tidyverse overview

Andrew Ghazi

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While we wait…

1. Install R from cran.r-project.org
2. Install Rstudio from rstudio.com
3. Install the tidyverse with this R command: `install.packages("tidyverse")`
4. If you'd like to follow along, get the slides (.html) and/or code (.R): github.com/andrewGhazi/tidy_overview

What is the tidyverse?

- A dialect of R
- A collection of R packages with a shared design philosophy

- Install it with this R command:
  `install.packages("tidyverse")`

Why use the tidyverse?

- Shared design philosophy → inter-package consistency
- Focused on data science and statistical analysis
- Easy to learn, write, and read
- It's ubiquitous

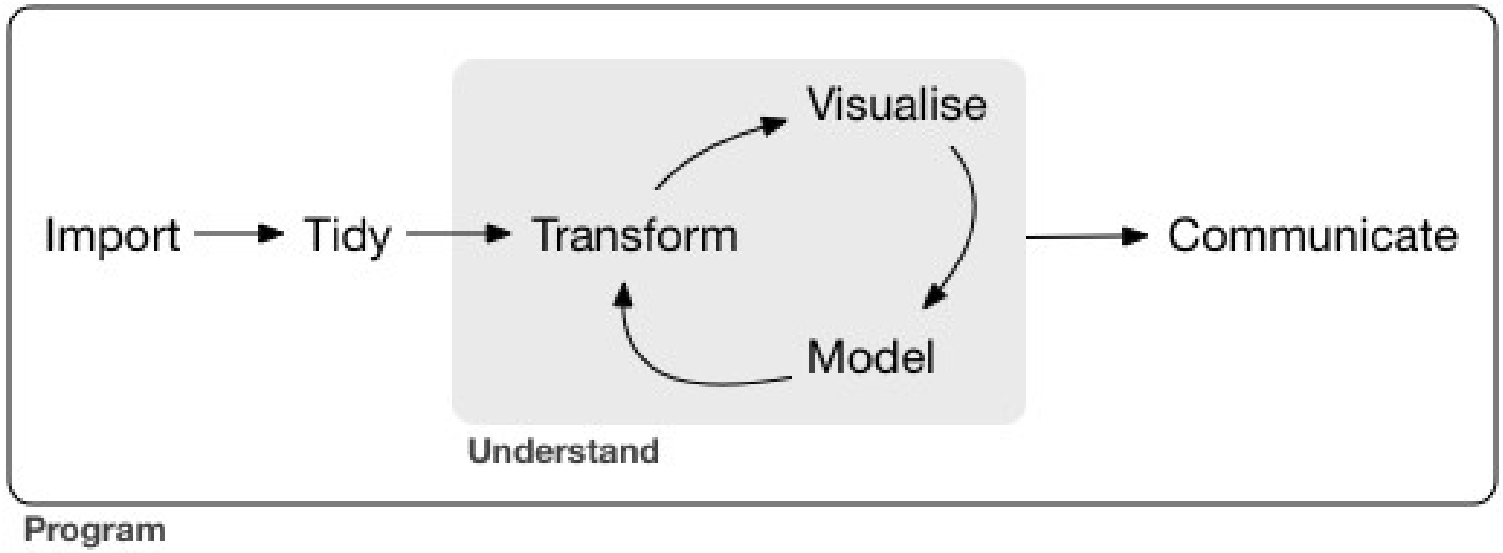


Diagram from R for Data Science by Wickham et al.

Outline

- Core concepts
- Package overview
- End-to-end example
- Questions

How to read these slides

- Lecture notes show up like this.

```
print("Console output has two pound symbols in front.")
```

```
## [1] "Console output has two pound symbols in front."
```

```
x = 5
```

- Assignment prints nothing.
- `package::function()` e.g. `dplyr::filter()`

Load the tidyverse

The startup message lists loaded packages and overwritten functions.

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.1.0     v dplyr   1.0.3
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
```

```
## Warning: package 'tibble' was built under R version 4.0.4
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

Core concepts

Data frames

- Used to store ordered collections of variables

```
diabetes
```

```
## # A tibble: 532 x 8
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     5    86    68    28  30.2 0.364    24 No
##  2     7   195    70    33  25.1 0.163    55 Yes
##  3     5    77    82    41  35.8 0.156    35 No
##  4     0   165    76    43  47.9 0.259    26 No
##  5     0   107    60    25  26.4 0.133    23 No
##  6     5    97    76    27  35.6 0.378    52 Yes
##  7     3    83    58    31  34.3 0.336    25 No
##  8     1   193    50    16  25.9 0.655    24 No
##  9     3   142    80    15  32.4 0.2      63 No
## 10     2   128    78    37  43.3 1.22     31 Yes
## # ... with 522 more rows
```

tidy data

- Columns are variables
- Rows are observations

```
## # A tibble: 532 x 8
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     5    86    68    28  30.2 0.364    24 No
##  2     7   195    70    33  25.1 0.163    55 Yes
##  3     5    77    82    41  35.8 0.156    35 No
##  4     0   165    76    43  47.9 0.259    26 No
##  5     0   107    60    25  26.4 0.133    23 No
##  6     5    97    76    27  35.6 0.378    52 Yes
##  7     3    83    58    31  34.3 0.336    25 No
##  8     1   193    50    16  25.9 0.655    24 No
##  9     3   142    80    15  32.4 0.2      63 No
## 10     2   128    78    37  43.3 1.22     31 Yes
## # ... with 522 more rows
```

tidyverse functions

- data frame in, data frame out
- Function names are *verbs*
  - e.g. `filter`, `arrange`, `mutate`

Pipes

- Pipes look like this: `%>%`
- They take the input from the left side, and hand it to the right side:

```
c(1,2,3,4) %>% mean
```

```
## [1] 2.5
```

- Verbalize as: “and then”.
- “Create this vector and then take the mean”.

Pipe example

Why are pipes useful?

Pipe example

Why are pipes useful?

Pipe example

Why are pipes useful?

Pipe example

Compare two ways of doing the same thing:

```
input = "potatoes"

stick(mash(boil(input)), where = 'stew')
```

```
## [1] "stewed, mashed, boiled potatoes"
```

Pipe example

Compare two ways of doing the same thing:

```
input = "potatoes"
```

```
stick(mash(boil(input)), where = 'stew')
```

```
## [1] "stewed, mashed, boiled potatoes"
```

```
input %>% boil() %>% mash() %>% stick(where = 'stew')
```

```
## [1] "stewed, mashed, boiled potatoes"
```

Pipe example

Why are pipes useful?

Because chained verbs look like English sentences.

```
input %>%
  boil() %>%
  mash() %>%
  stick(where = 'stew')
```

- Piped code is easier to write *and easier to read*.
- Keyboard shortcut: `ctrl + shift + M`

package overview

Import - `readr`

- Get the data into R as a data frame.
- Read data from a file on your computer or from a URL
- `read_csv()`, `read_tsv()`
- related package: `readxl`
- Read in the diabetes example dataset:

```
data_path = "data/diabetes.tsv"
diabetes = read_tsv(data_path)
```

Manipulate - `dplyr`

- Package for basic data manipulation
- Most important functions:
  `filter()`, `select()`, `arrange()`, `mutate()`, `group_by()`, `summarise()`
- Focused on data frames

dplyr::filter()

- Subset rows by a condition

```
diabetes %>%
  filter(npreg == 0)
```

```
## # A tibble: 77 x 8
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     0   165    76    43  47.9 0.259    26 No
##  2     0   107    60    25  26.4 0.133    23 No
##  3     0   137    40    35  43.1 2.29     33 Yes
##  4     0   139    62    17  22.1 0.207    21 No
##  5     0   101    64    17  21   0.252    21 No
##  6     0   140    65    26  42.6 0.431    24 Yes
##  7     0   121    66    30  34.3 0.203    33 Yes
##  8     0   102    86    17  29.3 0.695    27 No
##  9     0   119    66    27  38.8 0.259    22 No
## 10     0    86    68    32  35.8 0.238    25 No
## # ... with 67 more rows
```

dplyr::filter()

- Subset rows by a condition

```
diabetes %>%
  filter(bmi > 30)
```

```
## # A tibble: 342 x 8
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     5    86    68    28  30.2 0.364    24 No
##  2     5    77    82    41  35.8 0.156    35 No
##  3     0   165    76    43  47.9 0.259    26 No
##  4     5    97    76    27  35.6 0.378    52 Yes
##  5     3    83    58    31  34.3 0.336    25 No
##  6     3   142    80    15  32.4 0.2      63 No
##  7     2   128    78    37  43.3 1.22     31 Yes
##  8     0   137    40    35  43.1 2.29     33 Yes
##  9     9   154    78    30  30.9 0.164    45 No
## 10     1   189    60    23  30.1 0.398    59 Yes
## # ... with 332 more rows
```

dplyr::select()

- Subset columns
- Choose columns by name, index, or condition

```
diabetes %>%
  select(diabetic, npreg, age)
```

```
## # A tibble: 532 x 3
##    diabetic npreg   age
##    <chr>    <dbl> <dbl>
##  1 No           5    24
##  2 Yes          7    55
##  3 No           5    35
##  4 No           0    26
##  5 No           0    23
##  6 Yes          5    52
##  7 No           3    25
##  8 No           1    24
##  9 No           3    63
## 10 Yes          2    31
## # ... with 522 more rows
```

dplyr::select()

- Subset columns
- Choose columns by name, index, or condition

```
diabetes %>%
  select(8, 1, 7)
```

```
## # A tibble: 532 x 3
##    diabetic npreg   age
##    <chr>    <dbl> <dbl>
##  1 No           5    24
##  2 Yes          7    55
##  3 No           5    35
##  4 No           0    26
##  5 No           0    23
##  6 Yes          5    52
##  7 No           3    25
##  8 No           1    24
##  9 No           3    63
## 10 Yes          2    31
## # ... with 522 more rows
```

dplyr::select()

- Subset columns
- Choose columns by name, index, or condition

```
diabetes %>%
  select(starts_with('b'), matches('diab'))
```

```
## # A tibble: 532 x 3
##       bp   bmi diabetic
##    <dbl> <dbl> <chr>
##  1    68  30.2 No
##  2    70  25.1 Yes
##  3    82  35.8 No
##  4    76  47.9 No
##  5    60  26.4 No
##  6    76  35.6 Yes
##  7    58  34.3 No
##  8    50  25.9 No
##  9    80  32.4 No
## 10    78  43.3 Yes
## # ... with 522 more rows
```

dplyr::arrange()

- Reorder rows by a variable

```
diabetes %>% arrange(bmi)
```

```
## # A tibble: 532 x 8
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     1    97    64    19  18.2 0.299    21 No
##  2     1    97    70    15  18.2 0.147    21 No
##  3     3    99    80    11  19.3 0.284    30 No
##  4     1   103    80    11  19.4 0.491    22 No
##  5     1    92    62    25  19.5 0.482    25 No
##  6     1   100    74    12  19.5 0.149    28 No
##  7     1    95    66    13  19.6 0.334    25 No
##  8     6   129    90     7  19.6 0.582    60 No
##  9     0   105    68    22  20   0.236    22 No
## 10     2    68    62    13  20.1 0.257    23 No
## # ... with 522 more rows
```

dplyr::arrange()

- Reorder rows by a variable

```
diabetes %>% arrange(desc(age))
```

```
## # A tibble: 532 x 8
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     9   134    74    33  25.9 0.46     81 No
##  2     4   145    82    18  32.5 0.235    70 Yes
##  3     5   103   108    37  39.2 0.305    65 No
##  4     3   142    80    15  32.4 0.2      63 No
##  5     4   132    86    31  28   0.419    63 No
##  6    10   101    76    48  32.9 0.171    63 No
##  7    12   121    78    17  26.5 0.259    62 No
##  8     2   197    70    99  34.7 0.575    62 Yes
##  9     7   142    60    33  28.8 0.687    61 No
## 10     8   181    68    36  30.1 0.615    60 Yes
## # ... with 522 more rows
```

Quiz: What's the highest blood pressure observed in this data? (hint: desc())

`dplyr::mutate()`

- Add new columns
- Structure:

```
input_df %>%
  mutate(col_name = col_values)
```

dplyr::mutate()

- Add new columns
- Example: add an index

```
diabetes %>%
  mutate(index = 1:532)
```

```
## # A tibble: 532 x 9
##    npreg   glu    bp  skin   bmi   ped   age diabetic index
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>    <int>
##  1     5    86    68    28  30.2 0.364    24 No           1
##  2     7   195    70    33  25.1 0.163    55 Yes          2
##  3     5    77    82    41  35.8 0.156    35 No           3
##  4     0   165    76    43  47.9 0.259    26 No           4
##  5     0   107    60    25  26.4 0.133    23 No           5
##  6     5    97    76    27  35.6 0.378    52 Yes          6
##  7     3    83    58    31  34.3 0.336    25 No           7
##  8     1   193    50    16  25.9 0.655    24 No           8
##  9     3   142    80    15  32.4 0.2      63 No           9
## 10     2   128    78    37  43.3 1.22     31 Yes         10
## # ... with 522 more rows
```

dplyr::mutate()

- Refer to other columns by name
- Example: Calculate birth year as a function of age

```
diabetes %>%
  mutate(birth_year = 2021 - age)
```

```
## # A tibble: 532 x 9
##    npreg   glu    bp  skin   bmi   ped   age diabetic birth_year
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>         <dbl>
##  1     5    86    68    28  30.2 0.364    24 No             1997
##  2     7   195    70    33  25.1 0.163    55 Yes            1966
##  3     5    77    82    41  35.8 0.156    35 No             1986
##  4     0   165    76    43  47.9 0.259    26 No             1995
##  5     0   107    60    25  26.4 0.133    23 No             1998
##  6     5    97    76    27  35.6 0.378    52 Yes            1969
##  7     3    83    58    31  34.3 0.336    25 No             1996
##  8     1   193    50    16  25.9 0.655    24 No             1997
##  9     3   142    80    15  32.4 0.2      63 No             1958
## 10     2   128    78    37  43.3 1.22     31 Yes            1990
## # ... with 522 more rows
```

dplyr::mutate()

- Add new columns
- Example: Calculate birth year as a function of age

```
diabetes %>%
  mutate(birth_year = 2021 - age,
         is_mother = npreg > 0)
```

```
## # A tibble: 532 x 10
##    npreg   glu    bp  skin   bmi   ped   age diabetic birth_year is_mother
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>         <dbl> <lgl>
##  1     5    86    68    28  30.2 0.364    24 No             1997 TRUE
##  2     7   195    70    33  25.1 0.163    55 Yes            1966 TRUE
##  3     5    77    82    41  35.8 0.156    35 No             1986 TRUE
##  4     0   165    76    43  47.9 0.259    26 No             1995 FALSE
##  5     0   107    60    25  26.4 0.133    23 No             1998 FALSE
##  6     5    97    76    27  35.6 0.378    52 Yes            1969 TRUE
##  7     3    83    58    31  34.3 0.336    25 No             1996 TRUE
##  8     1   193    50    16  25.9 0.655    24 No             1997 TRUE
##  9     3   142    80    15  32.4 0.2      63 No             1958 TRUE
## 10     2   128    78    37  43.3 1.22     31 Yes            1990 TRUE
## # ... with 522 more rows
```

dplyr::group_by()

- Group a data frame
- Example: diabetic vs non-diabetic:

```
diabetes %>%
  group_by(diabetic)
```

```
## # A tibble: 532 x 8
## # Groups:   diabetic [2]
##    npreg   glu    bp  skin   bmi   ped   age diabetic
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
##  1     5    86    68    28  30.2 0.364    24 No
##  2     7   195    70    33  25.1 0.163    55 Yes
##  3     5    77    82    41  35.8 0.156    35 No
##  4     0   165    76    43  47.9 0.259    26 No
##  5     0   107    60    25  26.4 0.133    23 No
##  6     5    97    76    27  35.6 0.378    52 Yes
##  7     3    83    58    31  34.3 0.336    25 No
##  8     1   193    50    16  25.9 0.655    24 No
##  9     3   142    80    15  32.4 0.2      63 No
## 10     2   128    78    37  43.3 1.22     31 Yes
## # ... with 522 more rows
```

dplyr::summarise()

- Compute summary values by group

```
diabetes %>%
  group_by(diabetic) %>%
  summarise(mean_age = mean(age))
```

```
## # A tibble: 2 x 2
##   diabetic mean_age
## * <chr>       <dbl>
## 1 No           29.2
## 2 Yes          36.4
```

dplyr::summarise()

- Compute summary values by group

```
diabetes %>%
  group_by(diabetic) %>%
  summarise(mean_age = mean(age),
            group_size = n())
```

```
## # A tibble: 2 x 3
##   diabetic mean_age group_size
## * <chr>       <dbl>      <int>
## 1 No           29.2        355
## 2 Yes          36.4        177
```

dplyr::summarise()

- You can group by multiple variables

```
diabetes %>%
  mutate(is_mother = npreg > 0) %>%
  group_by(diabetic, is_mother)
```

```
## # A tibble: 532 x 9
## # Groups:   diabetic, is_mother [4]
##    npreg   glu    bp  skin   bmi   ped   age diabetic is_mother
##    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>    <lgl>
##  1     5    86    68    28  30.2 0.364    24 No       TRUE
##  2     7   195    70    33  25.1 0.163    55 Yes      TRUE
##  3     5    77    82    41  35.8 0.156    35 No       TRUE
##  4     0   165    76    43  47.9 0.259    26 No       FALSE
##  5     0   107    60    25  26.4 0.133    23 No       FALSE
##  6     5    97    76    27  35.6 0.378    52 Yes      TRUE
##  7     3    83    58    31  34.3 0.336    25 No       TRUE
##  8     1   193    50    16  25.9 0.655    24 No       TRUE
##  9     3   142    80    15  32.4 0.2      63 No       TRUE
## 10     2   128    78    37  43.3 1.22     31 Yes      TRUE
## # ... with 522 more rows
```

dplyr::summarise()

- You can group by multiple variables

```
diabetes %>%
  mutate(is_mother = npreg > 0) %>%
  group_by(diabetic, is_mother) %>%
  summarise(mean_age = mean(age))
```

```
## `summarise()` has grouped output by 'diabetic'. You can override using the `.groups` argumer
```

```
## # A tibble: 4 x 3
## # Groups:   diabetic [2]
##   diabetic is_mother mean_age
##   <chr>    <lgl>        <dbl>
## 1 No       FALSE         25.1
## 2 No       TRUE          29.9
## 3 Yes      FALSE         26.8
## 4 Yes      TRUE          38.1
```

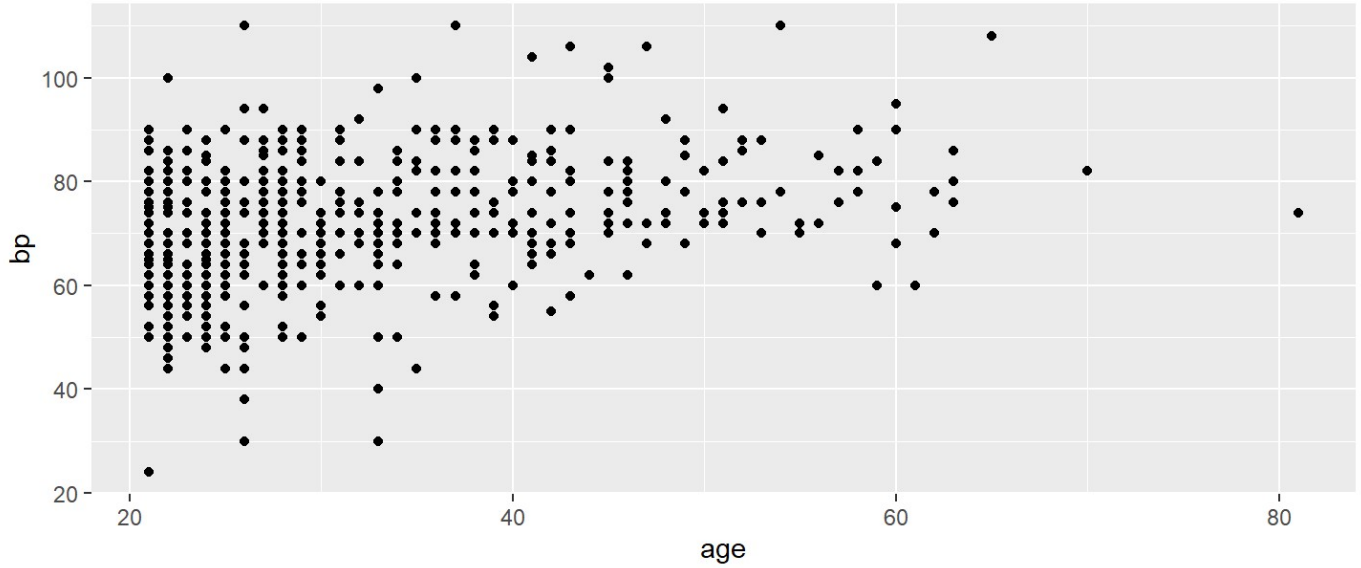
Visualize - `ggplot2`

- "Grammar of graphics"
- Core concepts:
  - Variables from tidy input data
  - Aesthetic mappings between variables and graphical elements: `aes()`
  - Add geometric objects to represent data via `geom_*()` e.g. `geom_point()`

Visualize - `ggplot2` example

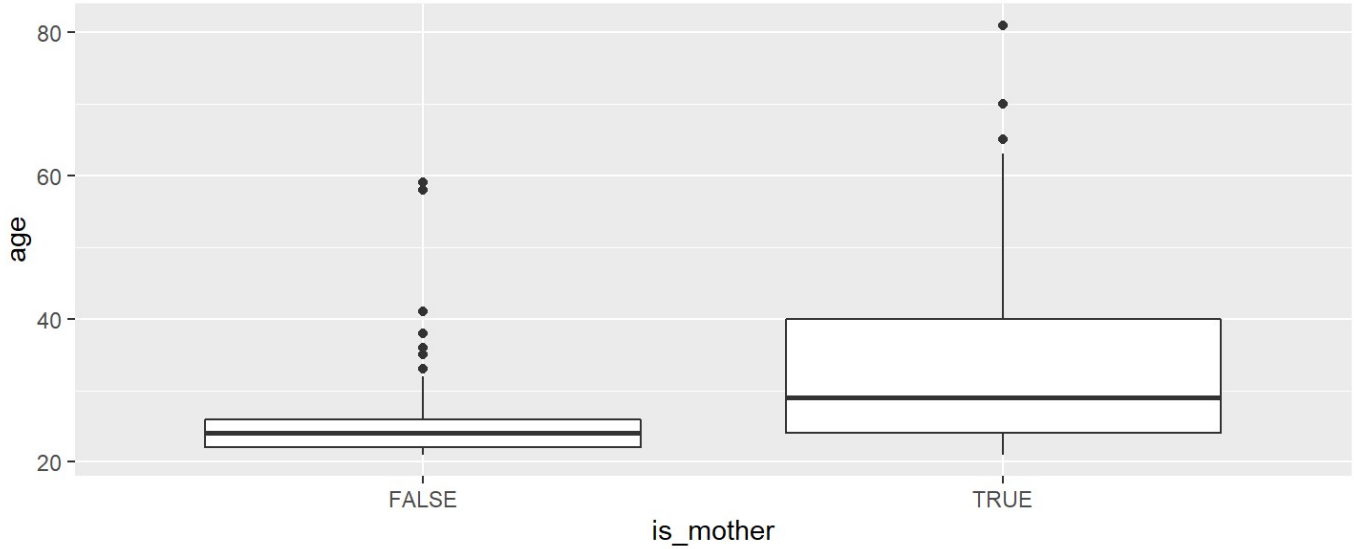
- Tidy input, aesthetic mapping, and a geom

```
diabetes %>%
  ggplot(mapping = aes(x = age, y = bp)) +
  geom_point()
```

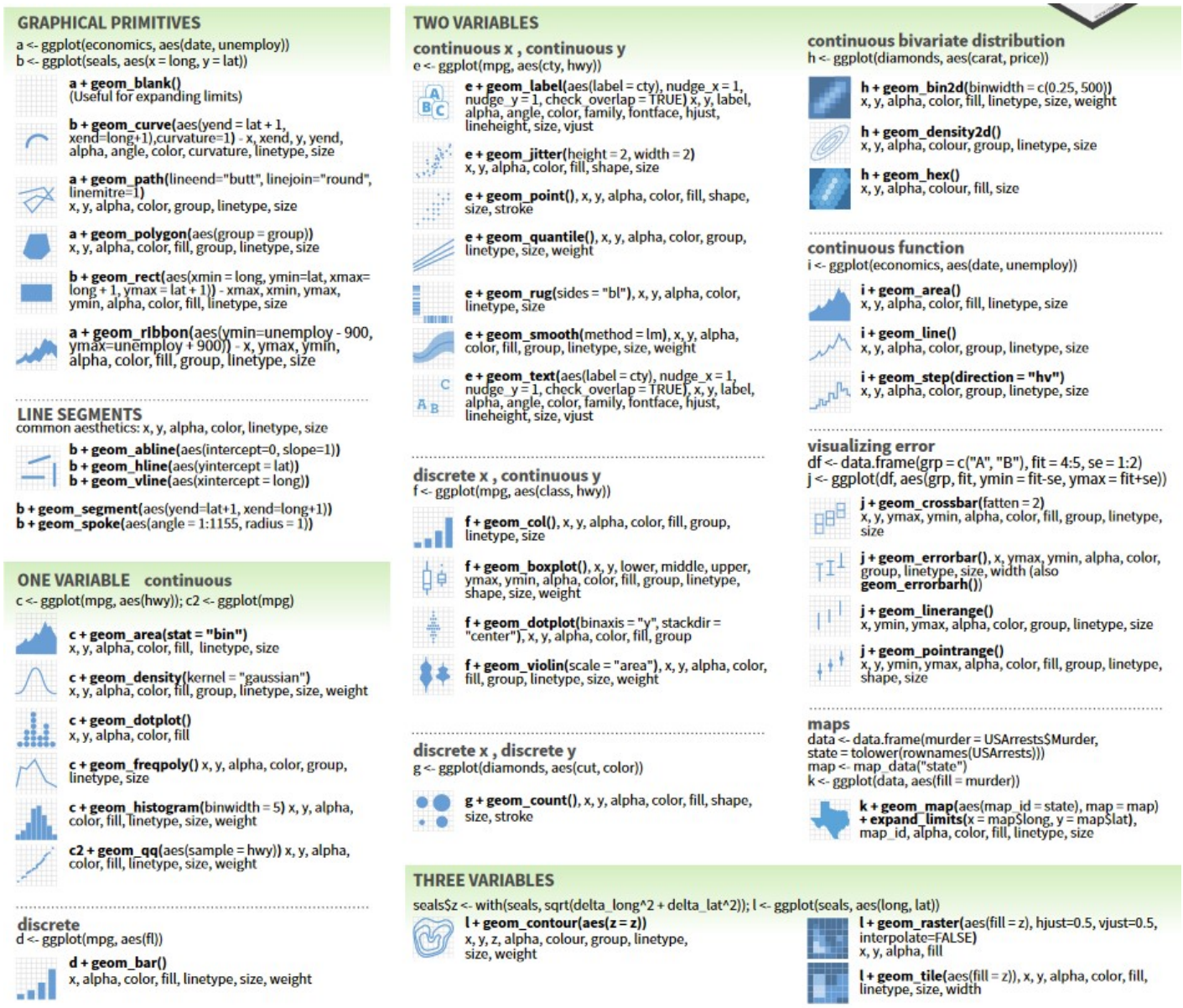


Visualize - ggplot2 example

```
diabetes %>%
  mutate(is_mother = npreg > 0) %>%
  ggplot(aes(is_mother, age)) +
  geom_boxplot()
```



Visualize - ggplot2's suite of geoms



GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank()
(Useful for expanding limits)

b + geom_curve(aes(yend = lat + 1, xend=long+1),curvature=1) - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend="butt", linejoin="round", linemitre=1)
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(group = group))
x, y, alpha, color, fill, group, linetype, size

b + geom_rect(aes(xmin = long, ymin=lat, xmax= long + 1, ymax = lat + 1)) - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin=unemploy - 900, ymax=unemploy + 900)) - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS
common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept=0, slope=1))
b + geom_hline(aes(yintercept = lat))
b + geom_vline(aes(xintercept = long))

b + geom_segment(aes(yend=lat+1, xend=long+1))
b + geom_spoke(aes(angle = 1:1155, radius = 1))

ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian")
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly() x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5) x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy)) x, y, alpha, color, fill, linetype, size, weight

discrete
d <- ggplot(mpg, aes(fl))

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

continuous x , continuous y
e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE) x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_jitter(height = 2, width = 2)
x, y, alpha, color, fill, shape, size

e + geom_point(), x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile(), x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl"), x, y, alpha, color, linetype, size

e + geom_smooth(method = lm), x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE), x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

discrete x , continuous y
f <- ggplot(mpg, aes(class, hwy))

f + geom_col(), x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot(), x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center"), x, y, alpha, color, fill, group

f + geom_violin(scale = "area"), x, y, alpha, color, fill, group, linetype, size, weight

discrete x , discrete y
g <- ggplot(diamonds, aes(cut, color))

g + geom_count(), x, y, alpha, color, fill, shape, size, stroke

continuous bivariate distribution
h <- ggplot(diamonds, aes(carat, price))

h + geom_bin2d(binwidth = c(0.25, 500))
x, y, alpha, color, fill, linetype, size, weight

h + geom_density2d()
x, y, alpha, colour, group, linetype, size

h + geom_hex()
x, y, alpha, colour, fill, size

continuous function
i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error
df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))

j + geom_crossbar(fatten = 2)
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar(), x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange()
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps
data <- data.frame(murder = USArrests$Murder, state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

k + geom_map(aes(map_id = state), map = map) **+ expand_limits(**x = map$long, y = map$lat), map_id, alpha, color, fill, linetype, size

THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2)); l <- ggplot(seals, aes(long, lat))

l + geom_contour(aes(z = z))
x, y, z, alpha, colour, group, linetype, size, weight

l + geom_raster(aes(fill = z), hjust=0.5, vjust=0.5, interpolate=FALSE)
x, y, alpha, fill

l + geom_tile(aes(fill = z)), x, y, alpha, color, fill, linetype, size, width

Report - `rmarkdown`

- Communicate analysis results
- Easily interweave notes, code, plots, and $\LaTeX$ in a single file
- Render as reports (.docx, .pdf, .html), slides (.html, .ppt), or web applications (Shiny)
- Rmd + Github = Digital lab notebook
- Demonstration at end of session 1 if there's time

COVID-19 example

COVID-19 data

- New York Times COVID-19 data on Github
- https://github.com/nytimes/covid-19-data
- Provides COVID-19 data by county, state, and nation-wide

Example: US COVID-19 state-level data

```
nyt_url = "https://raw.githubusercontent.com/nytimes/covid-19-data/master/us-states.csv"
state_covid = read_csv(nyt_url)
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   date = col_date(format = ""),
##   state = col_character(),
##   fips = col_character(),
##   cases = col_double(),
##   deaths = col_double()
## )
```

Example: Import state-level COVID-19 data

- Look at the data

```
state_covid
```

```
## # A tibble: 21,299 x 5
##    date       state      fips  cases deaths
##    <date>     <chr>      <chr> <dbl>  <dbl>
##  1 2020-01-21 Washington 53        1      0
##  2 2020-01-22 Washington 53        1      0
##  3 2020-01-23 Washington 53        1      0
##  4 2020-01-24 Illinois   17        1      0
##  5 2020-01-24 Washington 53        1      0
##  6 2020-01-25 California 06        1      0
##  7 2020-01-25 Illinois   17        1      0
##  8 2020-01-25 Washington 53        1      0
##  9 2020-01-26 Arizona    04        1      0
## 10 2020-01-26 California 06        2      0
## # ... with 21,289 more rows
```

Example: COVID-19 in California

- Plot one state over time

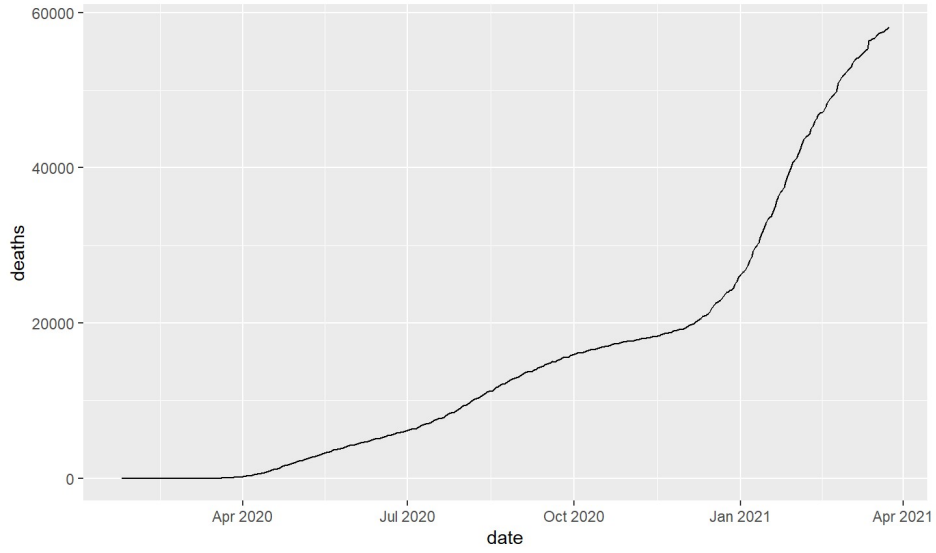
```
state_covid %>%
  filter(state == "California") %>%
  ggplot(aes(date, deaths)) +
  geom_line()
```

- What will the output of this command look like?

Example: COVID-19 in California

- Plot one state over time

```
state_covid %>%
  filter(state == "California") %>%
  ggplot(aes(date, deaths)) +
  geom_line()
```



Example: COVID-19 in California

- Want to define the CHANGE in deaths

```
state_covid %>%
  filter(state == "California", deaths > 0)
```

```
## # A tibble: 386 x 5
##    date       state      fips  cases deaths
##    <date>     <chr>      <chr> <dbl>  <dbl>
##  1 2020-03-04 California 06       55      1
##  2 2020-03-05 California 06       67      1
##  3 2020-03-06 California 06       81      1
##  4 2020-03-07 California 06      100      1
##  5 2020-03-08 California 06      112      1
##  6 2020-03-09 California 06      172      2
##  7 2020-03-10 California 06      179      3
##  8 2020-03-11 California 06      202      4
##  9 2020-03-12 California 06      252      4
## 10 2020-03-13 California 06      320      5
## # ... with 376 more rows
```

Example: COVID-19 in California

- Define daily added deaths using `diff()`

```
state_covid %>%
  filter(state == "California") %>%
  mutate(new_deaths = diff(deaths))
```

That didn't work

- Define daily added deaths using `diff()`

```
state_covid %>%
  filter(state == "California") %>%
  mutate(new_deaths = diff(deaths))
```

```
## Error: Problem with `mutate()` input `new_deaths`.
## x Input `new_deaths` can't be recycled to size 425.
## i Input `new_deaths` is `diff(deaths)`.
## i Input `new_deaths` must be size 425 or 1, not 424.
```

The fix

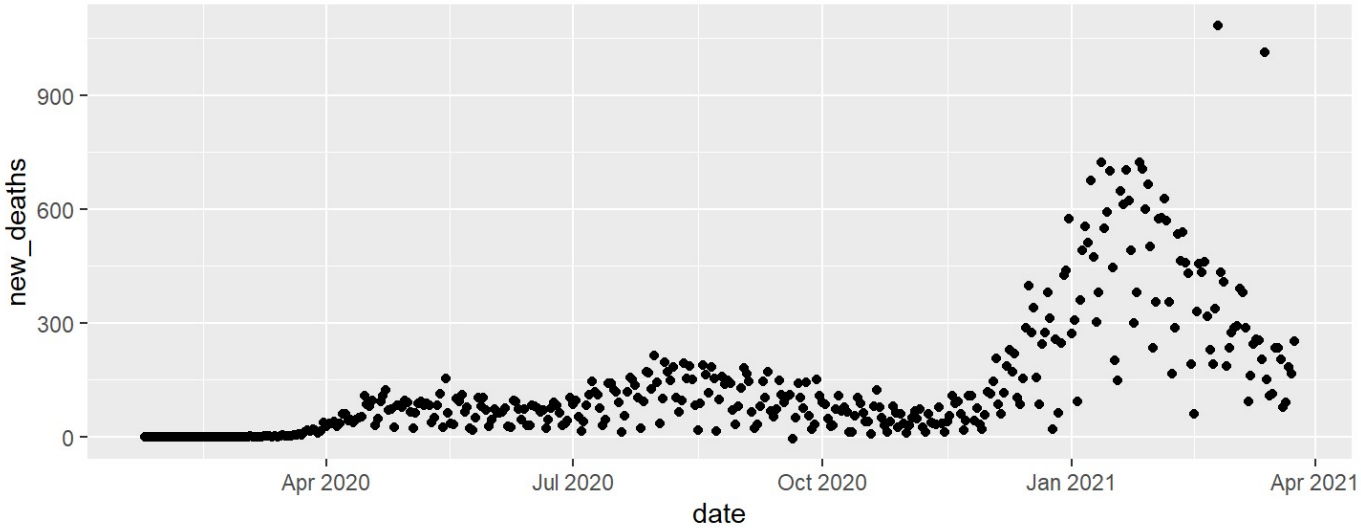
- `diff()` returns a vector that's one element too short – tack on the first observation at the start.

```
state_covid %>%
  filter(state == "California") %>%
  mutate(new_deaths = c(deaths[1], diff(deaths)))
```

```
## # A tibble: 425 x 6
##    date       state      fips  cases deaths new_deaths
##    <date>     <chr>      <chr> <dbl>  <dbl>      <dbl>
##  1 2020-01-25 California 06        1      0          0
##  2 2020-01-26 California 06        2      0          0
##  3 2020-01-27 California 06        2      0          0
##  4 2020-01-28 California 06        2      0          0
##  5 2020-01-29 California 06        2      0          0
##  6 2020-01-30 California 06        2      0          0
##  7 2020-01-31 California 06        3      0          0
##  8 2020-02-01 California 06        3      0          0
##  9 2020-02-02 California 06        6      0          0
## 10 2020-02-03 California 06        6      0          0
## # ... with 415 more rows
```

Example: New deaths over time

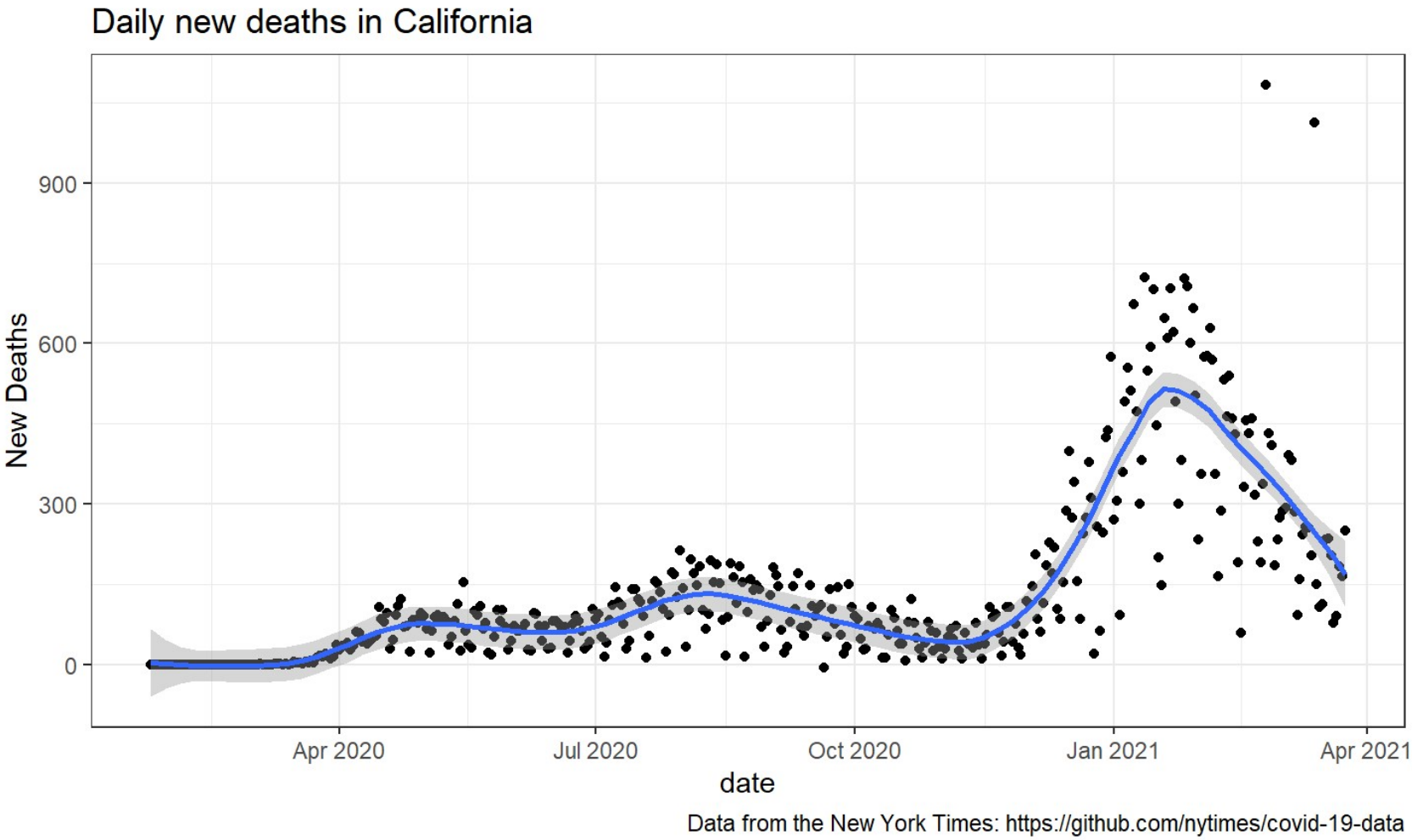
```
state_covid %>%
  filter(state == "California") %>%
  mutate(new_deaths = c(deaths[1], diff(deaths))) %>%
  ggplot(aes(date, new_deaths)) +
  geom_point()
```



Example: Adding bells and whistles to a plot

```
state_covid %>%
  filter(state == "California") %>%
  mutate(new_deaths = c(deaths[1], diff(deaths))) %>%
  ggplot(aes(date, new_deaths)) +
  geom_point() +
  geom_smooth(method = "loess", span = .2) +
  labs(title = "Daily new deaths in California",
       y = "New Deaths",
       caption = "Data from the New York Times: https://github.com/nytimes/covid-19-data") +
  theme_bw()
```

Example: COVID-19 in California



- Further enhancement with a trendline, labels, and theme
- Try plotting several states with different colors (hints: use `%in%` and `aes(color = ...)`)

Example: US COVID-19

- What states had the highest daily new deaths?

Example: US COVID-19

- What states had the highest daily new deaths?
- What do we need to do?

Example: US COVID-19

- What was the highest daily increase in death in any state?

```
state_covid %>%
  group_by(state) %>%
  mutate(new_deaths = c(deaths[1], diff(deaths))) %>%
  summarise(state_max = max(new_deaths)) %>%
  arrange(desc(state_max))
```

```
## # A tibble: 55 x 2
##    state        state_max
##    <chr>            <dbl>
##  1 Ohio              2559
##  2 New Jersey        1877
##  3 Indiana           1546
##  4 Texas             1202
##  5 California        1084
##  6 New York          1036
##  7 Georgia            466
##  8 Pennsylvania       401
##  9 Arizona            390
## 10 Virginia           383
## # ... with 45 more rows
```

- Note: `mutate()` is aware of groups!

Before switching to RStudio…

How to get help

- To look at the documentation for any function, use `?` or `help()`
  - `?summarise`
  - How to read help: https://socviz.co/appendix.html#a-little-more-about-r
- Package-specific walkthroughs: `vignette(package = "dplyr")`
- R tag on Stats Stack Exchange - stats.stackexchange.com

Resources

- R for Data Science - https://r4ds.had.co.nz/
- Cheat Sheets - https://rstudio.com/resources/cheatsheets/
- Tidy Tuesday - Weekly analysis screencasts on youtube

Questions?

Day 2

purrr

- Functional programming

map()

- Apply a function to each element of a list
- Example:

```
map(1:3, sqrt)
```

```
## [[1]]
## [1] 1
##
## [[2]]
## [1] 1.414214
##
## [[3]]
## [1] 1.732051
```

map()

- Apply a function to each element of a list
- Example:

```
map(1:3, sqrt)
```

```
## [[1]]
## [1] 1
##
## [[2]]
## [1] 1.414214
##
## [[3]]
## [1] 1.732051
```

```
map(datasets, ml_algorithm)
```

Anonymous functions

- Tilde + `.x`
- Use to easily define single-use functions

`map_*()` variants

- `map()` always returns a list
- Variants return a vector of a specific type

```
map_dbl(1:5, ~.x^2 + 1)
```

```
## [1]  2  5 10 17 26
```

```
map_lgl(1:5, ~.x == 3)
```

```
## [1] FALSE FALSE  TRUE FALSE FALSE
```

```
map_chr(letters[1:5], ~paste0(rep(.x, 3), collapse=''))
```

```
## [1] "aaa" "bbb" "ccc" "ddd" "eee"
```

purrr example: run many models

- Define each combination of two explanatory variables

```
formula_df = names(diabetes)[1:7] %>%
  combn(m = 2) %>%
  t %>%
  as_tibble %>%
  set_names(c('x1', 'x2')) %>%
  mutate(formula = paste("diabetic ~ ", x1, " + ", x2, sep = ''))
```

```
## Warning: The `x` argument of `as_tibble.matrix()` must have unique column names if `.name_re
## Using compatibility `.name_repair`.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was generated.
```

```
formula_df
```

```
## # A tibble: 21 x 3
##    x1    x2    formula
##    <chr> <chr> <chr>
##  1 npreg glu   diabetic ~ npreg + glu
##  2 npreg bp    diabetic ~ npreg + bp
##  3 npreg skin  diabetic ~ npreg + skin
##  4 npreg bmi   diabetic ~ npreg + bmi
##  5 npreg ped   diabetic ~ npreg + ped
```

purrr example: run many models

- Run a logistic regression on each combination of explanatory variables

```
formula_df %>%
  mutate(glm_result = map(formula,
                          ~glm(.x, data = diabetes, family = 'binomial')))
```

purrr example: run many models

- Extract the AIC of each model fit

```
formula_df %>%
  mutate(glm_result = map(formula,
                          ~glm(.x, data = diabetes, family = 'binomial')),
         aic = map_dbl(lm_result,
                       ~.x$aic))
```

purrr example: run many models

- See which model had the lowest AIC

```
formula_df %>%
  mutate(glm_result = map(formula,
                          ~glm(.x, data = diabetes, family = 'binomial')),
         aic = map_dbl(lm_result,
                       ~.x$aic)) %>%
  arrange(aic)
```

Organize - `tidyr`

- `pivot_longer()` and `pivot_wider()`
- `separate()` and `unite()`

Data tidying example: WHO TB data

- WHO tuberculosis case data
- realistically messy!
- Try running these commands:

```
?tidyr::who
dim(who)
names(who)
who[1:5, 1:8]
who
```

- We will tidy this data in 5 steps

WHO TB column names

- First part: “new” or “old”
- Second part: TB type (relapse, extrapulmonary, smear-positive, smear-negative)
- Third part: Sex and age group (e.g. f2534)

TB tidying 1/5: pivot wide to long

```
who1 = who %>%
  pivot_longer(new_sp_m014:newrel_f65,
               names_to = "key",
               values_to = "values",
               values_drop_na = TRUE)
who1
```

```
## # A tibble: 76,046 x 6
##    country     iso2  iso3   year key          values
##    <chr>       <chr> <chr> <int> <chr>         <int>
##  1 Afghanistan AF    AFG    1997 new_sp_m014       0
##  2 Afghanistan AF    AFG    1997 new_sp_m1524     10
##  3 Afghanistan AF    AFG    1997 new_sp_m2534      6
##  4 Afghanistan AF    AFG    1997 new_sp_m3544      3
##  5 Afghanistan AF    AFG    1997 new_sp_m4554      5
##  6 Afghanistan AF    AFG    1997 new_sp_m5564      2
##  7 Afghanistan AF    AFG    1997 new_sp_m65        0
##  8 Afghanistan AF    AFG    1997 new_sp_f014       5
##  9 Afghanistan AF    AFG    1997 new_sp_f1524     38
## 10 Afghanistan AF    AFG    1997 new_sp_f2534     36
## # ... with 76,036 more rows
```

TB tidying 2/5: fix inconsistent names

```
who2 = who1 %>%
  mutate(key = str_replace(key, "newrel", "new_rel"))
who2
```

```
## # A tibble: 76,046 x 6
##    country     iso2  iso3   year key          values
##    <chr>       <chr> <chr> <int> <chr>         <int>
##  1 Afghanistan AF    AFG    1997 new_sp_m014       0
##  2 Afghanistan AF    AFG    1997 new_sp_m1524     10
##  3 Afghanistan AF    AFG    1997 new_sp_m2534      6
##  4 Afghanistan AF    AFG    1997 new_sp_m3544      3
##  5 Afghanistan AF    AFG    1997 new_sp_m4554      5
##  6 Afghanistan AF    AFG    1997 new_sp_m5564      2
##  7 Afghanistan AF    AFG    1997 new_sp_m65        0
##  8 Afghanistan AF    AFG    1997 new_sp_f014       5
##  9 Afghanistan AF    AFG    1997 new_sp_f1524     38
## 10 Afghanistan AF    AFG    1997 new_sp_f2534     36
## # ... with 76,036 more rows
```

TB tidying 3/5: separate identifier components

```
who3 = who2 %>%
  separate(key, into = c("newold", "tb_type", "sexage"))
```

TB tidying 4/5: separate sex and age group

```
who4 = who3 %>%
  separate(sexage, into = c("sex", "age_group"), sep = 1)
```

TB tidying 5/5: remove redundant columns

```
who_final = who4 %>%
  select(-newold, -matches("iso"))
```

TB tidying: Final command

```
tidyr::who %>%
  pivot_longer(new_sp_m014:newrel_f65,
               names_to = "key",
               values_to = "values",
               values_drop_na = TRUE) %>%
  mutate(key = str_replace(key, "newrel", "new_rel")) %>%
  separate(key, into = c("newold", "tb_type", "sexage")) %>%
  separate(sexage, into = c("sex", "age_group"), sep = 1) %>%
  select(-newold, -matches("iso"))
```

```
## # A tibble: 76,046 x 6
##    country      year tb_type sex   age_group values
##    <chr>       <int> <chr>   <chr> <chr>      <int>
##  1 Afghanistan  1997 sp      m     014            0
##  2 Afghanistan  1997 sp      m     1524          10
##  3 Afghanistan  1997 sp      m     2534           6
##  4 Afghanistan  1997 sp      m     3544           3
##  5 Afghanistan  1997 sp      m     4554           5
##  6 Afghanistan  1997 sp      m     5564           2
##  7 Afghanistan  1997 sp      m     65             0
##  8 Afghanistan  1997 sp      f     014            5
##  9 Afghanistan  1997 sp      f     1524          38
## 10 Afghanistan  1997 sp      f     2534          36
## # ... with 76,036 more rows
```

Joins if there's time

Everything else

- `forcats` - work with factors
- `stringr` - work with strings
- `lubridate` - work with dates
- `tidymodels` - work with stats/ML algorithms
- `reticulate` - work with Python

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- Cheat Sheets - https://rstudio.com/resources/cheatsheets/
- Helpful cartoons - https://github.com/allisonhorst/stats-illustrations
- Tidy Tuesday - Weekly analysis screencasts on youtube