File I/O and basic data wrangling

John Tipton

Readings

- R for data science
  - Introduction
  - Chapters 3 (Data transformation with `dplyr`), 7 (Tibbles with `tibble`), 8 (Data import with `readr`), and 9 (Tidy data with `tidyr`)

The `dplyr` package

- The `dplyr` package can be loaded as part of the `tidyverse` library

```
library(tidyverse)
```

- Namespaces
    - Different modules might have the same name -- how does the computer know which function you meant?
    - In python, you can use the `mean()` function from the `statistics` module using `statistics.mean()`
    - In `R`, namespaces are defined using `::`
    - `dplyr::filter()` uses the `filter()` function in the `dplyr()` library

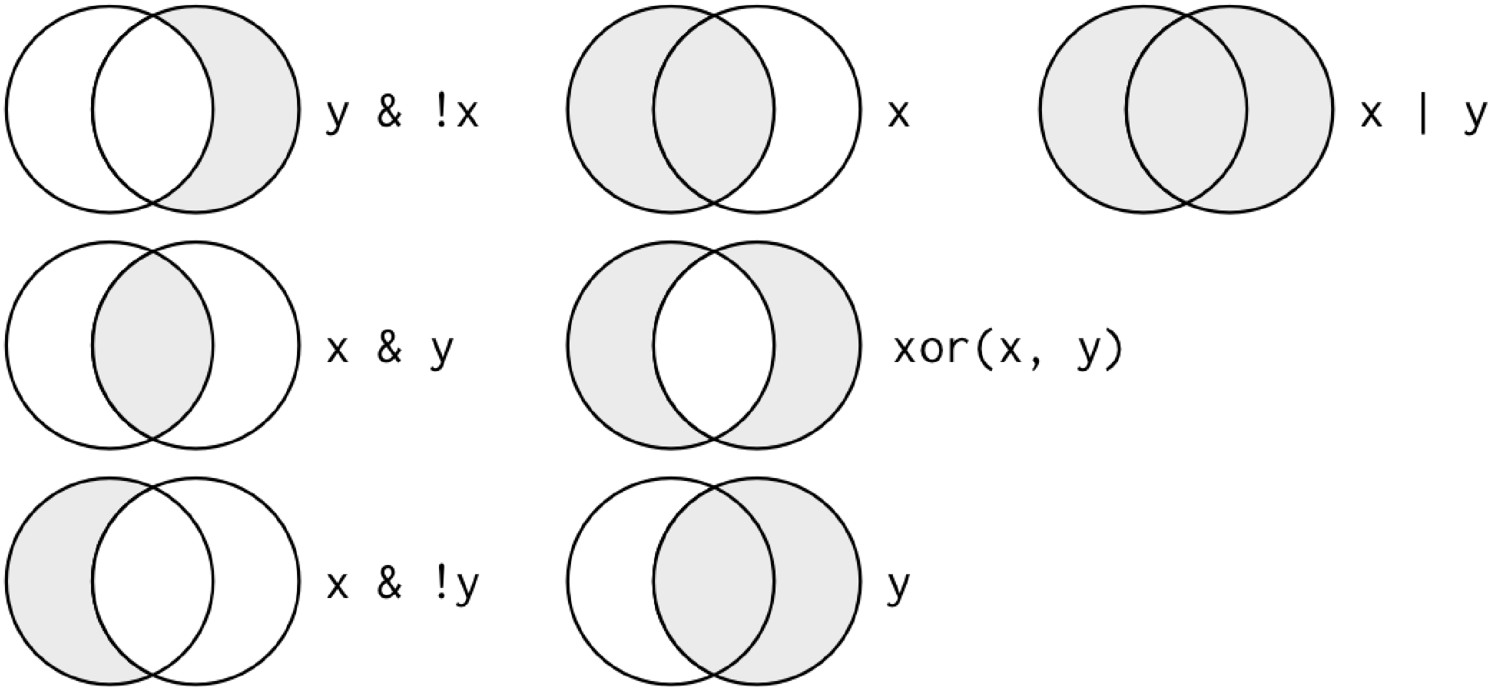
`dplyr` functions

- The big 5:
  - Choose observations (rows) based on conditional values with `filter()`
  - Reorder the variables with `arrange()`
  - Select variables by name with `select()`
  - Create new variables with `mutate()`
  - Create summary variables with `summarize()`
    - `summarise()` if you are British

Logical operators

- Test if A is greater than B `A > B`
- Test if A is less than B `A < B`
- Test if A is greater than or equal to B `A >= B`
- Test if A is less than or equal to B `A <= B`
- Test if A is equal to B `A == B`
- Test if A is not equal to B `A != B`
- Return TRUE if both A and B are TRUE `A & B`
- Return TRUE if A or B (or both) is TRUE `A | B`
- Return TRUE if A in B `A %in% B`

Logical operators



Penguins

```
library(palmerpenguins)
glimpse(penguins)
```

```
## Rows: 344
## Columns: 8
## $ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Ad
## $ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgersen, Torgersen, Torgerse
## $ bill_length_mm    <dbl> 39.10000000000000142109, 39.50000000000000000000, 40.29999999999999715783
## $ bill_depth_mm     <dbl> 18.69999999999999928946, 17.39999999999999857891, 18.00000000000000000000
## $ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186, 180, 182, 191, 198,
## $ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, 4250, 3300, 3700, 320
## $ sex               <fct> male, female, female, NA, female, male, female, male, NA, NA, NA, NA, fema
## $ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 20
```

Filter

- Choose only the penguins from the island Torgersen

```
penguins %>%
  filter(island == "Torgersen")
```

```
## # A tibble: 52 x 8
##    species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
##  2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
##  3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
##  4 Adelie  Torgersen           NA            NA                  NA          NA <NA>    2007
##  5 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
##  6 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
##  7 Adelie  Torgersen           38.9          17.8               181        3625 female  2007
##  8 Adelie  Torgersen           39.2          19.6               195        4675 male    2007
##  9 Adelie  Torgersen           34.1          18.1               193        3475 <NA>    2007
## 10 Adelie  Torgersen           42            20.2               190        4250 <NA>    2007
## # … with 42 more rows
```

Filter

- Choose only the penguins that are species `Gentoo`

```
penguins %>%
  filter(species == "Gentoo")
```

```
## # A tibble: 124 x 8
##    species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>           <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Gentoo  Biscoe           46.1          13.2               211        4500 female  2007
##  2 Gentoo  Biscoe           50            16.3               230        5700 male    2007
##  3 Gentoo  Biscoe           48.7          14.1               210        4450 female  2007
##  4 Gentoo  Biscoe           50            15.2               218        5700 male    2007
##  5 Gentoo  Biscoe           47.6          14.5               215        5400 male    2007
##  6 Gentoo  Biscoe           46.5          13.5               210        4550 female  2007
##  7 Gentoo  Biscoe           45.4          14.6               211        4800 female  2007
##  8 Gentoo  Biscoe           46.7          15.3               219        5200 male    2007
##  9 Gentoo  Biscoe           43.3          13.4               209        4400 female  2007
## 10 Gentoo  Biscoe           46.8          15.4               215        5150 male    2007
## # … with 114 more rows
```

Filter

- Choose only the penguins that are species `Chinstrap` and from the island `Biscoe`

```
penguins %>%
  filter(species == "Chinstrap" & island == "Biscoe")
```

```
## # A tibble: 0 x 8
## # … with 8 variables: species <fct>, island <fct>, bill_length_mm <dbl>, bill_depth_mm <dbl>, fl
```

- How many observations?

Filter

- Choose only the penguins that are species `Chinstrap` or from the island `Biscoe`

```
penguins %>%
  filter(species == "Chinstrap" | island == "Biscoe")
```

```
## # A tibble: 236 x 8
##    species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>           <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Biscoe           37.8          18.3               174        3400 female  2007
##  2 Adelie  Biscoe           37.7          18.7               180        3600 male    2007
##  3 Adelie  Biscoe           35.9          19.2               189        3800 female  2007
##  4 Adelie  Biscoe           38.2          18.1               185        3950 male    2007
##  5 Adelie  Biscoe           38.8          17.2               180        3800 male    2007
##  6 Adelie  Biscoe           35.3          18.9               187        3800 female  2007
##  7 Adelie  Biscoe           40.6          18.6               183        3550 male    2007
##  8 Adelie  Biscoe           40.5          17.9               187        3200 female  2007
##  9 Adelie  Biscoe           37.9          18.6               172        3150 female  2007
## 10 Adelie  Biscoe           40.5          18.9               180        3950 male    2007
## # … with 226 more rows
```

- How many observations?

Filter

- Choose only the penguins that are species `Gentoo` or not from the island `Torgersen`

```
penguins %>%
  filter(species == "Gentoo" | island != "Torgersen")
```

```
## # A tibble: 292 x 8
##    species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>           <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Biscoe           37.8          18.3               174        3400 female  2007
##  2 Adelie  Biscoe           37.7          18.7               180        3600 male    2007
##  3 Adelie  Biscoe           35.9          19.2               189        3800 female  2007
##  4 Adelie  Biscoe           38.2          18.1               185        3950 male    2007
##  5 Adelie  Biscoe           38.8          17.2               180        3800 male    2007
##  6 Adelie  Biscoe           35.3          18.9               187        3800 female  2007
##  7 Adelie  Biscoe           40.6          18.6               183        3550 male    2007
##  8 Adelie  Biscoe           40.5          17.9               187        3200 female  2007
##  9 Adelie  Biscoe           37.9          18.6               172        3150 female  2007
## 10 Adelie  Biscoe           40.5          18.9               180        3950 male    2007
## # … with 282 more rows
```

Filter

- Choose penguins that are from the islands of `Torgersen` or `Dream`

```
penguins %>%
  filter(island %in% c("Torgersen", "Dream"))
```

```
## # A tibble: 176 x 8
##    species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
##  2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
##  3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
##  4 Adelie  Torgersen           NA            NA                  NA          NA <NA>    2007
##  5 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
##  6 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
##  7 Adelie  Torgersen           38.9          17.8               181        3625 female  2007
##  8 Adelie  Torgersen           39.2          19.6               195        4675 male    2007
##  9 Adelie  Torgersen           34.1          18.1               193        3475 <NA>    2007
## 10 Adelie  Torgersen           42            20.2               190        4250 <NA>    2007
## # … with 166 more rows
```

Filter

- Choose penguins that have `bill_length_mm` between 36 than 48 mm (inclusive)

```
penguins %>%
  filter(bill_length_mm <= 48 & bill_length_mm>= 36)
```

```
## # A tibble: 226 x 8
##    species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
##  2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
##  3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
##  4 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
##  5 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
##  6 Adelie  Torgersen           38.9          17.8               181        3625 female  2007
##  7 Adelie  Torgersen           39.2          19.6               195        4675 male    2007
##  8 Adelie  Torgersen           42            20.2               190        4250 <NA>    2007
##  9 Adelie  Torgersen           37.8          17.1               186        3300 <NA>    2007
## 10 Adelie  Torgersen           37.8          17.3               180        3700 <NA>    2007
## # … with 216 more rows
```

Arrange

- Arrange the penguins based on `bill_length_mm` in increasing order

```
penguins %>%
  arrange(bill_length_mm)
```

```
## # A tibble: 344 x 8
##    species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Dream               32.1          15.5               188        3050 female  2009
##  2 Adelie  Dream               33.1          16.1               178        2900 female  2008
##  3 Adelie  Torgersen           33.5          19                 190        3600 female  2008
##  4 Adelie  Dream               34            17.1               185        3400 female  2008
##  5 Adelie  Torgersen           34.1          18.1               193        3475 <NA>    2007
##  6 Adelie  Torgersen           34.4          18.4               184        3325 female  2007
##  7 Adelie  Biscoe              34.5          18.1               187        2900 female  2008
##  8 Adelie  Torgersen           34.6          21.1               198        4400 male    2007
##  9 Adelie  Torgersen           34.6          17.2               189        3200 female  2008
## 10 Adelie  Biscoe              35            17.9               190        3450 female  2008
## # … with 334 more rows
```

Arrange

- Arrange the penguins based on `bill_length_mm` in decreasing order

```
penguins %>%
  arrange(desc(bill_length_mm))
```

```
## # A tibble: 344 x 8
##    species   island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>     <fct>           <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Gentoo    Biscoe            59.6          17                  230        6050 male    2007
##  2 Chinstrap Dream             58            17.8                181        3700 female  2007
##  3 Gentoo    Biscoe            55.9          17                  228        5600 male    2009
##  4 Chinstrap Dream             55.8          19.8                207        4000 male    2009
##  5 Gentoo    Biscoe            55.1          16                  230        5850 male    2009
##  6 Gentoo    Biscoe            54.3          15.7                231        5650 male    2008
##  7 Chinstrap Dream             54.2          20.8                201        4300 male    2008
##  8 Chinstrap Dream             53.5          19.9                205        4500 male    2008
##  9 Gentoo    Biscoe            53.4          15.8                219        5500 male    2009
## 10 Chinstrap Dream             52.8          20                  205        4550 male    2008
## # … with 334 more rows
```

Select

- Select the 3rd through 5th variables

```
penguins %>%
  select(3:5)
```

```
## # A tibble: 344 x 3
##    bill_length_mm bill_depth_mm flipper_length_mm
##             <dbl>         <dbl>             <int>
##  1           39.1          18.7               181
##  2           39.5          17.4               186
##  3           40.3          18                 195
##  4           NA            NA                  NA
##  5           36.7          19.3               193
##  6           39.3          20.6               190
##  7           38.9          17.8               181
##  8           39.2          19.6               195
##  9           34.1          18.1               193
## 10           42            20.2               190
## # … with 334 more rows
```

Select

- Select the variables `sex`, `island`, and `body_mass_g`

```
penguins %>%
  select(sex, island, body_mass_g)
```

```
## # A tibble: 344 x 3
##    sex    island    body_mass_g
##    <fct>  <fct>           <int>
##  1 male   Torgersen        3750
##  2 female Torgersen        3800
##  3 female Torgersen        3250
##  4 <NA>   Torgersen          NA
##  5 female Torgersen        3450
##  6 male   Torgersen        3650
##  7 female Torgersen        3625
##  8 male   Torgersen        4675
##  9 <NA>   Torgersen        3475
## 10 <NA>   Torgersen        4250
## # … with 334 more rows
```

Select

- Select all the variables except for `flipper_length_mm`, and `year`

```
penguins %>%
  select(-flipper_length_mm, -year)
```

```
## # A tibble: 344 x 6
##    species island    bill_length_mm bill_depth_mm body_mass_g sex
##    <fct>   <fct>              <dbl>         <dbl>       <int> <fct>
##  1 Adelie  Torgersen           39.1          18.7        3750 male
##  2 Adelie  Torgersen           39.5          17.4        3800 female
##  3 Adelie  Torgersen           40.3          18          3250 female
##  4 Adelie  Torgersen           NA            NA            NA <NA>
##  5 Adelie  Torgersen           36.7          19.3        3450 female
##  6 Adelie  Torgersen           39.3          20.6        3650 male
##  7 Adelie  Torgersen           38.9          17.8        3625 female
##  8 Adelie  Torgersen           39.2          19.6        4675 male
##  9 Adelie  Torgersen           34.1          18.1        3475 <NA>
## 10 Adelie  Torgersen           42            20.2        4250 <NA>
## # … with 334 more rows
```

Select

- Choose only variables starting with a string `starts_with()`
- Choose only variables ending with a string `ends_with()`
- Choose only variables containing a string `contains()`
- Choose only variables matching a regular expression `matches()`
- Choose only variables within a numeric range `num_range()`

Select

- Select all the variables ending with `mm` or beginning with `s`

```
penguins %>%
  select(ends_with("mm") | starts_with("s"))
```

```
## # A tibble: 344 x 5
##    bill_length_mm bill_depth_mm flipper_length_mm species sex
##             <dbl>         <dbl>             <int> <fct>   <fct>
##  1           39.1          18.7               181 Adelie  male
##  2           39.5          17.4               186 Adelie  female
##  3           40.3          18                 195 Adelie  female
##  4           NA            NA                  NA Adelie  <NA>
##  5           36.7          19.3               193 Adelie  female
##  6           39.3          20.6               190 Adelie  male
##  7           38.9          17.8               181 Adelie  female
##  8           39.2          19.6               195 Adelie  male
##  9           34.1          18.1               193 Adelie  <NA>
## 10           42            20.2               190 Adelie  <NA>
## # … with 334 more rows
```

Mutate

- Create a variable called `bill_area` that approximates bill surface area in mm (assume a rectangular bill) and select the three bill variables.

```
penguins %>%
  mutate(bill_area = bill_length_mm * bill_depth_mm) %>%
  select(starts_with("bill"))
```

```
## # A tibble: 344 x 3
##    bill_length_mm bill_depth_mm bill_area
##             <dbl>         <dbl>     <dbl>
##   1           39.1          18.7      731.
##   2           39.5          17.4      687.
##   3           40.3          18        725.
##   4           NA            NA         NA
##   5           36.7          19.3      708.
##   6           39.3          20.6      810.
##   7           38.9          17.8      692.
##   8           39.2          19.6      768.
##   9           34.1          18.1      617.
## 10           42            20.2      848.
## # … with 334 more rows
```

Transmute

- Keep only the created variable
- Create a variable called `bill_area` that approximates bill surface area in mm (assume a rectangular bill) and select the three bill variables.

```
penguins %>%
  transmute(bill_area = bill_length_mm * bill_depth_mm)
```

```
## # A tibble: 344 x 1
##    bill_area
##        <dbl>
##  1      731.
##  2      687.
##  3      725.
##  4       NA
##  5      708.
##  6      810.
##  7      692.
##  8      768.
##  9      617.
## 10      848.
## # … with 334 more rows
```

Transmute

- Keep only the created variable
- Create a variable called `bill_area` that approximates bill surface area on a log scale (assume a rectangular bill) and select the three bill variables (Why would you do this? No one knows…)

```
penguins %>%
  transmute(bill_area = log(bill_length_mm * bill_depth_mm))
```

```
## # A tibble: 344 x 1
##    bill_area
##        <dbl>
##  1      6.59
##  2      6.53
##  3      6.59
##  4     NA
##  5      6.56
##  6      6.70
##  7      6.54
##  8      6.64
##  9      6.43
## 10      6.74
## # … with 334 more rows
```

Summarize

- Calculate the average `bill_length_mm` and save as `mean_bill_length`

```
penguins %>%
  summarize(mean_bill_length_mm = mean(bill_length_mm))
```

```
## # A tibble: 1 x 1
##   mean_bill_length_mm
##                 <dbl>
## 1                  NA
```

- What happened?

```
penguins %>%
  summarize(mean_bill_length_mm = mean(bill_length_mm, na.rm = TRUE))
```

```
## # A tibble: 1 x 1
##   mean_bill_length_mm
##                 <dbl>
## 1                43.9
```

- What does `na.rm = TRUE` do?

Summarize

- What is the average `body_mass_g` by species?

```
penguins %>%
  group_by(species) %>%
  summarize(mean_body_mass_by_species = mean(body_mass_g, na.rm = TRUE))
```

```
## # A tibble: 3 x 2
##   species   mean_body_mass_by_species
##   <fct>                         <dbl>
## 1 Adelie                        3701.
## 2 Chinstrap                     3733.
## 3 Gentoo                        5076.
```

```
penguins %>%
  filter(!is.na(body_mass_g)) %>%
  group_by(species) %>%
  summarize(mean_body_mass_by_species = mean(body_mass_g))
```

```
## # A tibble: 3 x 2
##   species   mean_body_mass_by_species
##   <fct>                         <dbl>
## 1 Adelie                        3701.
## 2 Chinstrap                     3733.
## 3 Gentoo                        5076.
```

Summarize

```
data("starwars")
glimpse(starwars)
```

```
## Rows: 87
## Columns: 14
## $ name       <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", "Leia Organa", "Owen Lars'
## $ height     <int> 172, 167, 96, 202, 150, 178, 165, 97, 183, 182, 188, 180, 228, 180, 173, 175,
## $ mass       <dbl> 77.00000000000000000000, 75.00000000000000000000, 32.00000000000000000000, 13
## $ hair_color <chr> "blond", NA, NA, "none", "brown", "brown, grey", "brown", NA, "black", "aubur
## $ skin_color <chr> "fair", "gold", "white, blue", "white", "light", "light", "light", "white, re
## $ eye_color  <chr> "blue", "yellow", "red", "yellow", "brown", "blue", "blue", "red", "brown", '
## $ birth_year <dbl> 19.00000000000000000000, 112.00000000000000000000, 33.00000000000000000000, 4
## $ sex        <chr> "male", "none", "none", "male", "female", "male", "female", "none", "male", '
## $ gender     <chr> "masculine", "masculine", "masculine", "masculine", "feminine", "masculine",
## $ homeworld  <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Alderaan", "Tatooine", "Tatooin
## $ species    <chr> "Human", "Droid", "Droid", "Human", "Human", "Human", "Human", "Droid", "Huma
## $ films      <list> <"The Empire Strikes Back", "Revenge of the Sith", "Return of the Jedi", "A 
## $ vehicles   <list> <"Snowspeeder", "Imperial Speeder Bike">, <>, <>, <>, "Imperial Speeder Bike
## $ starships  <list> <"X-wing", "Imperial shuttle">, <>, <>, "TIE Advanced x1", <>, <>, <>, <>, '
```

Summarize

- Count using `n()`
- Important to make sure you check the group sample size

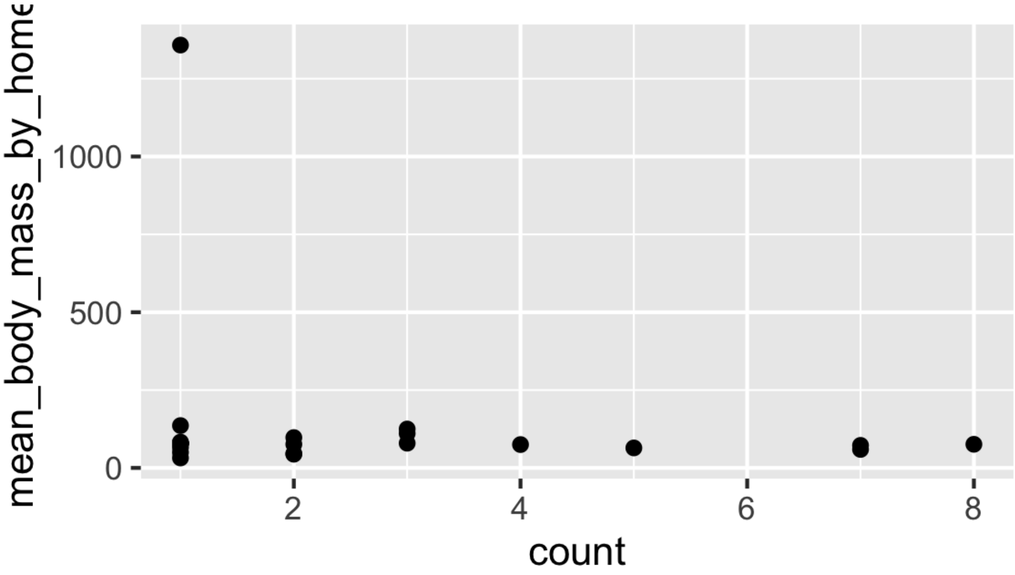
```
starwars %>%
  filter(!is.na(mass) & !is.na(films)) %>%
  group_by(films) %>%
  summarize(mean_body_mass_by_home = mean(mass),
            count = n())
```

```
## # A tibble: 23 x 3
##    films     mean_body_mass_by_home count
##    <list>                     <dbl> <int>
##  1 <chr [5]>                   79.3     3
##  2 <chr [6]>                   76       2
##  3 <chr [7]>                   32       1
##  4 <chr [4]>                  136       1
##  5 <chr [3]>                   97.5     2
##  6 <chr [1]>                   75       4
##  7 <chr [3]>                   75.9     8
##  8 <chr [4]>                   80       1
##  9 <chr [3]>                 1358       1
## 10 <chr [3]>                   77       1
## # … with 13 more rows
```

Summarize

- pipe output into `ggplot`

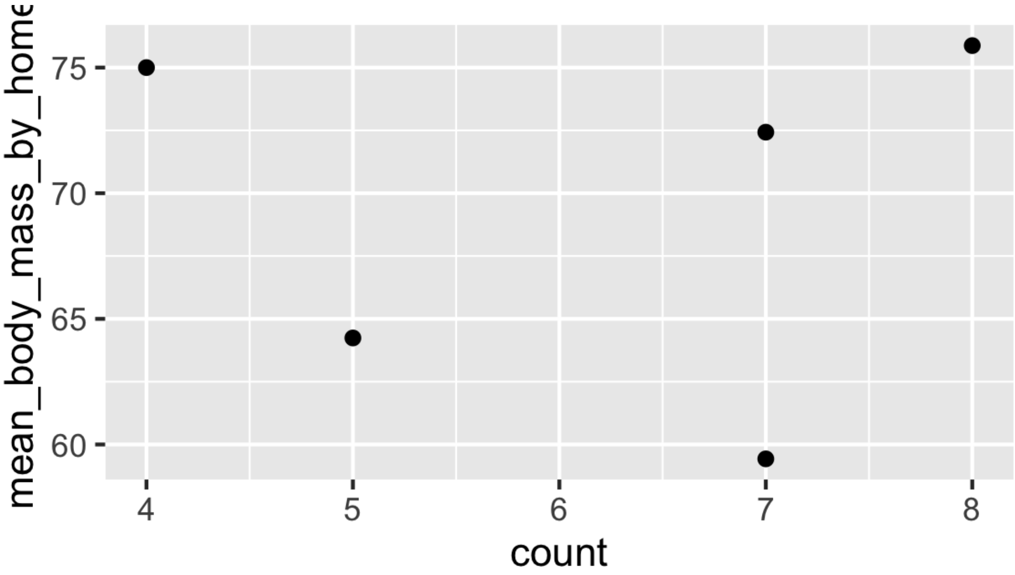
```
starwars %>%
  filter(!is.na(mass) & !is.na(films)) %>%
  group_by(films) %>%
  summarize(mean_body_mass_by_home = mean(mass),
            count = n()) %>%
  ggplot(aes(x = count, y = mean_body_mass_by_home)) +
  geom_point()
```



Summarize

- Only plot the average body masses for characters that appear in 4 or more movies

```
starwars %>%
  filter(!is.na(mass) & !is.na(films)) %>%
  group_by(films) %>%
  summarize(mean_body_mass_by_home = mean(mass),
            count = n()) %>%
  filter(count >= 4) %>%
  ggplot(aes(x = count, y = mean_body_mass_by_home)) +
  geom_point()
```



Question

- Which character has the highest body mass?

```
starwars %>%
  select(name, mass) %>%
  arrange(desc(mass))
```

```
## # A tibble: 87 x 2
##    name                   mass
##    <chr>                 <dbl>
##  1 Jabba Desilijic Tiure  1358
##  2 Grievous                159
##  3 IG-88                   140
##  4 Darth Vader             136
##  5 Tarfful                 136
##  6 Owen Lars               120
##  7 Bossk                   113
##  8 Chewbacca               112
##  9 Jek Tono Porkins        110
## 10 Dexter Jettster         102
## # … with 77 more rows
```

Question

- Plot the average `height` by species vs. the average `mass` by `species`

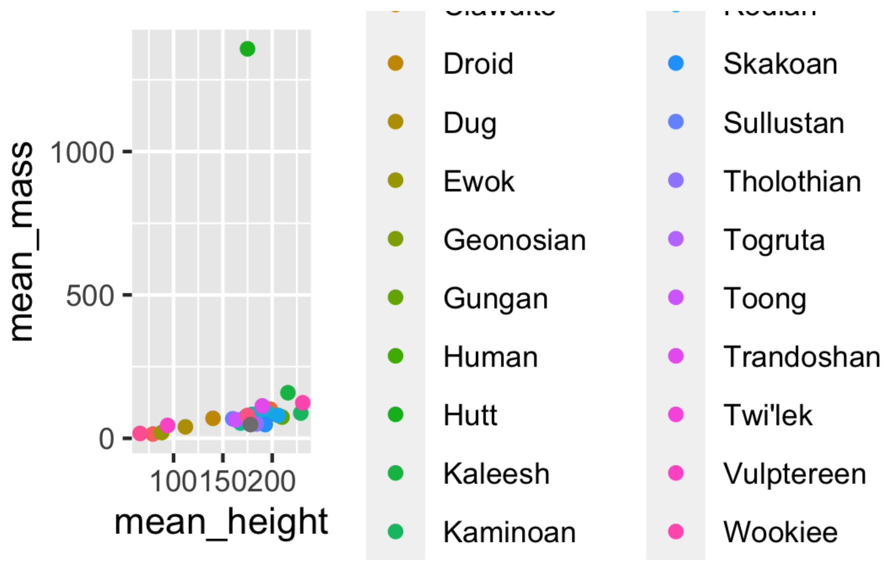
```
starwars %>%
  group_by(species) %>%
  filter(!is.na(height) & !is.na(mass)) %>%
  summarize(
    mean_height = mean(height),
    mean_mass = mean(mass),
    count = n()
  )
```

```
## # A tibble: 32 x 4
##    species   mean_height mean_mass count
##    <chr>           <dbl>     <dbl> <int>
##  1 Aleena            79       15       1
##  2 Besalisk         198      102       1
##  3 Cerean           198       82       1
##  4 Clawdite         168       55       1
##  5 Droid            140       69.8     4
##  6 Dug              112       40       1
##  7 Ewok              88       20       1
##  8 Geonosian        183       80       1
##  9 Gungan           210       74       2
## 10 Human            180.      82.8    22
## # … with 22 more rows
```

Question

- Plot the average `height` by species vs. the average `mass` by `species`

```
starwars %>%
  group_by(species) %>%
  filter(!is.na(height) & !is.na(mass)) %>%
  summarize(
    mean_height = mean(height),
    mean_mass = mean(mass)
  ) %>%
  ggplot(aes(x = mean_height, y = mean_mass, color = species)) +
  geom_point()
```



Grouping

- Can `group_by()` multiple variables
- Count the number of penguins observed from each `species` and `island`

```
penguins %>%
  group_by(species, island) %>%
  summarize(count = n())
```

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

```
## # A tibble: 5 x 3
## # Groups:   species [3]
##   species   island    count
##   <fct>     <fct>     <int>
## 1 Adelie    Biscoe       44
## 2 Adelie    Dream        56
## 3 Adelie    Torgersen    52
## 4 Chinstrap Dream        68
## 5 Gentoo    Biscoe      124
```

Grouping

- Then `ungroup()` to resume the calculations

```
penguins %>%
  group_by(species, island) %>%
  summarize(count = n()) %>%
  ungroup() %>%
  summarize(total = sum(count))
```

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

```
## # A tibble: 1 x 1
##   total
##   <int>
## 1   344
```

Grouping

- Filter the data to only contain penguin species have 100 observations or more?

```
penguins %>%
  group_by(species) %>%
  filter(n() >= 100)
```

```
## # A tibble: 276 x 8
## # Groups:   species [2]
##    species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
##  2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
##  3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
##  4 Adelie  Torgersen           NA            NA                  NA          NA <NA>    2007
##  5 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
##  6 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
##  7 Adelie  Torgersen           38.9          17.8               181        3625 female  2007
##  8 Adelie  Torgersen           39.2          19.6               195        4675 male    2007
##  9 Adelie  Torgersen           34.1          18.1               193        3475 <NA>    2007
## 10 Adelie  Torgersen           42            20.2               190        4250 <NA>    2007
## # … with 266 more rows
```

Grouping

- Is there a difference in mean `body_mass_g` between penguin `species` on the different `islands`?

```
penguins %>%
  group_by(species, island) %>%
  filter(!is.na(body_mass_g)) %>%
  summarize(mean_mass = mean(body_mass_g),
            count = n())
```

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

## # A tibble: 5 x 4
## # Groups:   species [3]
##   species   island    mean_mass count
##   <fct>     <fct>         <dbl> <int>
## 1 Adelie    Biscoe        3710.    44
## 2 Adelie    Dream         3688.    56
## 3 Adelie    Torgersen     3706.    51
## 4 Chinstrap Dream         3733.    68
## 5 Gentoo    Biscoe        5076.   123
```

`data.frame`s and `tibble`s

- The default data object in `R` is the `data.frame`
- A `tibble` is a `data.frame` with extra bells and whistles

```
data("iris")
class(iris)
```

```
## [1] "data.frame"
```

```
iris_tibble <- as_tibble(iris)
class(iris_tibble)
```

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

Creating `tibbles`

```
dat <- data.frame(x = 1:5, y = rnorm(5), z = letters[1:5])
glimpse(dat)
```

```
## Rows: 5
## Columns: 3
## $ x <int> 1, 2, 3, 4, 5
## $ y <dbl> -1.07908605196321638608481, -0.01375981518563124117449, 0.73639613403315984374586, -0.
## $ z <chr> "a", "b", "c", "d", "e"
```

```
dat_tibble <- tibble(x = 1:5, y = rnorm(5), z = letters[1:5])
glimpse(dat_tibble)
```

```
## Rows: 5
## Columns: 3
## $ x <int> 1, 2, 3, 4, 5
## $ y <dbl> -0.5636274879810749816045, 0.9625499602714389091318, -1.1225359576985030063412, 0.3231
## $ z <chr> "a", "b", "c", "d", "e"
```

Working with `tibbles`

- Better printing of data
- Easier to perform grouping and nesting operations
- Subsetting tibbles
    - `$` and `[[`
    - `[[` can subset by variable name or index (counting base starts at 1)
    - `$` subsets by variable name only

```
starwars$name
```

```
##  [1] "Luke Skywalker"        "C-3PO"                 "R2-D2"                 "Darth Vader"
##  [8] "R5-D4"                 "Biggs Darklighter"     "Obi-Wan Kenobi"        "Anakin Skywalker"
## [15] "Greedo"                "Jabba Desilijic Tiure" "Wedge Antilles"        "Jek Tono Porkins"
## [22] "IG-88"                 "Bossk"                 "Lando Calrissian"      "Lobot"
## [29] "Wicket Systri Warrick" "Nien Nunb"             "Qui-Gon Jinn"          "Nute Gunray"
## [36] "Rugor Nass"            "Ric Olié"              "Watto"                 "Sebulba"
## [43] "Bib Fortuna"           "Ayla Secura"           "Dud Bolt"              "Gasgano"
## [50] "Kit Fisto"             "Eeth Koth"             "Adi Gallia"            "Saesee Tiin"
## [57] "Gregar Typho"          "Cordé"                 "Cliegg Lars"           "Poggle the Lesser"
## [64] "Dooku"                 "Bail Prestor Organa"   "Jango Fett"            "Zam Wesell"
## [71] "Jocasta Nu"            "Ratts Tyerell"         "R4-P17"                "Wat Tambor"
## [78] "Tarfful"               "Raymus Antilles"       "Sly Moore"             "Tion Medon"
## [85] "BB8"                   "Captain Phasma"        "Padmé Amidala"
```

```
starwars[["name"]]
```

```
##  [1] "Luke Skywalker"        "C-3PO"                 "R2-D2"                 "Darth Vader"
##  [8] "R5-D4"                 "Biggs Darklighter"     "Obi-Wan Kenobi"        "Anakin Skywalker"
## [15] "Greedo"                "Jabba Desilijic Tiure" "Wedge Antilles"        "Jek Tono Porkins"
## [22] "IG-88"                 "Bossk"                 "Lando Calrissian"      "Lobot"
## [29] "Wicket Systri Warrick" "Nien Nunb"             "Qui-Gon Jinn"          "Nute Gunray"
## [36] "Rugor Nass"            "Ric Olié"              "Watto"                 "Sebulba"
## [43] "Bib Fortuna"           "Ayla Secura"           "Dud Bolt"              "Gasgano"
## [50] "Kit Fisto"             "Eeth Koth"             "Adi Gallia"            "Saesee Tiin"
## [57] "Gregar Typho"          "Cordé"                 "Cliegg Lars"           "Poggle the Lesser"
## [64] "Dooku"                 "Bail Prestor Organa"   "Jango Fett"            "Zam Wesell"
## [71] "Jocasta Nu"            "Ratts Tyerell"         "R4-P17"                "Wat Tambor"
## [78] "Tarfful"               "Raymus Antilles"       "Sly Moore"             "Tion Medon"
## [85] "BB8"                   "Captain Phasma"        "Padmé Amidala"
```

```r
starwars[[1]]
```

```
##  [1] "Luke Skywalker"        "C-3PO"                 "R2-D2"                 "Darth Vader"
##  [8] "R5-D4"                 "Biggs Darklighter"     "Obi-Wan Kenobi"        "Anakin Skywalker"
## [15] "Greedo"                "Jabba Desilijic Tiure" "Wedge Antilles"        "Jek Tono Porkins"
## [22] "IG-88"                 "Bossk"                 "Lando Calrissian"      "Lobot"
## [29] "Wicket Systri Warrick" "Nien Nunb"             "Qui-Gon Jinn"          "Nute Gunray"
## [36] "Rugor Nass"            "Ric Olié"              "Watto"                 "Sebulba"
## [43] "Bib Fortuna"           "Ayla Secura"           "Dud Bolt"              "Gasgano"
## [50] "Kit Fisto"             "Eeth Koth"             "Adi Gallia"            "Saesee Tiin"
## [57] "Gregar Typho"          "Cordé"                 "Cliegg Lars"           "Poggle the Lesser"
## [64] "Dooku"                 "Bail Prestor Organa"   "Jango Fett"            "Zam Wesell"
## [71] "Jocasta Nu"            "Ratts Tyerell"         "R4-P17"                "Wat Tambor"
## [78] "Tarfful"               "Raymus Antilles"       "Sly Moore"             "Tion Medon"
## [85] "BB8"                   "Captain Phasma"        "Padmé Amidala"
```

```r
starwars %>%
  .$name
```

```
##  [1] "Luke Skywalker"        "C-3PO"                 "R2-D2"                 "Darth Vader"
##  [8] "R5-D4"                 "Biggs Darklighter"     "Obi-Wan Kenobi"        "Anakin Skywalker"
## [15] "Greedo"                "Jabba Desilijic Tiure" "Wedge Antilles"        "Jek Tono Porkins"
## [22] "IG-88"                 "Bossk"                 "Lando Calrissian"      "Lobot"
## [29] "Wicket Systri Warrick" "Nien Nunb"             "Qui-Gon Jinn"          "Nute Gunray"
## [36] "Rugor Nass"            "Ric Olié"              "Watto"                 "Sebulba"
## [43] "Bib Fortuna"           "Ayla Secura"           "Dud Bolt"              "Gasgano"
## [50] "Kit Fisto"             "Eeth Koth"             "Adi Gallia"            "Saesee Tiin"
## [57] "Gregar Typho"          "Cordé"                 "Cliegg Lars"           "Poggle the Lesser"
## [64] "Dooku"                 "Bail Prestor Organa"   "Jango Fett"            "Zam Wesell"
## [71] "Jocasta Nu"            "Ratts Tyerell"         "R4-P17"                "Wat Tambor"
## [78] "Tarfful"               "Raymus Antilles"       "Sly Moore"             "Tion Medon"
## [85] "BB8"                   "Captain Phasma"        "Padmé Amidala"
```

Reading files

- Many options to read files
  - Different file types can have different methods to read files
- Base `R` options
  - `read.table()`, `read.csv()`, `read.csv2()`, `read.delim()`, `read.delim2()`
- Excel file type methods using the `readxl` package
  - `read_excel()`, `read_xls()`, `read_xlsx()`
- Reading files using the `readr` package
  - `read_csv()` reads comma separated value (csv) files
    - `read_csv2()` reads semicolon separated files (Europeans and others use `,` instead of `.` in decimal numbers)
  - `read_tsv()` reads tab delimited files
  - `read_delim()` reads generic delimiter files

Reading files

- Player performance for NHL players

```
file_path <- here::here("data", "game_goals.csv")
file_path
```

```
## [1] "/Users/tips/dasc1104-teaching/data/game_goals.csv"
```

```
dat <- read_csv(file_path)
```

```
##
## ── Column specification ────────────────────────────────────────────────
## cols(
##   .default = col_double(),
##   player = col_character(),
##   date = col_date(format = ""),
##   age = col_character(),
##   team = col_character(),
##   at = col_character(),
##   opp = col_character(),
##   location = col_character(),
##   outcome = col_character()
## )
## ℹ Use `spec()` for the full column specifications.
```

```
glimpse(dat)
```

```
## Rows: 49,384
## Columns: 25
## $ player            <chr> "Alex Ovechkin", "Alex Ovechkin", "Alex Ovechkin", "Alex Ovechkin", "A
## $ season            <dbl> 2006, 2006, 2006, 2006, 2006, 2006, 2006, 2006, 2006, 2006, 2006, 2006
## $ rank              <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,
## $ date              <date> 2005-10-05, 2005-10-07, 2005-10-08, 2005-10-10, 2005-10-12, 2005-10-1
## $ game_num          <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,
## $ age               <chr> "20-018", "20-020", "20-021", "20-023", "20-025", "20-026", "20-029",
## $ team              <chr> "WSH", "WSH", "WSH", "WSH", "WSH", "WSH", "WSH", "WSH", "WSH", "WSH",
## $ at                <chr> NA, NA, "@", NA, "@", NA, NA, "@", NA, "@", "@", "@", NA, NA, "@", NA,
## $ opp               <chr> "CBJ", "ATL", "ATL", "NYR", "CAR", "NYI", "TBL", "FLA", "CAR", "BUF",
## $ location          <chr> "Home", "Home", "Away", "Home", "Away", "Home", "Home", "Away", "Home"
## $ outcome           <chr> "W", "L", "L", "W", "L", "L", "W", "L", "L", "W", "L", "L", "W", "W",
## $ goals             <dbl> 2, 0, 0, 1, 1, 0, 0, 2, 0, 0, 2, 0, 0, 2, 2, 1, 0, 1, 1, 0, 0, 0, 0, 0
## $ assists           <dbl> 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1
## $ points            <dbl> 2, 1, 1, 1, 1, 1, 1, 2, 0, 1, 2, 0, 0, 2, 2, 1, 0, 1, 2, 0, 1, 1, 1, 1
## $ plus_minus        <dbl> 1, -2, 0, 1, 0, -1, 1, 1, 0, 0, 0, -2, 1, -1, -2, 0, 0, 0, -1, 1, 1, -
## $ penalty_min       <dbl> 2, 0, 4, 2, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 4, 0, 0, 0, 2, 0, 0, 0, 0, 0
## $ goals_even        <dbl> 1, 0, 0, 0, 1, 0, 0, 2, 0, 0, 1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0
## $ goals_powerplay   <dbl> 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0
## $ goals_short       <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0
## $ goals_gamewinner  <dbl> 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0
## $ assists_even      <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA
## $ assists_powerplay <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA
## $ assists_short     <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA
## $ shots             <dbl> 5, 1, 3, 6, 6, 5, 2, 10, 2, 5, 4, 7, 7, 8, 7, 5, 3, 9, 7, 5, 4, 0, 9,
## $ shot_percent      <dbl> 40.000000000000000000000, 0.000000000000000000000, 0.00000000000000000
```

- For players who took at least 100 shots in the 2014 season, which play had the highest mean shot percentage?

```
dat %>%
  filter(season == 2014) %>%
  group_by(player) %>%
  filter(!is.na(shots) & !is.na(shot_percent)) %>%
  summarize(total_shots = sum(shots),
            mean_shot_percent = mean(shot_percent)) %>%
  filter(total_shots >= 100) %>%
  arrange(desc(mean_shot_percent))
```

```
## # A tibble: 29 x 3
##    player          total_shots mean_shot_percent
##    <chr>                 <dbl>             <dbl>
##  1 Steven Stamkos          124              20.5
##  2 Anze Kopitar            200              19.1
##  3 Joe Pavelski            225              17.0
##  4 Corey Perry             280              16.9
##  5 Jarome Iginla           209              16.0
##  6 Brad Marchand           149              15.9
##  7 Ryan Getzlaf            204              15.5
##  8 Patrick Kane            227              14.9
##  9 Jamie Benn              279              14.8
## 10 Jaromir Jagr            231              14.3
## # … with 19 more rows
```

- Data about measles vaccine

```
file_path <- here::here("data", "measles.csv")
file_path
```

```
## [1] "/Users/tips/dasc1104-teaching/data/measles.csv"
```

```
dat <- read_csv(file_path)
```

```
##
## ── Column specification ────────────────────────────────────────────────
## cols(
##   index = col_double(),
##   state = col_character(),
##   year = col_character(),
##   name = col_character(),
##   type = col_character(),
##   city = col_character(),
##   county = col_character(),
##   district = col_logical(),
##   enroll = col_double(),
##   mmr = col_double(),
##   overall = col_double(),
##   xrel = col_logical(),
##   xmed = col_double(),
##   xper = col_double(),
##   lat = col_double(),
##   lng = col_double()
## )
```

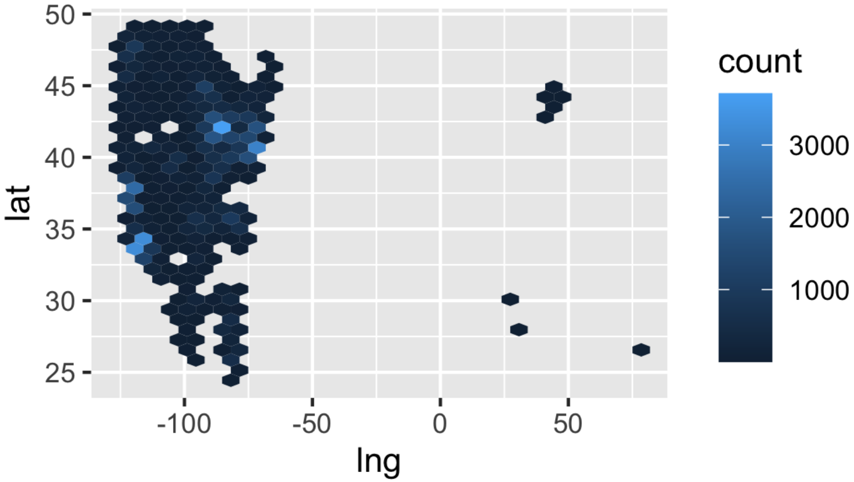
```
glimpse(dat)
```

```
## Rows: 66,113
## Columns: 16
## $ index    <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 10, 11, 12, 13, 14, 15, 15, 16, 17, 18, 19, 20,
## $ state    <chr> "Arizona", "Arizona", "Arizona", "Arizona", "Arizona", "Arizona", "Arizona", "A
## $ year     <chr> "2018-19", "2018-19", "2018-19", "2018-19", "2018-19", "2018-19", "2018-19", "2
## $ name     <chr> "A J Mitchell Elementary", "Academy Del Sol", "Academy Del Sol - Hope", "Academ
## $ type     <chr> "Public", "Charter", "Charter", "Charter", "Charter", "Public", "Charter", "Cha
## $ city     <chr> "Nogales", "Tucson", "Tucson", "Phoenix", "Phoenix", "Phoenix", "Phoenix", "Yum
## $ county   <chr> "Santa Cruz", "Pima", "Pima", "Maricopa", "Maricopa", "Maricopa", "Maricopa", "
## $ district <lgl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
## $ enroll   <dbl> 51, 22, 85, 60, 43, 36, 24, 22, 26, 78, 78, 35, 54, 54, 34, 57, 57, 47, 54, 98,
## $ mmr      <dbl> 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100,
## $ overall  <dbl> -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1,
## $ xrel     <lgl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
## $ xmed     <dbl> NA, NA, NA, NA, 2.33000000000000071054, NA, NA, NA, NA, NA, NA, 2.8599999999999
## $ xper     <dbl> NA, NA, NA, NA, 2.33000000000000071054, NA, 4.16999999999999928946, NA, NA, N
## $ lat      <dbl> 31.34781890000000004193, 32.22192150000000054888, 32.13049319999999653419, 33.4
## $ lng      <dbl> -110.93803139999999998487, -110.89610310000000048152, -111.11700480000000036836, -
```

- Plot the locations of measles outbreaks

```
dat %>%
  ggplot(aes(x = lng, y = lat)) +
  geom_hex()
```

```
## Warning: Removed 1549 rows containing non-finite values (stat_binhex).
```



- A subset of speeches at Trump rallies

```
file_path <- here::here("data", "Trump_rallies")
all_files <- list.files(file_path, pattern = ".txt")

dat <- list()

for (i in 1:length(all_files)) {
  dat[[i]] <- read_file(paste(file_path, all_files[i], sep = "/"))
}
```

- Trump rally speeches

```
glimpse(dat)
```

```
## List of 35
##  $ : chr "Thank you. Thank you. Thank you to Vice President Pence. He's a good guy. We've done a
##  $ : chr "There's a lot of people. That's great. Thank you very much. Thank you very much. That'
##  $ : chr "Thank you. Thank you. Thank you. All I can say is that the fake news just doesn't get
##  $ : chr "I want to thank you very much. North Carolina, thank you very much. I'm thrilled to ba
##  $ : chr "Thank you all. Thank you very much. Thank you to Vice President Mike Pence, and hello
##  $ : chr "Hello Colorado. We love Colorado, most beautiful place And I'm thrilled to be back in
##  $ : chr "Thank you. Thank you very much. Hello Dallas. It's great to be with you tonight. Thank
##  $ : chr "I worked so hard for this state. I worked so hard. You just got two of the greatest tr
##  $ : chr "What a crowd, what a crowd. Get those people over here. See me. Let them come over. Wh
##  $ : chr " Thank you everybody. Thank you and Vice President Mike Pence, thank you very much. In
##  $ : chr "We brought you a lot of car plants, Michigan. We brought you a lot of car plants. You
##  $ : chr "Thank you very much. Thank you. Thank you. Thank you to Greenville, North Carolina, I
##  $ : chr "Thank you, thank you. Wow. Wow, and I'm thrilled to be here with you in Henderson. Tho
##  $ : chr " Well, thank you to Vice President Pence. Thank you, Mike. And hello Pennsylvania. Hel
##  $ : chr "Well, thank you very much. And hello Las Vegas. Great to be with you. They have a big
##  $ : chr "So thank you Pennsylvania, very much. I'm thrilled to be in Latrobe, the home of the l
##  $ : chr "Thank you very much and thank you to the original Lee Greenwood. Thank you. Thank you,
##  $ : chr "Well thank you very much. And I'm thrilled to be back in Wisconsin where we had a very
##  $ : chr "Well, I thank you very much. So I want to start by saying, \"Hello, Nevada. How are yo
##  $ : chr "Thank you very much. Thank you, Minnesota. This is a great state. We are going to win
##  $ : chr "Thank you, thank you very much. Thank you very much. That is a beautiful site right be
##  $ : chr " Thank you very much everybody. Thank you. Wow. I will never, ever let you down, that
##  $ : chr "Hello, everybody. Hello, everybody. Wow. Hello, everybody. Thank you. Thank you. And I
##  $ : chr "Hello, Manchester, and I am thrilled to be in the great state of New Hampshire with th
##  $ : chr " Wow, thank you. Thank you, New Mexico. Thank you. We love being with you. We love bei
##  $ : chr "Wow, that's a big crowd. This is a big crowd. Thank you very much, everybody. Hello to
##  $ : chr " Thank you very much, Phoenix. We love to be back. We'll be back a lot. We're going to
##  $ : chr "Doesn't have the power. Doesn't have the staying power. You see what's happening in Ca
##  $ : chr "Hello, Houston. I am so thrilled to be here in the great state of Texas with one of Am
```

- examine the fist speech

```r
library(tidytext)
# examine the fist speech
dat[[1]] %>%
  tibble(text = .) %>%
  drop_na() %>%
  unnest_tokens(word, text) %>%
  group_by(word) %>%
  summarize(count = n()) %>%
  arrange(desc(count))## from tidytext package
```

```
## # A tibble: 2,113 x 2
##    word  count
##    <chr> <int>
##  1 the     702
##  2 i       508
##  3 and     497
##  4 you     480
##  5 to      427
##  6 a       366
##  7 they    318
##  8 of      311
##  9 it      279
## 10 that    260
## # … with 2,103 more rows
```

- examine the fist speech (remove the "stop" words)

```r
library(tidytext)
dat[[1]] %>%
  tibble(text = .) %>%
  drop_na() %>%
  unnest_tokens(word, text) %>%
  anti_join(stop_words) %>%
  group_by(word) %>%
  summarize(count = n()) %>%
  arrange(desc(count))## from tidytext package
```

```
## Joining, by = "word"

## # A tibble: 1,693 x 2
##    word      count
##    <chr>     <int>
##  1 people      112
##  2 michigan     50
##  3 country      47
##  4 time         42
##  5 lot          39
##  6 president    38
##  7 love         33
##  8 deal         30
##  9 remember     27
## 10 democrats    24
## # … with 1,683 more rows
```

Examine the fist speech with a word cloud

```r
library(tidytext)
library(wordcloud2)
dat[[1]] %>%
  tibble(text = .) %>%
  drop_na() %>%
  unnest_tokens(word, text) %>% ## from tidytext package
  anti_join(stop_words) %>%     ## from tidytext package
  group_by(word) %>%
  summarize(count = n()) %>%
  wordcloud2()
```

Examine the fist speech with a word cloud

```
<div id="htmlwidget-766398535c149d60ef72" style="width:60%;height:648px;" class="wordclo
<script type="application/json" data-for="htmlwidget-766398535c149d60ef72">{"x":{"word":
```

File I/O

- Data about Jelle's Marble Run

```
filename <- here::here("data", "marbles.csv")
dat <- read_csv(filename)
```

```
##
## ── Column specification ──────────────────────────────────────────────
## cols(
##   `# Data from Jelle's Marble Run https://www.youtube.com/channel/UCYJdpnjuSWVOLgGT9fIzL0g` = co
## )

## Warning: 257 parsing failures.
## row col  expected    actual                                            file
##   1  -- 1 columns 14 columns '/Users/tips/dasc1104-teaching/data/marbles.csv'
##   2  -- 1 columns 14 columns '/Users/tips/dasc1104-teaching/data/marbles.csv'
##   3  -- 1 columns 14 columns '/Users/tips/dasc1104-teaching/data/marbles.csv'
##   4  -- 1 columns 14 columns '/Users/tips/dasc1104-teaching/data/marbles.csv'
##   5  -- 1 columns 14 columns '/Users/tips/dasc1104-teaching/data/marbles.csv'
## ... ... ......... .......... ..............................................
## See problems(...) for more details.
```

- What went wrong?

```
glimpse(dat)
```

```
## Rows: 257
## Columns: 1
## $ `# Data from Jelle's Marble Run https://www.youtube.com/channel/UCYJdpnjuSWVOLgGT9fIzL0g` <chr
```

- Let's look at the file in the terminal using the head command

```
head ./data/marbles.csv
```

```
# Data from Jelle's Marble Run https://www.youtube.com/channel/UCYJdpnjuSWVOLgGT9fIzL0g
date,race,site,source,marble_name,team_name,time_s,pole,points,track_length_m,number_laps,avg_time_
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Clementin,O'rangers,28.11,P1,NA,1
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Starry,Team Galactic,28.37,P2,NA,
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Momo,Team Momo,28.4,P3,NA,12.81,1
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Yellow,Mellow Yellow,28.7,P4,NA,1
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Snowy,Snowballs,28.71,P5,NA,12.81
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Razzy,Raspberry Racers,28.72,P6,N
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Prim,Team Primary,28.96,P7,NA,12.
15-Feb-20,S1Q1,Savage Speedway,https://youtu.be/JtsQ_UydjEI?t=356,Vespa,Hornets,29.11,P8,NA,12.81,1
```

- There is a line before the variable names!

Skipping lines when reading files

```r
filename <- here::here("data", "marbles.csv")
dat <- read_csv(filename, skip = 1)
```

```
##
## ── Column specification ──────────────────────────────────────────────────
## cols(
##   date = col_character(),
##   race = col_character(),
##   site = col_character(),
##   source = col_character(),
##   marble_name = col_character(),
##   team_name = col_character(),
##   time_s = col_double(),
##   pole = col_character(),
##   points = col_double(),
##   track_length_m = col_double(),
##   number_laps = col_double(),
##   avg_time_lap = col_double(),
##   host = col_character(),
##   notes = col_character()
## )
```

Parsing vectors

- The `parse_*()` functions

```
parse_logical(c(TRUE, FALSE, "TRUE", "FALSE", 1, 0, NA, "ABC"))
```

```
## Warning: 1 parsing failure.
## row col           expected actual
##   8  -- 1/0/T/F/TRUE/FALSE    ABC

## [1]  TRUE FALSE  TRUE FALSE  TRUE FALSE    NA    NA
## attr(,"problems")
## # A tibble: 1 x 4
##     row   col expected           actual
##   <int> <int> <chr>              <chr>
## 1     8    NA 1/0/T/F/TRUE/FALSE ABC
```

```
parse_double(c(2.4, "5.7", 22/7, NA, "ABC"))
```

```
## Warning: 1 parsing failure.
## row col expected actual
##   5  -- a double    ABC

## [1] 2.39999999999999911182 5.70000000000000177636 3.14285714285714012916                      NA
## attr(,"problems")
## # A tibble: 1 x 4
##     row   col expected actual
##   <int> <int> <chr>    <chr>
## 1     5    NA a double ABC
```

Parsing vectors

```
parse_integer(c(1, "3", 4.5, NA, "ABC"))
```

```
## Warning: 2 parsing failures.
## row col               expected actual
##   3  -- no trailing characters    4.5
##   5  -- an integer                ABC

## [1]  1  3 NA NA NA
## attr(,"problems")
## # A tibble: 2 x 4
##     row   col expected               actual
##   <int> <int> <chr>                  <chr>
## 1     3    NA no trailing characters 4.5
## 2     5    NA an integer             ABC
```

```
parse_factor(c("A", "B", "C", "A"))
```

```
## [1] A B C A
## Levels: A B C
```

Parsing vectors

```
parse_date(c("2020-10-31", "2020/10/28", NA))
```

```
## [1] "2020-10-31" "2020-10-28" NA
```

```
parse_date("02/18/2020", "%m/%d/%Y")
```

```
## [1] "2020-02-18"
```

```
parse_time(c("6:22:16", "22:16"))
```

```
## 06:22:16
## 22:16:00
```

Parsing a file

- When you load a file using `read_*()` functions, `R` guesses which `parse_*()` functions should be applied to each column

```
guess_parser(c(2.5, 7))
```

```
## [1] "double"
```

```
guess_parser(c(2.5, "3"))
```

```
## [1] "double"
```

```
guess_parser(c("ABC", "FALSE"))
```

```
## [1] "character"
```

```
guess_parser(c(TRUE, FALSE, NA))
```

```
## [1] "logical"
```

Writng to files

- Use `write_csv()` to write data to a csv file
  - Can load the data with `read_csv()`
- Use `write_rds()` and `read_rds()` to save and load compressed R data files
  - very useful when running long code to save the output to a file
- Use the `feather` package for file types that are compatible with both `R` and `python`
  - Cross-language and very fast
- Can check if a directory exists and create it if it doesn't

```r
if(!dir.exists(here::here("results"))) {
  dir.create(here::here("results"))
}
```

Writng to files

```
write_csv(dat, path = here::here("results", "marbles-clean.csv"))
```

```
write_rds(dat, path = here::here("results", "marbles-clean.rds"))
```

```
# remove the data.frame
rm(dat)
glimpse(dat)
```

```
## Error in glimpse(dat): object 'dat' not found
```

```
# useful for saving long-running chunks of code
dat <- read_rds(here::here("results", "marbles-clean.rds"))
```

```
glimpse(dat)
```

```
## Rows: 256
## Columns: 14
## $ date          <chr> "15-Feb-20", "15-Feb-20", "15-Feb-20", "15-Feb-20", "15-Feb-20", "15-Feb-20"
## $ race          <chr> "S1Q1", "S1Q1", "S1Q1", "S1Q1", "S1Q1", "S1Q1", "S1Q1", "S1Q1", "S1Q1", "S1Q
## $ site          <chr> "Savage Speedway", "Savage Speedway", "Savage Speedway", "Savage Speedway", "
## $ source        <chr> "https://youtu.be/JtsQ_UydjEI?t=356", "https://youtu.be/JtsQ_UydjEI?t=356", "
## $ marble_name   <chr> "Clementin", "Starry", "Momo", "Yellow", "Snowy", "Razzy", "Prim", "Vespa", "
## $ team_name     <chr> "O'rangers", "Team Galactic", "Team Momo", "Mellow Yellow", "Snowballs", "Ra
## $ time_s        <dbl> 28.10999999999999943157, 28.37000000000000099476, 28.39999999999999857891, 28
## $ pole          <chr> "P1", "P2", "P3", "P4", "P5", "P6", "P7", "P8", "P9", "P10", "P11", "P12", "P
## $ points        <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 25, 18, 15, 
## $ track_length_m <dbl> 12.81000000000000049738, 12.81000000000000049738, 12.81000000000000049738, 12
```

Tidy data

- Consistent data formats make analysis much easier
- Tidy data has each observation as a row and each variable as a column

Tall vs. wide data

- "Tall" data

```
tall_data <- read.table(header=TRUE, text
 subject sex condition measurement
       1   M   control         7.9
       1   M     cond1        12.3
       1   M     cond2        10.7
       2   F   control         6.3
       2   F     cond1        10.6
       2   F     cond2        11.1
       3   F   control         9.5
       3   F     cond1        13.1
       3   F     cond2        13.8
       4   M   control        11.5
       4   M     cond1        13.4
       4   M     cond2        12.9
')
# Make sure the subject column is a facto
tall_data$subject <- factor(tall_data$sub
```

- "Wide" data

```
wide_data <- read.table(header=TRUE, text
 subject sex control cond1 cond2
       1   M     7.9  12.3  10.7
       2   F     6.3  10.6  11.1
       3   F     9.5  13.1  13.8
       4   M    11.5  13.4  12.9
')
# Make sure the subject column is a facto
wide_data$subject <- factor(wide_data$sub
```

Tall vs. wide data

```
tall_data
```

```
##    subject sex condition              measurement
## 1        1   M   control  7.900000000000000355271
## 2        1   M     cond1 12.300000000000000710543
## 3        1   M     cond2 10.699999999999999289457
## 4        2   F   control  6.299999999999999822364
## 5        2   F     cond1 10.599999999999999644729
## 6        2   F     cond2 11.099999999999999644729
## 7        3   F   control  9.500000000000000000000
## 8        3   F     cond1 13.099999999999999644729
## 9        3   F     cond2 13.800000000000000710543
## 10       4   M   control 11.500000000000000000000
## 11       4   M     cond1 13.400000000000000355271
## 12       4   M     cond2 12.900000000000000355271
```

```
wide_data
```

```
##   subject sex                  control
## 1       1   M  7.900000000000000355271 12.3000000
## 2       2   F  6.299999999999999822364 10.5999999
## 3       3   F  9.500000000000000000000 13.0999999
## 4       4   M 11.500000000000000000000 13.4000000
```

Tall vs. wide data

- In general, tall data is preferred
    - Easier to generate summaries of the data
    - Can generate key-value pairs (dictionaries)
    - Most statistical models require long data for inputs

Convert from tall to wide

```
tall_data
```

```
##    subject sex condition              measurement
## 1        1   M   control  7.900000000000000355271
## 2        1   M     cond1 12.300000000000000710543
## 3        1   M     cond2 10.699999999999999289457
## 4        2   F   control  6.299999999999999822364
## 5        2   F     cond1 10.599999999999999644729
## 6        2   F     cond2 11.099999999999999644729
## 7        3   F   control  9.500000000000000000000
## 8        3   F     cond1 13.099999999999999644729
## 9        3   F     cond2 13.800000000000000710543
## 10       4   M   control 11.500000000000000000000
## 11       4   M     cond1 13.400000000000000355271
## 12       4   M     cond2 12.900000000000000355271
```

```
tall_data %>%
  pivot_wider(names_from = condition, values_from = measurement)
```

```
## # A tibble: 4 x 5
##   subject sex   control cond1 cond2
##   <fct>   <chr>   <dbl> <dbl> <dbl>
## 1 1       M         7.9  12.3  10.7
## 2 2       F         6.3  10.6  11.1
## 3 3       F         9.5  13.1  13.8
## 4 4       M        11.5  13.4  12.9
```

Convert from wide to tall

```
wide_data
```

```
##   subject sex                 control                   cond1                   cond2
## 1       1   M  7.90000000000000355271 12.30000000000000071054 10.69999999999999928946
## 2       2   F  6.29999999999999822364 10.59999999999999964473 11.09999999999999964473
## 3       3   F  9.50000000000000000000 13.09999999999999964473 13.80000000000000071054
## 4       4   M 11.50000000000000000000 13.40000000000000035527 12.90000000000000035527
```

```
wide_data %>%
  pivot_longer(cols = c(control, cond1, cond2), names_to = "measurement")
```

```
## # A tibble: 12 x 4
##    subject sex   measurement value
##    <fct>   <chr> <chr>       <dbl>
##  1 1       M     control       7.9
##  2 1       M     cond1        12.3
##  3 1       M     cond2        10.7
##  4 2       F     control       6.3
##  5 2       F     cond1        10.6
##  6 2       F     cond2        11.1
##  7 3       F     control       9.5
##  8 3       F     cond1        13.1
##  9 3       F     cond2        13.8
## 10 4       M     control      11.5
## 11 4       M     cond1        13.4
## 12 4       M     cond2        12.9
```

Completing data

- The `tibble` below does not have data for every case

```
df <- tibble(
  group = c(1:2, 1),
  item_id = c(1:2, 2),
  item_name = c("a", "b", "b"),
  value1 = 1:3,
  value2 = 4:6
)
```

- Complete the group variable so that `item_id` and `item_name` have all their possible combinations filled in

```
df %>% complete(group, nesting(item_id, item_name))
```

```
## # A tibble: 4 x 5
##   group item_id item_name value1 value2
##   <dbl>   <dbl> <chr>      <int>  <int>
## 1     1       1 a              1      4
## 2     1       2 b              3      6
## 3     2       1 a             NA     NA
## 4     2       2 b              2      5
```

Completing data

- Fill in the completed values

```
df %>%
  complete(group, nesting(item_id, item_name),
           fill = list(value1 = "foo", value2 = "bar"))
```

```
## # A tibble: 4 x 5
##   group item_id item_name value1 value2
##   <dbl>   <dbl> <chr>     <chr>  <chr> 
## 1     1       1 a         1      4     
## 2     1       2 b         3      6     
## 3     2       1 a         foo    bar   
## 4     2       2 b         2      5     
```