DataCamp Covid-19 Project

DSC 205 Introduction to Advanced Data Science

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README

- Demo of ggplot2 using early pandemic COVID data
- The material covered comes from the following DataCamp courses:
  - Data Visualization with ggplot2 (a graphics package for R)
  - Intermediate Data Visualization with ggplot2
  - Data Manipulation with dplyr (a table manipulation package in R)
  - Introduction to Importing Data in R (using `read.table`)
- To look at the whole project at once see here.
- We'll revisit some topics in our gapminder project

Aspects of this project (discussion)

The table 1 lists some (**variable**) aspects of this project. In practice, you would revisit these before, during and after the project.

ASPECT	CONTENT	DECISIONS
Technical	R packages	Base R, ggplot2
Scientific	Data science pipeline	Data quality, presentation
Political	Policy	Funding, trust, future
Personal	Pro or Con	Do it or don't, dig deeper

Which aspects did you find interesting and why (not)?

Personal

- Alright - "we've talked about COVID a lot"

- These plots were new?
- I somewhat disliked this project

Technical

- Fun to create fancy graphs with little effort
- Is ggplot2 really necessary?
- dplyr - table manipulation (similar to SQL)
- linear modeling with the glm() family of functions

Scientific

- You should always try to go to the source of the data (In this case: JHU)
- Data quality in this area needs to be questioned
- Issues are: collection procedures and measures

Political

- Ongoing issue (with every new variant)

Example: getting the data for your own project

- I found this dataset via
    1. Google search of `datasets/confirmed_cases_worldwide.csv`
    2. The site ourworldindata.org uses JHU as the main data source
    3. Data import from GitHub - you need the raw source
- Or you can select the Jan-Mar 17, 2020 timeline and download the CSV data from the "COVID-19 Data Explorer", a graphical dashboard.

- From the "COVID-19 Data Explorer".

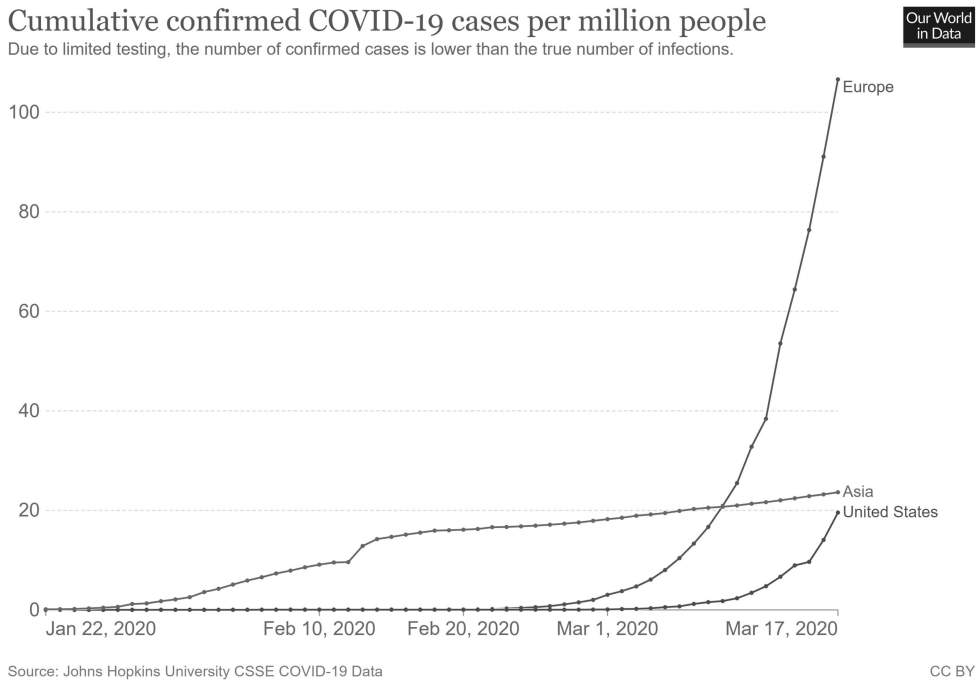


Figure 1: Cumulative cases (Asia, Europe, USA) Jan-March 17, 2020 (Source: OWID)

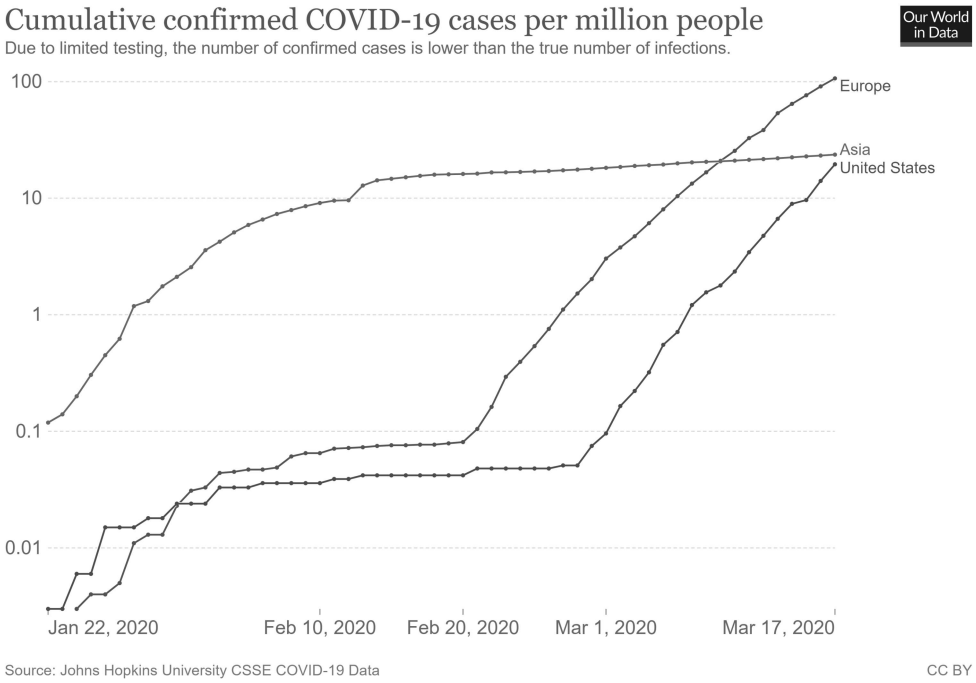


Figure 2: Cumulative cases (Asia, Europe, USA) Jan-March 17, 2020 (Source: OWID)

- [ ] What's wrong with just using such a nice dashboard solution?

From epidemic to pandemic

Load packages

- We load three different packages - for data import (readr), graphics (ggplot2) and table manipulation (dplyr).
- They're contained in the "Tidyverse" package but it's preferable to load them individually.
- [X]

  Why is it better to load packages individually?

```
## Load the readr, ggplot2, and dplyr packages
library(readr)
library(ggplot2)
library(dplyr)
```

- Answer: performance and memory issues aside, packages rely on a limited supply of function names. When different packages use the same name, the function name of the older (less recently installed) package is masked - usually this is the base R function name. This can lead to confusion or error.

Reading data into a data frame using `readr::read_csv`

- We use readr::read_csv to read a (local) CSV file into a data frame
- [X]

  What's a data frame again? Can you define it?

  > "A data frame is … a list of variables of the same number of rows with unique row names, given class "data.frame". If no variables are included, the row names determine the number of rows." (`data.frame` help page)
  >
  > Alternative definition: "A data frame is a table or a two-dimensional array-like structure in which each column contains values of one variable and each row contains one set of values from each column." (tutorialspoint.com)

- [X]

  The command creates a number of substructures

```
## Read datasets/confirmed_cases_worldwide.csv into confirmed_cases_worldwide
confirmed_cases_worldwide <- read_csv("data/covid.csv")

## Try to fix tibble display problems in Emacs + ESS
## Source: https://github.com/emacs-ess/ESS/issues/810
options(crayon.enabled = FALSE)

## Print out confirmed_cases_worldwide
str(confirmed_cases_worldwide)
class(confirmed_cases_worldwide)
```

```
Rows: 169173 Columns: 4
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (2): Entity, Code
dbl  (1): Total confirmed cases of COVID-19
date (1): Day

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
spec_tbl_df [169,173 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
 $ Entity                           : chr [1:169173] "Afghanistan" "Afghanistan" "Afghanis
 $ Code                             : chr [1:169173] "AFG" "AFG" "AFG" "AFG" ...
 $ Day                              : Date[1:169173], format: "2020-02-24" "2020-02-25" ..
 $ Total confirmed cases of COVID-19: num [1:169173] 5 5 5 5 5 5 5 5 5 5 ...
 - attr(*, "spec")=
  .. cols(
  ..   Entity = col_character(),
  ..   Code = col_character(),
  ..   Day = col_date(format = ""),
  ..   `Total confirmed cases of COVID-19` = col_double()
  .. )
 - attr(*, "problems")=<

[1] "spec_tbl_df" "tbl_df"      "tbl"         "data.frame"
```

readr::read_csv

"The goal of readr is to provide a fast and friendly way to read rectangular data from delimited files, such as comma-separated values (CSV) and tab-separated values (TSV). It is designed to parse many types of data found in the wild, while providing an informative problem report when parsing leads to unexpected results. If you are new to readr, the best place to start is the data import chapter in R for Data Science." (online documentation)

- [X] Check the documentation for `read_csv` and its many options.
- [X] Test the claims made in the quote 1 by reading the Pima indians diabetes data set (download via Kaggle).
- [X] Try to extract the ZIP file itself first, then the unzipped CSV file
- [X] After extraction, print the data structure and the first few lines (each block should have three statements).
- [X]

  Read the archive ZIP file first. Do you think it'll work?

```
pima_archive <- read_csv("data/archive.zip")
str(pima)
head(pima_archive)
```

```
Rows: 767 Columns: 9
-- Column specification --------------------------------------------------------
Delimiter: ","
dbl (9): 6, 148, 72, 35, 0, 33.6, 0.627, 50, 1

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
Error in str(pima) : object 'pima' not found
# A tibble: 6 x 9
    `6` `148`  `72`  `35`   `0` `33.6` `0.627`  `50`   `1`
  <
<
<
<
<
 <
  <
<
<dbl>
1     1    85    66    29     0   26.6   0.351    31     0
2     8   183    64     0     0   23.3   0.672    32     1
3     1    89    66    23    94   28.1   0.167    21     0
4     0   137    40    35   168   43.1   2.29     33     1
5     5   116    74     0     0   25.6   0.201    30     0
6     3    78    50    32    88   31     0.248    26     1
```

- [X]

  Next, read the CSV file.

```
pima <- read_csv("data/pima-indians-diabetes.csv")
str(pima)
head(pima)
```

```
Rows: 767 Columns: 9
-- Column specification --------------------------------------------------------
Delimiter: ","
dbl (9): 6, 148, 72, 35, 0, 33.6, 0.627, 50, 1

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
spec_tbl_df [767 x 9] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
 $ 6    : num [1:767] 1 8 1 0 5 3 10 2 8 4 ...
 $ 148  : num [1:767] 85 183 89 137 116 78 115 197 125 110 ...
 $ 72   : num [1:767] 66 64 66 40 74 50 0 70 96 92 ...
 $ 35   : num [1:767] 29 0 23 35 0 32 0 45 0 0 ...
 $ 0    : num [1:767] 0 0 94 168 0 88 0 543 0 0 ...
 $ 33.6 : num [1:767] 26.6 23.3 28.1 43.1 25.6 31 35.3 30.5 0 37.6 ...
 $ 0.627: num [1:767] 0.351 0.672 0.167 2.288 0.201 ...
 $ 50   : num [1:767] 31 32 21 33 30 26 29 53 54 30 ...
 $ 1    : num [1:767] 0 1 0 1 0 1 0 1 1 0 ...
 - attr(*, "spec")=
  .. cols(
  ..   `6` = col_double(),
  ..   `148` = col_double(),
  ..   `72` = col_double(),
  ..   `35` = col_double(),
  ..   `0` = col_double(),
  ..   `33.6` = col_double(),
  ..   `0.627` = col_double(),
  ..   `50` = col_double(),
  ..   `1` = col_double()
  .. )
 - attr(*, "problems")=<

# A tibble: 6 x 9
    `6` `148`  `72`  `35`   `0` `33.6` `0.627`  `50`   `1`
  <
<
<
<
<
 <
  <
<
<dbl>
1     1    85    66    29     0   26.6   0.351    31     0
2     8   183    64     0     0   23.3   0.672    32     1
3     1    89    66    23    94   28.1   0.167    21     0
4     0   137    40    35   168   43.1   2.29     33     1
5     5   116    74     0     0   25.6   0.201    30     0
6     3    78    50    32    88   31     0.248    26     1
```

- [X]

  For comparison, extract the archive and the CSV data using the Base R function `read.csv`.

  Start with the CSV file "pima-indians-diabetes.csv".

```
pima_base <- read.csv("data/pima-indians-diabetes.csv", header=TRUE)
str(pima_base)
head(pima_base)
```

```
'data.frame':   767 obs. of  9 variables:
 $ X6    : int  1 8 1 0 5 3 10 2 8 4 ...
 $ X148  : int  85 183 89 137 116 78 115 197 125 110 ...
 $ X72   : int  66 64 66 40 74 50 0 70 96 92 ...
 $ X35   : int  29 0 23 35 0 32 0 45 0 0 ...
 $ X0    : int  0 0 94 168 0 88 0 543 0 0 ...
 $ X33.6 : num  26.6 23.3 28.1 43.1 25.6 31 35.3 30.5 0 37.6 ...
 $ X0.627: num  0.351 0.672 0.167 2.288 0.201 ...
 $ X50   : int  31 32 21 33 30 26 29 53 54 30 ...
 $ X1    : int  0 1 0 1 0 1 0 1 1 0 ...
  X6 X148 X72 X35  X0 X33.6 X0.627 X50 X1
1  1   85  66  29   0  26.6  0.351  31  0
2  8  183  64   0   0  23.3  0.672  32  1
3  1   89  66  23  94  28.1  0.167  21  0
4  0  137  40  35 168  43.1  2.288  33  1
5  5  116  74   0   0  25.6  0.201  30  0
6  3   78  50  32  88  31.0  0.248  26  1
```

- [ ] There is a mistake in the code block 1. Fix it and run the block again.

- [ ]

  Convince yourself that the Base R function cannot read the ZIP file. I have specified `:results silent`, otherwise Emacs will get confused by spurious characters in the ZIP file - you see the output in the echo area of the mini buffer.

```
pima_base_archive <- read.csv("data/archive.zip")
str(pima_base_archive)
head(pima_base_archive)
```

Reading data into a data frame using Base R's `read.csv`

- [ ]

  We use `read.csv` to read a (local) CSV file into a data frame. The result is formatted much simpler than before.

```
## Read data into cases
cases <- read.csv("data/covid.csv")

## Print out confirmed_cases_worldwide
str(cases)
class(cases)
```

```
'data.frame':   169173 obs. of  4 variables:
 $ Entity                          : chr  "Afghanistan" "Afghanistan" "Afghanistan" "Afgh
 $ Code                            : chr  "AFG" "AFG" "AFG" "AFG" ...
 $ Day                             : chr  "2020-02-24" "2020-02-25" "2020-02-26" "2020-02
 $ Total.confirmed.cases.of.COVID.19: int  5 5 5 5 5 5 5 5 5 5 ...
[1] "data.frame"
```

utils::read.table

The `read.csv` command belongs to the `read.table` family of functions as calling the help function will tell you.

> "Reads a file in table format and creates a data frame from it, with cases corresponding to lines (rows) and variables to fields (columns) in the file."

- Cases or records, and variables or vectors are the corresponding names for the data structure (data frame)
- It is often important to distinguish between data in the real world (usually the result of real observations) and their representation by a machine

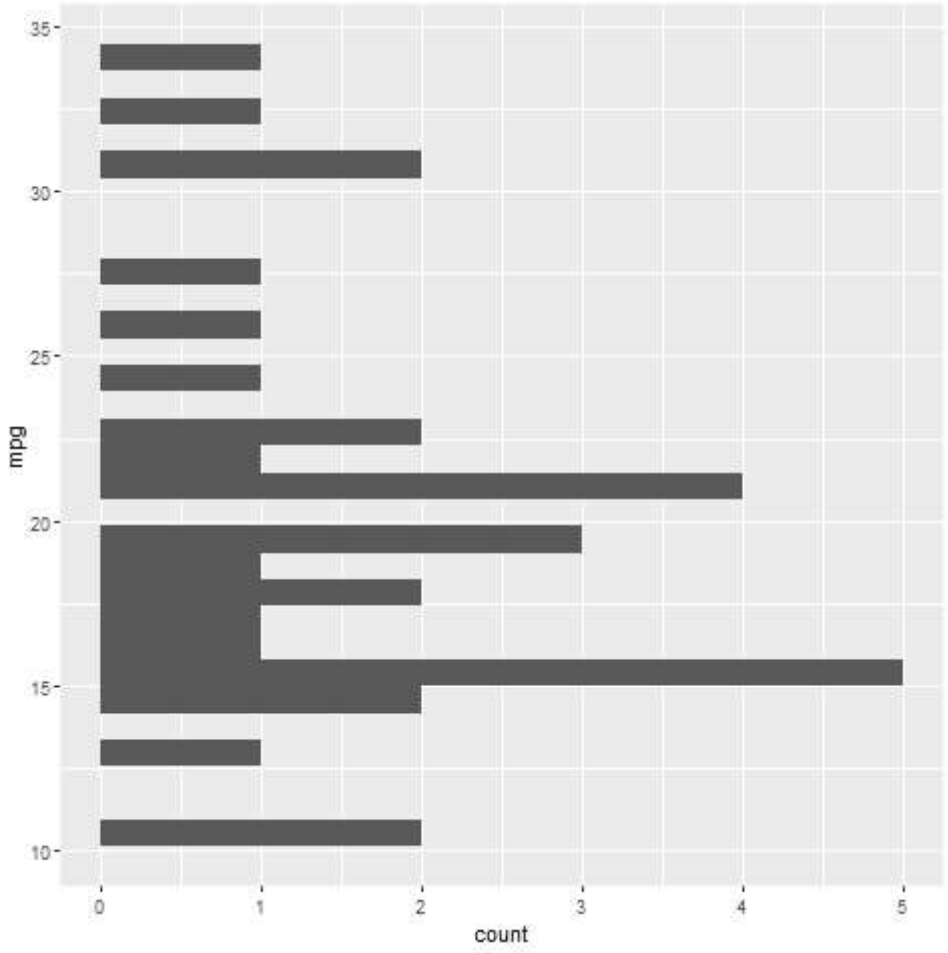
Confirmed cases throughout the world

Basics: data and layout (aes and geom)

- To get this plot from the downloaded data, the `aes` argument has to be adapted accordingly.
- Remember: `aes`[thetics] means data, as in x and y for 2d plots, while `geom`[etry] means layout
- `[ ]` What does ggplot do if only one argument is given to `aes`?
- `[ ]` Answer: Depends on the layout function! `geom_hist` works (counts occurrences), and so does `geom_boxplot`, but `geom_point()` does not.

- Histogram:

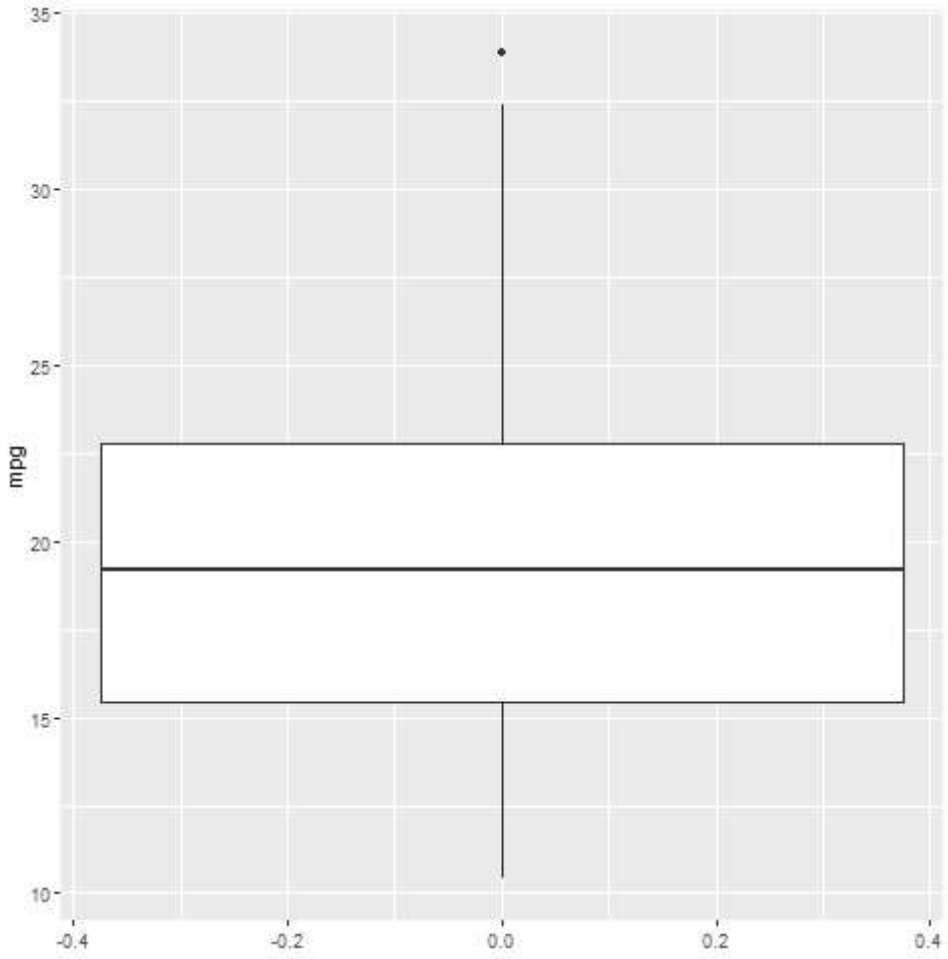
```
ggplot(data=mtcars, aes(y=mpg)) +
  geom_histogram()
```



    - [ ] what is the default binwidth?
    - [ ] Change it to 5. Tip: `binwidth=5` is a layout parameter.
    - [ ] How would you turn the plot by 90 degrees? Do it!
- [ ]

  Boxplot:

```
ggplot(data=mtcars, aes(y=mpg)) +
  geom_boxplot()
```



  Note that the x-axis shows a scale [-0.5,0.5].

    - [ ] To remove the x scale, add a layer `scale_x_discrete()` and run the code again.

Emacs tip

- [ ]

  Emacs info: you can change the HTML and screen layout of a plot with meta data - e.g. `#+attr_html: :width 400px` would restrict the width of the following inline image to 400px.

Try that with the last inline image - set the width to 200px.

To open/close inline images, use the key sequence C-c C-x C-v (or the command M-x org-toggle-inline-images).

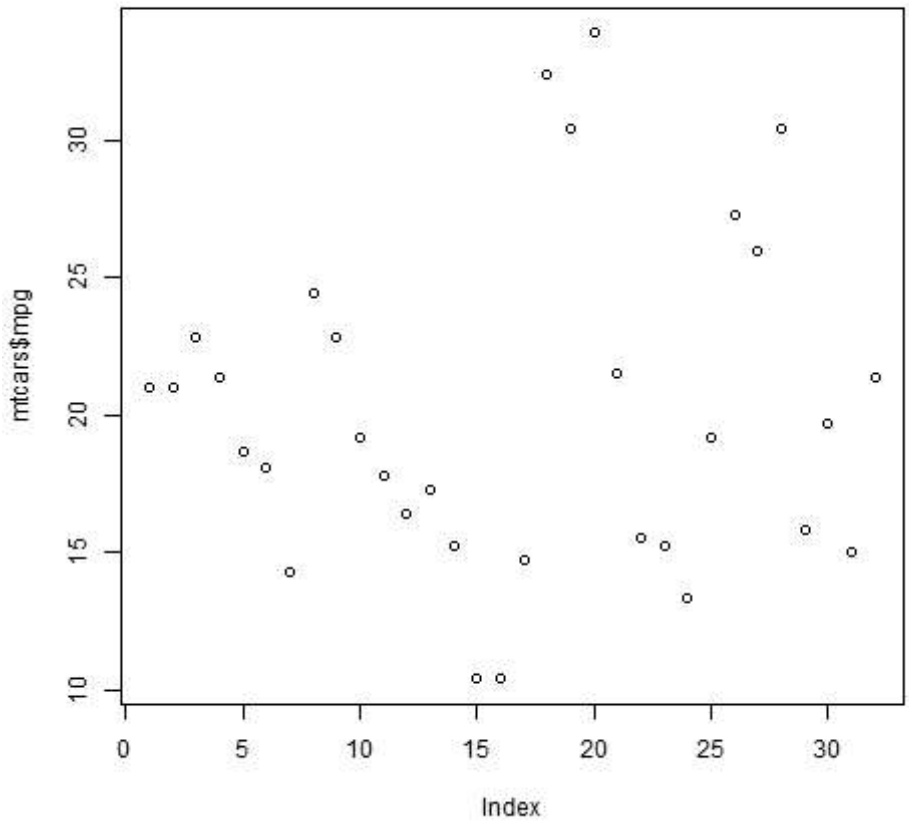
base::plot is generic

- [X]

  Compare this with `base::plot`, which is a generic function capable of adapting to different data structures.

  Scatterplot: plot the variable `mpg` of the data frame `mtcars`.

```
plot(mtcars$mpg)
```



- [X]

  To see which data structures `plot` can digest, call the function `methods(plot)`.

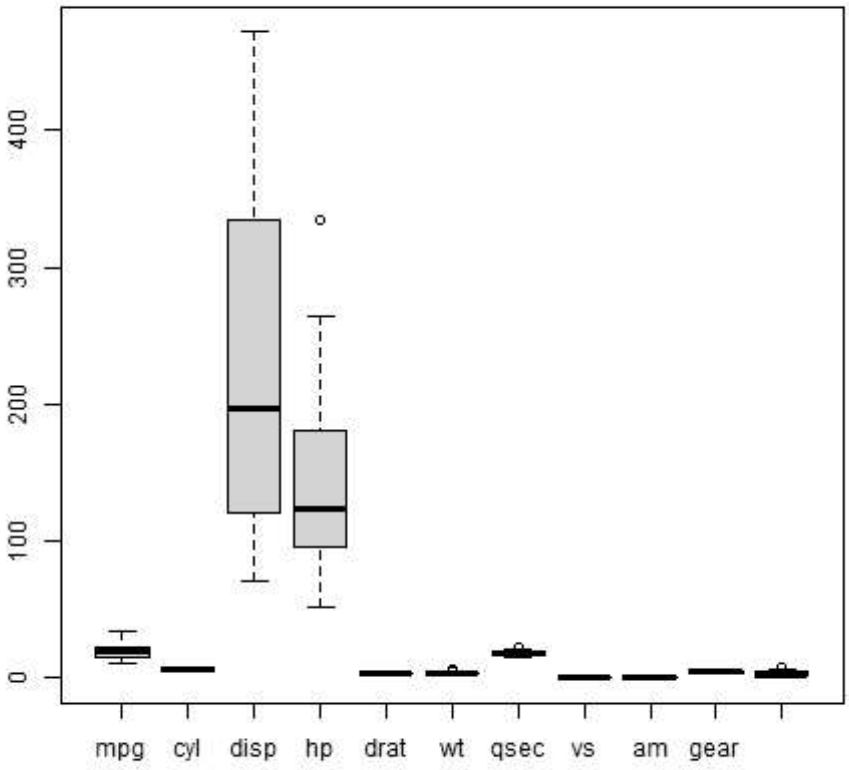
```
methods(plot)
```

```
 [1] plot,ANY-method     plot,color-method   plot.acf*
 [4] plot.data.frame*    plot.decomposed.ts* plot.default
 [7] plot.dendrogram*    plot.density*       plot.ecdf
[10] plot.factor*        plot.formula*       plot.function
[13] plot.ggplot*        plot.gtable*        plot.hcl_palettes*
[16] plot.hclust*        plot.histogram*     plot.HoltWinters*
[19] plot.isoreg*        plot.lm*            plot.medpolish*
[22] plot.mlm*           plot.ppr*           plot.prcomp*
[25] plot.princomp*      plot.profile.nls*   plot.R6*
[28] plot.raster*        plot.spec*          plot.stepfun
[31] plot.stl*           plot.table*         plot.trans*
[34] plot.ts             plot.tskernel*      plot.TukeyHSD*
see '?methods' for accessing help and source code
```

- `[X]`

  The boxplot function will display every available numerical variable. Make a boxplot of `mtcars`.

```
boxplot(mtcars)
```

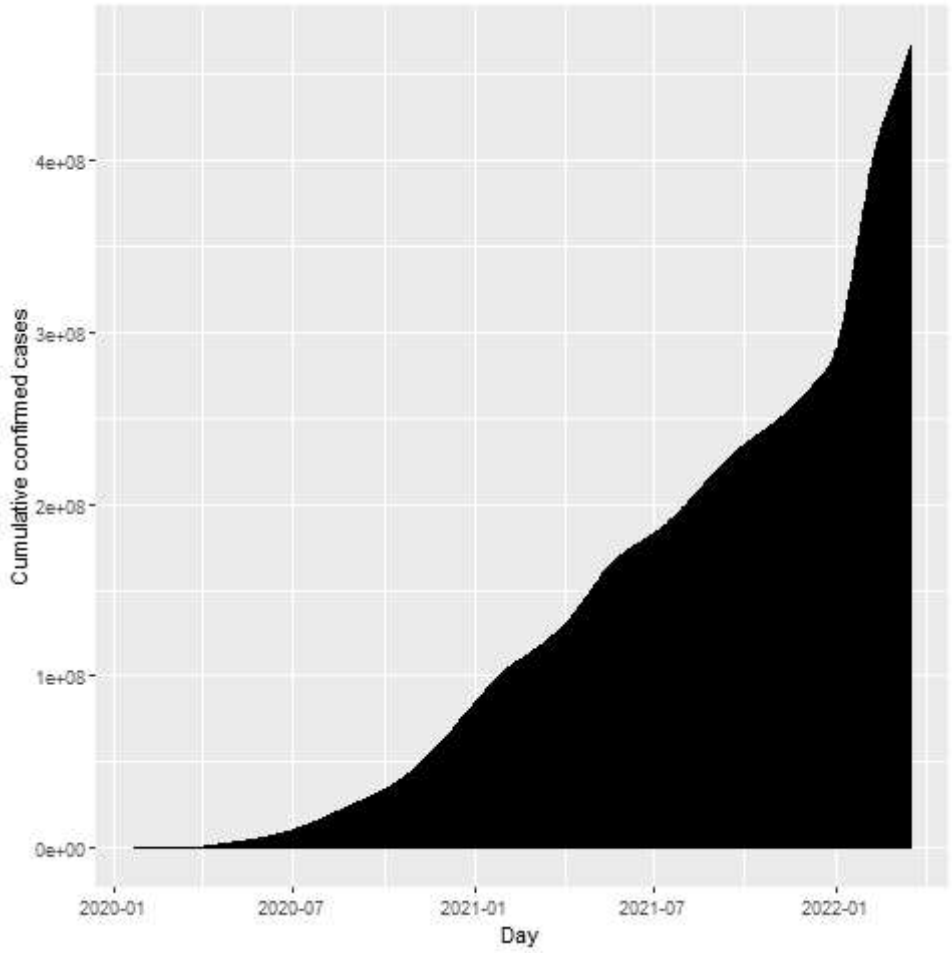


Plotting a line graph straight from the full data set

- [X]

  Let's first run this code in 1 using the full, current data set.

```
## Draw a line plot of cumulative cases vs. date
## Label the y-axis
ggplot(
  confirmed_cases_worldwide,
  aes(x=Day, y=`Total confirmed cases of COVID-19`)) +
  geom_line() +
  ylab("Cumulative confirmed cases")
```



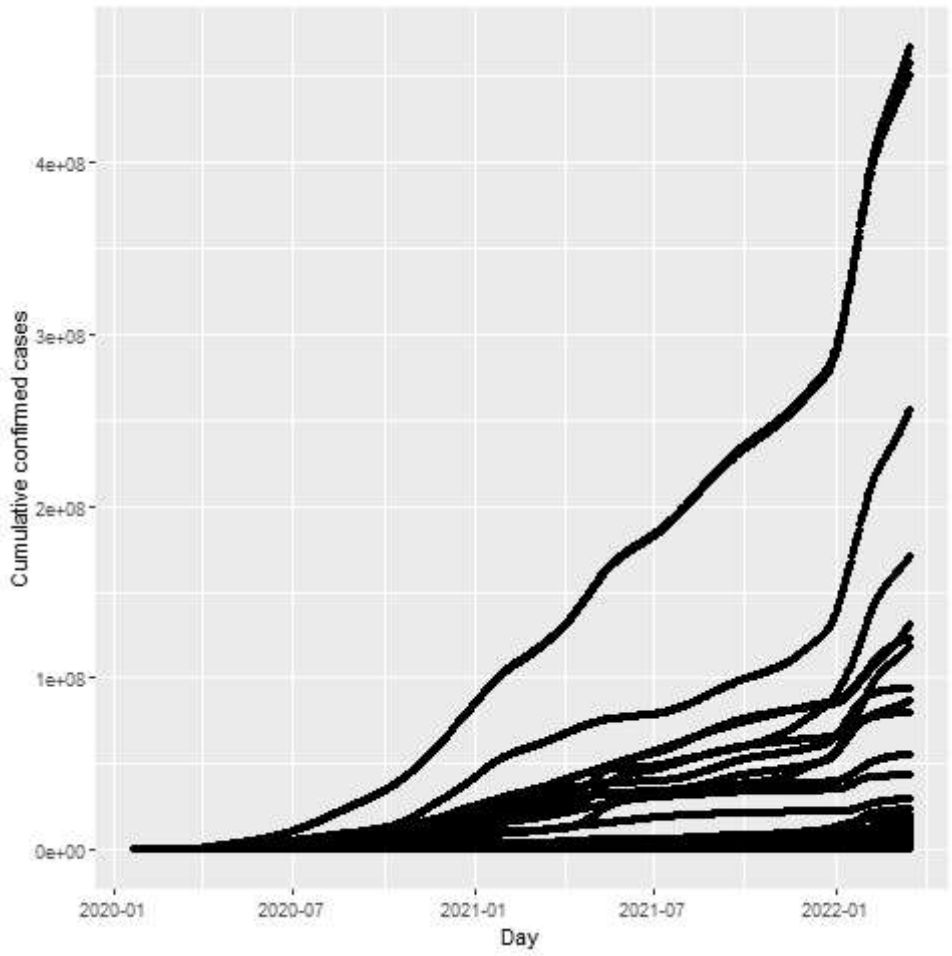
Plot points not lines

- [X]

  If you change `geom_line()` to `geom_point()`, you see the individual lines (for each entity, or country): the cumulative case line is the enveloping line for all of them.

```
## Draw a line plot of cumulative cases vs. date
## Label the y-axis
ggplot(confirmed_cases_worldwide,
```

```
      aes(x=Day,
          y=`Total confirmed cases of COVID-19`))+
  geom_point() +
  ylab("Cumulative confirmed cases")
```



Limit the data set by filtering

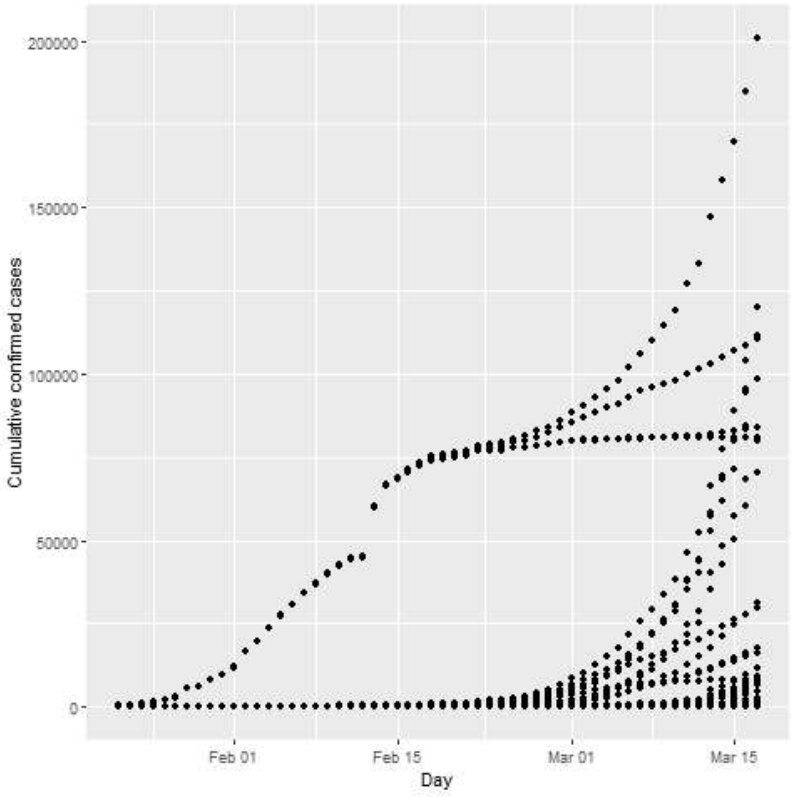
- [X]

  To narrow the data to the day range covered by the DataCamp project, you can use `dplyr::filter` applied to the `Day` variable. This function filters all values for which the argument is `TRUE`.

  - Use `geom_point` for the plot layout.
  - Pipe the data set into `filter()`
  - Filter those records earlier than March 18, 2020

```
## Draw a point plot of cases vs. date
## Label the y-axis
confirmed_cases_worldwide %>%
  filter(Day < "2020-03-18") %>%
  ggplot(
    aes(
      x=Day,
```

```
      y=`Total confirmed cases of COVID-19`)) +
  geom_point() +
  ylab("Cumulative confirmed cases")
```



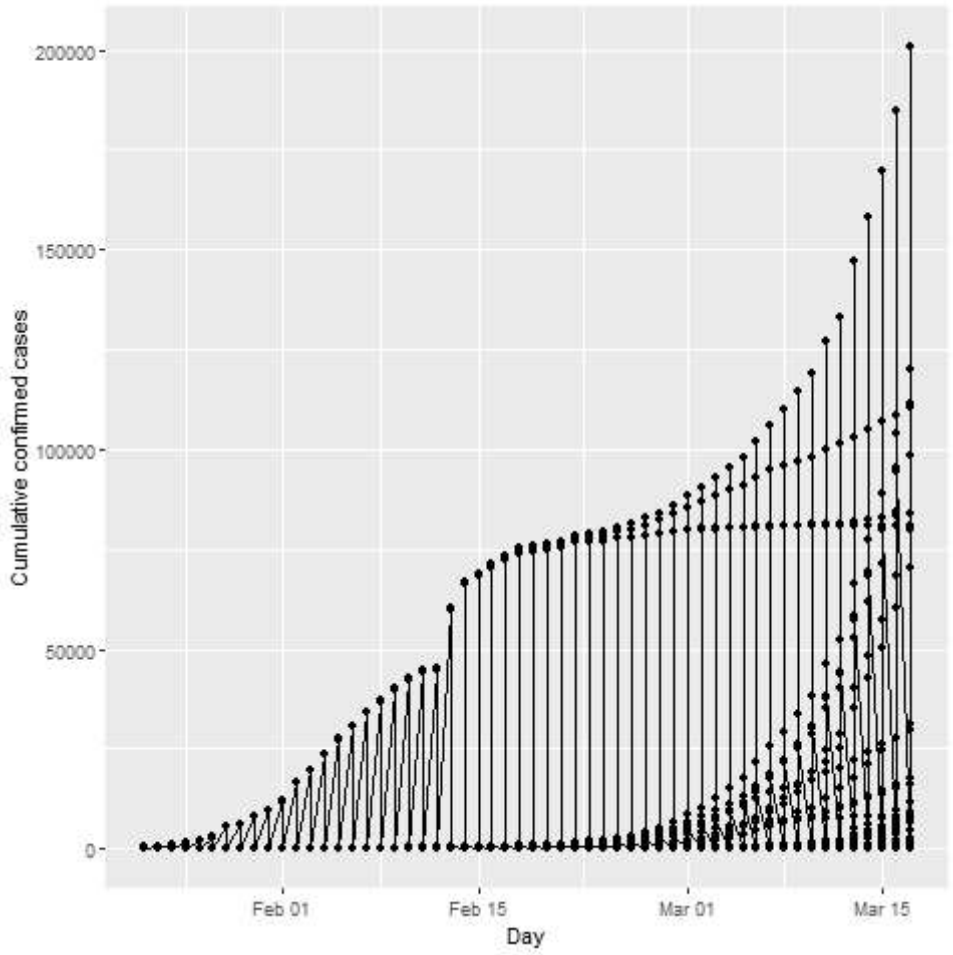
Use both lines and points

- [X]

  Experiment with mixing both point and line layout: use both layouts in the same plot! Remember that layouts are layered.

  Below is the code from above. Alter it accordingly and run it.

```
## Draw a plot of cumulative cases vs. date
## Label the y-axis
confirmed_cases_worldwide %>%
  filter(Day < "2020-03-18") %>%
  ggplot(
    aes(
      x=Day,
      y=`Total confirmed cases of COVID-19`)) +
  geom_line() +
  geom_point() +
  ylab("Cumulative confirmed cases")
```

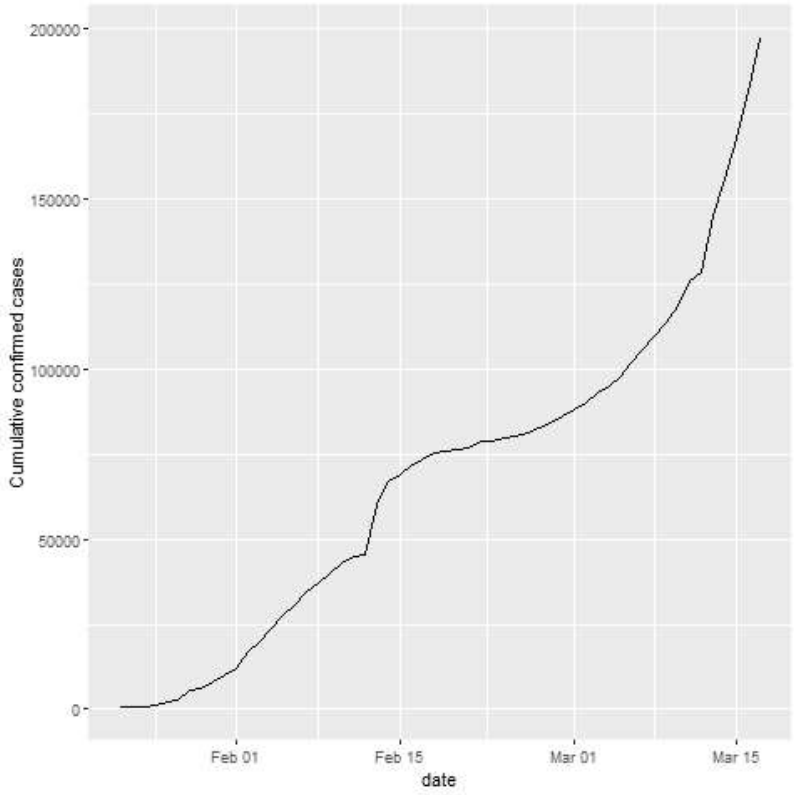


Compare with the DataCamp plot

We're now using the DataCamp data sets.

```
confirmed_cases_worldwide <- read_csv('data/confirmed_cases_worldwide.csv')

## Draw a line plot of cumulative cases vs. date
## Label the y-axis
ggplot(confirmed_cases_worldwide,
       aes(y=cum_cases, x=date)) +
  geom_line() +
  ylab('Cumulative confirmed cases')
```



- [ ] How can you remove the shading under the curve in our plot from the code block 1 above? (Extra credit question!)

Further reading

- ggplot2 line plot : Quick start guide (2018)
- Create a line graph with ggplot (2020)

China compared to the rest of the world

- [X]

  Load data.

```
## Read in datasets/confirmed_cases_china_vs_world.csv
confirmed_cases_china_vs_world <-
  read_csv('data/confirmed_cases_china_vs_world.csv')
```

```
Rows: 112 Columns: 4
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (1): is_china
dbl  (2): cases, cum_cases
date (1): date
```

```
i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Glimpse of the data

- [X]

  What does dplyr::glimpse do?

  Same thing (almost) as `str` but "it tries to show you as much data as possible" (documentation). Run `glimpse` on the data frame `mtcars` and compare with `str`.

```
glimpse(mtcars)
str(mtcars)
```

```
Rows: 32
Columns: 11
$ mpg  <
21.0, 21.0, 22.8, 21.4, 18.7, 18.1, 14.3, 24.4, 22.8, 19.2, 17.8,~
$ cyl  <
6, 6, 4, 6, 8, 6, 8, 4, 4, 6, 6, 8, 8, 8, 8, 8, 8, 4, 4, 4, 4, 8,~
$ disp <
160.0, 160.0, 108.0, 258.0, 360.0, 225.0, 360.0, 146.7, 140.8, 16~
$ hp   <
110, 110, 93, 110, 175, 105, 245, 62, 95, 123, 123, 180, 180, 180~
$ drat <
3.90, 3.90, 3.85, 3.08, 3.15, 2.76, 3.21, 3.69, 3.92, 3.92, 3.92,~
$ wt   <
2.620, 2.875, 2.320, 3.215, 3.440, 3.460, 3.570, 3.190, 3.150, 3.~
$ qsec <
16.46, 17.02, 18.61, 19.44, 17.02, 20.22, 15.84, 20.00, 22.90, 18~
$ vs   <
0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0,~
$ am   <
1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 0,~
$ gear <
4, 4, 4, 3, 3, 3, 3, 4, 4, 4, 4, 3, 3, 3, 3, 3, 3, 4, 4, 4, 3, 3,~
$ carb <
4, 4, 1, 1, 2, 1, 4, 2, 2, 4, 4, 3, 3, 3, 4, 4, 4, 1, 2, 1, 1, 2,~
'data.frame':   32 obs. of  11 variables:
 $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
 $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
 $ disp: num  160 160 108 258 360 ...
 $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
 $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
 $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
 $ qsec: num  16.5 17 18.6 19.4 17 ...
 $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
 $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
 $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
 $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

- [X]

  Glimpse at the Chinese COVID cases. The output is slightly different.

```
glimpse(confirmed_cases_china_vs_world)
```

```
Rows: 112
Columns: 4
$ is_china  <
"China", "China", "China", "China", "China", "China", "China~
$ date      <
2020-01-22, 2020-01-23, 2020-01-24, 2020-01-25, 2020-01-26,~
$ cases     <
548, 95, 277, 486, 669, 802, 2632, 578, 2054, 1661, 2089, 47~
$ cum_cases <
548, 643, 920, 1406, 2075, 2877, 5509, 6087, 8141, 9802, 118~
```

Aesthetics inside a geometry of the plot

- [ ] What's the effect of putting `aes` into the geometry instead of into the `ggplot` call?
- [ ] Answer: The geometry is responsible for the drawing - putting the aes in a geom function means that we only draw on the data specified in the geom function call.

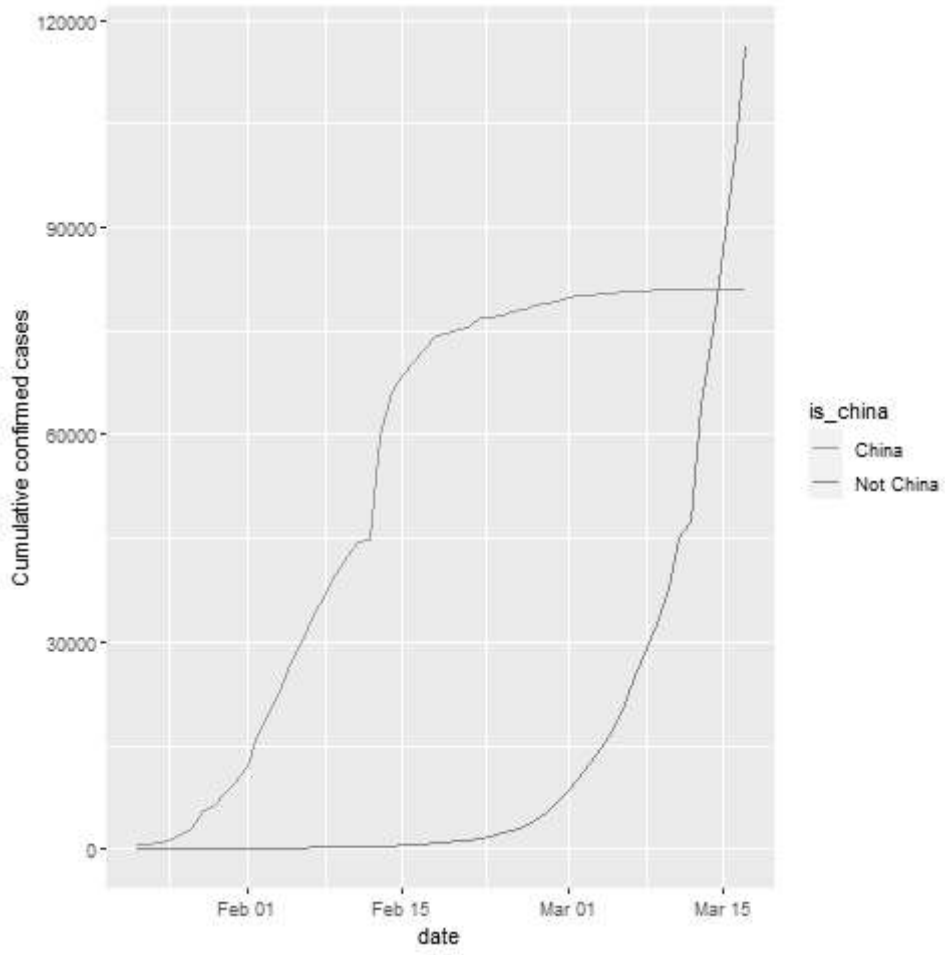
Plot China data

- [ ]

  Line plot of China data and store the plot in an object.

```
## Draw a line plot of cumulative cases vs. date, grouped and colored by is_china
## Define aesthetics within the line geom
plt_cum_confirmed_cases_china_vs_world <-
  ggplot(confirmed_cases_china_vs_world) +
  geom_line(aes(x=date, y=cum_cases, group = is_china, color=is_china)) +
  ylab("Cumulative confirmed cases")

## See the plot
plt_cum_confirmed_cases_china_vs_world
```



- The attribute `group` removes the default grouping and splits the data into Chinese and non-Chinese data (using the variable `$Entity` in the original data frame)
- None of these changes are permanent - they are only valid for the creation of the graphical object (better: save data in a separate data structure)
- The attribute `color` colors both categorical variables of the underlying data set
- `[X]`

  What kind of R object is the plot? Check class and structure.

```
class(plt_cum_confirmed_cases_china_vs_world)
str(plt_cum_confirmed_cases_china_vs_world)
```

```
[1] "gg"     "ggplot"
List of 9
 $ data       : spec_tbl_df [112 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
  ..$ is_china : chr [1:112] "China" "China" "China" "China" ...
  ..$ date     : Date[1:112], format: "2020-01-22" "2020-01-23" ...
  ..$ cases    : num [1:112] 548 95 277 486 669 ...
  ..$ cum_cases: num [1:112] 548 643 920 1406 2075 ...
  ..- attr(*, "spec")=
  .. .. cols(
  .. ..   is_china = col_character(),
  .. ..   date = col_date(format = ""),
```

```
  .. ..   cases = col_double(),
  .. ..   cum_cases = col_double()
  .. .. )
  ..- attr(*, "problems")=<

 $ layers     :List of 1
  ..$ :Classes 'LayerInstance', 'Layer', 'ggproto', 'gg' <ggproto object: Class LayerInsta
    aes_params: list
    compute_aesthetics: function
    compute_geom_1: function
    compute_geom_2: function
    compute_position: function
    compute_statistic: function
    computed_geom_params: list
    computed_mapping: uneval
    computed_stat_params: list
    data: waiver
    draw_geom: function
    finish_statistics: function
    geom: <ggproto object: Class GeomLine, GeomPath, Geom, gg>
        aesthetics: function
        default_aes: uneval
        draw_group: function
        draw_key: function
        draw_layer: function
        draw_panel: function
        extra_params: na.rm orientation
        handle_na: function
        non_missing_aes:
        optional_aes:
        parameters: function
        required_aes: x y
        setup_data: function
        setup_params: function
        use_defaults: function
        super:  <ggproto object: Class GeomPath, Geom, gg>
    geom_params: list
    inherit.aes: TRUE
    layer_data: function
    map_statistic: function
    mapping: uneval
    position: <ggproto object: Class PositionIdentity, Position, gg>
        compute_layer: function
        compute_panel: function
        required_aes:
        setup_data: function
        setup_params: function
        super:  <ggproto object: Class Position, gg>
    print: function
    setup_layer: function
    show.legend: NA
    stat: <ggproto object: Class StatIdentity, Stat, gg>
        aesthetics: function
        compute_group: function
        compute_layer: function
        compute_panel: function
        default_aes: uneval
        extra_params: na.rm
        finish_layer: function
        non_missing_aes:
        optional_aes:
        parameters: function
        required_aes:
        retransform: TRUE
        setup_data: function
        setup_params: function
```

```
        setup_params: function
        super:  <ggproto object: Class Stat, gg>
    stat_params: list
    super:  <ggproto object: Class Layer,

$ scales     :Classes 'ScalesList', 'ggproto', 'gg' <ggproto object: Class ScalesList, gg
    add: function
    clone: function
    find: function
    get_scales: function
    has_scale: function
    input: function
    n: function
    non_position_scales: function
    scales: list
    super:  <ggproto object: Class ScalesList,

$ mapping    : Named list()
 ..- attr(*, "class")= chr "uneval"
$ theme      : list()
$ coordinates:Classes 'CoordCartesian', 'Coord', 'ggproto', 'gg' <ggproto object: Class C
    aspect: function
    backtransform_range: function
    clip: on
    default: TRUE
    distance: function
    expand: TRUE
    is_free: function
    is_linear: function
    labels: function
    limits: list
    modify_scales: function
    range: function
    render_axis_h: function
    render_axis_v: function
    render_bg: function
    render_fg: function
    setup_data: function
    setup_layout: function
    setup_panel_guides: function
    setup_panel_params: function
    setup_params: function
    train_panel_guides: function
    transform: function
    super:  <ggproto object: Class CoordCartesian, Coord,

$ facet      :Classes 'FacetNull', 'Facet', 'ggproto', 'gg' <ggproto object: Class FacetN
    compute_layout: function
    draw_back: function
    draw_front: function
    draw_labels: function
    draw_panels: function
    finish_data: function
    init_scales: function
    map_data: function
    params: list
    setup_data: function
    setup_params: function
    shrink: TRUE
    train_scales: function
    vars: function
    super:  <ggproto object: Class FacetNull, Facet,

$ plot_env   :<environment: R_

$ labels     :List of 4
```

```
 $ labels    :List of 4
  ..$ y     : chr "Cumulative confirmed cases"
  ..$ x     : chr "date"
  ..$ group : chr "is_china"
  ..$ colour: chr "is_china"
 - attr(*, "class")= chr [1:2] "gg" "ggplot"
```

Let's annotate!

- You've already seen annotation in the test data analysis when we drew vertical lines for the average values.
- We want to annotate by drawing vertical lines over dates and giving them text labels.

Date and text data frame

- [X]

  who_events is a data frame with two variables. Create this data frame using these data - not as a "tribble" but using the Base R tools that you already know. Call it df.

```
"2020-01-30" "Global health\nemergency declared"
"2020-03-11" "Pandemic\ndeclared"
"2020-02-13" "China reporting\nchange"
```

```
df <- data.frame(
  date = c("2020-01-30",
           "2020-03-11",
           "2020-02-13"),
  event = c("Global health\nemergency declared",
            "Pandemic\ndeclared",
            "China reporting\nchange"))
df
```

```
        date                              event
1 2020-01-30 Global health\nemergency declared
2 2020-03-11                Pandemic\ndeclared
3 2020-02-13           China reporting\nchange
```

- The functions geom_vline and geom_text are drawn using the data frame and their own attributes. The Base R equivalents are abline (drawing a line from a to b, horizontally or vertically), and text.

DataCamp plot

- The DataCamp example uses a data frame formatted as a "tribble" and created with the tribble function instead of data.frame.
- The dplyr::mutate function attaches a new variable date to the data frame.

```
who_events <- tribble(
  ~ date, ~ event,
  "2020-01-30", "Global health\nemergency declared",
  "2020-03-11", "Pandemic\ndeclared",
  "2020-02-13", "China reporting\nchange"
```

```
) %>%
  mutate(date = as.Date(date))
who_events
```

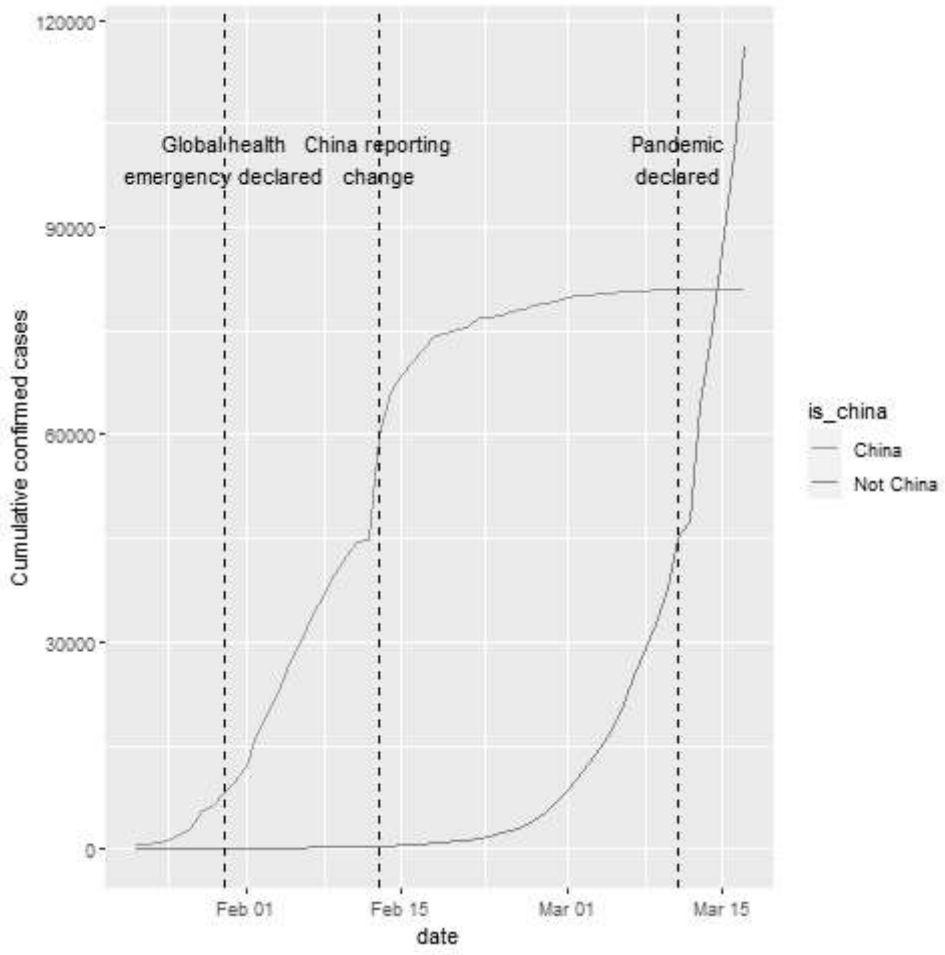
```
# A tibble: 3 x 2
  date       event
  <
    <

1 2020-01-30 "Global health\nemergency declared"
2 2020-03-11 "Pandemic\ndeclared"
3 2020-02-13 "China reporting\nchange"
```

- [X]

  Annotate the stored plot. I have broken the lines differently than DataCamp to clarify the layers and arguments within each layer.

```
## Using who_events, add vertical dashed lines with an xintercept at date
## and text at date, labeled by event, and at 100000 on the y-axis
plt_cum_confirmed_cases_china_vs_world +
  geom_vline(
    data=who_events,
    aes(xintercept=date),
    linetype="dashed") +
  geom_text(
    data = who_events,
    aes(x=date, label=event),
    y=1e5)
```



Adding a trend line to China

- You can use dplyr::filter to filter data set lines / rows that fulfil a set of logical conditions.

```
## Filter for China, from Feb 15
china_after_feb15 <- confirmed_cases_china_vs_world %>%
  filter(is_china == "China" & date >= '2020-02-15')
```

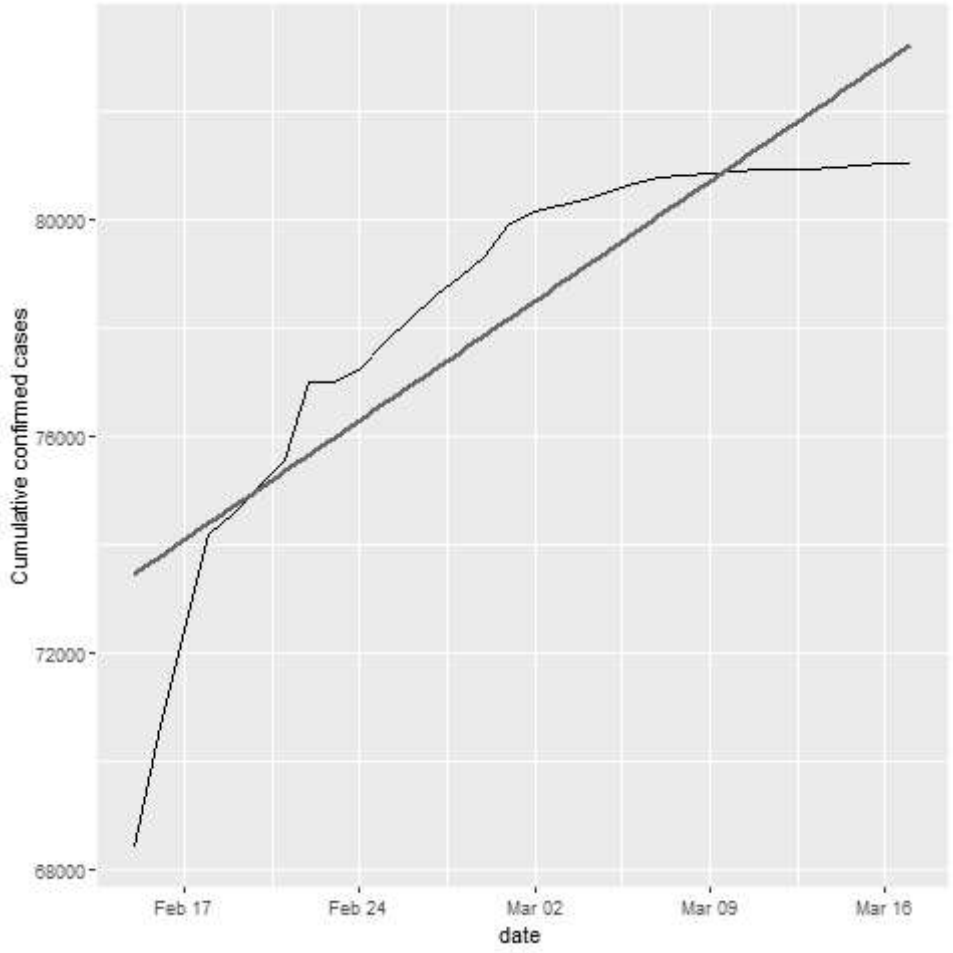
- `geom_smooth` implements a linear model.

  > "Calculation is performed by the (currently undocumented) `predictdf` generic and its methods. For most methods the standard error bounds are computed using the `predict()` method - the exceptions are `loess` which uses a t-based approximation, and `glm` where the normal confidence interval is constructed on the link scale, and then back-transformed to the response scale." (ggplot2 doc)

- `[X]` what does the attribute `se=FALSE` mean? (Answer: see doc)
- For more information and a demo, see `??predict` and run the `glm()` demo with examples.
- Better: separate modeling and creation of pretty plots. Understand functions like `glm()` before blindly applying them (needlessly, in this case - the linear modeling adds nothing to the plot).

- Trend plot with `lm`

```
## Using china_after_feb15, draw a line plot cum_cases vs. date
## Add a smooth trend line using linear regression, no error bars
ggplot(china_after_feb15, aes(x=date, y=cum_cases)) +
  geom_line() +
  geom_smooth(method='lm', se=FALSE) +
  ylab("Cumulative confirmed cases")
```



And the rest of the world?

- `[X]`

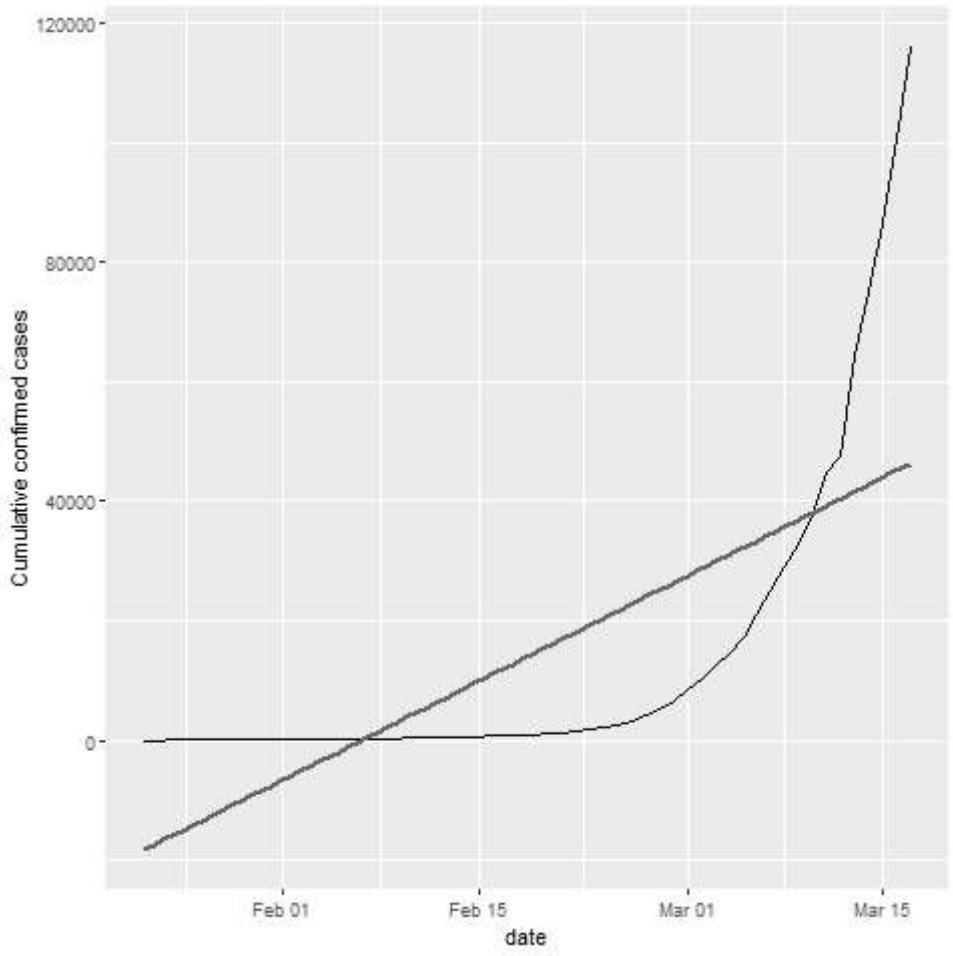
  Same thing for the rest of the world.

```
## Filter confirmed_cases_china_vs_world for not China
not_china <- confirmed_cases_china_vs_world %>%
  filter(is_china == 'Not China')

## Using not_china, draw a line plot cum_cases vs. date
                                        # Add a smooth trend line using linear regression,
plt_not_china_trend_lin <- ggplot(not_china, aes(x=date, y=cum_cases)) +
```

```
  geom_line() +
  geom_smooth(method='lm', se=FALSE) +
  ylab("Cumulative confirmed cases")

## See the result
plt_not_china_trend_lin
```

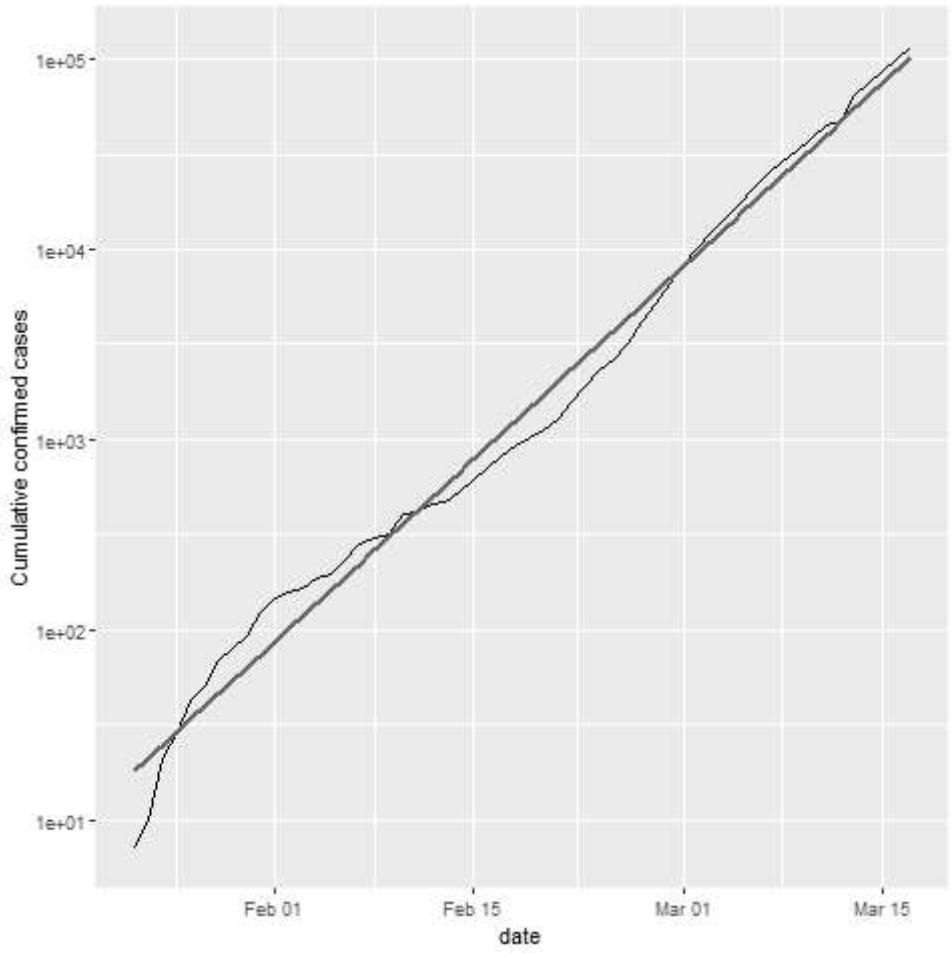


Adding a logarithmic scale

- [ ] What does the image suggest to not data-literate viewers?
- [ ] What does it mean "we get a much closer fit of the data?"
- [ ]

What do you think of the graph (in terms of communication)?

```
## Modify the plot to use a logarithmic scale on the y-axis
plt_not_china_trend_lin +
  scale_y_log10()
```



Which countries outside of China have been hit hardest?

- New input data.

```
## Run this to get the data for each country
confirmed_cases_by_country <-
  read_csv("data/confirmed_cases_by_country.csv")
```

- Glimpse at the data

```
glimpse(confirmed_cases_by_country)
```

```
Rows: 13272 Columns: 5
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (2): country, province
dbl  (2): cases, cum_cases
date (1): date

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
Rows: 13,272
Columns: 5
$ country   <
"Afghanistan", "Albania", "Algeria", "Andorra", "Antigua and~
$ province  <
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ date      <
2020-01-22, 2020-01-22, 2020-01-22, 2020-01-22, 2020-01-22,~
$ cases     <
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ cum_cases <
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
```

- [ ] What does dplyr:group_by do?
- [ ]

  What does dplyr::summarize do?

```
## Group by country, summarize to calculate total cases, find the top 7
top_countries_by_total_cases <- confirmed_cases_by_country %>%
  group_by(country) %>%
  summarize(total_cases = max(cum_cases)) %>%
  top_n(7)

## See the result
top_countries_by_total_cases
```

```
Selecting by total_cases
# A tibble: 7 x 2
  country      total_cases
  <
            <dbl>
1 France              7699
2 Germany             9257
3 Iran               16169
4 Italy              31506
5 Korea, South        8320
6 Spain              11748
7 US                  6421
```

Plotting hardest hit countries as of Mid-March 2020

- [ ] Why do we move the aesthetic mapping back into the main function?
- New input data.

```
## Run this to get the data for the top 7 countries
confirmed_cases_top7_outside_china <-
  read_csv('data/confirmed_cases_top7_outside_china.csv')
```

- Glimpse.

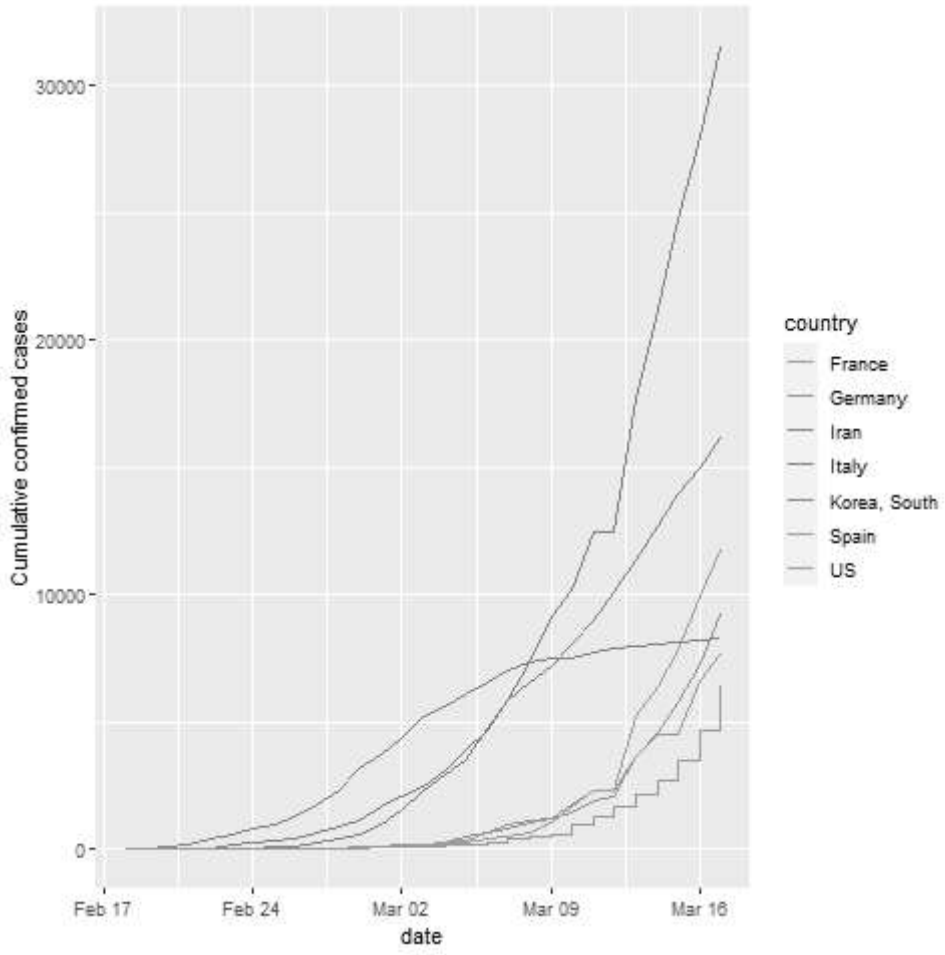
```
glimpse(confirmed_cases_top7_outside_china)
```

```
Rows: 2030 Columns: 3
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (1): country
dbl  (1): cum_cases
date (1): date

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
Rows: 2,030
Columns: 3
$ country   <
"Germany", "Iran", "Italy", "Korea, South", "Spain", "US", "~
$ date      <
2020-02-18, 2020-02-18, 2020-02-18, 2020-02-18, 2020-02-18,~
$ cum_cases <
16, 0, 3, 31, 2, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13,~
```

- Plot

```
## Using confirmed_cases_top7_outside_china, draw a line plot of
## cum_cases vs. date, grouped and colored by country
ggplot(confirmed_cases_top7_outside_china, aes(x=date, y=cum_cases, group=country, color=c
  geom_line()+
  ylab('Cumulative confirmed cases')
```



References

- Wickham H, Hester J, Bryan J (2022). readr: Read Rectangular Text Data. https://readr.tidyverse.org, https://github.com/tidyverse/readr.
- R Core Team (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.r-project.org/.

Author: DataCamp Covid-19 Project / M Birkenkrahe

Created: 2022-03-30 Wed 18:50

Validate