

Intro to Tidyverse!



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Intro

- Familiar w/ R and ggplot? Introduce yourself briefly!
 - Who you are | Name, affiliation
 - Do you have the same version of
 - R (4.1+), RStudio & Tidyverse?
 - NO? Installation time!

Need help? Raise your hand!

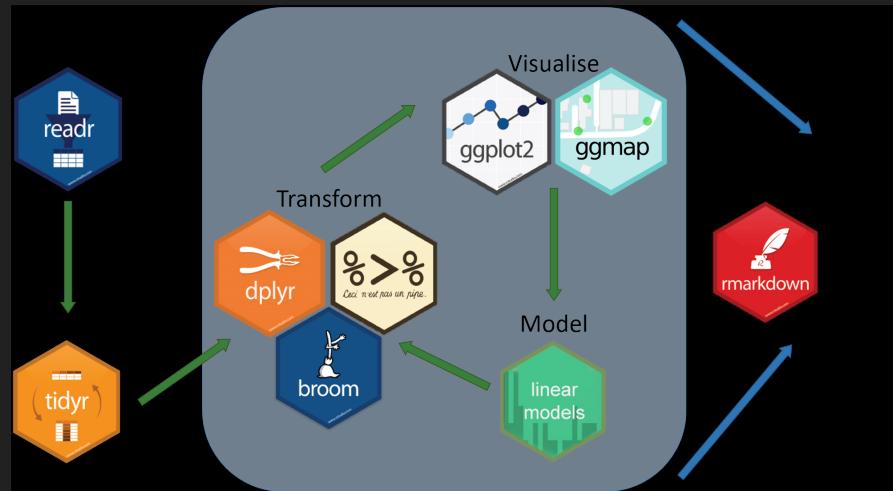


OR ask on chat!



Today!

- Workshop
 - Intro to Tidyverse



Welcome to *tidyverse*

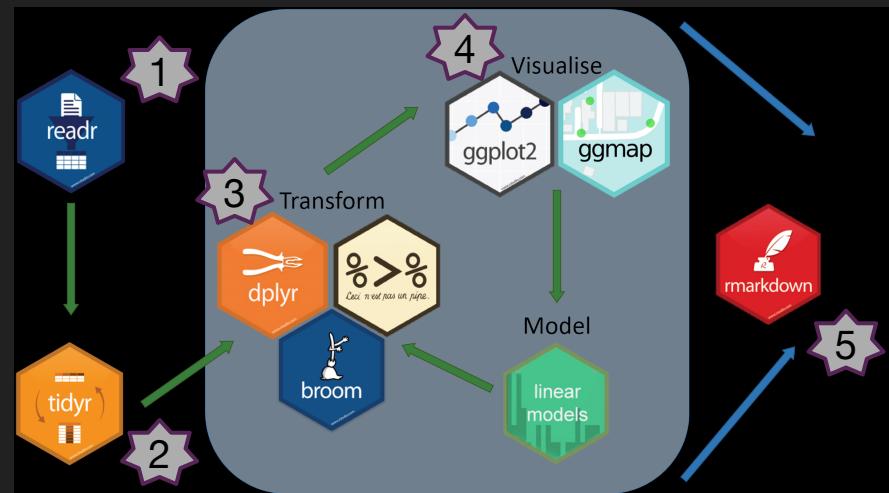
P1: Getting Started w/ `readr`

P2: Reshaping data w/ `tidyr`

P3: Data wrangling w/ `dplyr`

P4: DataViz w/ `ggplot`

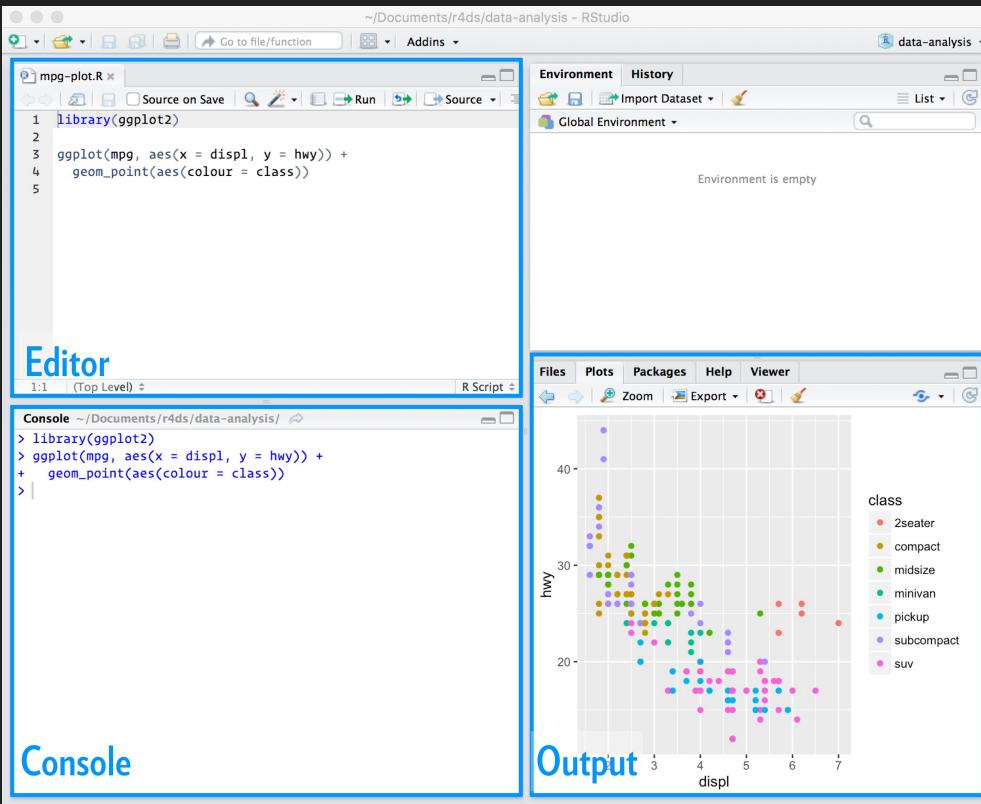
P5: Wrap-up w/ RMarkdown



Part 1: Getting Started: Environment

- ✓ Installing RStudio, R
- ✓ Installing tidyverse

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



Getting Started: Data, your data

1. Import your data

```
library(tidyverse)
read_csv(file="my_data.csv",
         col_names=T)      # comma-separated values
read_delim(file="my_data.txt", col_names=T,
            delim="//")   # any delimiter
# Other useful packages
# readxl by Jenny Bryan
read_excel(path="path/to/excel.xls",
           sheet=1,
           range="A1:D50",
           col_names=T)
```

Getting Started: Today's Dataset

A resource of ribosomal RNA-depleted RNA-Seq data from different normal adult and fetal human tissues

Jocelyn Y.H. Choy, Priscilla L.S. Boon, Nicolas Bertin & Melissa J. Fullwood ✉

Scientific Data 2, Article number: 150063
(2015)

doi:10.1038/sdata.2015.63

Download Citation

Development RNA sequencing

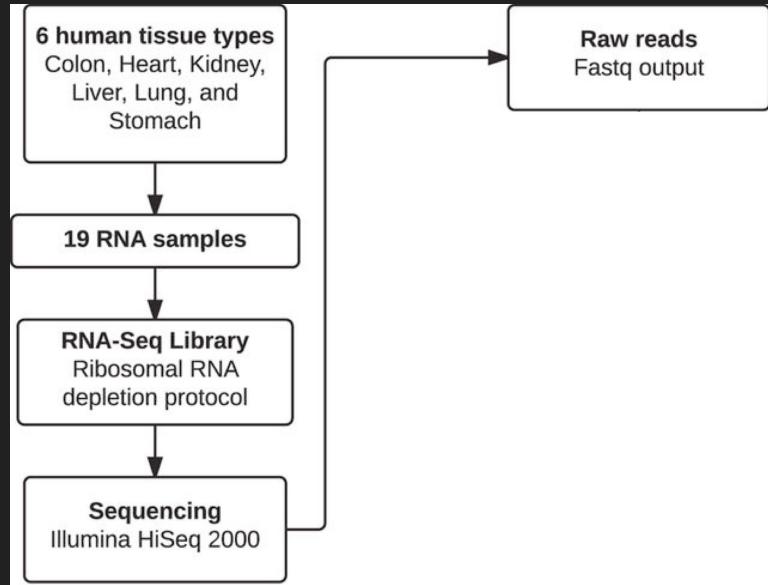
Transcriptomics

Received: 10 June 2015

Accepted: 07 October 2015

Published online: 10 November 2015

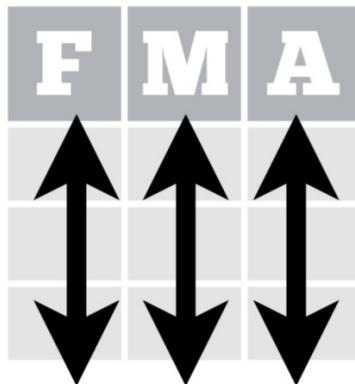
Design Type(s)	parallel group design • replicate design • organism development design
Measurement Type(s)	transcription profiling assay
Technology Type(s)	next generation sequencing
Factor Type(s)	tissue specimen • life cycle stage
Sample Characteristic(s)	Homo sapiens • colon • stomach • heart • kidney • liver • lung



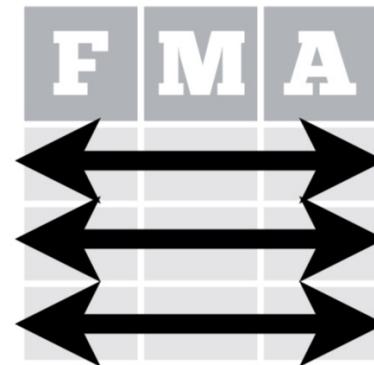
<https://www.nature.com/articles/sdata201563>

Back to RStudio

Part 2: Reshaping data w/ *tidyR*



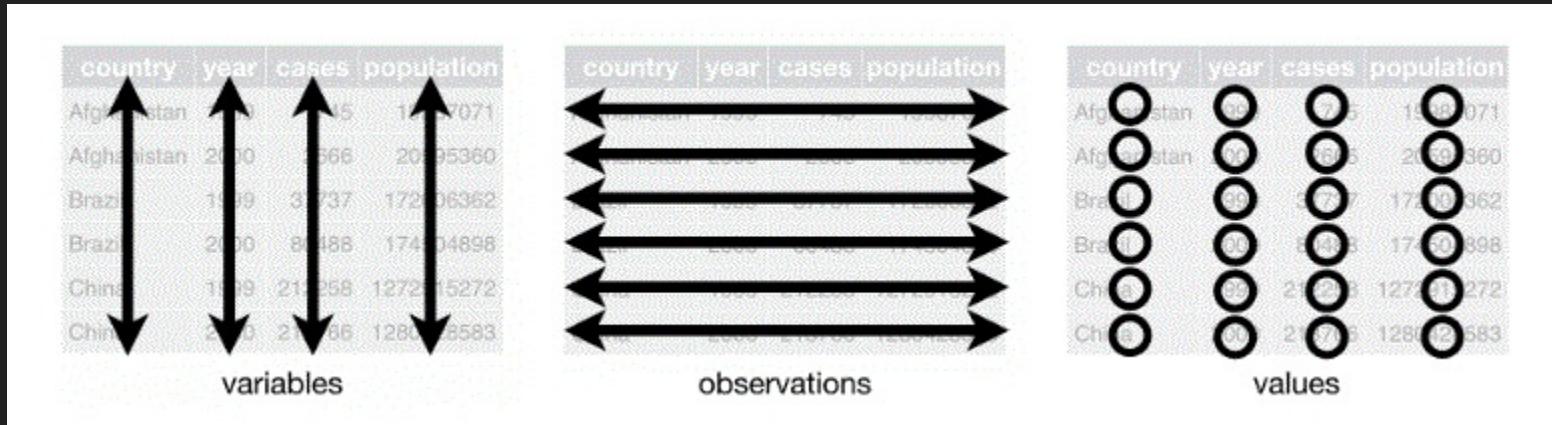
Each **variable** is saved
in its own **column**



Each **observation** is
saved in its own **row**

Tidy Data ... In a ‘Tidy’ dataset, ...

Part 2: What is tidy data?



- Each variable in the data set is placed in its own column.
- Each observation is placed in its own row.
- Each value is placed in its own cell.

Part 2: In a ‘Tidy’ dataset, ...

		wide	long					
		id	x	y	z	id	key	val
1	a	c	e	x	y	z	1	a
	b	d	f				2	b
2	x	y	z	1	c	e	1	c
				2	d	f	2	d

Part 2: Reshaping data w/ *tidyverse*

```
pivot_longer()      # Gather COLUMNS -> ROWS  
pivot_wider()       # Spread ROWS -> COLUMNS  
separate()          # Separate 1 COLUMN -> many COLUMNS  
unite()             # Unite several COLUMNS -> 1 COLUMN
```

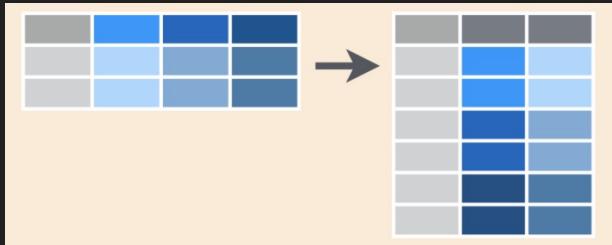
Part 2: Reshaping data w/ *tidyverse*

Tidy data

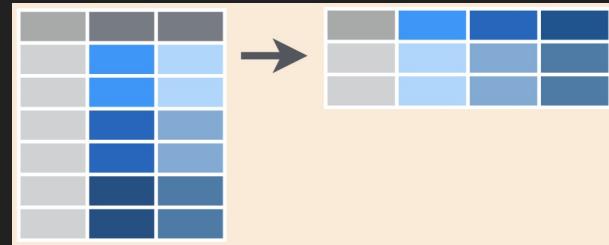
		wide		
		x	y	z
id				
1	a		c	e
	b		d	f



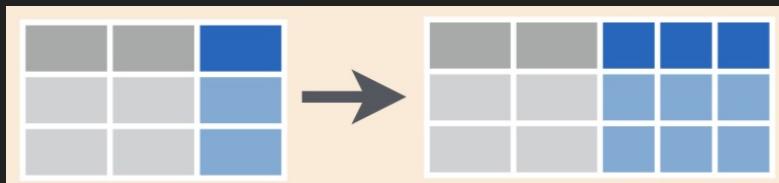
Part 2: Reshaping data w/ *tidyverse*



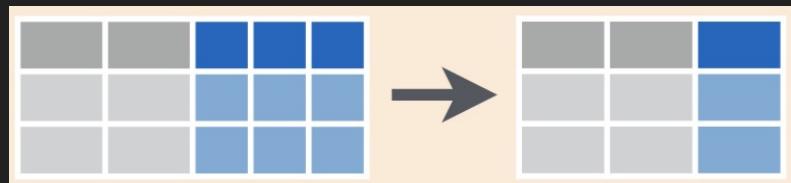
`pivot_longer`



`pivot_wider`



`separate`



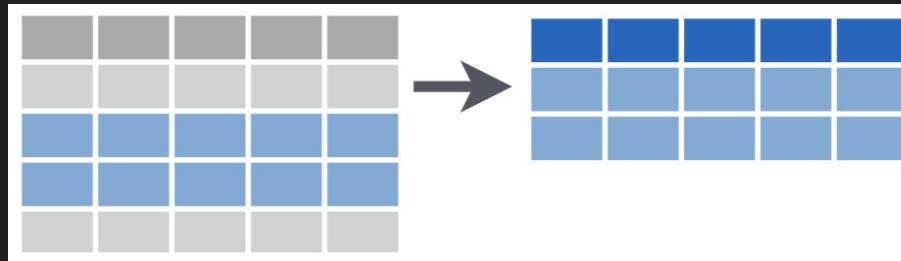
`unite`

Back to RStudio

Part 3: Wrangling data w/ *dplyr*

```
filter()    # PICK observations by their values | ROWS  
select()    # PICK variables by their names | COLUMNS  
mutate()    # CREATE new variables w/ functions of existing variables | COLUMNS  
transmute() # COMPUTE 1 or more COLUMNS but drop original columns  
arrange()   # REORDER the ROWS  
summarize() # COLLAPSE many values to a single SUMMARY  
group_by()  # GROUP data into rows with the same value of variable (COLUMN)
```

Part 3: Wrangling data w/ *dplyr*

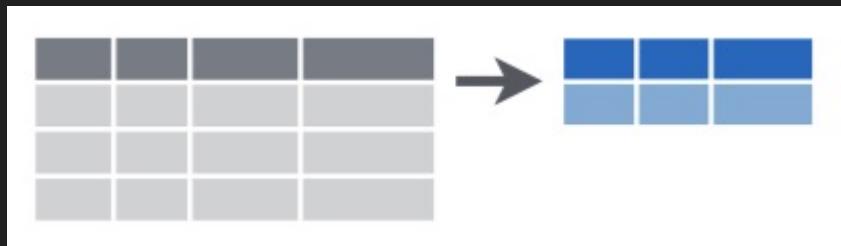


`filter`



`select`

Part 3: Wrangling data w/ *dplyr*



summarise



group_by

Part 3: Wrangling data w/ *dplyr*

Mutating joins

a	
x1	x2
A	1
B	2
C	3

b	
x1	x3
A	T
B	F
D	T

left_join()

x1	x2	x3
A	1	T
B	2	F
C	3	NA

right_join()

x1	x3	x2
A	T	1
B	F	2
D	T	NA

inner_join()

x1	x2	x3
A	1	T
B	2	F

outer_join()

x1	x2	x3
A	1	T
B	2	F
C	3	NA
D	NA	T

Part 3: Wrangling data w/ *dplyr*

Mutating joins

left_join(x, y)			
1	x1	1	y1
2	x2	2	y2
3	x3	4	y4



Part 3: Wrangling data w/ *dplyr*

Mutating joins

right_join(x, y)

1	x1	1	y1
2	x2	2	y2
3	x3	4	y4



Part 3: Wrangling data w/ *dplyr*

Mutating joins

inner_join(x, y)

1	x1	1	y1
2	x2	2	y2
3	x3	4	y4



Part 3: Wrangling data w/ *dplyr*

Mutating joins

full_join(x, y)			
1	x1	1	y1
2	x2	2	y2
3	x3	4	y4



Part 3: Wrangling data w/ *dplyr*

Set operations

y	
x1	x2
A	1
B	2
C	3

+

z	
x1	x2
B	2
C	3
D	4

=

intersect()

x1	x2
B	2
C	3

union()

x1	x2
A	1
B	2
C	3
D	4

setdiff()

x1	x2
A	1
D	4

Part 3: Wrangling data w/ *dplyr*

Set operations

intersect(x, y)

1	a
1	b
2	a

1	a
2	b



Part 3: Wrangling data w/ *dplyr*

Set operations

union(x, y)

1	a	1	a
1	b	2	b
2	a		



Part 3: Wrangling data w/ *dplyr*

Binding

y		Z	
x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4



bind_rows()

x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4

x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4

bind_cols()

Back to RStudio

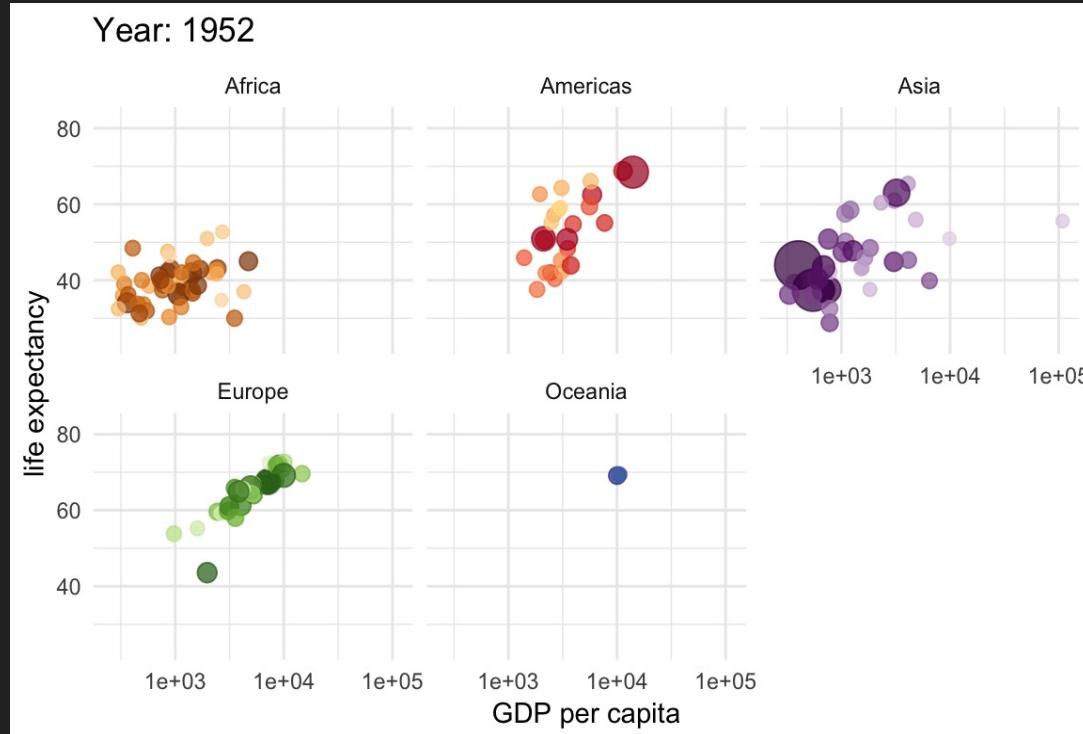
Part 4: Visualizing tidy data w/ ggplot2

Geometry of graphics

- **data**: Must be a data frame
- **aesthetics**: How your data are represented visually
 - x, y, color, size, shape, etc.
- **geometry**: Geometries of plotted objects
 - points, lines, boxplot, polygons, etc.
- and *other customizations*

Part 4: Visualizing tidy data w/ ggplot2

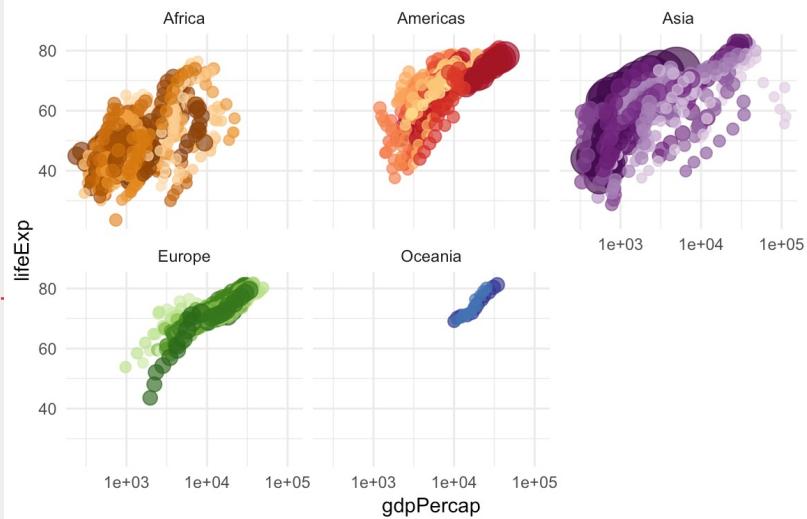
gganimate: aha!



Part 4: Visualizing tidy data w/ ggplot2

gapminder: static plot

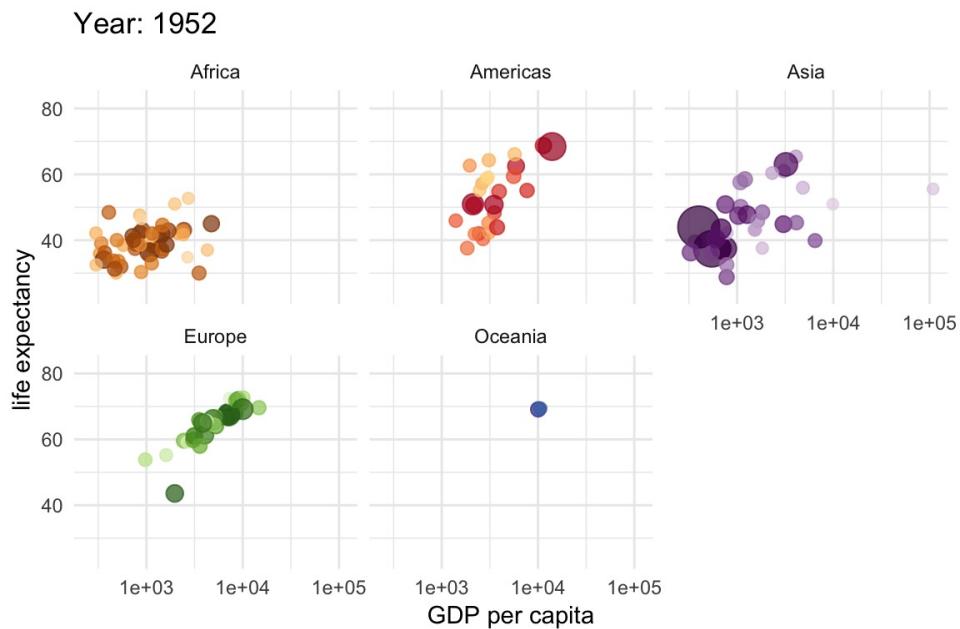
```
library(gapminder)
ggplot(gapminder,
       aes(gdpPerCap, lifeExp,
           size=pop, colour=country)) +
  geom_point(alpha = 0.7,
             show.legend = FALSE) +
  scale_colour_manual(values=country_colors) +
  scale_size(range=c(2, 12)) +
  scale_x_log10() +
  facet_wrap(~continent) +
  theme_minimal()
```



Part 4: Visualizing tidy data w/ ggplot2

gapminder: dynamic plot

```
ggplot(gapminder,  
       aes(gdpPercap, lifeExp,  
            size=pop, colour=country)) +  
... ... ... +  
theme_minimal() +  
# Here comes the gganimate part!  
labs(title = 'Year: {frame_time}',  
     x = 'GDP per capita',  
     y = 'life expectancy') +  
transition_time(year) +  
ease_aes('linear')
```



Part 5: Export & Wrap-up

`ggsave` — Save your plots

`write_delim` — Save your data

Back to RStudio

Tidyverse Recap

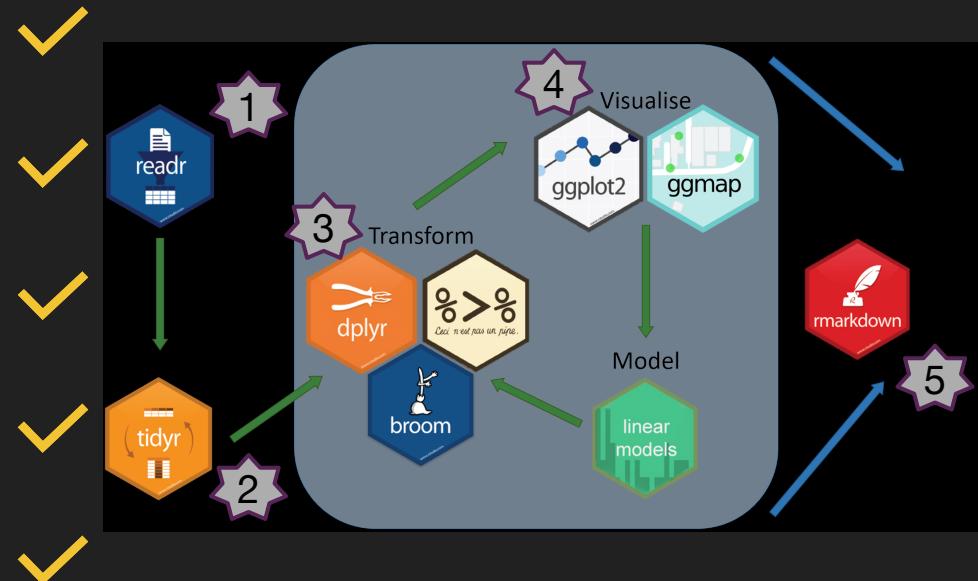
P1: Getting Started w/ readr ✓

P2: Reshaping data w/ tidyr ✓

P3: Data wrangling w/ dplyr ✓

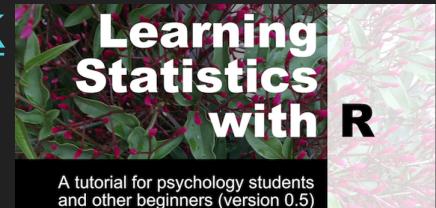
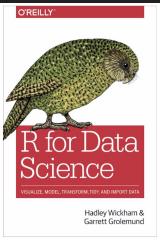
P4: DataViz w/ ggplot ✓

P5: Wrap-up w/ RMarkdown ✓



Resources

- Hands-On Programming with R: *Grolemund* #HOPR
 - <https://rstudio-education.github.io/hopr/>
- R for Data Science: *Wickham & Grolemund* #R4DS
 - <https://r4ds.had.co.nz>
- R Programming for Data Science: Peng
 - <https://leanpub.com/rprogramming>
- Learning Statistics with R: Navarro
 - <https://learningstatisticswithr.com/book>



More Resources

 **R-Ladies EL material:** github.com/r-ladies-eastlansing

 **#TidyTuesday** challenges

 **gganimate:** thomasp85/gganimate

 **tidyexplain:** gadenbuie/tidyexplain

- **Distill (theme for RMarkdown):** <https://rstudio.github.io/distill>
- Google & <https://stackoverflow.com/> are your best friends!



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- Arjun Krishnan, CMSE & BMB, MSU
- R-Ladies EL & my previous talks!
- JRaviLab & the Krishnan Lab
- The R&DS books
- The R-Ladies Global community



Questions? Comments?

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