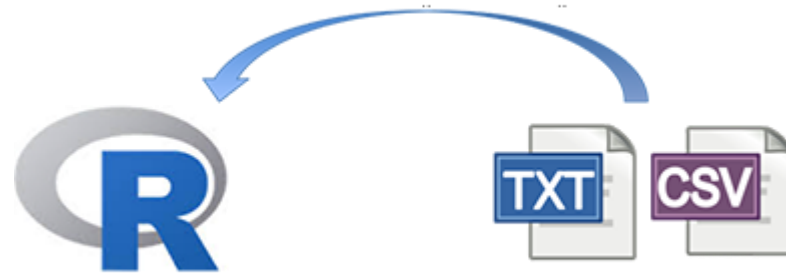
Trinity 2021

# INTRO TO R FOR BIOLOGISTS

## ► Data exploration

- Reading and writing data files
- Managing working directory
- Functions to explore data
- Cleaning data
- Functions to modify a data.frame
- Basic plots to visualize data
- Basic statistics
- Filtering data

# Reading data into R



## Base functions:

- **read.table**(file, header = FALSE, sep = "", quote = "\"'", dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"), row.names, col.names, as.is = !stringsAsFactors, na.strings = "NA", colClasses = NA, nrows = -1, skip = 0, ...)
- **read.csv**(file, header = TRUE, sep = ",", quote = "\"", dec = ".", fill = TRUE, comment.char = "", ...)
- **read.delim**(file, header = TRUE, sep = "\t", quote = "\"", dec = ".", fill = TRUE, comment.char = "", ...)

# Reading data into R



```
install.packages("readxl") - install the package  
library(readxl) - load the package
```

- **read\_excel**(**path**, sheet = NULL, range = NULL, col\_names = TRUE, col\_types = NULL, na = "", trim\_ws = TRUE, ...)
- **read\_xls**(**path**, sheet = NULL, range = NULL, col\_names = TRUE, col\_types = NULL, na = "", trim\_ws = TRUE, ...)
- **read\_xlsx**(**path**, sheet = NULL, range = NULL, col\_names = TRUE, col\_types = NULL, na = "", trim\_ws = TRUE, ...)

<https://www.rdocumentation.org>

More examples (over 21 000 packages)

# Managing working directory

The **working directory** is a file path on your computer that sets the default location of any files you read into **R**, or save out of **R**.

`getwd()` - returns the current working directory

`setwd("path/to/your_new_wd")` - changes the working directory

`list.files()` - displays the list of all the files in wd

**Note:** `getwd()` function has no arguments!

# Write files from R



## Base functions:

- `write.table(my_data, file = "my_data.txt", append = FALSE, sep = " ", dec = ".", row.names = TRUE, col.names = TRUE)`  
**Set separator to `sep = "\t"` to get tab separated txt file**
- `write.csv(my_data, file = "my_data.csv")` - comma-separated csv files

# Write files from R



xls, xlsx files

```
install.packages("xlsx") - install the package
```

```
library(xlsx) - load the package
```

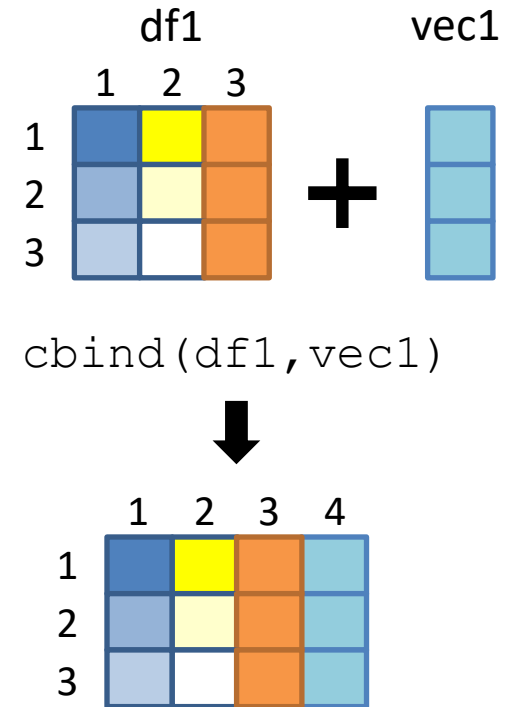
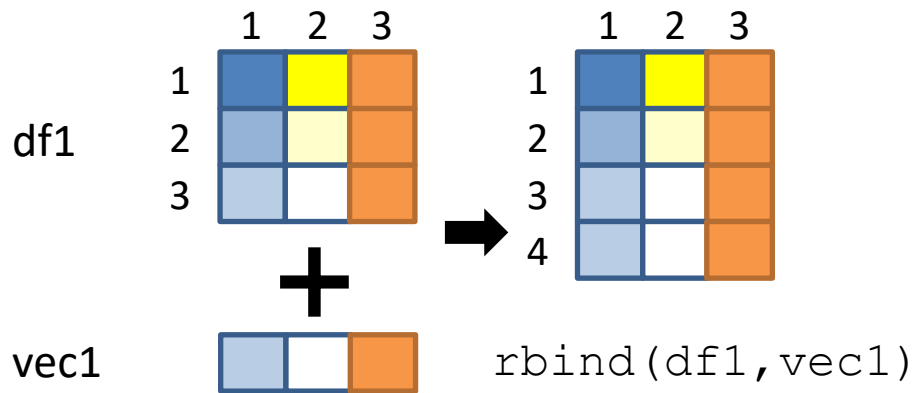
```
write.xlsx(my_data, file = "result.xlsx", sheetName =  
"Sheet1", col.names = TRUE, row.names = TRUE, append = FALSE)
```

**Let's  
explore  
practically**





# Adding rows or columns to a data.frame



# Migration and morphology data

## scientific data

[Explore content](#) [Journal information](#) [Publish with us](#)

[nature](#) > [scientific data](#) > [data descriptors](#) > [article](#)

[Open Access](#) | Published: 01 March 2017

## Systematic high-content genome-wide RNAi screens of endothelial cell migration and morphology

Steven P. Williams, Cathryn M. Gould, Cameron J. Nowell, Tara Karnezis, Marc G. Achen, Kaylene J. Simpson & Steven A. Stacker [✉](#)

*Scientific Data* **4**, Article number: 170009 (2017) | [Cite this article](#)

**747** Accesses | **12** Citations | **6** Altmetric | [Metrics](#)

### Abstract

Many cell types undergo migration during embryogenesis and disease. Endothelial cells line blood vessels and lymphatics, which migrate during development as part of angiogenesis, lymphangiogenesis and other types of vessel remodelling. These processes are also important in wound healing, cancer metastasis and cardiovascular conditions. However, the molecular control of endothelial cell migration is poorly understood. Here, we present a dataset containing siRNA screens that identify known and novel components of signalling pathways regulating migration of lymphatic endothelial cells. These components are compared to signalling in blood vascular endothelial cells. Further, using high-content microscopy, we captured a dataset of images of migrating cells following transfection with a genome-wide siRNA library. These datasets are suitable for the identification and analysis of genes involved

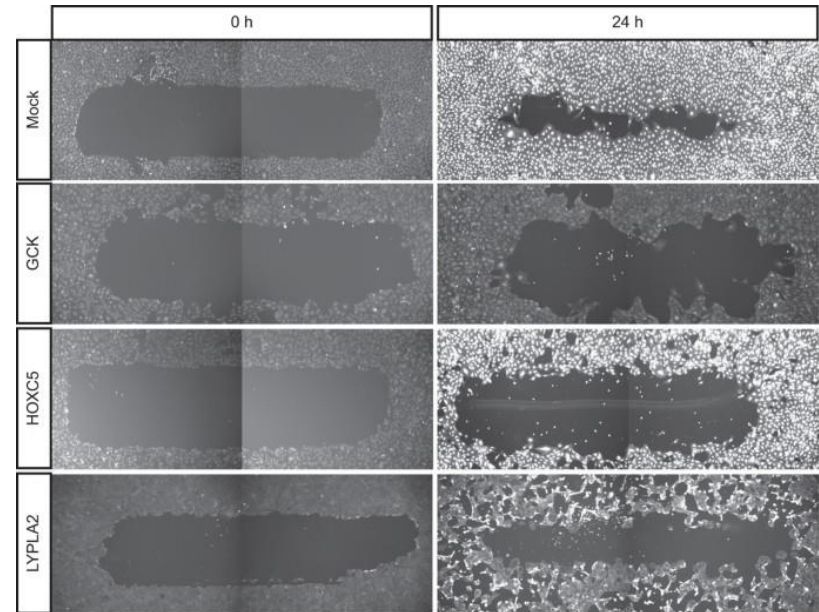


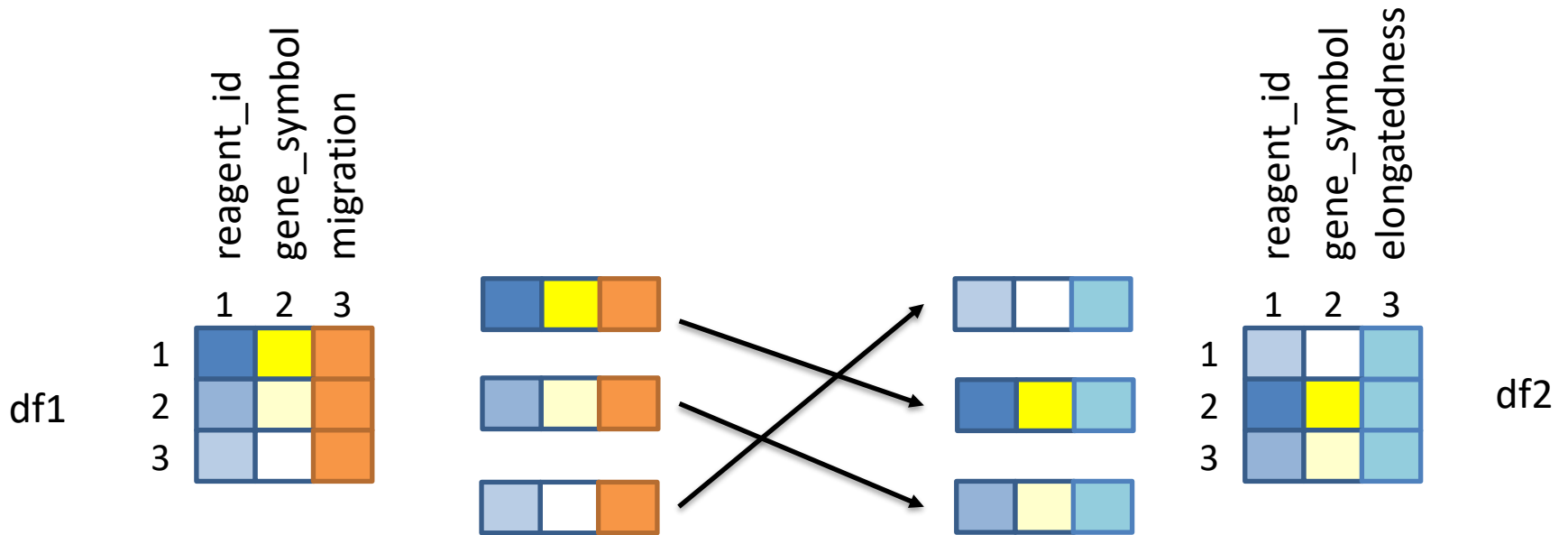
Table 1: Migration data

col1: reagent\_id  
col2: gene\_symbol  
col3: migration

Table 2: Morphology data

col1: reagent\_id  
col2: gene\_symbol  
col3: elongatedness

# Merging data.frames



```
merge(df1, df2, by =  
c("reagent_id", "gene_symbol"))
```

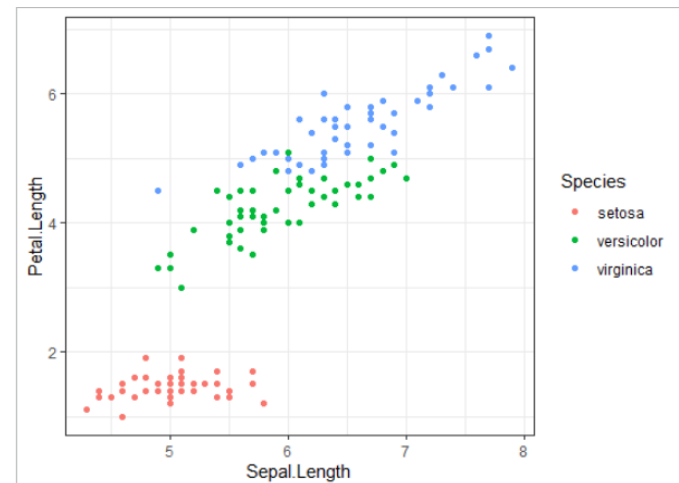
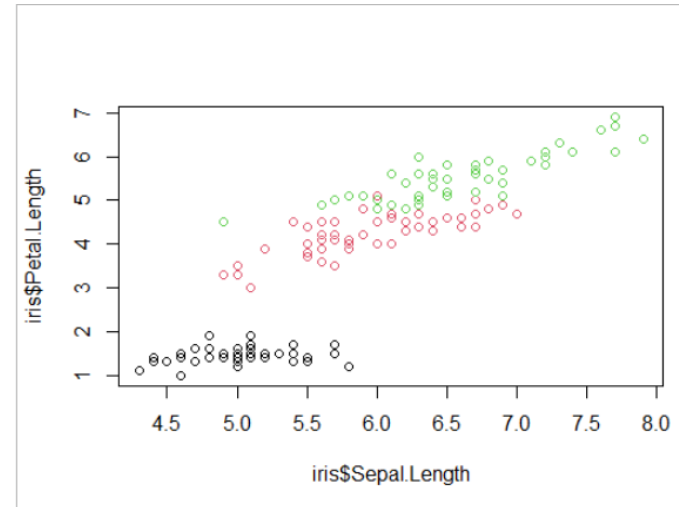
reagent_id	gene_symbol	migration	elongatedness
1	2	3	3
1	2	3	3
1	2	3	3

# Data exploration and cleaning

- Look at the data
  - `head()`, `tail()`, `class()`, `str()`, `View()`
- Are the data types correct? If not, convert to appropriate type
  - `as.numeric()`, `as.character()`, `as.logical()`
- Is there any missing data? NA or NaN are missing data
  - `na.omit()`, `complete.cases()`
- Is there unnecessary data? Rows or columns you don't need?
  - Subset the data
  - Filter the data
- Visualise the data with graphs

# Visualising data

- Base R plotting
  - Great for initial exploration
  - Quick
  - Simple syntax – many things can be plotted with just `plot()`
  - Not easy to modify colours, aesthetics, etc.
- ggplot2 package
  - Modular – graphs can be built element-by-element
  - Need to remember a few different functions
  - Possible to produce publication quality figures with relative ease



**Let's  
explore  
practically**



# Filtering data

- Keep/remove data that satisfies one or more conditions

```
> my_vec = c(1, 2, 3, 4, 5, 6)
> my_vec < 4
TRUE TRUE TRUE FALSE FALSE FALSE
> my_vec[my_vec < 4]
1 2 3
```

- For more than one condition, we need to use logical operators
  - & (AND)
  - | (OR)

# Logical operators

- TRUE & TRUE    # evaluates to TRUE
- TRUE & FALSE    # evaluates to FALSE
- FALSE & FALSE    # evaluates to FALSE
- TRUE | FALSE    # evaluates to TRUE

```
> my_vec = c(1, 2, 3, 4, 5, 6)
> my_vec < 4 & my_vec > 2
FALSE FALSE TRUE FALSE FALSE FALSE
> my_vec[my_vec < 4 & my_vec > 2]
3
```



**Let's  
explore  
practically**



# Loop functions

- `lapply()` – perform an action on each element of a vector: returns list
- `sapply()` – as above, returns a simplified object (variable)
- `apply()` – loop over rows or columns of a matrix or df
- `tapply()` – loop over a vector, split based on a factor
- `mapply()` – loop over more than one vector

```
> my_list = list(a = c(1, 2, 3), b = c(4, 5, 6), c = c(7, 8, 9))
```

```
> lapply(my_list, mean)
```

```
$a
```

```
[1] 2
```

```
$b
```

```
[1] 5
```

```
$c
```

```
[1] 8
```

# Useful reference

- [R Programming for Data Science \(Roger Peng\)](#) – Ch. 3, 4, 5, 9
- [Swirl](#) – Interactive learning