R-eproducible workflows

1-day workshop
Morning overview

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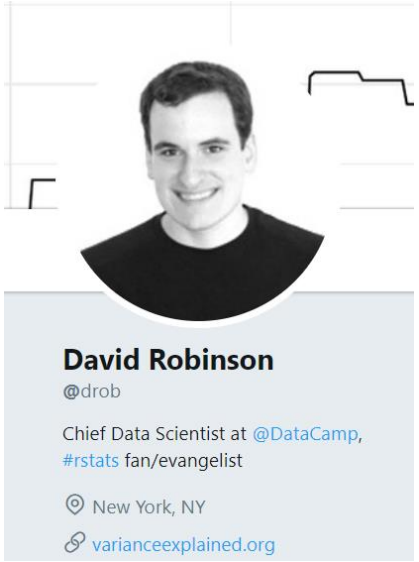
UCC
University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

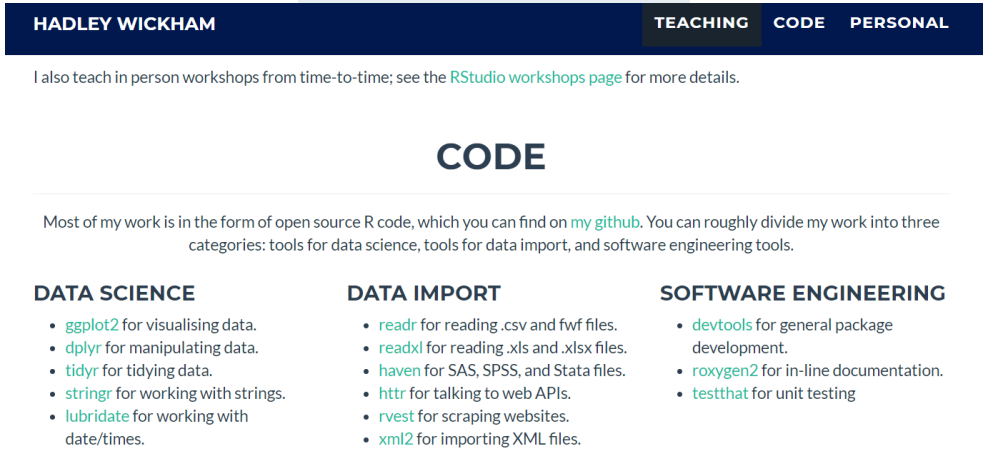
CRF-C
HRB Clinical Research Facility Cork

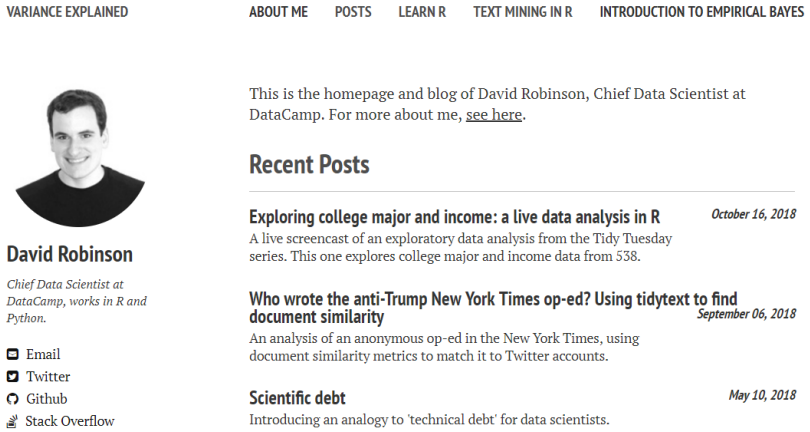
HRB
Health Research Board

Disclaimer

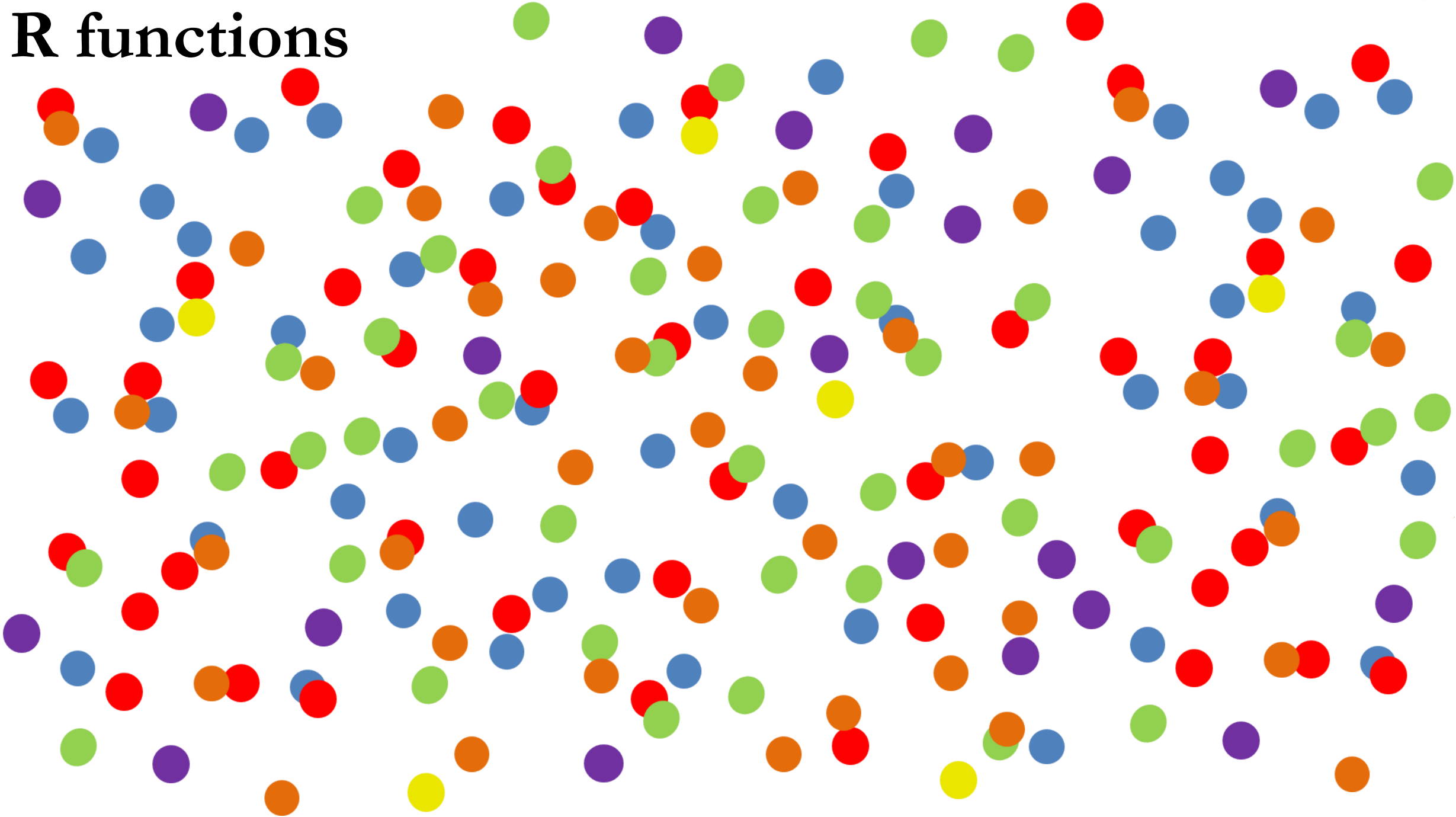
- Hadley Wickham and David Robinson are the go-to resources for most of the content in this session



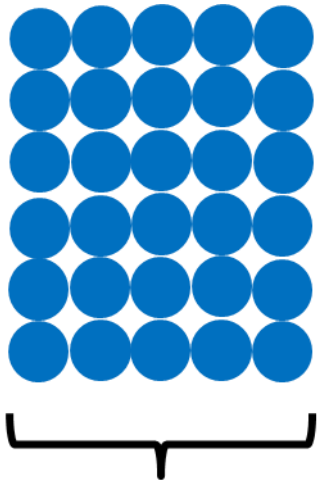




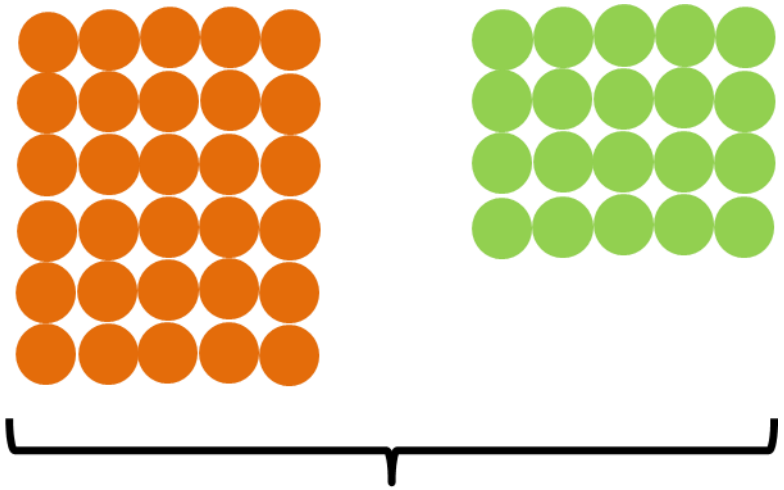
R functions



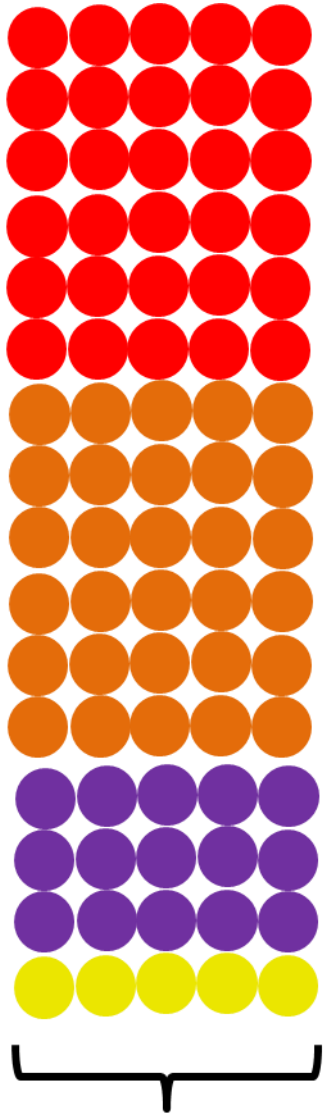
R packages



Base R:
Comes
pre-
loaded

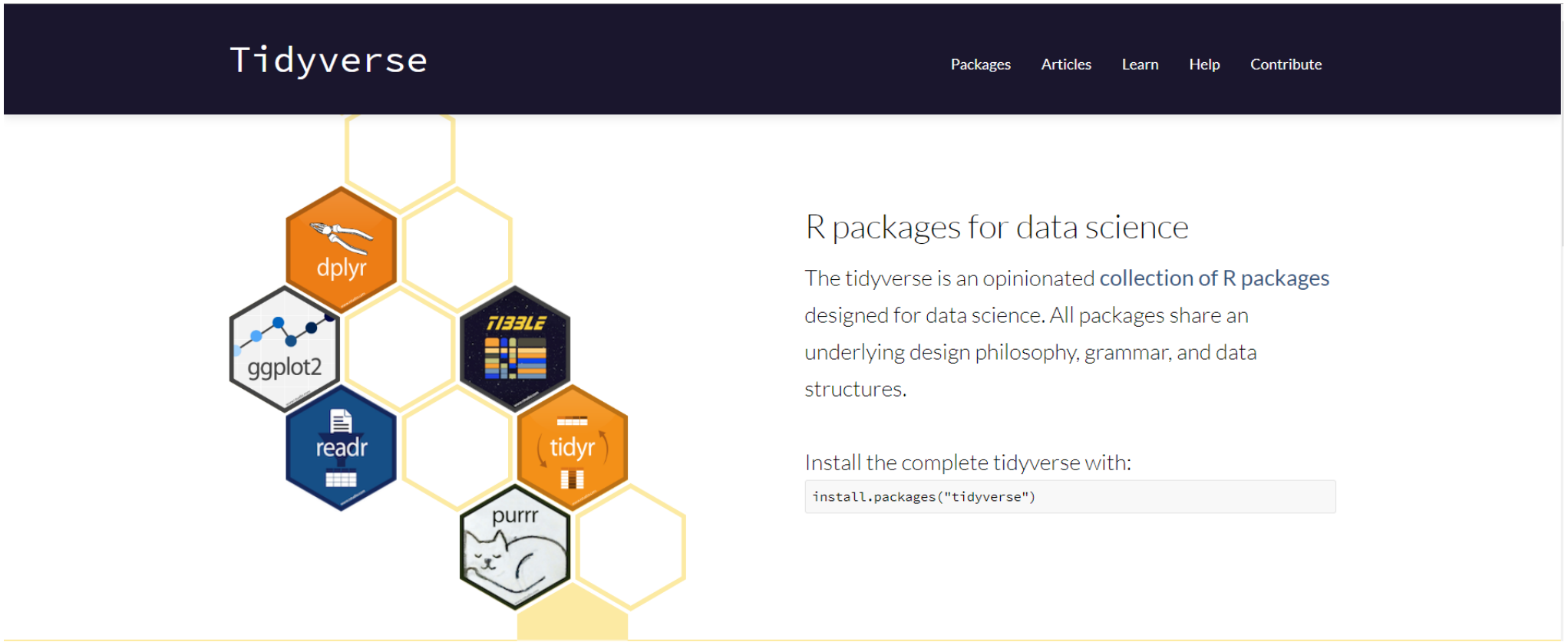


Other packages:
Install once
Update regularly
Load each session



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
```

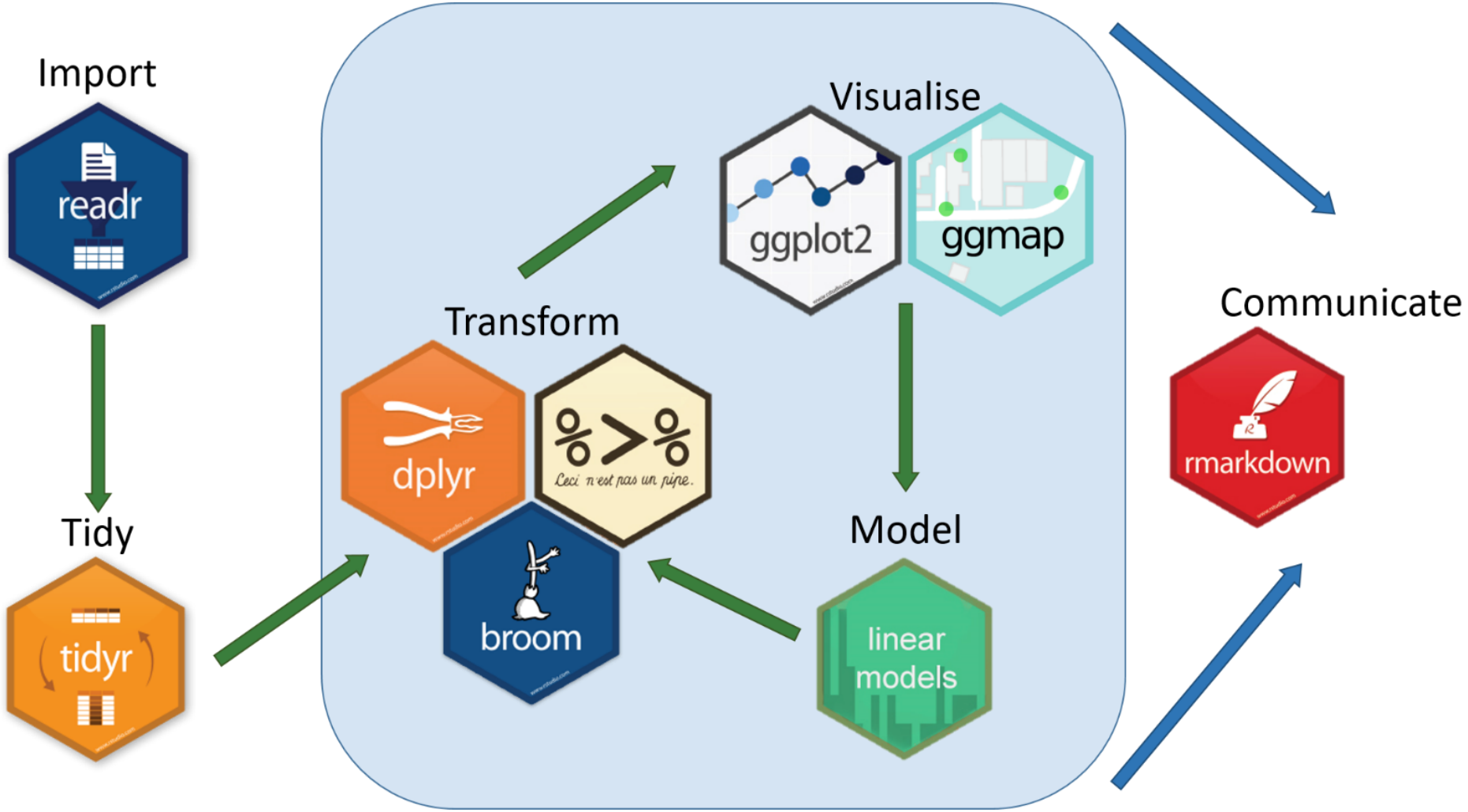
- ggplot2 → Data visualisation
- tibble → Modern version of data frames
- tidyr → Data tidying
- readr → Data import
- purrr → Functional programming
- dplyr → Data manipulation

The tidyverse Oct 2018

```
> library("tidyverse")
-- Attaching packages --------------------------------------- tidyverse 1.2.1 --
v ggplot2 3.0.0     v purrr   0.2.5
v tibble  1.4.2     v dplyr   0.7.6
v tidyr   0.8.1     v stringr 1.3.1
v readr   1.1.1     v forcats 0.3.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
> |
```

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

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

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ws1_script1_stepwise_Bauer_dataset_an... *

```
raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")

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 != "")
```

15:1 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:
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

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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
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

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ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")

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 != "")
```

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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)
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+                               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

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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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house_completions.csv	4 KB	Sep 28, 2017, 1:35 PM
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raw_house_completions.csv	16.2 KB	Aug 25, 2017, 3:45 PM
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Line by line

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ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

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

Console | Terminal

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```
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Environment | History | Connections

Import Dataset | Grid

Global Environment

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

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>
```

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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

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Go to file/function | Addins | workshop_1_project — 8_weeks_Oct-Dec_17

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")

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 != "")
```

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

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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
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Line by line

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Go to file/function | Addins | workshop_1_project — 8_weeks_Oct-Dec_17

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
raw_gene_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t")

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 != "")
```

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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Name	Size	Modified
..		
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Line by line

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Go to file/function | Addins | workshop_1_project — 8_weeks_Oct-Dec_17

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```
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 != "")
```

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
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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Brauer2008_DataSet1.tds	1.6 MB	Sep 28, 2017, 10:22 AM
house_completions.csv	4 KB	Sep 28, 2017, 1:35 PM
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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

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Go to file/function | Addins | workshop_1_project — 8_weeks_Oct-Dec_17

ws1_script1_stepwise_Bauer_dataset_an... *

Source on Save | Run | Source

```r
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 != "")
```

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

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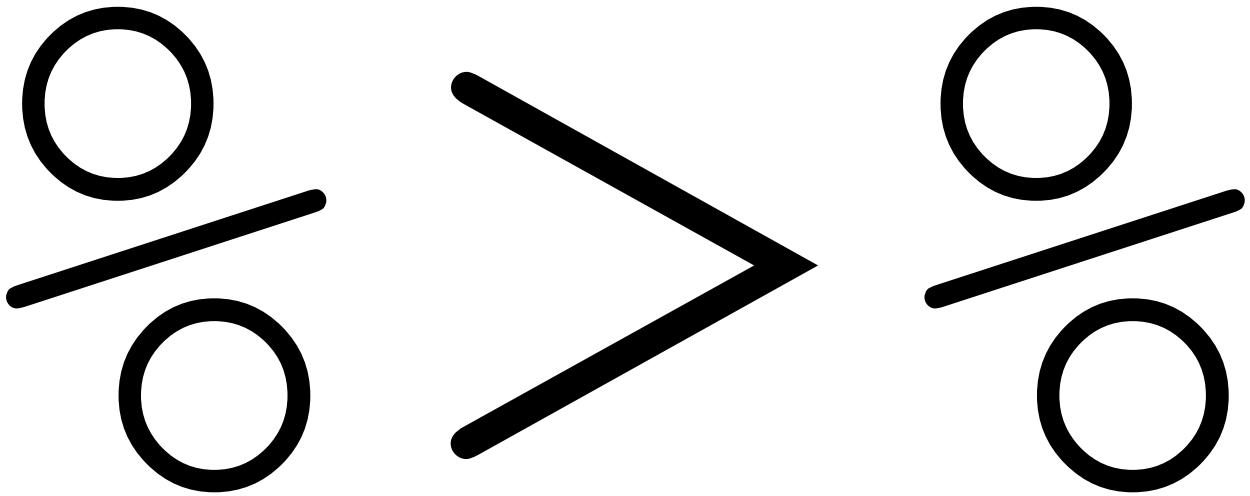
ws1_script2_Bauer_dataset_analysis.R	2 KB	Dec 6, 2017, 2:33 PM
ws1_script3_house_completions.R	2.4 KB	Oct 2, 2017, 3:53 PM

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

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

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ws1_script1_stepwise_Bauer_dataset_an... | ws1_script2_Bauer_dataset_analysis.R*

```r
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 != ""
         )
```

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...

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ws1_script3_house_completions.R	2.4 KB	Oct 2, 2017, 3:53 PM

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 != ""
         )
```

The moral of the story…….

You can go from this

To this!!

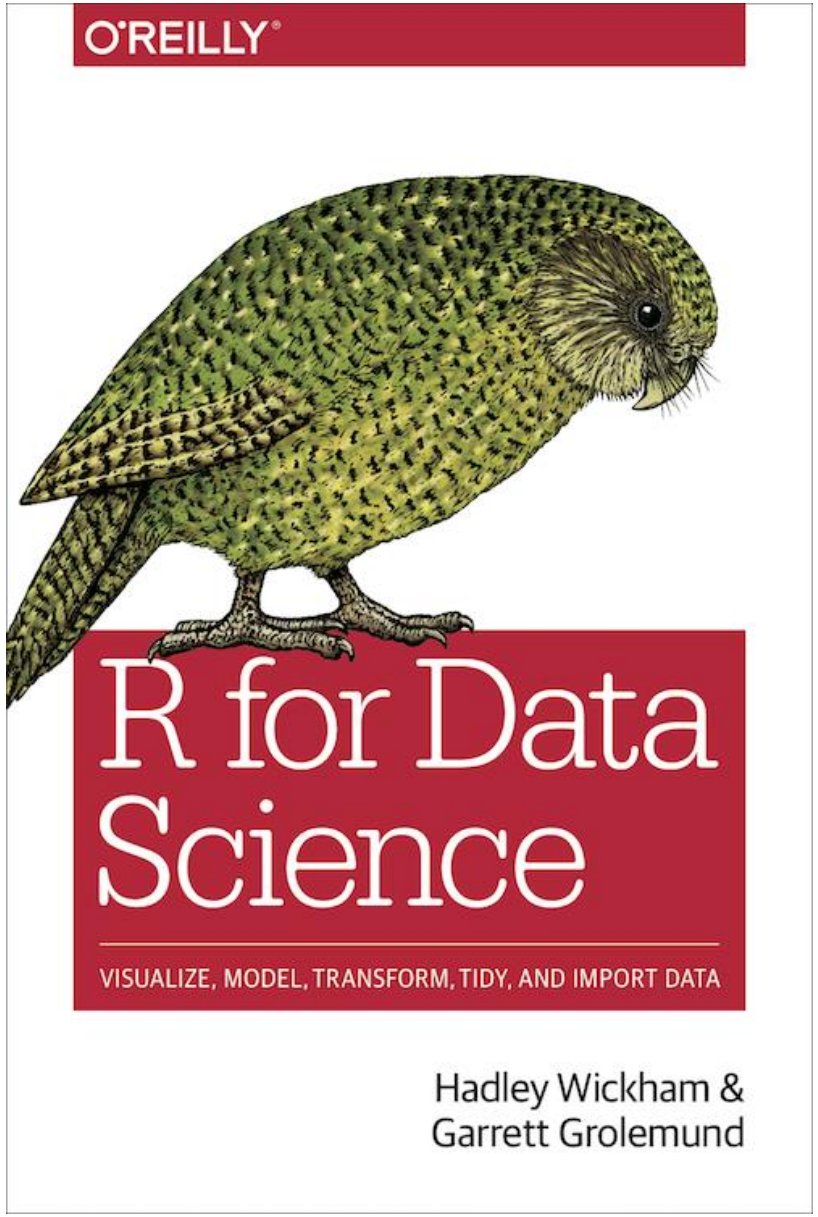
+

tidyverse

www.rstudio.com

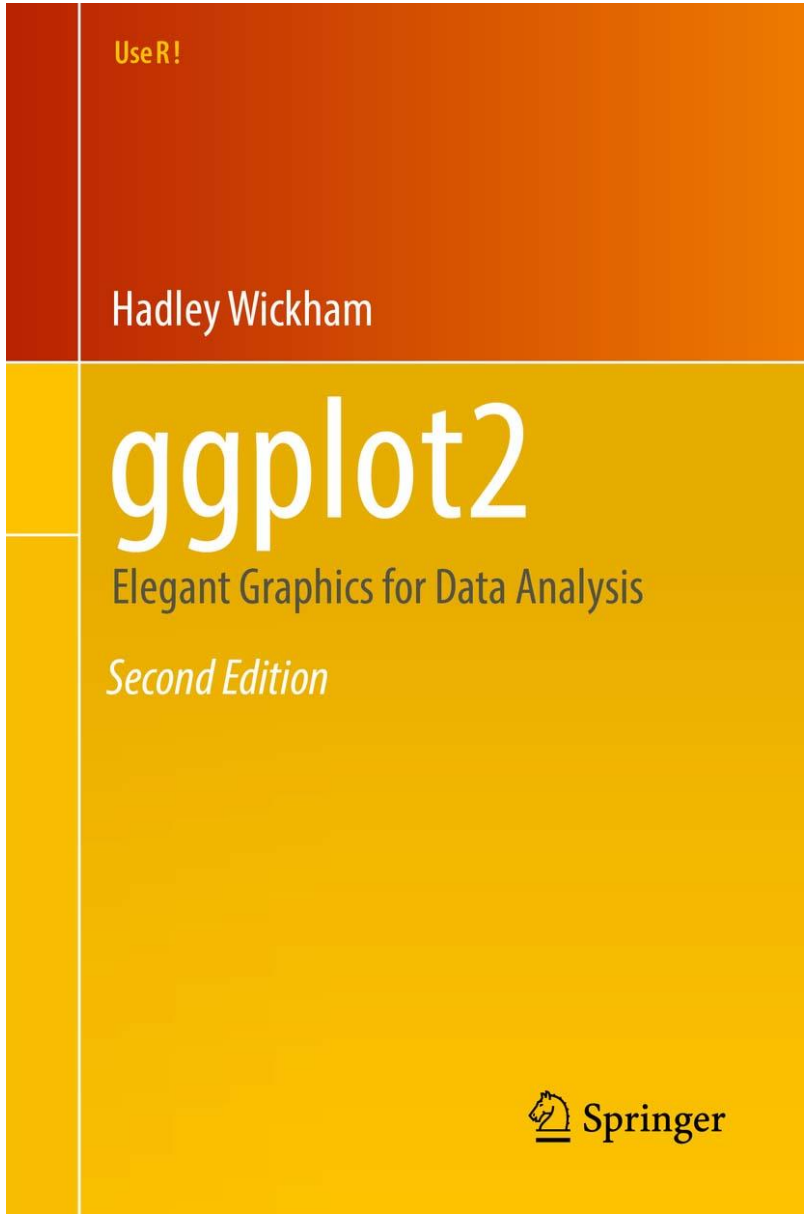
=

You could write a book on that!!



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

And on this!!


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