R: The tidyverse and beyond

1-day workshop
Afternoon lecture

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UCC
University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

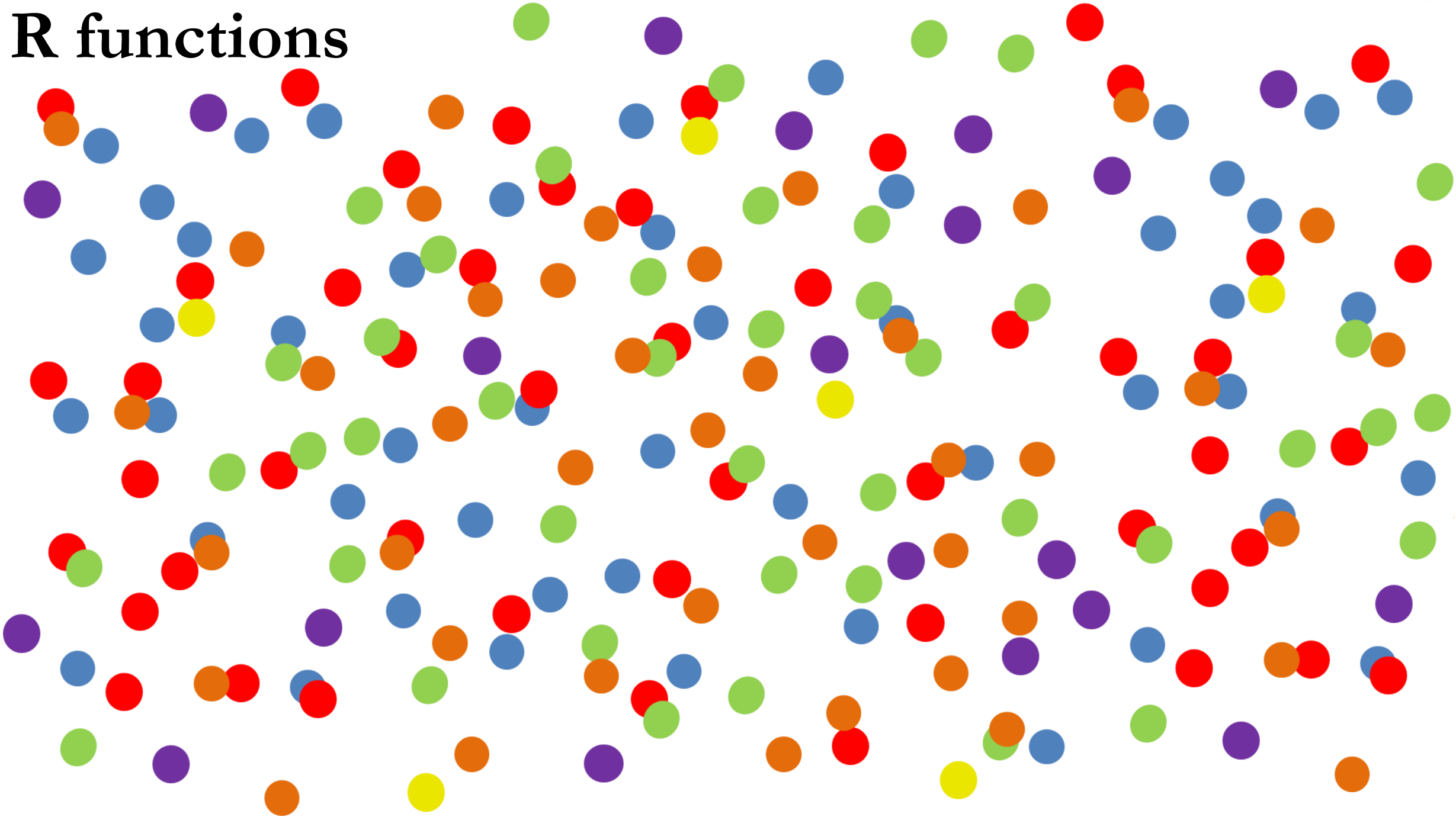
CRF-C
HRB Clinical Research Facility Cork

HRB
Health Research Board

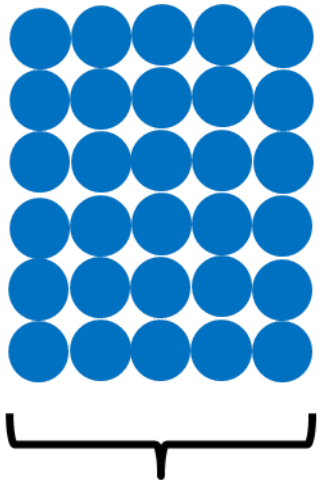
To understand R, remember the following

- **Everything that exists is an object**
- **Everything that happens is a function**

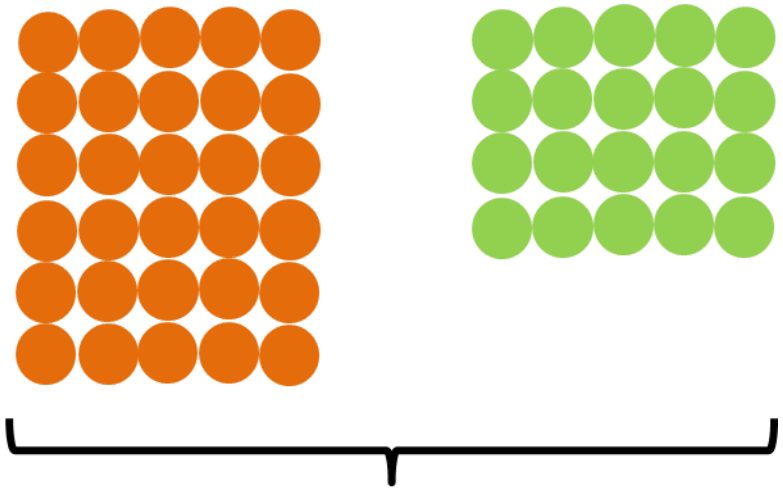
R functions



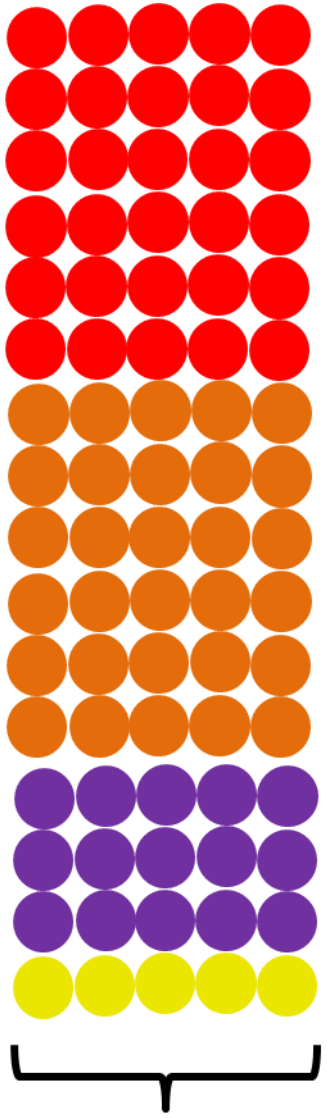
R packages



Base R:
Comes
pre-
loaded

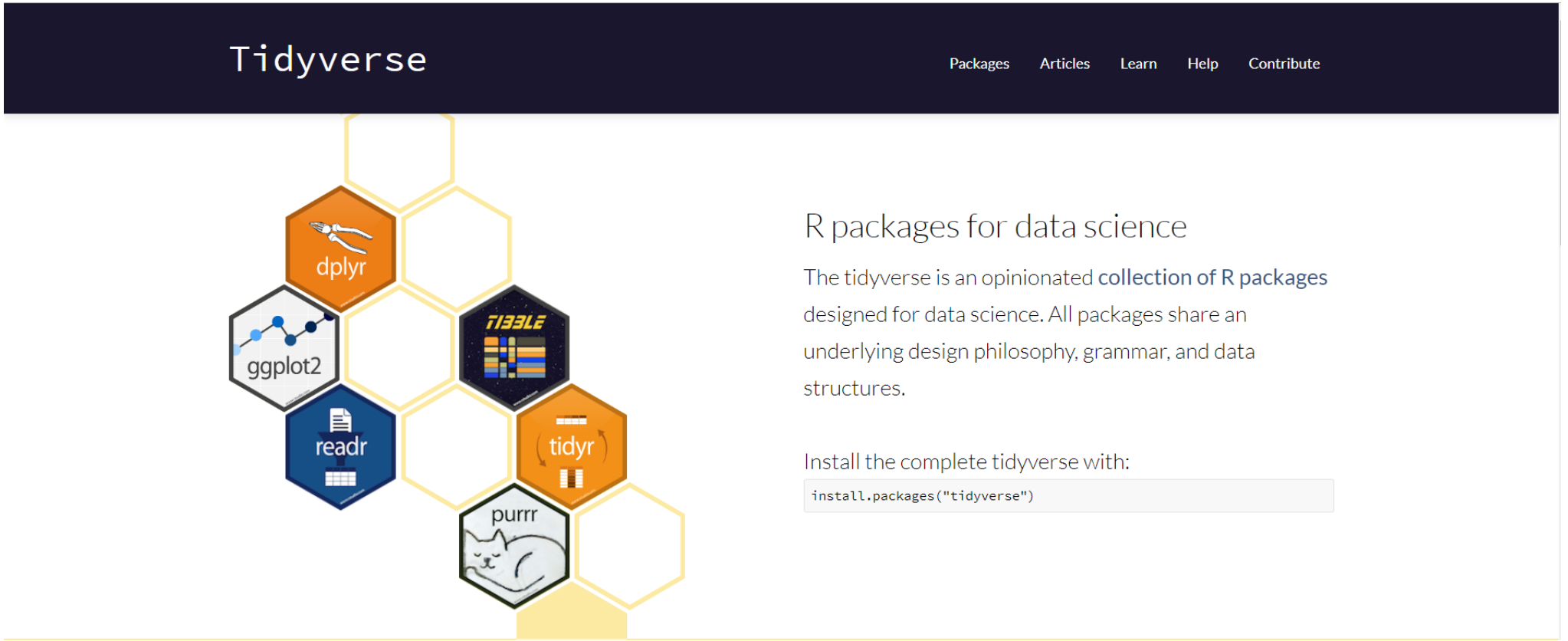


Other packages:
Install once
Update regularly
Load each session



core
tidyverse

What is the tidyverse?



- Joined up collection of packages for data analysis
    - Consistent functions
    - Uses (tidy) data
    - Supports end-to-end workflows

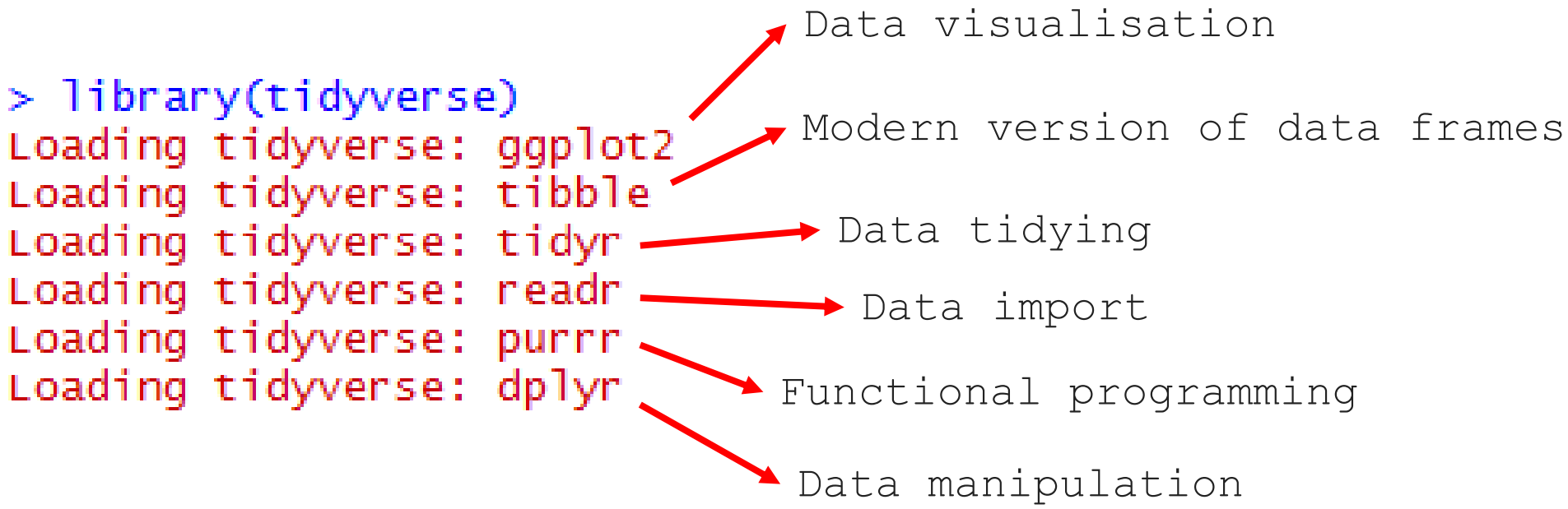
What is the tidyverse?

```
> install.packages(c("broom", "cli2", "crayon",
"dbplyr", "dplyr", "forcats", "ggplot2", "haven",
"hms", "httr", "jsonlite", "lubridate",
"magrittr", "modelr", "pillar", "purrr", "readr",
"readxl", "reprex", "rlang", "rstudioapi",
"rvest", "stringr", "tibble", "tidyr", "xml2")
```

```
> install.packages("tidyverse")
```

The tidyverse Oct 2017

```
> library(tidyverse)
Loading tidyverse: ggplot2
Loading tidyverse: tibble
Loading tidyverse: tidyr
Loading tidyverse: readr
Loading tidyverse: purrr
Loading tidyverse: dplyr
```



The tidyverse May 2019

```
> library(tidyverse)
-- Attaching packages ------------------------------------ tidyverse 1.2.1 --
v ggplot2 3.1.1       v purrr   0.3.2
v tibble  2.1.1       v dplyr   0.8.0.1
v tidyr   0.8.3       v stringr 1.4.0
v readr   1.3.1       v forcats 0.4.0
-- Conflicts --------------------------------------- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```

FYI, the latest R release was last week!

R-3.6.0 for Windows (32/64 bit)

Download R 3.6.0 for Windows (80 megabytes, 32/64 bit)

Installation and other instructions
New features in this version

If you want to double-check that the package you have downloaded matches the package distributed by CRAN, you can compare the md5sum of the .exe to the fingerprint on the master server. You will need a version of md5sum for windows: both graphical and command line versions are available.

Frequently asked questions

- Does R run under my version of Windows?
- How do I update packages in my previous version of R?
- Should I run 32-bit or 64-bit R?

Please see the R FAQ for general information about R and the R Windows FAQ for Windows-specific information.

Other builds

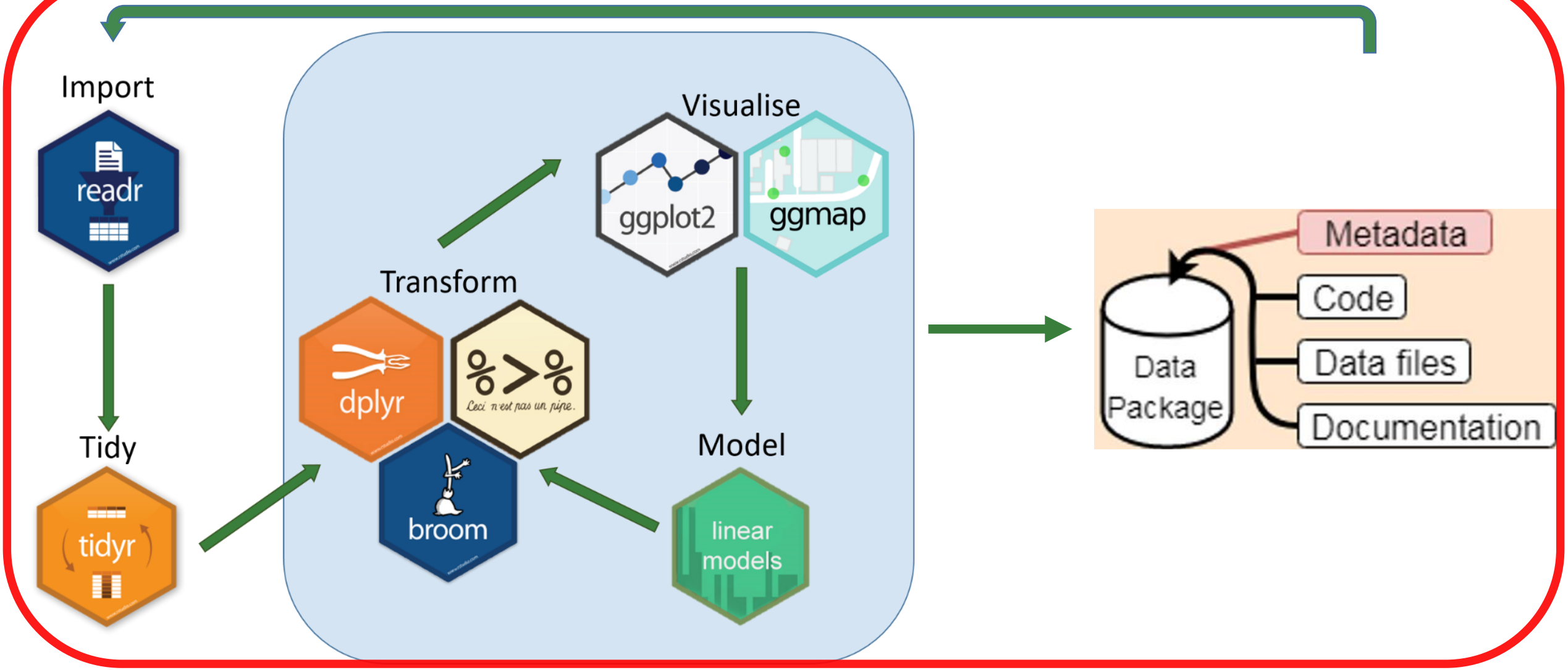
- Patches to this release are incorporated in the r-patched snapshot build.
- A build of the development version (which will eventually become the next major release of R) is available in the r-devel snapshot build.
- Previous releases

Note to webmasters: A stable link which will redirect to the current Windows binary release is <CRAN MIRROR>/bin/windows/base/release.htm.

Last change: 2019-04-26

Putting the pieces together

- Data analysis in a tidyverse nutshell



Tidyverse works best with tidy data

- Each variable forms a column
- Each observation forms a row

Problems with Brauer et al., data…

Column headers contain values

Multiple variables are stored in one column

e.g. column "NAME" contains values such as;

SFB2 || ER to Golgi transport || molecular function unknown || YNL049C || 1082129

These need to be split up

G0.05 - letter identifies a compound
      - number is the concentration of that compound

Code structure v1

```
separated_gene <- separate(raw_gene, NAME, c("name", "BP", "MF", "systematic_name", "number"), sep = "\\|\\|")
```

```
separated_gene                  - the new tibble you will create

<-                              - the assign operator

separate                        - the function you are calling on

(raw_gene,                      - the tibble to be used

NAME,                           - the column to be altered

c("name", "BP", "MF", "systematic_name", "number"),
                                - new columns IDs for the new columns

sep = "\\|\\|")                 - identify the separator to be used
```

Filter

	GID	YORF	NAME	GWEIGHT	G0.05	G0.1	G0.15	G0.2	G0.25	G0.3
1	GENE1331X	A_06_P5820	SFB2 || ER to Golgi transport || molecular function unknown || YNL049C || 108...	1	-0.24	-0.13	-0.21	-0.15	-0.05	-0.05
2	GENE4924X	A_06_P5866	|| biological process unknown || molecular function unknown || YNL095C || 1...	1	0.28	0.13	-0.40	-0.48	-0.11	0.17
3	GENE4690X	A_06_P1834	QRI7 || proteolysis and peptidolysis || metalloendopeptidase activity || YDL104...	1	-0.02	-0.27	-0.27	-0.02	0.24	0.25
4	GENE1177X	A_06_P4928	CFT2 || mRNA polyadenylylation* || RNA binding || YLR115W || 1081958	1	-0.33	-0.41	-0.24	-0.03	-0.03	0.00
5	GENE511X	A_06_P5620	SSO2 || vesicle fusion* || t-SNARE activity || YMR183C || 1081214	1	0.05	0.02	0.40	0.34	-0.13	-0.14
6	GENE2133X	A_06_P5307	PSP2 || biological process unknown || molecular function unknown || YML01...	1	-0.69	-0.03	0.23	0.20	0.00	-0.27
7	GENE1002X	A_06_P6258	RIB2 || riboflavin biosynthesis || pseudouridylate synthase activity* || YOL066C...	1	-0.55	-0.30	-0.12	-0.03	-0.16	-0.11
8	GENE5478X	A_06_P7082	VMA13 || vacuolar acidification || hydrogen-transporting ATPase activity, rota...	1	-0.75	-0.12	-0.07	0.02	-0.32	-0.41
9	GENE2065X	A_06_P2554	EDC3 || deadenylylation-independent decapping || molecular function unkno...	1	-0.24	-0.22	0.14	0.06	0.00	-0.13
10	GENE2440X	A_06_P6431	VPS5 || protein retention in Golgi* || protein transporter activity || YOR069W || ...	1	-0.16	-0.38	0.05	0.14	-0.04	-0.01
11	GENE4180X	A_06_P6220	|| biological process unknown || molecular function unknown || YOL029C || 1...	1	-0.22	-0.18	0.27	0.18	0.03	-0.04
12	GENE5247X	A_06_P1410	AMN1 || negative regulation of exit from mitosis* || protein binding || YBR158...	1	0.18	0.61	1.55	1.34	0.23	-0.03
13	GENE2121X	A_06_P2983	SCW11 || cytokinesis, completion of separation || glucan 1,3-beta-glucosidas...	1	-0.67	-0.47	1.16	1.05	-0.18	-0.68
14	GENE1985X	A_06_P3720	DSE2 || cell wall organization and biogenesis* || glucan 1,3-beta-glucosidase ...	1	-0.59	-0.17	1.17	0.85	-0.12	-0.61
15	GENE4728X	A_06_P2774	COX15 || cytochrome c oxidase complex assembly* || oxidoreductase activity,...	1	-0.28	-0.81	-0.39	0.24	0.01	0.01
16	GENE3153X	A_06_P4597	SPE1 || pantothenate biosynthesis* || ornithine decarboxylase activity || YKL18...	1	-0.19	0.24	0.03	0.17	0.00	-0.01
17	GENE3704X	A_06_P5667	MTF1 || transcription from mitochondrial promoter || S-adenosylmethionine-...	1	-0.42	-0.43	-0.36	-0.12	0.05	0.24
18	GENE2141X	A_06_P3260	KSS1 || invasive growth (sensu Saccharomyces)* || MAP kinase activity || YGR...	1	-0.76	-0.32	-0.05	-0.27	-0.31	-0.01
19	GENE2978X	A_06_P3607	|| biological process unknown || molecular function unknown || YHR036W || 1...	1	-0.91	-0.43	-0.05	-0.09	-0.27	-0.45
20	GENE1203X	A_06_P5929	|| biological process unknown || molecular function unknown || YNL158W || 1...	1	-0.47	-0.43	-0.15	0.08	-0.26	-0.25

Try to limit “uninformative” data

“GWEIGHT” contains the same information in every cell

- This isn’t going to add to our analysis

“GID” and “YORF” appear to be study specific IDs

“NAME” column contains a lot of information

Going back to the previous example;

SFB2 || ER to Golgi transport || molecular function unknown || YNL049C || 1082129

SFB2: Gene names, but not present in all cases
ER to Golgi transport: Biological process
molecular function unknown: Molecular function
YNL049C: Gene ID listed on public repositories
1082129: Another identifier that does not appear to be useful

Line by line

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
12
13 raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")
14
15 separated_gene_df <- separate(raw_gene_df, NAME,
16                              c("name", "BP", "MF", "systematic_name",
17                                "number"),
18                              sep = "\\|\\|")
19
20 mutated_gene_df <- mutate_at(separated_gene_df,
21                              vars(name:systematic_name),
22                              funs(trimws)
23                              )
24
25 selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
26
27 gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
28
29 nearly_there_df <- separate(gathered_gene_df, sample,
30                             c("nutrient", "rate"), sep = 1, convert = TRUE)
31
32 nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
33                     S = "Sulfate", N = "Ammonia", U = "Uracil")
34
35 cleaned_genes_df <- mutate(nearly_there_df,
36                            nutrient = plyr::revalue(nutrient, nutrient_names)
37                            ) %>%
38   filter(!is.na(expression), systematic_name != "")
```

15:1 | Section 1: Data import, tidying and transformation | R Script

Console | Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/

```
> raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")
Parsed with column specification:
cols(
  .default = col_double(),
  GID = col_character(),
  YORF = col_character(),
  NAME = col_character(),
  GWEIGHT = col_integer()
)
See spec(...) for full column specifications.
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

Name	Type	Length	Size	Value
raw_gene_df	tbl_df	40	3.3 MB	5537 obs. of 40 variables

Files | Plots | Packages | Help | Viewer

New Folder | Delete | Rename | More

Home > R_Users_Workshop > 8_weeks_Oct-Dec_17 > Workshop_1 > workshop_1_project

Name	Size	Modified
..		
.RData	2.5 KB	Oct 2, 2017, 1:49 PM
.Rhistory	20.3 KB	Dec 6, 2017, 3:43 PM
Brauer2008_DataSet1.csv	1.6 MB	Sep 27, 2017, 11:32 PM
Brauer2008_DataSet1.tds	1.6 MB	Sep 28, 2017, 10:22 AM
house_completions.csv	4 KB	Sep 28, 2017, 1:35 PM
irish_population.csv	315 B	Aug 28, 2017, 4:21 PM
raw_house_completions.csv	16.2 KB	Aug 25, 2017, 3:45 PM
workshop_1.Rproj	217 B	Oct 18, 2018, 12:18 PM
ws1_script1_stepwise_Bauer_dataset_analysis.R	6.1 KB	Dec 5, 2017, 12:19 PM
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ws1_script3_house_completions.R	2.4 KB	Oct 2, 2017, 3:53 PM

Line by line

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
12
13 raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")
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15 separated_gene_df <- separate(raw_gene_df, NAME,
16                              c("name", "BP", "MF", "systematic_name",
17                                "number"),
18                              sep = "\\|\\|")
19
20 mutated_gene_df <- mutate_at(separated_gene_df,
21                              vars(name:systematic_name),
22                              funs(trimws)
23                              )
24
25 selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
26
27 gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
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29 nearly_there_df <- separate(gathered_gene_df, sample,
30                             c("nutrient", "rate"), sep = 1, convert = TRUE)
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32 nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
33                     S = "Sulfate", N = "Ammonia", U = "Uracil")
34
35 cleaned_genes_df <- mutate(nearly_there_df,
36                            nutrient = plyr::revalue(nutrient, nutrient_names)
37                            ) %>%
38   filter(!is.na(expression), systematic_name != "")
```

20:1 | Section 1: Data import, tidying and transformation | R Script

Console | Terminal

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```
> raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")
Parsed with column specification:
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  NAME = col_character(),
  GWEIGHT = col_integer()
)
See spec(...) for full column specifications.
> separated_gene_df <- separate(raw_gene_df, NAME,
+                              c("name", "BP", "MF", "systematic_name",
+                                "number"),
+                              sep = "\\|\\|")
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

Name	Type	Length	Size	Value
raw_gene_df	tbl_df	40	3.3 MB	5537 obs. of 40 variables
separated_gene...	tbl_df	44	3.6 MB	5537 obs. of 44 variables

Files | Plots | Packages | Help | Viewer

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Line by line

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

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20 mutated_gene_df <- mutate_at(separated_gene_df,
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23                              )
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25 selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
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27 gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
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29 nearly_there_df <- separate(gathered_gene_df, sample,
30                             c("nutrient", "rate"), sep = 1, convert = TRUE)
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32 nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
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35 cleaned_genes_df <- mutate(nearly_there_df,
36                            nutrient = plyr::revalue(nutrient, nutrient_names)
37                            ) %>%
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```

27:1 | Section 1: Data import, tidying and transformation | R Script

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```
Parsed with column specification:
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See spec(...) for full column specifications.
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+                              c("name", "BP", "MF", "systematic_name",
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+                             vars(name:systematic_name),
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+                             )
> selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

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selected_gene_df	tbl_df	40	2.4 MB	5537 obs. of 40 variables
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23                               )
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27  gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
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29  hearly_there_df <- separate(gathered_gene_df, sample,
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32  nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
33                      S = "Sulfate", N = "Ammonia", U = "Uracil")
34
35  cleaned_genes_df <- mutate(nearly_there_df,
36                             nutrient = plyr::revalue(nutrient, nutrient_names)
37                             ) %>%
38    filter(!is.na(expression), systematic_name != "")
```

29:1 | Section 1: Data import, tidying and transformation | R Script

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+                              )
> selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
> gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
>
```

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Global Environment

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raw_house_completions.csv	16.2 KB	Aug 25, 2017, 3:45 PM
workshop_1.Rproj	217 B	Oct 18, 2018, 12:18 PM
ws1_script1_stepwise_Bauer_dataset_analysis.R	6.1 KB	Dec 5, 2017, 12:19 PM
ws1_script2_Bauer_dataset_analysis.R	2 KB	Dec 6, 2017, 2:33 PM
ws1_script3_house_completions.R	2.4 KB	Oct 2, 2017, 3:53 PM

Line by line

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
12
13  raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")
14
15  separated_gene_df <- separate(raw_gene_df, NAME,
16                                c("name", "BP", "MF", "systematic_name",
17                                  "number"),
18                                sep = "\\|\\|")
19
20  mutated_gene_df <- mutate_at(separated_gene_df,
21                               vars(name:systematic_name),
22                               funs(trimws)
23                               )
24
25  selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
26
27  gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
28
29  nearly_there_df <- separate(gathered_gene_df, sample,
30                              c("nutrient", "rate"), sep = 1, convert = TRUE)
31
32  nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
33                      S = "Sulfate", N = "Ammonia", U = "Uracil")
34
35  cleaned_genes_df <- mutate(nearly_there_df,
36                             nutrient = plyr::revalue(nutrient, nutrient_names)
37                             ) %>%
38    filter(!is.na(expression), systematic_name != "")
```

32:1 | Section 1: Data import, tidying and transformation | R Script

Console | Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/

```
  GID = col_character(),
  YORF = col_character(),
  NAME = col_character(),
  GWEIGHT = col_integer()
)
See spec(...) for full column specifications.
> separated_gene_df <- separate(raw_gene_df, NAME,
+                               c("name", "BP", "MF", "systematic_name",
+                                 "number"),
+                               sep = "\\|\\|")
> mutated_gene_df <- mutate_at(separated_gene_df,
+                              vars(name:systematic_name),
+                              funs(trimws)
+                              )
> selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
> gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
> nearly_there_df <- separate(gathered_gene_df, sample,
+                             c("nutrient", "rate"), sep = 1, convert = TRUE)
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

Name	Type	Length	Size	Value
gathered_gene_df	tbl_df	6	9.8 MB	199332 obs. of 6 variables
mutated_gene_df	tbl_df	44	3.5 MB	5537 obs. of 44 variables
nearly_there_df	tbl_df	7	11.3 MB	199332 obs. of 7 variables
raw_gene_df	tbl_df	40	3.3 MB	5537 obs. of 40 variables
selected_gene_df	tbl_df	40	2.4 MB	5537 obs. of 40 variables
separated_gene...	tbl_df	44	3.6 MB	5537 obs. of 44 variables

Files | Plots | Packages | Help | Viewer

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Home > R_Users_Workshop > 8_weeks_Oct-Dec_17 > Workshop_1 > workshop_1_project

Name	Size	Modified
..		
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Line by line

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
12
13 raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")
14
15 separated_gene_df <- separate(raw_gene_df, NAME,
16                              c("name", "BP", "MF", "systematic_name",
17                                "number"),
18                              sep = "\\|\\|")
19
20 mutated_gene_df <- mutate_at(separated_gene_df,
21                              vars(name:systematic_name),
22                              funs(trimws)
23                              )
24
25 selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
26
27 gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
28
29 nearly_there_df <- separate(gathered_gene_df, sample,
30                             c("nutrient", "rate"), sep = 1, convert = TRUE)
31
32 nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
33                     S = "Sulfate", N = "Ammonia", U = "Uracil")
34
35 cleaned_genes_df <- mutate(nearly_there_df,
36                            nutrient = plyr::revalue(nutrient, nutrient_names)
37                            ) %>%
38   filter(!is.na(expression), systematic_name != "")
```

35:1 | Section 1: Data import, tidying and transformation | R Script

Console | Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/

```
  NAME = col_character(),
  GWEIGHT = col_integer()
)
See spec(...) for full column specifications.
> separated_gene_df <- separate(raw_gene_df, NAME,
+                               c("name", "BP", "MF", "systematic_name",
+                                 "number"),
+                               sep = "\\|\\|")
> mutated_gene_df <- mutate_at(separated_gene_df,
+                              vars(name:systematic_name),
+                              funs(trimws)
+                              )
> selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
> gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
> nearly_there_df <- separate(gathered_gene_df, sample,
+                             c("nutrient", "rate"), sep = 1, convert = TRUE)
> nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
+                     S = "Sulfate", N = "Ammonia", U = "Uracil")
> |
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

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gathered_gene_df	tbl_df	6	9.8 MB	199332 obs. of 6 variables
mutated_gene_df	tbl_df	44	3.5 MB	5537 obs. of 44 variables
nearly_there_df	tbl_df	7	11.3 MB	199332 obs. of 7 variables
nutrient_names	character	6	984 B	Named chr [1:6] "Glucose" "...
raw_gene_df	tbl_df	40	3.3 MB	5537 obs. of 40 variables
selected_gene_df	tbl_df	40	2.4 MB	5537 obs. of 40 variables
separated_gene...	tbl_df	44	3.6 MB	5537 obs. of 44 variables

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Home > R_Users_Workshop > 8_weeks_Oct-Dec_17 > Workshop_1 > workshop_1_project

Name	Size	Modified
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Line by line

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
15 separated_gene_df <- separate(raw_gene_df, NAME,
16                               c("name", "BP", "MF", "systematic_name",
17                                 "number"),
18                               sep = "\\|\\|")
19
20 mutated_gene_df <- mutate_at(separated_gene_df,
21                               vars(name:systematic_name),
22                               funs(trimws)
23                               )
24
25 selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
26
27 gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
28
29 nearly_there_df <- separate(gathered_gene_df, sample,
30                              c("nutrient", "rate"), sep = 1, convert = TRUE)
31
32 nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
33                     S = "Sulfate", N = "Ammonia", U = "Uracil")
34
35 cleaned_genes_df <- mutate(nearly_there_df,
36                            nutrient = plyr::revalue(nutrient, nutrient_names)
37                            ) %>%
38   filter(!is.na(expression), systematic_name != "")
39
40
41
```

44:1 | Section 1: Data import, tidying and transformation | R Script

Console | Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/

```
> separated_gene_df <- separate(raw_gene_df, NAME,
+                               c("name", "BP", "MF", "systematic_name",
+                                 "number"),
+                               sep = "\\|\\|")
> mutated_gene_df <- mutate_at(separated_gene_df,
+                              vars(name:systematic_name),
+                              funs(trimws)
+                              )
> selected_gene_df <- select(mutated_gene_df, -number, -GID, -YORF, -GWEIGHT)
> gathered_gene_df <- gather(selected_gene_df, sample, expression, G0.05:U0.3)
> nearly_there_df <- separate(gathered_gene_df, sample,
+                             c("nutrient", "rate"), sep = 1, convert = TRUE)
> nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
+                     S = "Sulfate", N = "Ammonia", U = "Uracil")
> cleaned_genes_df <- mutate(nearly_there_df,
+                            nutrient = plyr::revalue(nutrient, nutrient_names)
+                            ) %>%
+   filter(!is.na(expression), systematic_name != "")
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

Name	Type	Length	Size	Value
cleaned_genes_df	tbl_df	7	11.3 MB	198430 obs. of 7 variables
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mutated_gene_df	tbl_df	44	3.5 MB	5537 obs. of 44 variables
nearly_there_df	tbl_df	7	11.3 MB	199332 obs. of 7 variables
nutrient_names	character	6	984 B	Named chr [1:6] "Glucose" "...
raw_gene_df	tbl_df	40	3.3 MB	5537 obs. of 40 variables
selected_gene_df	tbl_df	40	2.4 MB	5537 obs. of 40 variables
separated_gene...	tbl_df	44	3.6 MB	5537 obs. of 44 variables

Files | Plots | Packages | Help | Viewer

New Folder | Delete | Rename | More

Home > R_Users_Workshop > 8_weeks_Oct-Dec_17 > Workshop_1 > workshop_1_project

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Brauer2008_DataSet1.tds	1.6 MB	Sep 28, 2017, 10:22 AM
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ws1_script2_Bauer_dataset_analysis.R	2 KB	Dec 6, 2017, 2:33 PM
ws1_script3_house_completions.R	2.4 KB	Oct 2, 2017, 3:53 PM

Nested

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
1  nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
2                      S = "Sulfate", N = "Ammonia", U = "Uracil")
3
4  cleaned_genes_df <-
5    filter(
6      mutate(
7        separate(
8          gather(
9            select(
10             mutate_at(
11               separate(
12                 read_delim("Brauer2008_DataSet1.tds", delim = "\t"),
13                 NAME,
14                 c("name", "BP", "MF", "systematic_name",  "number"),
15                 sep = "\\|\\|"), vars(name:systematic_name),
16               funs(trimws)),
17             -number, -GID, -YORF, -GWEIGHT),
18           sample, expression, G0.05:U0.3),
19         sample,
20         c("nutrient", "rate"),
21         sep = 1, convert = TRUE),
22       nutrient = plyr::revalue(nutrient, nutrient_names)),
23     !is.na(expression), systematic_name != "")
24
```

24:1 (Top Level) R Script

Console Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/

```
+                sep = "\\|\\|"), vars(name:systematic_name),
+              funs(trimws)),
+            -number, -GID, -YORF, -GWEIGHT),
+          sample, expression, G0.05:U0.3),
+        sample,
+        c("nutrient", "rate"),
+        sep = 1, convert = TRUE),
+      nutrient = plyr::revalue(nutrient, nutrient_names)),
+    !is.na(expression), systematic_name != "")
Parsed with column specification:
cols(
  .default = col_double(),
  GID = col_character(),
  YORF = col_character(),
  NAME = col_character(),
  GWEIGHT = col_integer()
)
See spec(...) for full column specifications.
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

Name	Type	Length	Size	Value
cleaned_genes_df	tbl_df	7	11.3 MB	198430 obs. of 7 variables
nutrient_names	character	6	984 B	Named chr [1:6] "Glucose" "Le...

Files | Plots | Packages | Help | Viewer

New Folder | Delete | Rename | More

Home > R_Users_Workshop > 8_weeks_Oct-Dec_17 > Workshop_1 > workshop_1_project

Name	Size	Modified
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ws1_script2_Bauer_dataset_analysis.R	2 KB	Dec 6, 2017, 2:33 PM
ws1_script3_house_completions.R	2.4 KB	Oct 2, 2017, 3:53 PM

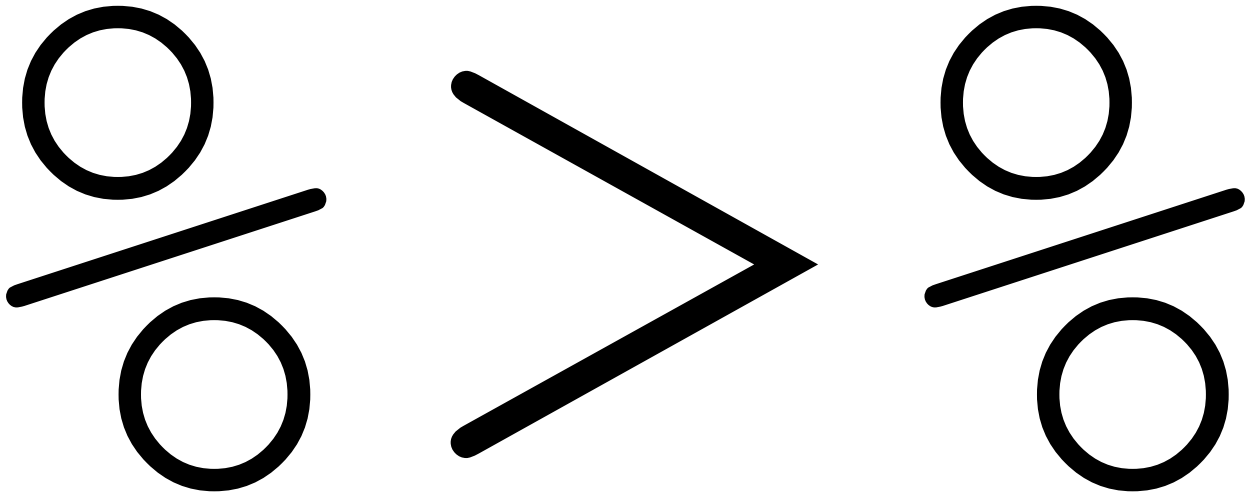
Nested

```
nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
                    S = "Sulfate", N = "Ammonia", U = "Uracil")

cleaned_genes_df <-
  filter(
    mutate(
      separate(
        gather(
          select(
            mutate_at(
              separate(
                read_delim("Brauer2008_DataSet1.tds", delim = "\t"),
                NAME,
                c("name", "BP", "MF", "systematic_name",  "number"),
                sep = "\\|\\|"), vars(name:systematic_name),
              funs(trimws)),
            -number, -GID, -YORF, -GWEIGHT),
          sample, expression, G0.05:U0.3),
        sample,
        c("nutrient", "rate"),
        sep = 1, convert = TRUE),
      nutrient = plyr::revalue(nutrient, nutrient_names)),
    !is.na(expression), systematic_name != "")

```

Putting the pieces together



Code structure v2

```
separated_gene <- raw_gene %>%
    separate(NAME,
        c("name", "BP", "MF", "systematic_name", "number"),
        sep = "\\|\\|"
        )
```

Here the input data is outside the function

First argument is no longer the data

Piped

ws1_script1_stepwise_Bauer_dataset_an... | ws1_script2_Bauer_dataset_analysis.R*

Source on Save | Run | Source

```
1  nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
2                      S = "Sulfate", N = "Ammonia", U = "Uracil"
3                      )
4
5  cleaned_genes_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t"
6                                 ) %>%
7
8    separate(NAME, c("name", "BP", "MF", "systematic_name", "number"), sep = "\\|\\|"
9            )  %>%
10
11   mutate_at(vars(name:systematic_name), funs(trimws)
12             ) %>%
13
14   select(-number, -GID, -YORF, -GWEIGHT
15          ) %>%
16
17   gather(sample, expression, G0.05:U0.3
18          ) %>%
19
20   separate(sample, c("nutrient", "rate"), sep = 1, convert = TRUE
21            ) %>%
22
23   mutate(nutrient = plyr::revalue(nutrient, nutrient_names)
24          ) %>%
25
26   filter(!is.na(expression), systematic_name != ""
27          )
```

9:18 (Top Level) R Script

Console | Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/

```
+
+   separate(sample, c("nutrient", "rate"), sep = 1, convert = TRUE
+            ) %>%
+
+   mutate(nutrient = plyr::revalue(nutrient, nutrient_names)
+          ) %>%
+
+   filter(!is.na(expression), systematic_name != ""
+          )
Parsed with column specification:
cols(
  .default = col_double(),
  GID = col_character(),
  YORF = col_character(),
  NAME = col_character(),
  GWEIGHT = col_integer()
)
See spec(...) for full column specifications.
>
```

Environment | History | Connections

Import Dataset | Grid

Global Environment

Name	Type	Length	Size	Value
cleaned_genes_df	tbl_df	7	11.3 MB	198430 obs. of 7 variables
nutrient_names	character	6	984 B	Named chr [1:6] "Glucose" "Le...

Files | Plots | Packages | Help | Viewer

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Piped

```
nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
                    S = "Sulfate", N = "Ammonia", U = "Uracil"
                    )

cleaned_genes_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t"
                               ) %>%

  separate(NAME, c("name", "BP", "MF", "systematic_name", "number"), sep = "\\|\\|"
           )  %>%

  mutate_at(vars(name:systematic_name), funs(trimws)
            ) %>%

  select(-number, -GID, -YORF, -GWEIGHT
         ) %>%

  gather(sample, expression, G0.05:U0.3
         ) %>%

  separate(sample, c("nutrient", "rate"), sep = 1, convert = TRUE
           ) %>%

  mutate(nutrient = plyr::revalue(nutrient, nutrient_names)
         ) %>%

  filter(!is.na(expression), systematic_name != ""
         )
```

magrittr package

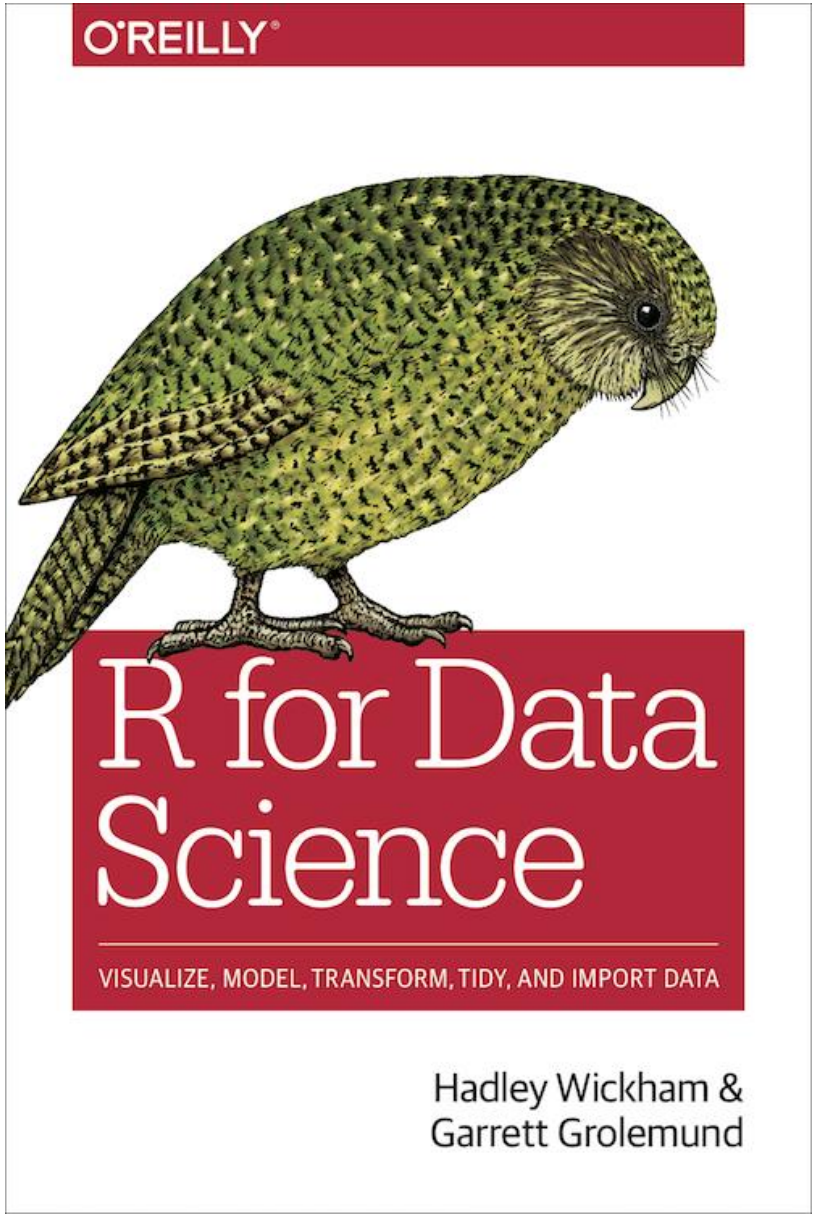
- Tidyverse packages automatically make %>% available
- magrittr has other tools that you might find useful

%$%

%T>%

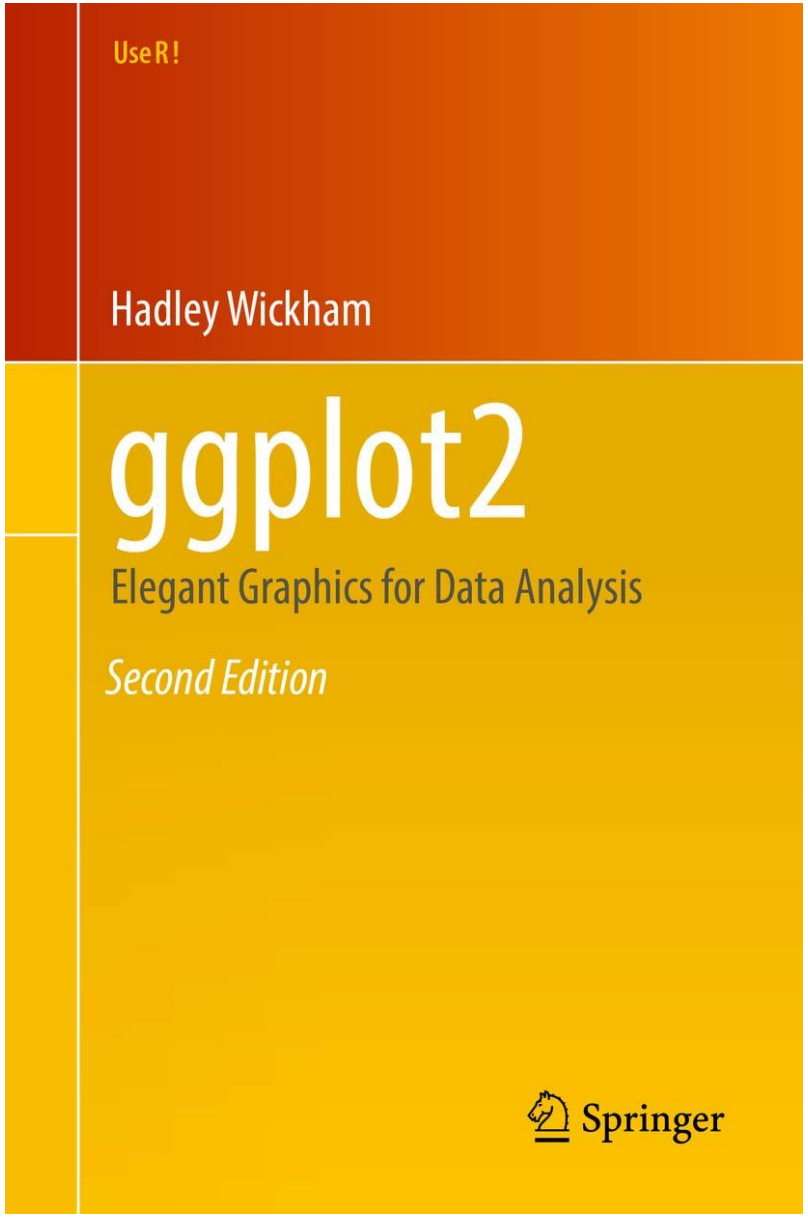
- Open the script magrittr.R

You could write a book on that!!



https://r4ds.had.co.nz/

And on this!!


Use R!
Hadley Wickham
ggplot2
Elegant Graphics for Data Analysis
Second Edition
Springer