

R-reproducible workflows

Half-day workshop

(after 2.5 days of intense R training!!)



Brendan Palmer, University College Cork
Adam Kane, University College Dublin
Enrico Pirotta, Washington State University



Cork (Ireland) R-Users Group



Disclaimer



Jenny Bryan

@JennyBryan

Software engineer @rstudio, humane
#rstats, adjunct prof @UBC where I
created @STAT545, part of @opencsci

STAT
545

Home FAQ Syllabus Topics People

Data wrangling, exploration, and analysis with R

UBC STAT 545A and 547M

Learn how to

- explore, groom, visualize, and analyze data
- make all of that reproducible, reusable, and shareable
- using R

Hadley Wickham

@hadleywickham

R, data, visualisation.

⌚ Houston, TX

🔗 hadley.nz

TEACHING CODE PERSONAL

I also teach in person workshops from time-to-time; see the [RStudio workshops page](#) for more details.

CODE

Most of my work is in the form of open source R code, which you can find on [my github](#). You can roughly divide my work into three categories: tools for data science, tools for data import, and software engineering tools.

DATA SCIENCE

- [ggplot2](#) for visualising data.
- [dplyr](#) for manipulating data.
- [tidyverse](#) for tidying data.
- [stringr](#) for working with strings.
- [lubridate](#) for working with date/times.

DATA IMPORT

- [readr](#) for reading .csv and fwf files.
- [readxl](#) for reading .xls and .xlsx files.
- [haven](#) for SAS, SPSS, and Stata files.
- [httr](#) for talking to web APIs.
- [rvest](#) for scraping websites.
- [xml2](#) for importing XML files.

SOFTWARE ENGINEERING

- [devtools](#) for general package development.
- [roxygen2](#) for in-line documentation.
- [testthat](#) for unit testing

VARIANCE EXPLAINED

David Robinson

@drob

Chief Data Scientist at [@DataCamp](#),
#rstats fan/evangelist

⌚ New York, NY

🔗 varianceexplained.org

ABOUT ME POSTS LEARN R TEXT MINING IN R INTRODUCTION TO EMPIRICAL BAYES

This is the homepage and blog of David Robinson, Chief Data Scientist at DataCamp. For more about me, [see here](#).



David Robinson

Chief Data Scientist at
DataCamp, works in R and
Python.

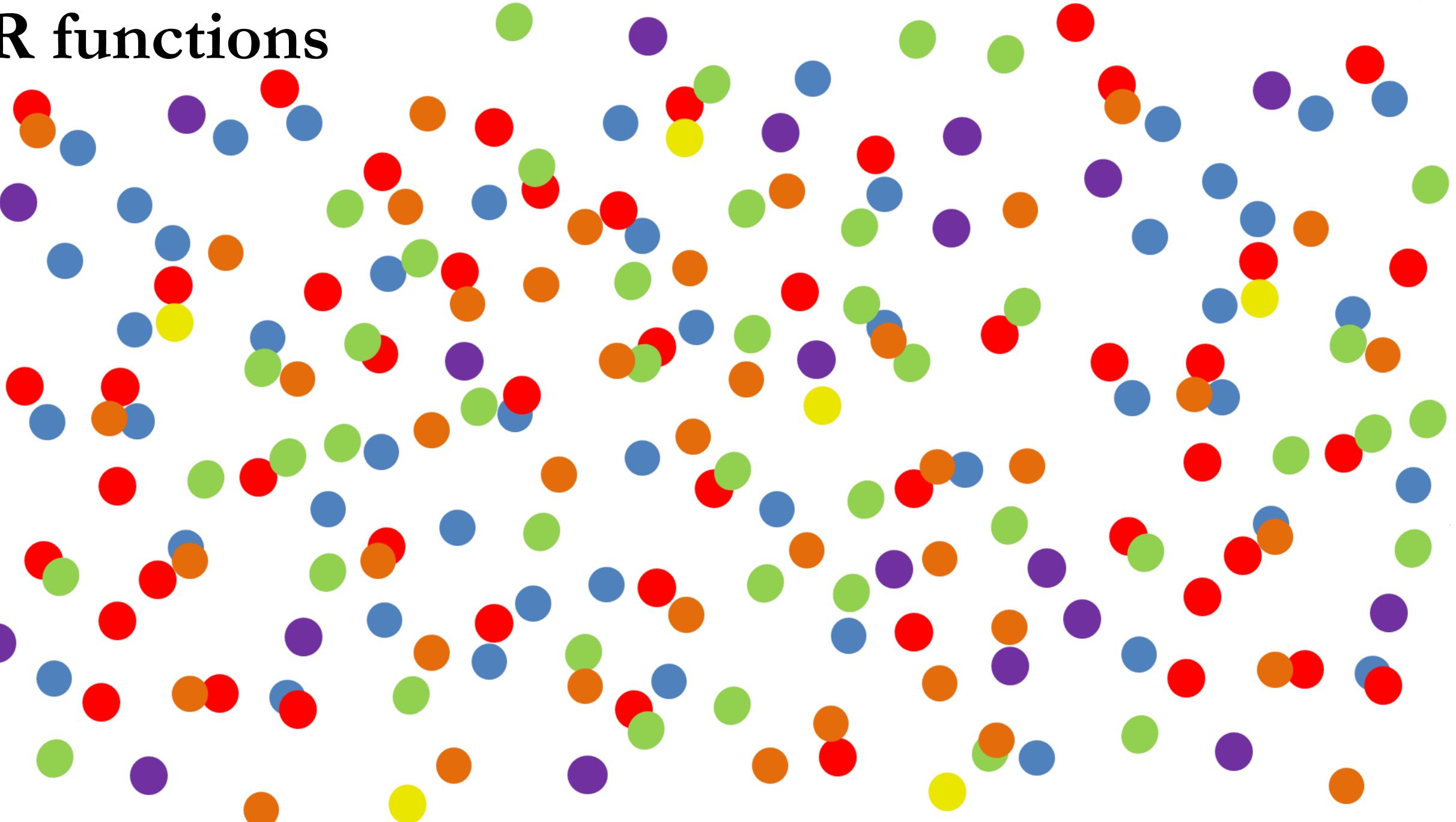
- ✉ Email
- ⌚ Twitter
- ⌚ Github
- 🌐 Stack Overflow

Exploring college major and income: a live data analysis in R
October 16, 2018
A live screencast of an exploratory data analysis from the Tidy Tuesday series. This one explores college major and income data from 538.

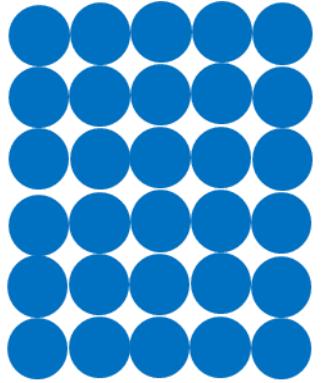
Who wrote the anti-Trump New York Times op-ed? Using tidytext to find document similarity
September 06, 2018
An analysis of an anonymous op-ed in the New York Times, using document similarity metrics to match it to Twitter accounts.

Scientific debt
May 10, 2018
Introducing an analogy to 'technical debt' for data scientists.

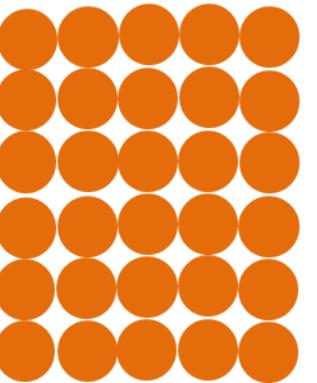
R functions



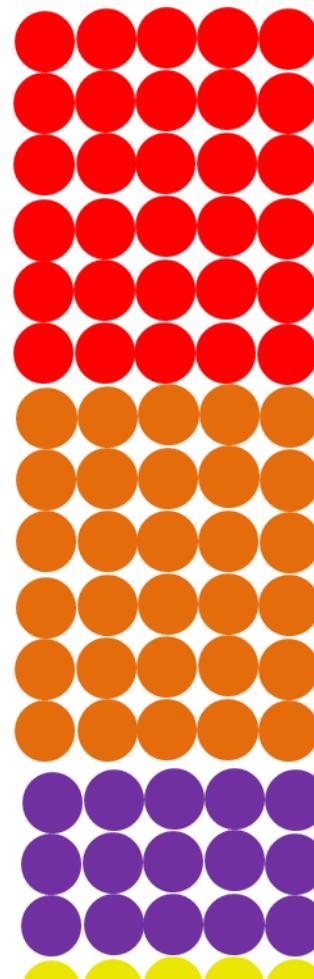
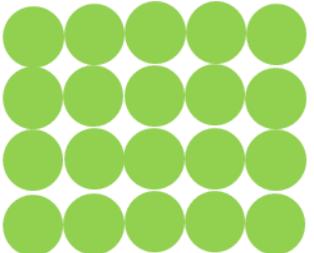
R packages



Base R:
Comes
pre-
loaded



Other packages:
Install once
Update regularly
Load each session



core
tidyverse

What is the tidyverse?

Tidyverse

Packages Articles Learn Help Contribute

R packages for data science

The tidyverse is an opinionated collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures.

Install the complete tidyverse with:

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

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

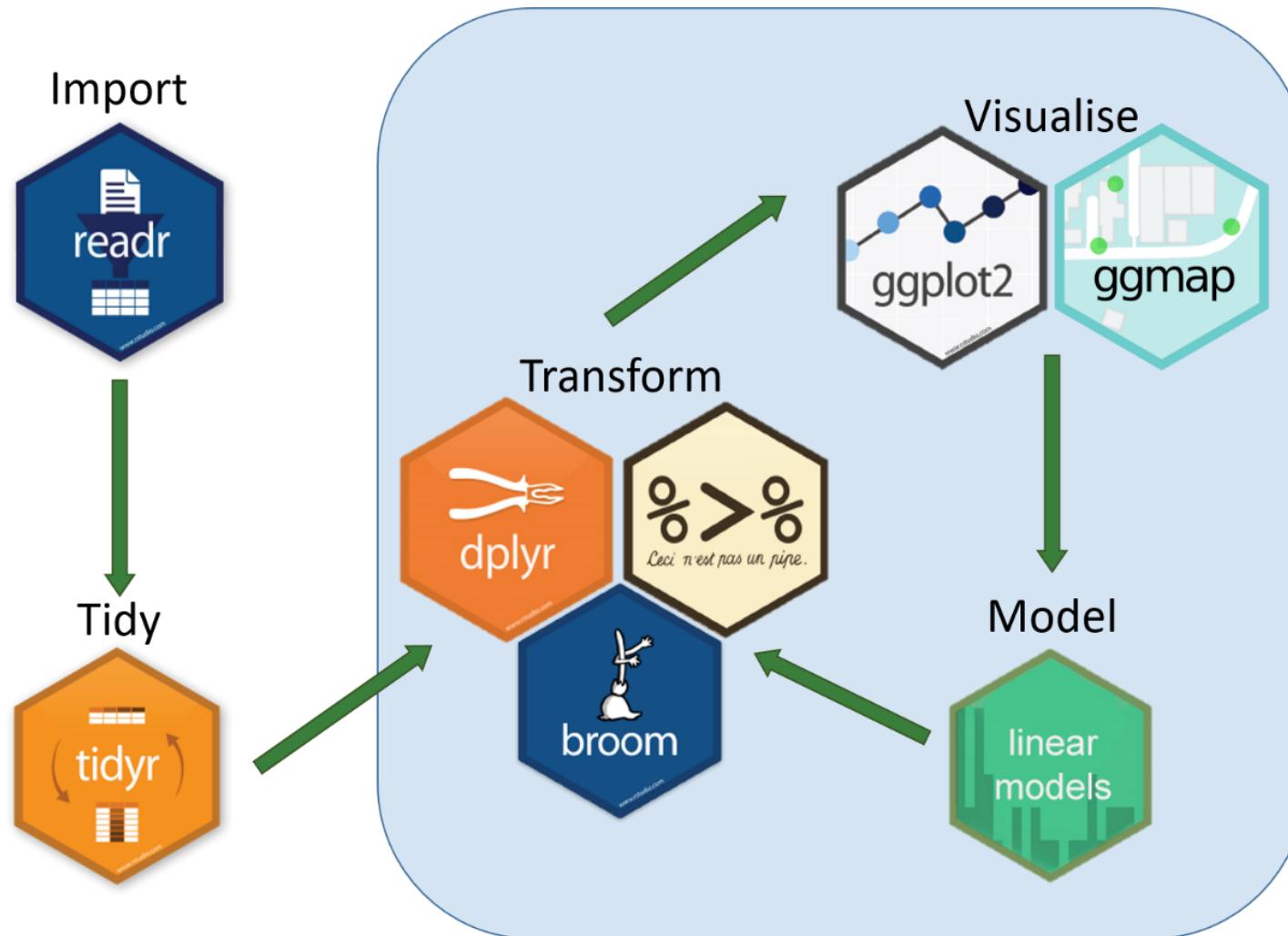
What is the tidyverse?

```
> 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", "tidyverse", "xml2"))

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

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

	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 polyadenylation* 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 <i>Saccharomyces</i>)* 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

```

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

Console Terminal

> 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.

> |

Line by line

workshop_1_project — 8_weeks_Oct-Dec_17

Environment History Connections

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
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house_completions.csv	4 KB	Sep 28, 2017, 1:35 PM
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```

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21                               )
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38 filter(!is.na(expression), systematic_name != "")

```

20:1 Section 1: Data import, tidying and transformation

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")
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See spec(...) for full column specifications.
> separated_gene_df <- separate(raw_gene_df, NAME,
+                               c("name", "BP", "MF", "systematic_name",
+                                 "number"),
+                               sep = "\\|\\|\\|")
> |

```

Line by line

Environment History Connections

Import Dataset

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

New Folder Delete Rename More

Name	Size	Modified
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```

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```

27:1 Section 1: Data import, tidying and transformation

Console Terminal

```

~/R_Users_Workshop/8_weeks_Oct-Dec_17/Workshop_1/workshop_1_project/ ↵
Parsed with column specification:
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See spec(...) for full column specifications.
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>

```

Line by line

Environment History Connections

Global Environment

Name	Type	Length	Size	Value
mutated_gene_df	tbl_df	44	3.5 MB	5537 obs. of 44 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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29:1 Section 1: Data import, tidying and transformation

```

Console Terminal

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

CTRL

```

.default = col_double(),
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```

See spec(...) for full column specifications.

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```

Line by line

Environment History Connections

Import Dataset

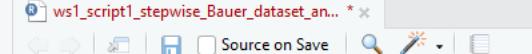
Global Environment

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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
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25                               c("nutrient", "rate"), sep = 1, convert = TRUE)
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27                       S = "Sulfate", N = "Ammonia", U = "Uracil")
28 cleaned_genes_df <- mutate(nearly_there_df,
29                               nutrient = plyr::revalue(nutrient, nutrient_names)
30                               ) %>%
31 filter(!is.na(expression), systematic_name != "")
32
33 Section 1: Data import, tidying and transformation

```

```

Console Terminal x
~/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)
>

```

Line by line

workshop_1_project — 8_weeks_Oct-Dec_17

Environment History Connections

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

New Folder Delete Rename More

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
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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

```

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

Line by line

Environment History Connections

Global Environment

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nutrient_names	character	6	984 B	Named chr [1:6] "Glucose" ...
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Line by line

ws1_script1_stepwise_Bauer_dataset_analysis.R

```

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 < Section 1: Data import, tidying and transformation
42
43
44:1

```

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

Name	Type	Length	Size	Value
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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" ...
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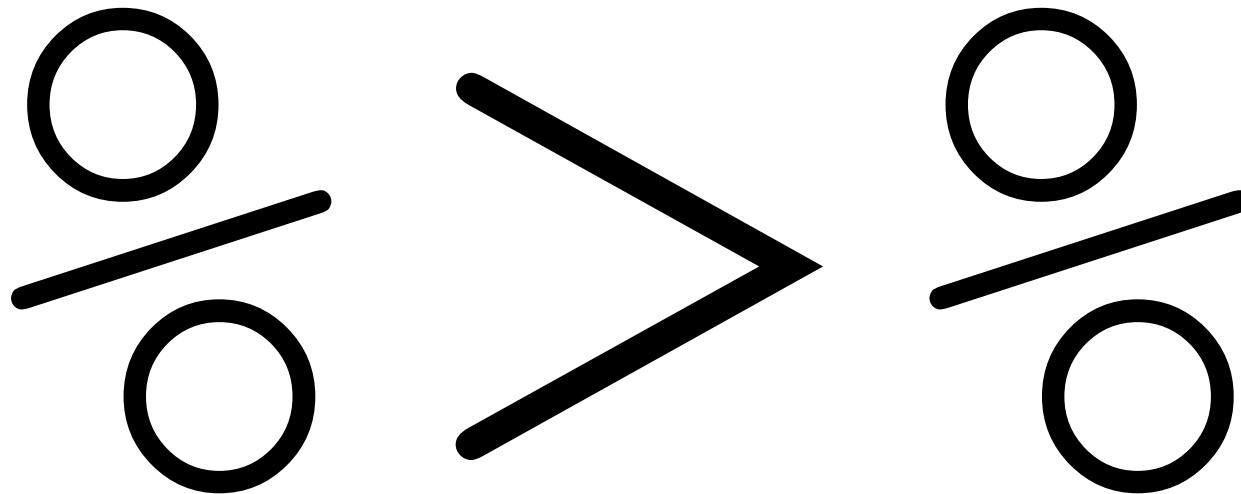
Files Plots Packages Help Viewer

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
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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

Putting the pieces together



Code structure v2

```
separated_gene <- raw_gene %>%  
  separate(NAME,           ← First argument is no longer the data  
    c("name", "BP", "MF", "systematic_name", "number"),  
    sep = "\\|\\|"  
  )
```

Here the input data is outside the function

```

1 nutrient_names <- c(G = "Glucose", L = "Leucine", P = "Phosphate",
2                     S = "Sulfate", N = "Ammonia", U = "Uracil")
3
4 cleaned_genes_df <- read_delim("Brauer2008_DataSet1.tds", delim = "\t"
5                                 ) %>%
6
7   separate(NAME, c("name", "BP", "MF", "systematic_name", "number"), sep = "\\|\\|\\|")
8
9   mutate_at(vars(name:systematic_name), funs(trimws))
10
11 select(-number, -GID, -YORF, -GWEIGHT)
12
13 gather(sample, expression, G0.05:U0.3
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```

9:18 (Top Level) ▾

Console Terminal

~/R_Users_Workshop/8_weeks_Oct-Dec_17/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.

> |

Piped

workshop_1_project — 8_weeks_Oct-Dec_17

Environment History Connections

Import Dataset

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

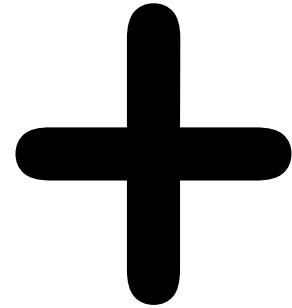
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Piped

```
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  select(-number, -GID, -YORF, -GWEIGHT
14         ) %>%
15
16  gather(sample, expression, G0.05:U0.3
17         ) %>%
18
19  separate(sample, c("nutrient", "rate"), sep = 1, convert = TRUE
20         ) %>%
21
22  mutate(nutrient = plyr::revalue(nutrient, nutrient_names)
23         ) %>%
24
25  filter(!is.na(expression), systematic_name != ""
26         )
```

The moral of the story.....

You can go from this

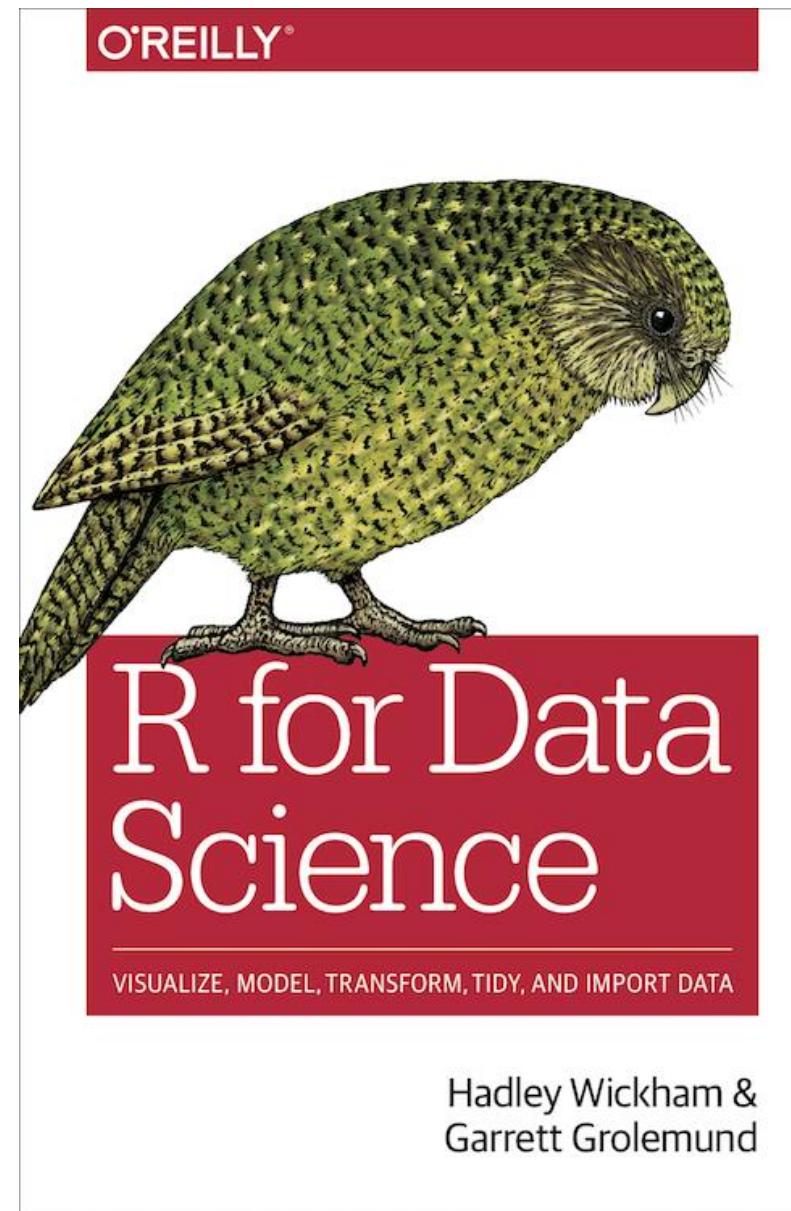


Completely ordinary

To this!!

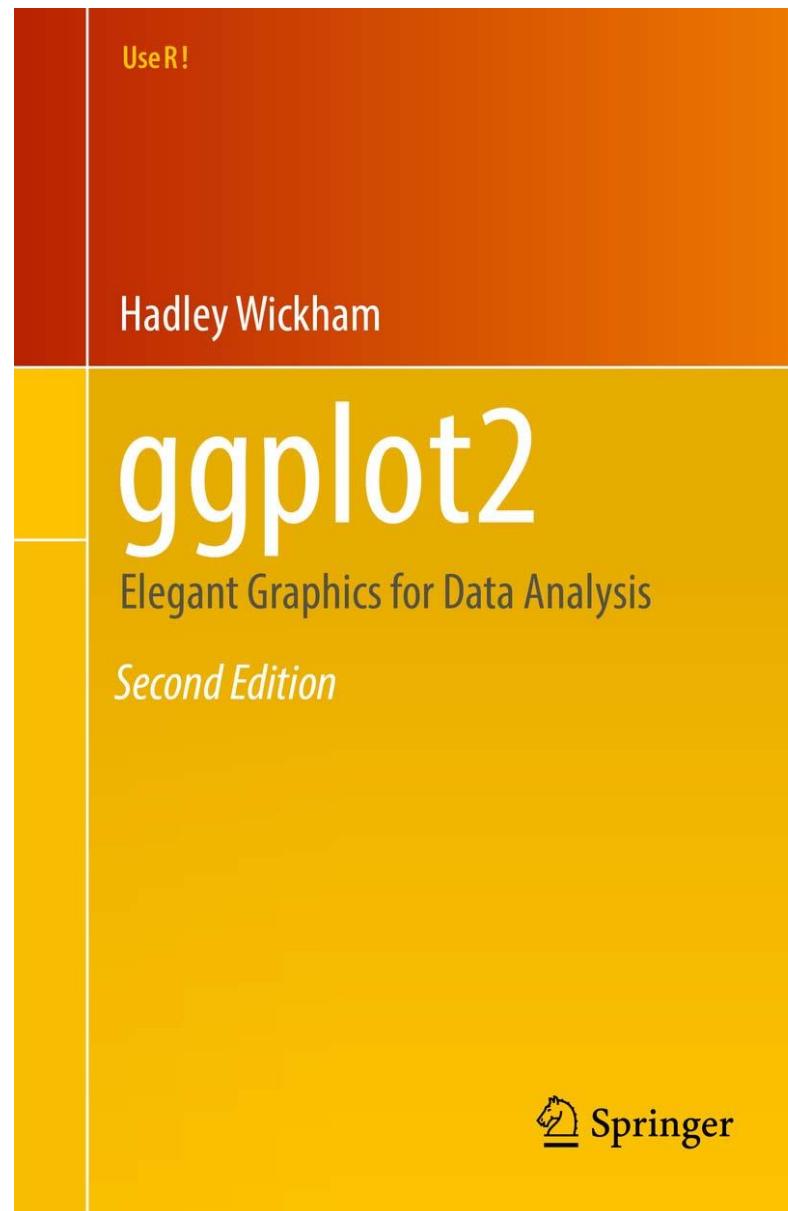
Master Builder!

You could write a book on that!!



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

And on this!!



A: Tibbles



- The tidyverse equivalent of data.frames

4 main points of difference:

1. Printing in the console
2. Subsetting (The use of a placeholder ("."))
3. Interacting with older code
4. Tibbles don't change the input

- Open the script 01_tibbles.R

A: `readr` and more



- fast way to read rectangular data (like `csv`, `tsv`)
- `read_csv()`: comma separated (CSV) files
- `read_tsv()`: tab separated files
- `read_delim()`: general delimited files

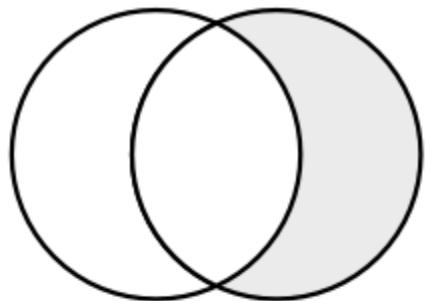


- `readxl` supports both the legacy `.xls` format and the modern XML-based `.xlsx` format
- Need to load explicitly

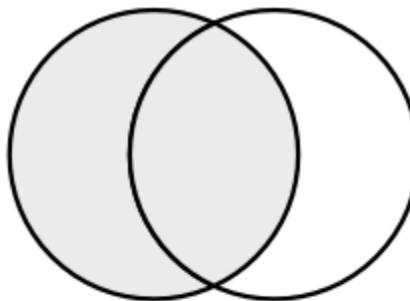


- `read_sas()`: SAS files
- `read_sav()`: SPSS files
- `read_dta()`: Stata files
- Also need to load explicitly
- Open the script `02_readr.R`

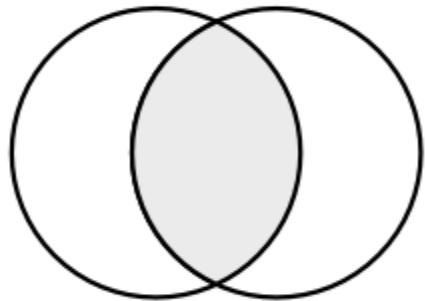
Logical operators and conditional subsetting



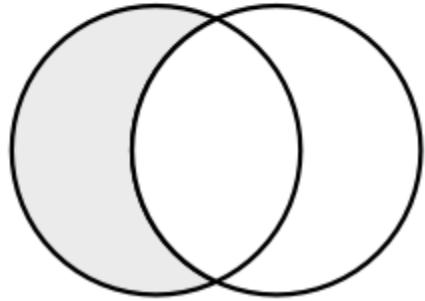
$y \& \neg x$



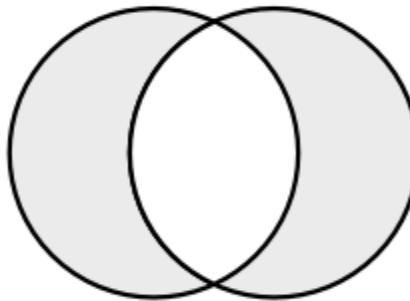
x



$x \& y$



$x \& \neg y$



$\text{xor}(x, y)$

- $\&$ -> AND
- $|$ -> OR (inclusive)
- $!$ -> NOT
- $==$ -> EQUAL (identity)
- $!=$ -> NOT EQUAL



A: tidyverse



- The goal is to create tidy data
 1. Each variable a column
 2. Each observation a row
 3. Each value is a cell

Main functions:

- `gather()`
- `separate()`
- Open the script `03_tidyverse.R`



Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II. <http://www.jstatsoft.org/>

Tidy Data

Hadley Wickham
RStudio

Abstract

A huge amount of effort is spent cleaning data to get it ready for analysis, but there has been little research on how to make data cleaning as easy and effective as possible. This paper tackles a small, but important, component of data cleaning: data tidying. Tidy datasets are easy to manipulate, model and visualise, and have a specific structure: each variable is a column, each observation is a row, and each type of observational unit is a table. This framework makes it easy to tidy messy datasets because only a small set of tools are needed to deal with a wide range of un-tidy datasets. This structure also makes it easier to develop tidy tools for data analysis, tools that both input and output tidy datasets. The advantages of a consistent data structure and matching tools are demonstrated with a case study free from mundane data manipulation chores.

Keywords: data cleaning, data tidying, relational databases, R.

DOI: [10.18637/jss.v059.i10](https://doi.org/10.18637/jss.v059.i10)

B: dplyr for data transformation



- Solves the most common data manipulation challenges

Main functions:

- select()
 - filter()
 - mutate()
 - group_by()
 - summarise()
 - and many many more
-
- Open the script 04_dplyr.R

Time for some hands on application

- Open the script 05_practise.R



C: ggplot2



- Data visualisation based on "The Grammar of Graphics"

`ggplot(data = <DATA>) +`

`<GEOM_FUNCTION>(mapping = aes(<MAPPINGS>)) +`

linear model +

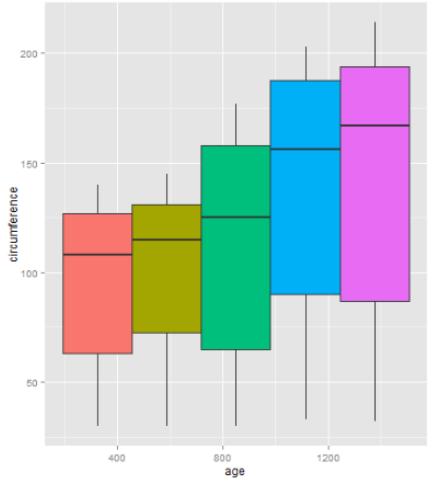
axes formatting +

legend formatting +

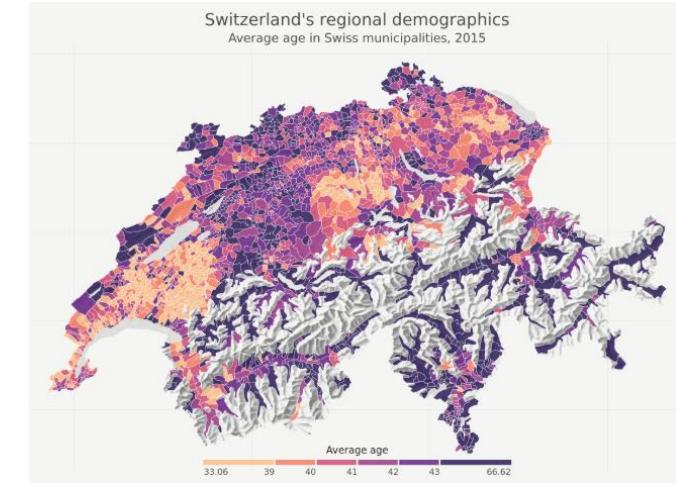
title + etc. etc.

C: ggplot2

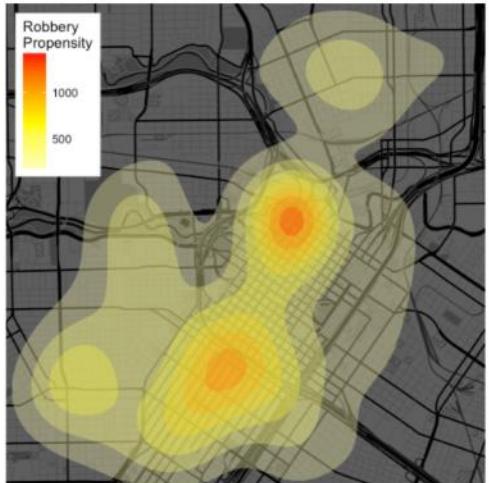
- Very versatile
- Allows you to go from
- Lots of add-on packages



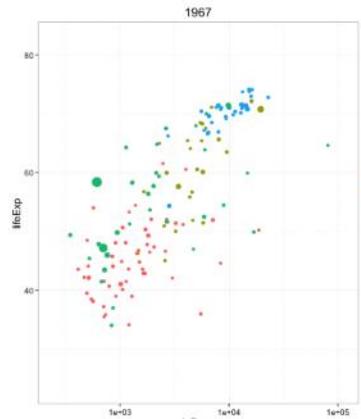
to



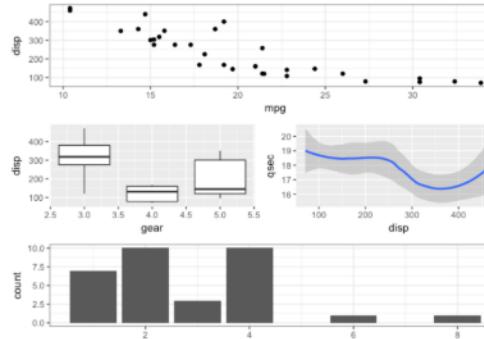
ggmap



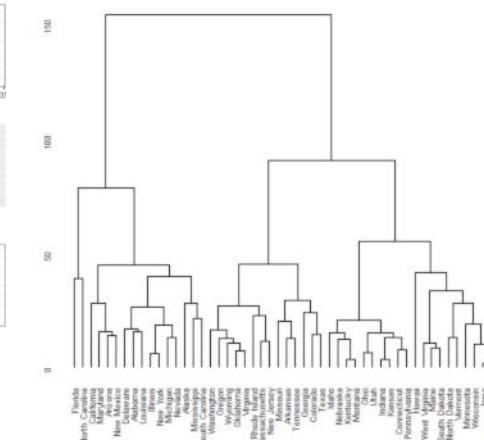
ggridge



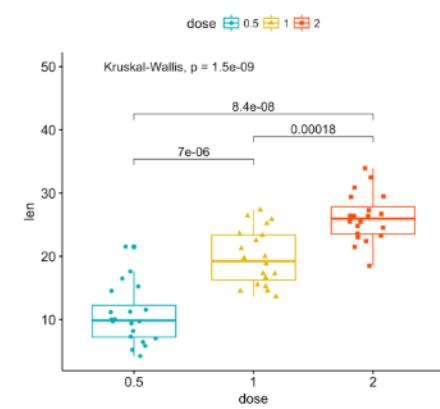
patchwork



ggdendro



ggpubr



Whistle-stop tour of ggplot2

Main features:

1. The data
2. The geoms
3. The mappings (x, y, colour, shape etc.)
4. Legends
5. Labels
6. Themes

and many many more

- Open the script 06_ggplot2.R
- Open the script 07_practise_plots.R

Putting the pieces together

- Project structure
 - Naming conventions
 - Scripted workflows
 - Reproducible research

How is research presented?

Theses

Papers



Network Analysis of the Chronic Hepatitis C Virome Defines Hypervariable Region 1 Evolutionary Phenotypes in the Context of Humoral Immune Responses

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Molecular Virology Diagnostic & Research Laboratory, Department of Medicine, University College Cork, Cork, Ireland; Division of Viral Hepatitis, Centers for Disease Control and Prevention, Atlanta, Georgia, USA; Department of Reproductive, Cork University Hospital, Cork, Ireland

ABSTRACT
Hypervariable region 1 (HVR1) of hepatitis C virus (HCV) comprises the first 27 N-terminal amino acid residues of E2. It is classically recognized as the major antigenic determinant of HCV envelope glycoprotein E2. We performed a deep sequencing of a cohort of treatment-naïve, chronically infected patients over a short, 16-week period. Organization of the sequence set into connected components that represented single nucleotide substitution events revealed a network dominated by highly connected, centrally positioned master sequences. HVR1 phenotypes were observed to be under strong purifying (stationary) and strong positive (antigenic drift) selection pressures, which were consistent with advancing patient age and diagnosis of cirrhosis. It was found that the HVR1 network structure was dominated by stationary variants, which were composed from conservative single amino acid substitution events. We present evidence to suggest that neutralization antibody efficacy was diminished for stationary-virome HVR1 variants. Our results identify the HVR1 network structure during chronic hepatitis C as the predominant dominance of a single variant within a narrow sequence space.

IMPORTANCE
Hepatitis C virus is often asymptomatic, and chronic infection is generally well established in advance of initial diagnosis and subsequent treatment. HVR1 can undergo rapid sequence evolution during acute infection, and the variant pool is typically seen to diverge away from ancestral sequences as infection progresses from the acute to the chronic phase. In this report, we describe HVR1 viromes in chronically infected patients that are defined by a dominant epitope located centrally within a narrow variant pool. Our findings suggest that weakened humoral immune activity, as a consequence of persistent chronic infection, allows for the acquisition and maintenance of host-specific adaptive mutations at HVR1 that reflect virus fitness.

Hepatitis C virus (HCV) infection is a global health burden and a major etiological agent of liver related disease worldwide. In the United States alone, the estimated prevalence of HCV represents approximately 2% of the global adult (15 years of age and older) population (1). Following transmission, HCV infection is often asymptomatic and may remain undetected for many years, allowing for infections initially passing undetected (2). It is estimated that up to 4 million Americans are living with the virus, the majority of whom became infected prior to the first clinical identification of the virus (3, 4). Consequently, the U.S. Centers for Disease Control and Prevention now recommend that Americans born from 1945 to 1965 be screened for the presence of the virus, as well as all individuals at risk of contracting HCV (5).

HCV is a single-stranded positive-sense RNA virus of considerable genomic heterogeneity. A recent reclassification defines the major genotypes 1a and 1b and 67 subtypes within genotypes 1 and 5 accounting for the majority of infections worldwide (6, 7). An error-prone RNA-dependent RNA polymerase, together with an inherent propensity of defining hypervariable regions (HVRs), is responsible for much of this variability. These HVRs are located within the envelope glycoprotein E2. The greatest heterogeneity has been identified at the 27-amino-acid HVR1 (residues 456–482) located at the N-terminal end of the E2 glycoprotein (8). Recent studies indicated that the central region of E2 (residues 456 to 656) is globular and surprisingly compact, whereas the first 80 amino acids (including

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B.A.O'F and D.S.M. contributed equally to this article.
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Books



Talks



2318 *Infect Dis Ther* April 2016 Volume 90 Number 7

Pioneering new approaches to woodland ecology and human activity in medieval Ireland (c. 500 – 1550 AD): An investigation using archaeological charcoal

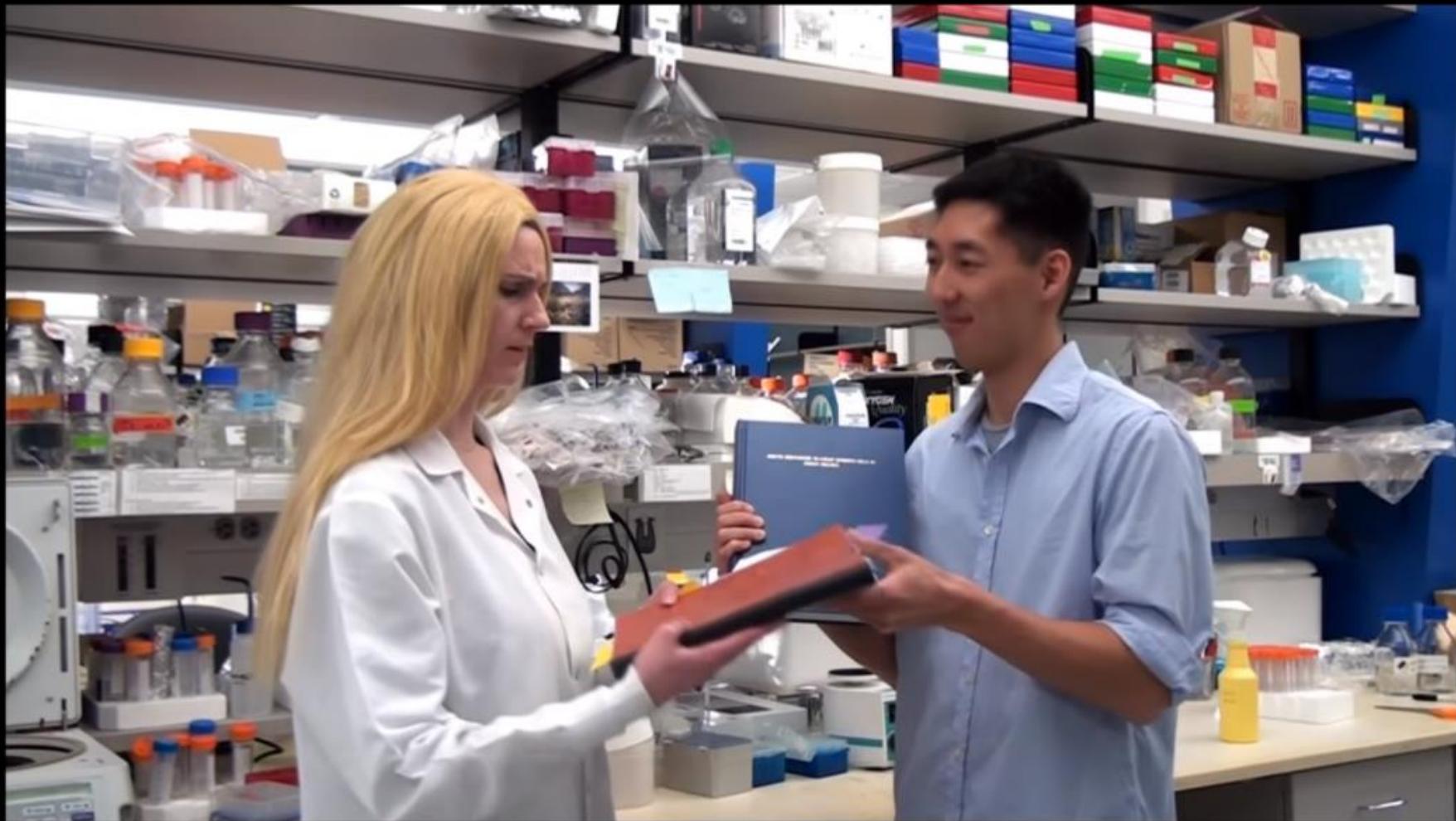
SUSAN LYONS

Posters



But what does it look like under the bonnet?

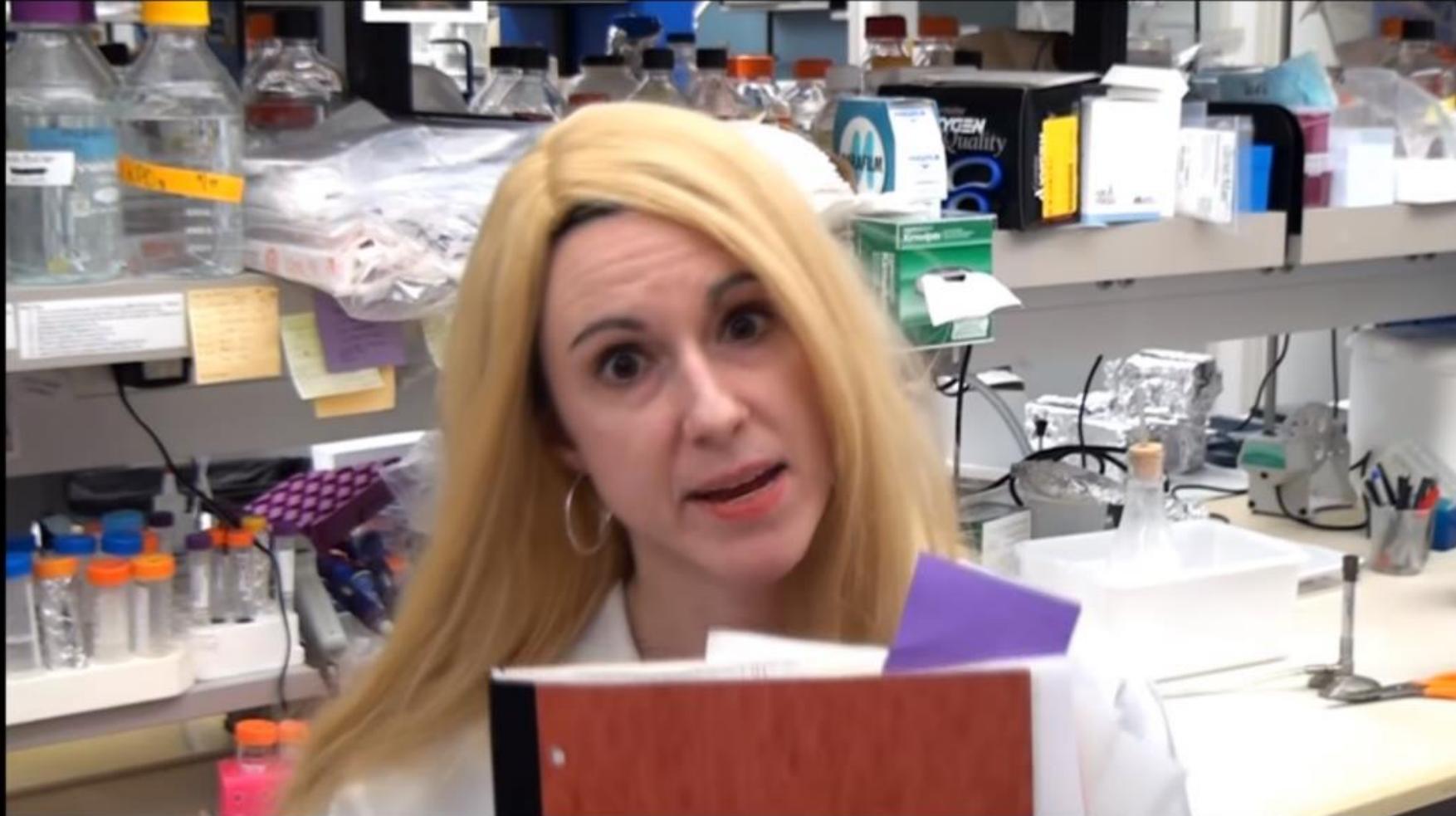




You were defending, one foot out the door



I got your project and its problems galore



I hate my life,

DON'T WORRY,
YOU DON'T HAVE
TO START YOUR
CODE FROM
SCRATCH.

YOU CAN REUSE THE
SOFTWARE THAT THE
PREVIOUS PERSON
ON THE PROJECT
WROTE SEVERAL
YEARS AGO.

ARE THERE
INSTRUCTIONS FOR
HOW TO USE IT?

I DOUBT IT.

IS THE CODE
COMMENTED?

NOT LIKELY.

WHERE ARE
THE FILES?

WHO KNOWS.

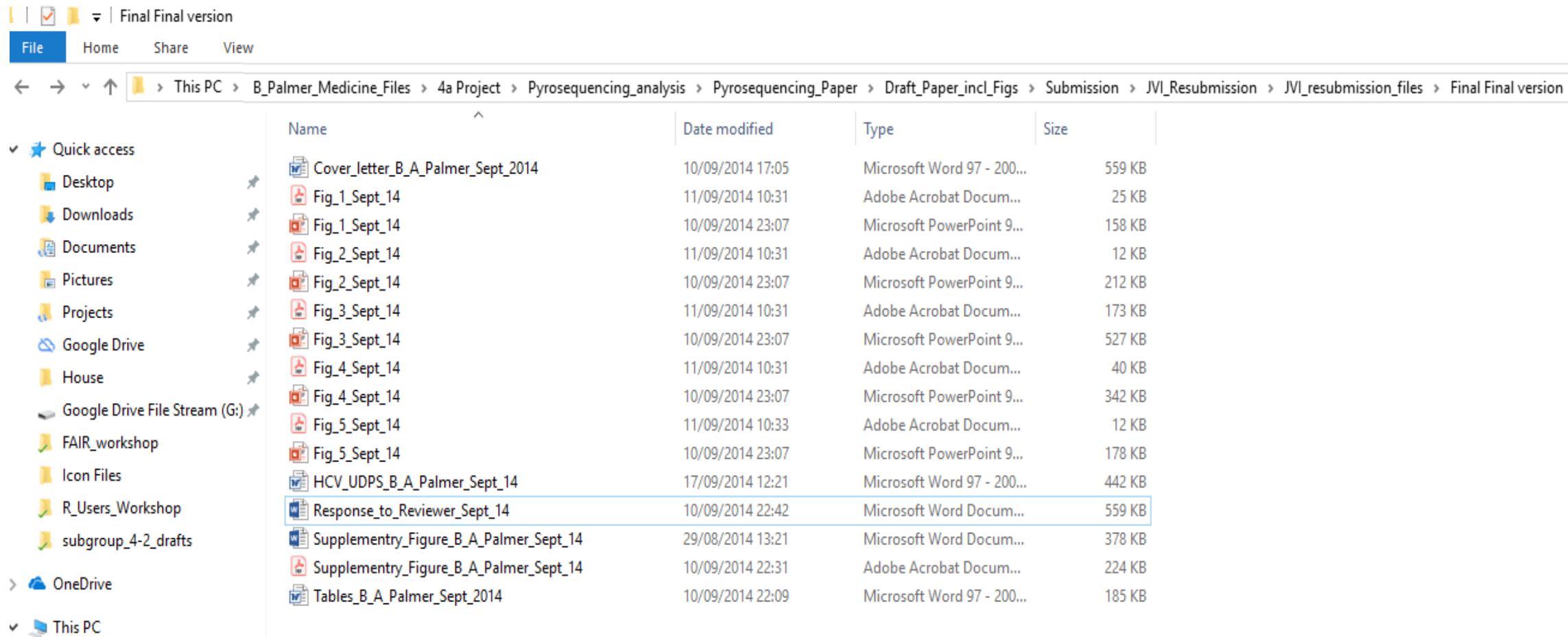
THIS IS GOING
TO BE PAINFUL,
ISN'T IT?

JUST A
SCRATCH.

THIS PERSON IS likely to be YOU BTW!!

D: Still haven't found what I'm looking for

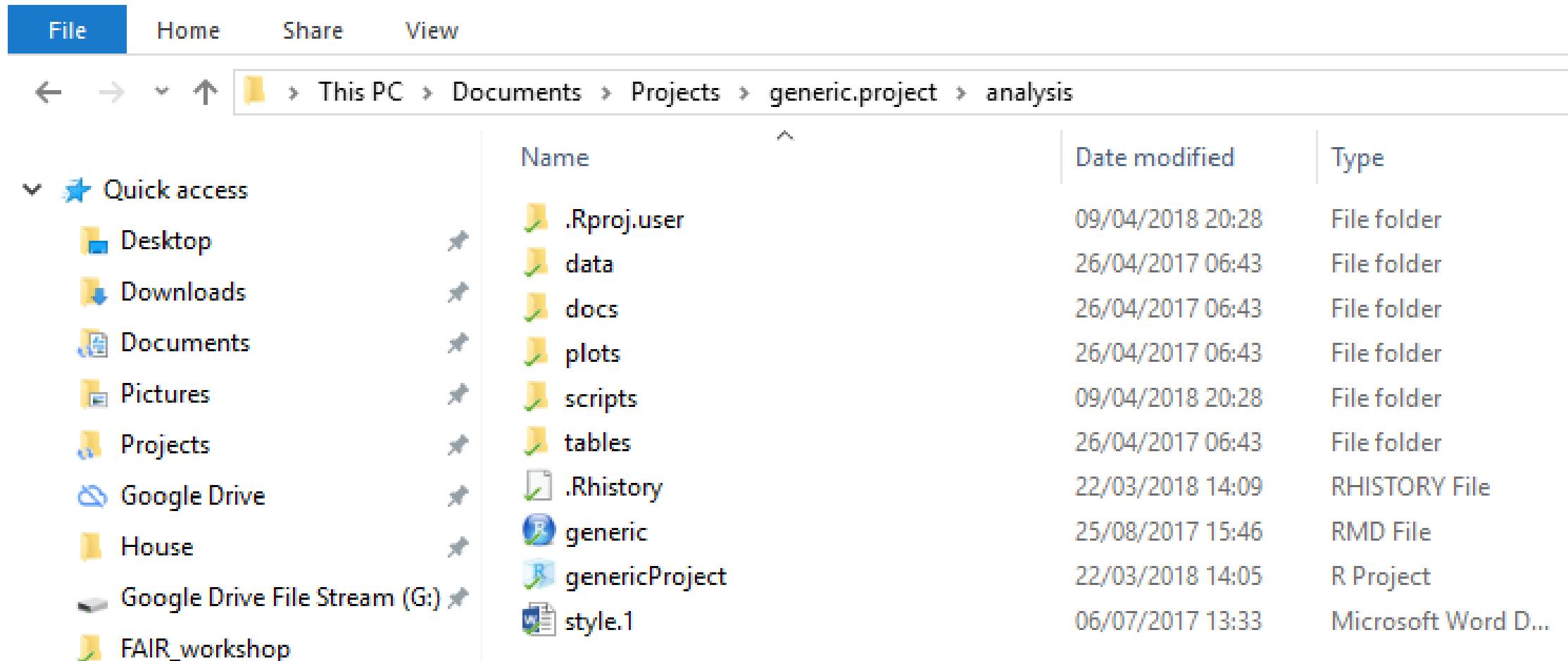
- Help your future-self



	Name	Date modified	Type	Size
Quick access	Cover_letter_B_A_Palmer_Sept_2014	10/09/2014 17:05	Microsoft Word 97 - 200...	559 KB
	Fig_1_Sept_14	11/09/2014 10:31	Adobe Acrobat Docum...	25 KB
	Fig_1_Sept_14	10/09/2014 23:07	Microsoft PowerPoint 9...	158 KB
	Fig_2_Sept_14	11/09/2014 10:31	Adobe Acrobat Docum...	12 KB
	Fig_2_Sept_14	10/09/2014 23:07	Microsoft PowerPoint 9...	212 KB
	Fig_3_Sept_14	11/09/2014 10:31	Adobe Acrobat Docum...	173 KB
	Fig_3_Sept_14	10/09/2014 23:07	Microsoft PowerPoint 9...	527 KB
	Fig_4_Sept_14	11/09/2014 10:31	Adobe Acrobat Docum...	40 KB
	Fig_4_Sept_14	10/09/2014 23:07	Microsoft PowerPoint 9...	342 KB
	Fig_5_Sept_14	11/09/2014 10:33	Adobe Acrobat Docum...	12 KB
	Fig_5_Sept_14	10/09/2014 23:07	Microsoft PowerPoint 9...	178 KB
	HCV_UDPS_B_A_Palmer_Sept_14	17/09/2014 12:21	Microsoft Word 97 - 200...	442 KB
	Response_to_Reviewer_Sept_14	10/09/2014 22:42	Microsoft Word Docum...	559 KB
	Supplementary_Figure_B_A_Palmer_Sept_14	29/08/2014 13:21	Microsoft Word Docum...	378 KB
	Supplementary_Figure_B_A_Palmer_Sept_14	10/09/2014 22:31	Adobe Acrobat Docum...	224 KB
	Tables_B_A_Palmer_Sept_2014	10/09/2014 22:09	Microsoft Word 97 - 200...	185 KB

Define a generic project structure

- STEP 1: Give your research projects a shared structure



The screenshot shows a Windows File Explorer window with the following details:

- File Explorer ribbon:** File, Home, Share, View.
- Address bar:** This PC > Documents > Projects > generic.project > analysis
- Left sidebar (Quick access):** Desktop, Downloads, Documents, Pictures, Projects, Google Drive, House, Google Drive File Stream (G:), FAIR_workshop.
- Right pane (File list):**

Name	Date modified	Type
.Rproj.user	09/04/2018 20:28	File folder
data	26/04/2017 06:43	File folder
docs	26/04/2017 06:43	File folder
plots	26/04/2017 06:43	File folder
scripts	09/04/2018 20:28	File folder
tables	26/04/2017 06:43	File folder
.Rhistory	22/03/2018 14:09	RHISTORY File
generic	25/08/2017 15:46	RMD File
genericProject	22/03/2018 14:05	R Project
style.1	06/07/2017 13:33	Microsoft Word D...

Give your files informative names

- STEP 1: Give your research projects a shared structure

The screenshot shows a Windows File Explorer window with the following details:

- File Bar:** File, Home, Share, View.
- Address Bar:** This PC > Documents > Projects > 18.04.27-WP3_Feeding_Trial > analysis > data
- Left Sidebar:** Quick access, Desktop, Downloads, Documents, Pictures, Projects.
- Table View:** A list of files in the "data" folder.

Name	Date modified
raw_files_password_protected	27/09/2018 11:54
master_database	12/06/2018 12:22
nutritics_food_level	09/05/2018 14:25
nutritics_grouped	09/05/2018 14:27
nutritics_grouped_reduced	14/05/2018 01:14

Everything in its right place

- STEP 2: Make your file names machine readable, human readable and work with default ordering

NO

Name
All unique 4a amino acid Sequences (B-N).fas
All unique 4a amino acid Sequences (B-N).meg
All_AA_haplotypes.meg
All_AA_haplotypes_with_clonal_sequences.meg
BS100_AA_with_clones
BS100_AA_with_clones.nwk
BS1000_AA_pyro&clones
BS1000_AA_pyro&clones.nwk
BS1000_AA_pyro_only
BS1000_AA_pyro_only.nwk
BS1000_Uncalibrated_Clonal_AA
BS1000_Uncalibrated_Clonal_AA.nwk
BS1000_Uncalibrated_Pyro_AA
BS1000_Uncalibrated_Pyro_AA.nwk
pic

Yes

Documents > Projects > 18.04.27-WP3_Feeding_Trial > analysis > scripts		
	Name	Date modified
...	01_data_import_and_tidying_master_file	02/10/2018 18:51
...	02_data_import_and_tidying_nutritics_grouped	19/10/2018 19:47
...	03_figures	17/10/2018 16:40
...	04_tables	22/05/2018 12:26
...	05_study_overview	19/10/2018 23:06
...	functions	13/05/2018 23:13

Outline a file naming convention

Machine readable:

- Inherent order
- Avoid spaces
- Avoid punctuation
- Remove case-sensitivity

Human readable:

- Contains info on content
- Avoid spaces
- Avoid punctuation
- Remove case sensitivity

Metadata:

Separate with underscores ("_")

- Avoid punctuation
- Remove case-sensitivity

01_marshall-data.r

02_pre-dea-filtering.r

03_dea-with-limma-voom.r

04_explore-dea-results.r

90_limma-model-term-name-fiasco.r

helper01_load-counts.r

helper02_load-exp-des.r

helper03_load-focus-statinf.r

helper04_extract-and-tidy.r

Outline a file naming convention

Chronological order:

```
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_H01.csv  
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_H02.csv  
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_H03.csv  
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_platefile.csv  
2014-02-26_BRAFWTNEGASSAY_FFPEDNA-CRC-1-41_A01.csv  
2014-02-26_BRAFWTNEGASSAY_FFPEDNA-CRC-1-41_A02.csv  
2014-02-26_BRAFWTNEGASSAY_FFPEDNA-CRC-1-41_A03.csv  
2014-02-26_BRAFWTNEGASSAY_FFPEDNA-CRC-1-41_A04.csv
```

Logical order:

```
01_marshall-data.r  
02_pre-dea-filtering.r  
03_dea-with-limma-voom.r  
04_explore-dea-results.r  
90_limma-model-term-name-fiasco.r  
helper01_load-counts.r  
helper02_load-exp-des.r  
helper03_load-focus-statinf.r  
helper04_extract-and-tidy.r
```

Joined up thinking

- The R scripts you generate should be human readable
 - Annotate the code
 - Break up the scripts into dedicated tasks
 - Interlink with other within project scripts

```
1 # Data ----
2 # Eight tibbles returned from the 01_data_import_and_tidying_master_file.R
3 # 1. fgf23_data => FGF23 readings from study centres 01-03
4 # 2. food_level_data => Food diary entries
5 # 3. grouped_data => Dialysis and nondialysis diary entries by component
6 # 4. k_data => Serum potassium
7 # 5. master_data_clean => all the clean master file data if required
8 # 6. p_data => Serum phosphate
9 # 7. pth_data => Parathyroid hormone readings
10 # 8. pulses_nuts_data
11
12 source("scripts/01_data_import_and_tidying_master_file.R")
```

Is too much choice good or bad?

Toothpaste & Jam: The Psychology of Choice



Something as simple as buying toothpaste can be overwhelming. Do you want the anti-tartar kind or the cavity-busting option? Sensitive enamel protection or the one with whitening? Fluoride, non-fluoride? Then there's flavor: crystal mint, intense mint, fresh mint or sparkling mint - and that's just mint.

Inconsistent function names, inconsistent syntax

- R is a very versatile language
 - Sometimes it can be too versatile
 - Do you want to use.....
 - Names or colnames
 - row.names or rownames
 - rowSums or rowsum
 - Sys.time, system.time
- Is it written as.....
 - newobject or new.Object
 - x = 5 or x <- 5
 - mapping=aes(x,y) or mapping = aes(x, y)

Variable selection

```
summary(starwars$name)
```

```
summary(starwars$"name")
```

```
summary(starwars ["name"] )
```

```
summary(starwars [, "name"] )
```

```
summary(starwars[1])
```

```
summary(starwars[, 1])
```

```
summary(starwars[[1]])
```

- Open the script 08_too_much.choice.R

Writing clearer code

- Annotation
- Object names
 - should use only lowercase letters, numbers, and “_”
- Spacing
 - Put a space before and after =
 - Put a space after a ,
 - Operators should be surrounded by spaces e.g. ==, <-, +
- For a more complete list visit
 - <http://style.tidyverse.org/syntax.html>
- Open the script 09_good_habits.R

E: Everything in its right place

- To finish up, we're going to explore the benefits of using R projects for our data analysis tasks
- Open the script 10_project_clean_data.R
- Open the script 11_project_project_data.R

Don't Do What Donny Don't Does!!



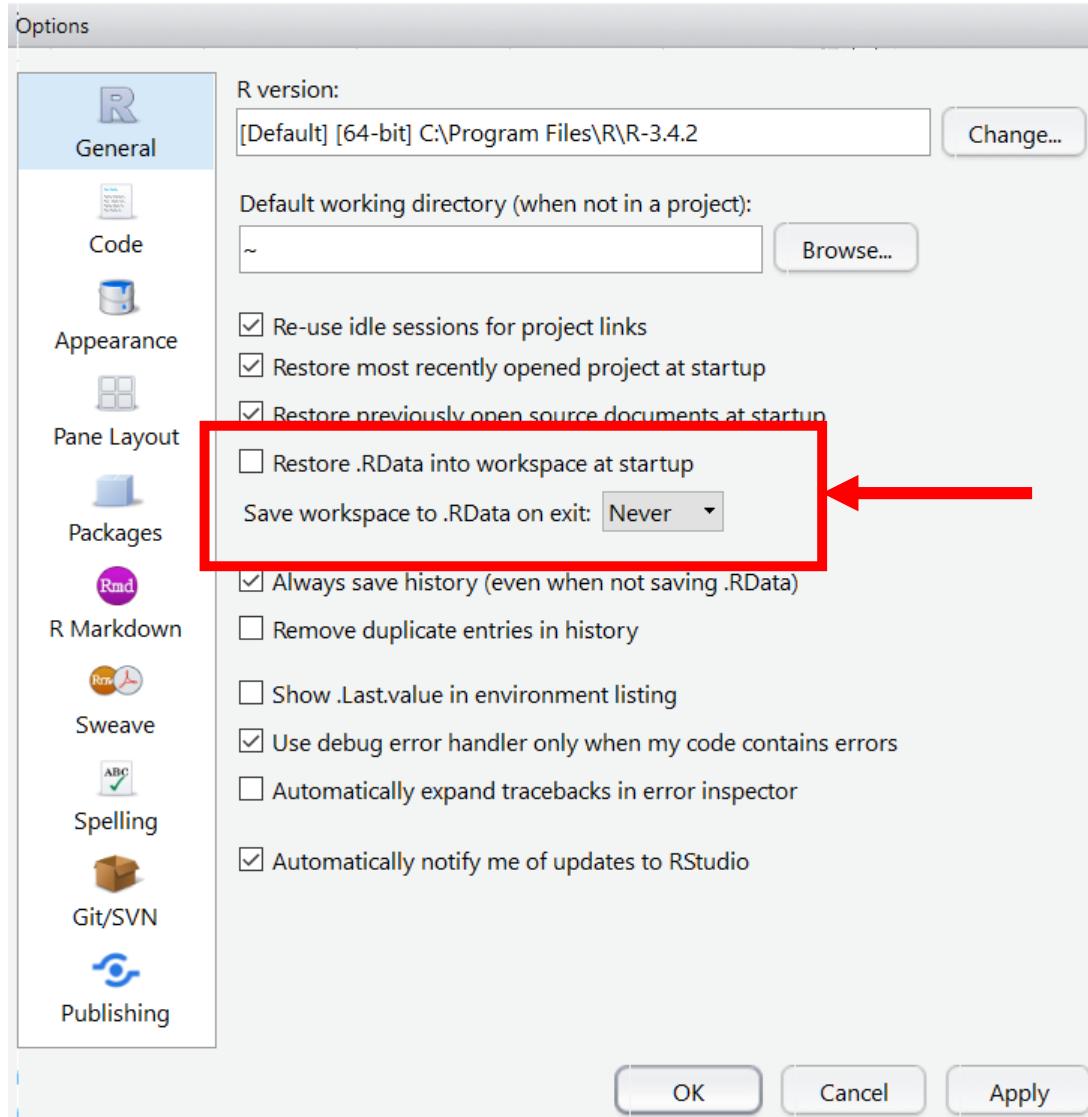
Donny Don't:

- Start your script with...
`setwd()`

Donny Don't:

- Start your script with...
`rm(list = ls())`

Other points to note



- You might consider your environment as “real”
- If you continue to use R, it is better for you to consider your R scripts as “real”, as these should recreate the environment
- You may suffer short term pain
- This will prevent long term agony