Summarising and Plotting Data in R

Advanced Data Visualisation and Putting it All Together

Glenn Williams

University of Sunderland

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Exploring Different Geoms

We aren't restricted to dot plots in R, but we can make many different plots by using different geoms. For example:

- **Bar plots**: for displaying **count data**. Often used for scale data too (only safe is normally distributed with few outliers). Height of bar shows where scores lie.
- **Box plots**: for displaying **continuous (e.g. scale) data**. Shows interquartile range, median, and outliers.
- **Violin Plots**: like box plots, but shows **density of scores** (i.e. where scores are most common).
- **Density Plots**: for checking **distributions of data** (e.g. checking normality).
- **Histograms**: the same as density plots, but more **useful with fewer observations**.

```r
data(starwars) # load data first
starwars <- filter(starwars, mass < 300) # filter out Jabba the Hutt
```

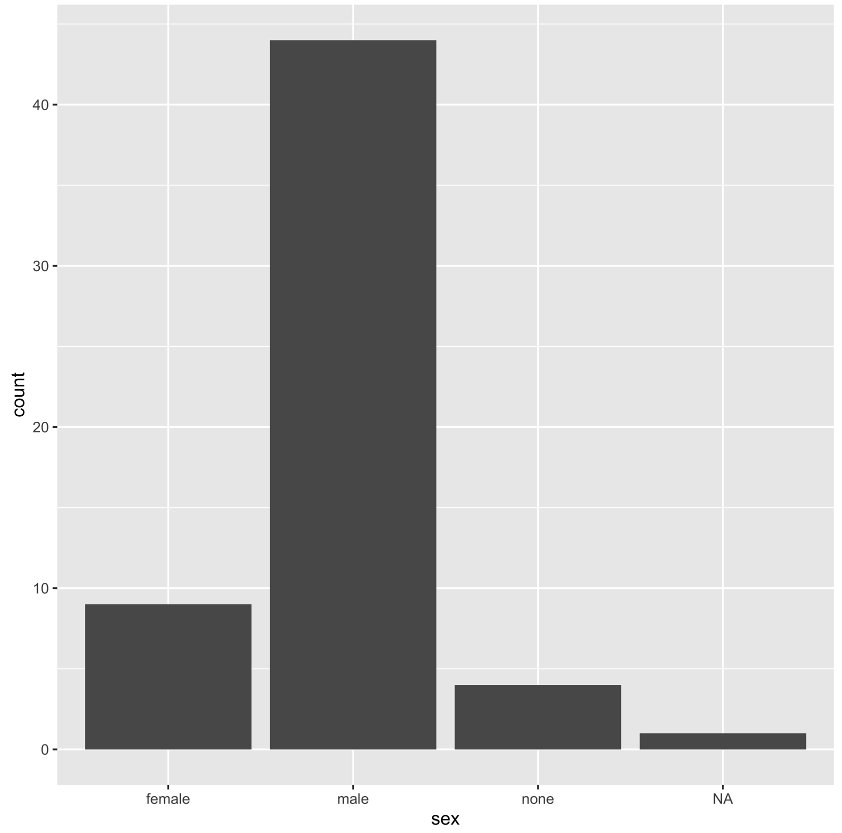
Bar Plots for Count Data

For a **bar plot of count data**, we just need to pass a column of data to the aesthetics, and say it should appear on the x-axis.

We then use `geom_bar()` to make the bar plot.

This is what this looks like for counting up characters of different sexes.

```
ggplot(data = starwars, mapping = aes(x = sex)) +
  geom_bar()
```



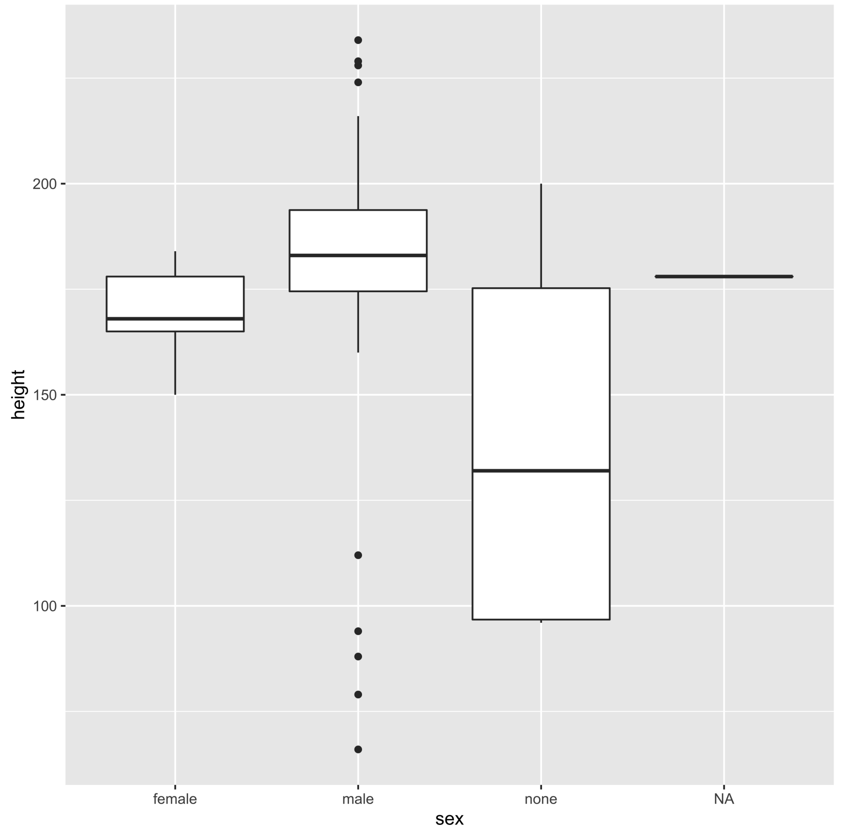
Box Plots

What if we want to display a **continuous variable** across groups? A **boxplot** is handy here.

Let's get heights of characters from each sex. Now, we just add height to the y-axis, and change `geom_bar()` to `geom_boxplot()`

```
ggplot(
  data = starwars,
  mapping = aes(x = sex,y = height)
) +
  geom_boxplot()
```

Remember, the dark line is the median, the box the middle 50% of scores.



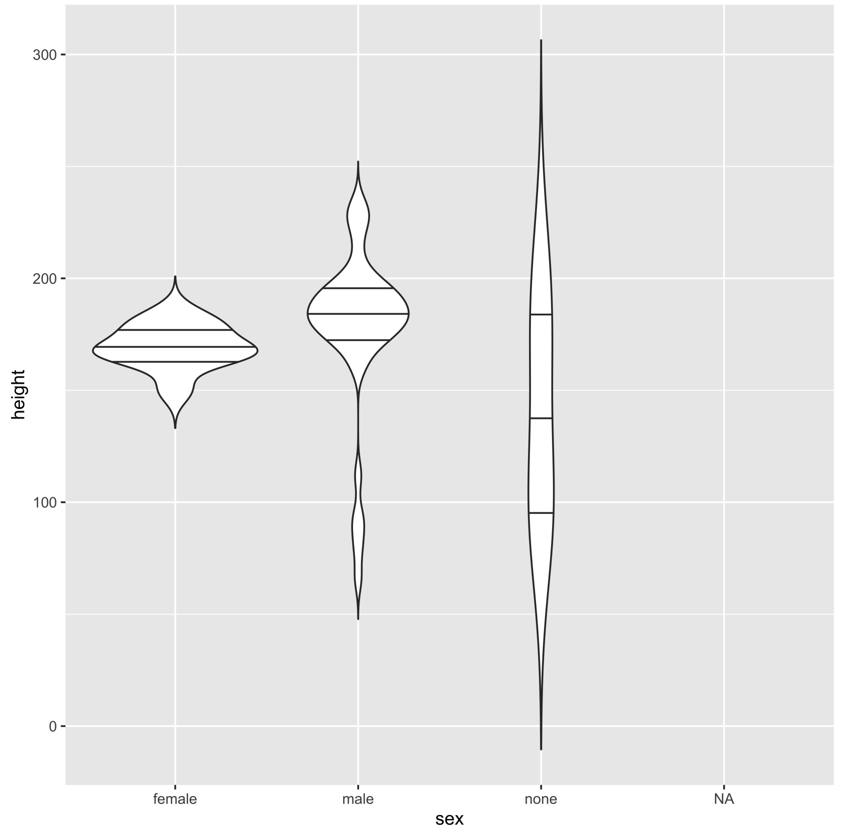
Lines represent the remainder, and dots represent outliers.

Violin Plots

We can keep all code the same in the `ggplot()` call, but change the geom to `geom_violin()`.

```
ggplot(
  data = starwars,
  aes(x = sex, y = height)
) +
  geom_violin(
    trim = FALSE,
    draw_quantiles = c(0.25, 0.5, 0.75)
  )
```

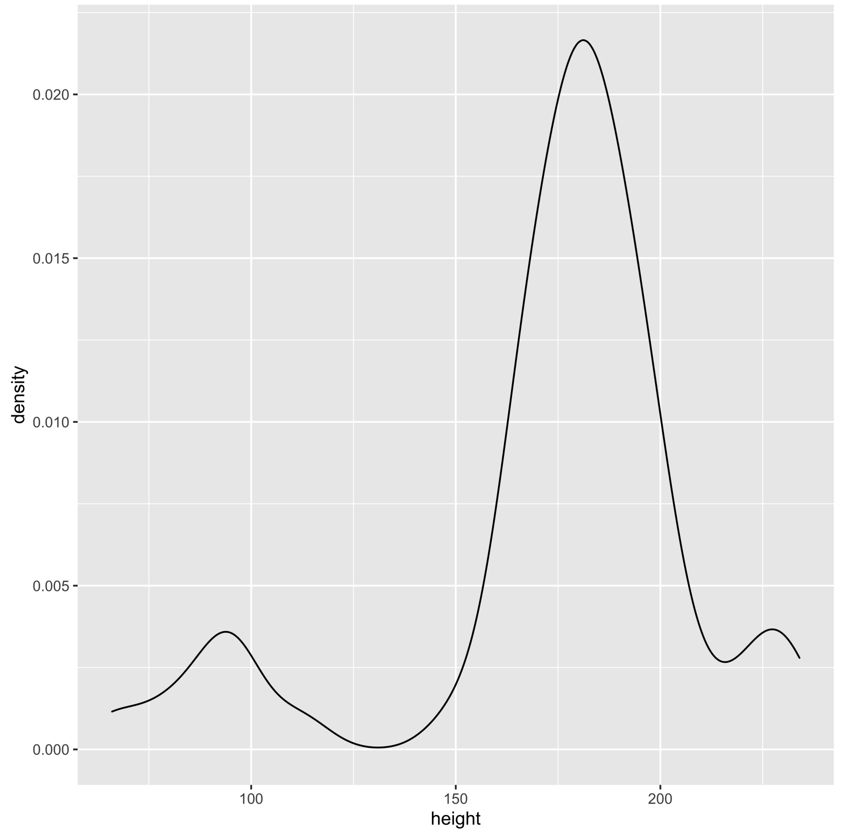
This takes some **optional arguments**. Here, I've told it to not trim the tails of scores, and to draw lines at the .25, .50, and .75 quantiles to be similar to a boxplot.



Density Plots

We can see how a variable is distributed by making a **density plot**. Use `geom_density()` and only have variable mapped to the x-axis. (The y-axis is reserved for density.)

```
ggplot(
  data = starwars,
  aes(x = height)
) +
  geom_density()
```

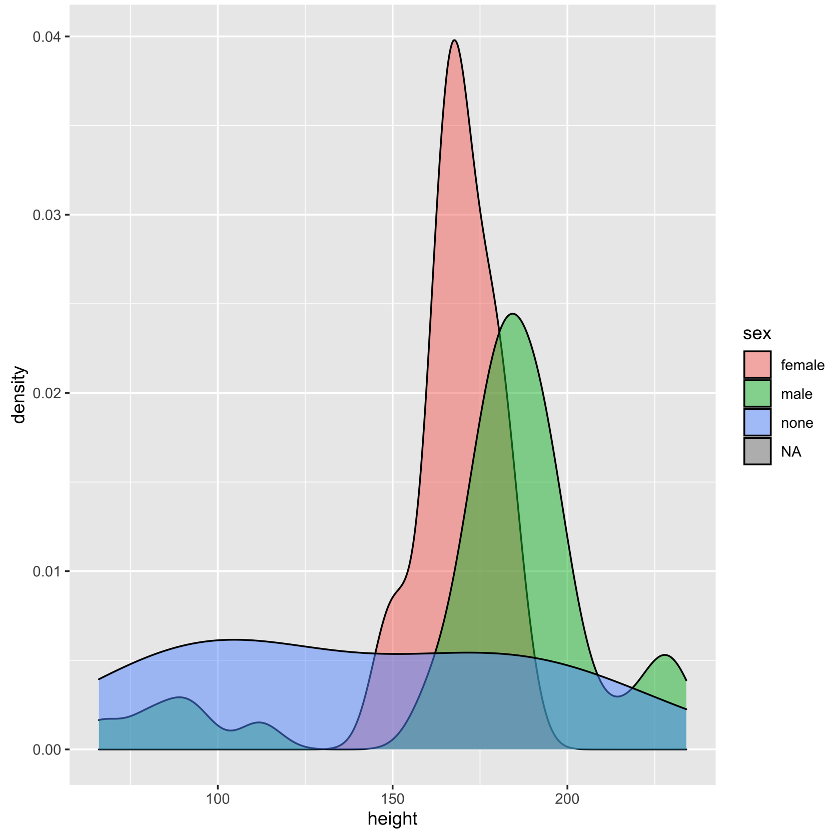


Density Plots by Group

We can see many categories for the variable by adding a variable to the `fill` argument.

I've also changed the alpha (opacity) in `geom_density()` so we can see overlapping data.

```
ggplot(
  data = starwars,
  aes(x = height,fill = sex)
) +
  geom_density(alpha = 0.5)
```



Histograms

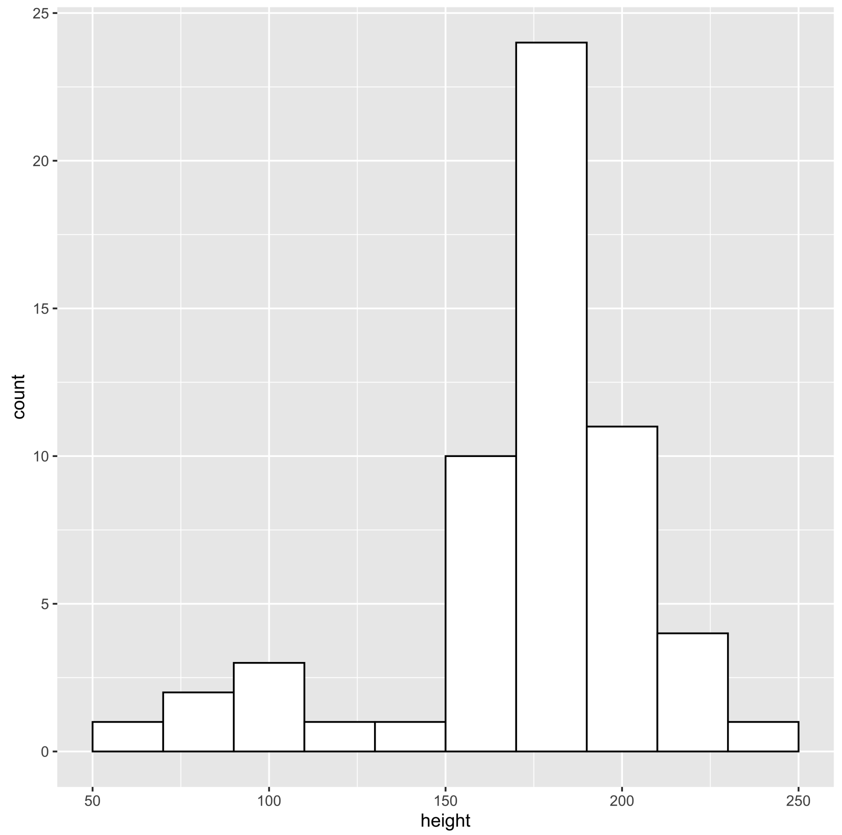
This is usually used with few observations, but we'll use the same data here.

Change `geom_density()` to `geom_histogram()`.

I've changed some the looks of the bars too using fill and colour arguments.

```
ggplot(
  data = starwars,
  mapping = aes(x = height)
) +
  geom_histogram(
    binwidth = 20,
    fill = "white",
    colour = "black"
  )
```

We have to set the binwidth here, which is how we group continuous scores into bars. **Large bins** = **big bars**. We'll remove sex from the fill aesthetic too.



Faceting

Faceting allows us to **split our plots up into many panels**.

This is useful if we want to show patterns in data within groups.

There are two main facets, or ways of splitting data, in `ggplot2`:

- **facet_wrap()**: Split your data in to groups and automate how it will be displayed.
- **facet_grid()**: Split your data and define how it will be laid out in a grid.

Both take variables as arguments as such:

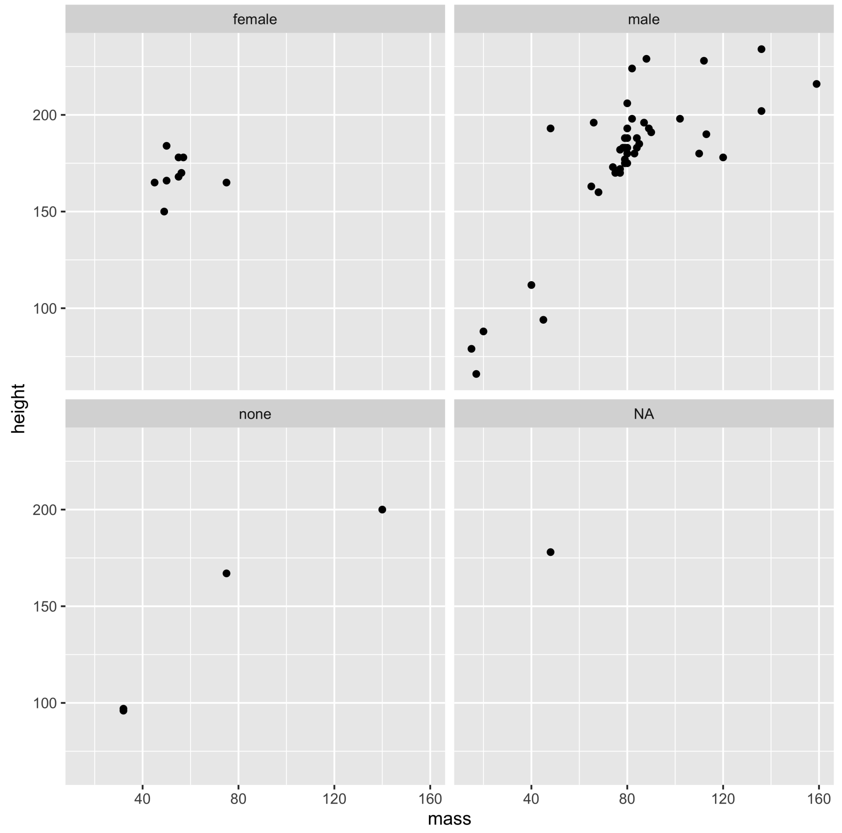
e.g. `facet_wrap(rows ~ columns)`. Variables in **rows** will be presented stacked vertically. Variables in **columns** will be presented side by side horizontally.

If you don't have a variable to present in e.g. **rows**, then put a full stop there, e.g. `facet_wrap(.~columns)`.

Facet Wrap

Facet wrap wraps plots next to each other only for cases where we have the data to make a plot. It tries to **maximise plotting space**.

```
ggplot(
  data = starwars,
  mapping = aes(x = mass,y = height)
) +
  geom_point() +
  facet_wrap(.~sex)
```

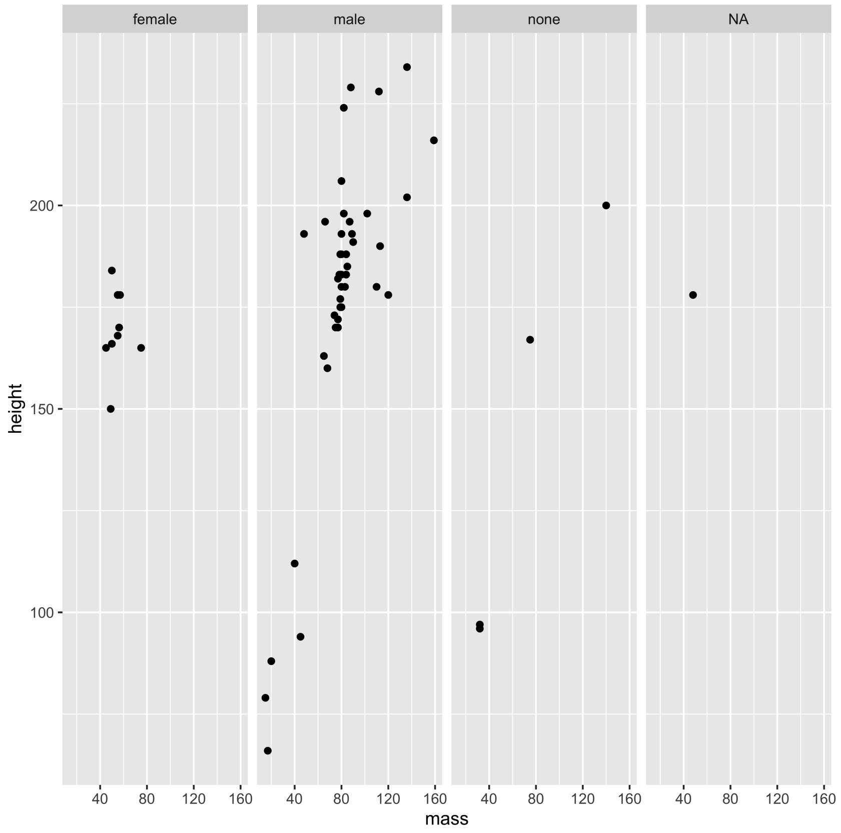


Facet Grid

Facet grid **completes cases** in your panel. So even missing combinations of data get a pane.

```
ggplot(
  data = starwars,
  mapping = aes(x = mass,y = height)
) +
  geom_point() +
  facet_grid(.~sex)
```

Data is only presented in dimensions that you ask it to be presented in (e.g. columns here).



Saving Plots

We can save graphics from R using a number of methods, but for plots produced in `ggplot2`, we can use `ggsave()`.

We can either make our plot without assigning it to a variable, and then save it as follows:

```r
ggplot(data = starwars, aes(x = height)) +
  geom_density()

ggsave(here("myplot.png"), last_plot())
```

Or we can make a plot and assign it to a variable, and save it as follows:

```r
my_plot <- ggplot(data = starwars, aes(x = height)) +
  geom_density()

ggsave(here("myplot.png"), my_plot)
```

I prefer the latter. Why? Once a plot is stored as a variable, you can change it by adding `ggplot` arguments! For example...

```r
my_plot + coord_cartesian(xlim = c(0, 180))
```

Putting it Together

We can make a summary of our data using tidyverse functions.

```
descriptives <- starwars %>%
  group_by(species) %>%
  summarise(
    total_n = n(),
    mean_height = mean(height, na.rm = TRUE),
    sd_height = sd(height, na.rm = TRUE)
  ) %>%
  filter(total_n > 1) %>%
  mutate(se_height = sd_height/sqrt(total_n))

# inspect our summary
descriptives
```

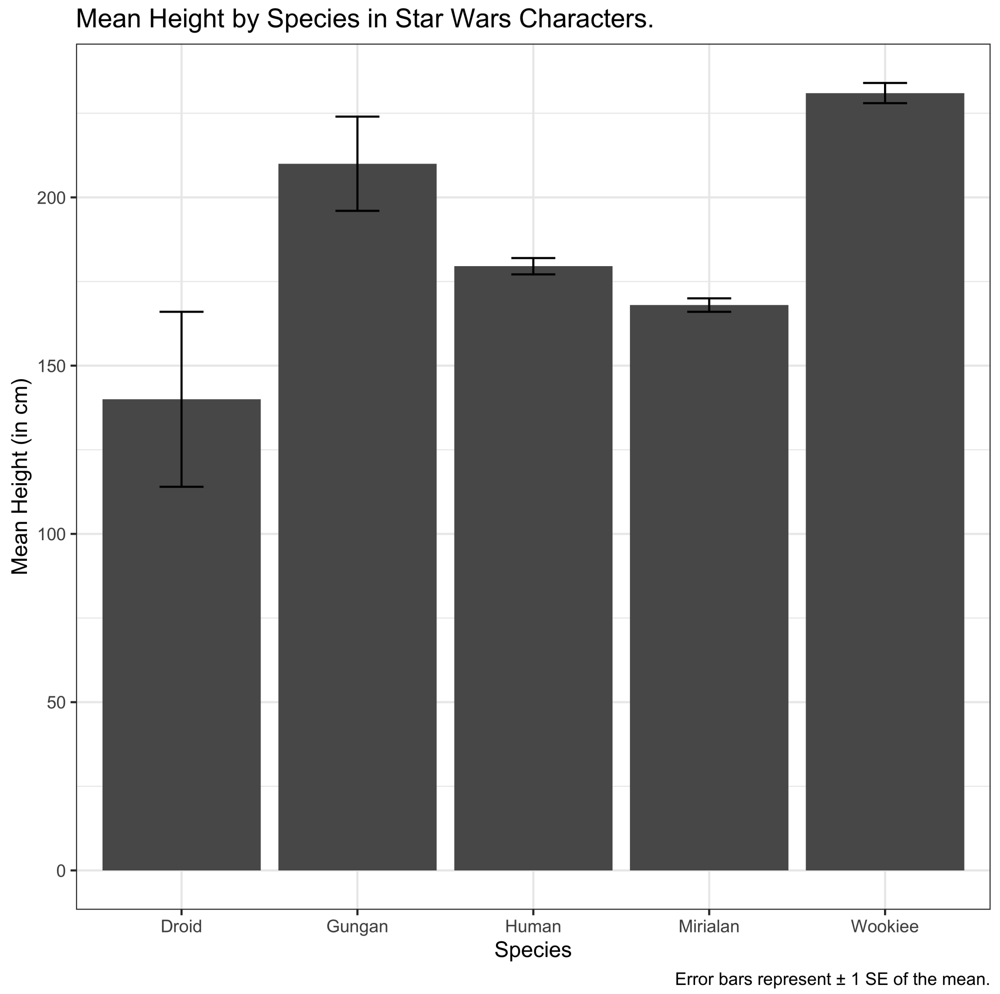
```
## # A tibble: 5 x 5
##   species  total_n mean_height sd_height se_height
##   <chr>      <int>       <dbl>     <dbl>     <dbl>
## 1 Droid          4        140      52.0      26.0 
## 2 Gungan         2        210      19.8      14.0 
## 3 Human         22        180.     11.4       2.43
## 4 Mirialan       2        168       2.83      2
```

Putting it Together

…and use this summary in plotting, or pipe it directly into `ggplot2`.

```r
ggplot(
  data = descriptives,
  mapping = aes(x = species, y = mean_height)
) +
  geom_bar(stat = "identity") +
  geom_errorbar(
    aes(
      ymin = mean_height - se_height,
      ymax = mean_height + se_height
      ),
    width = 0.25
  ) +
  labs(
    title = "Mean Height by Species in Star Wars Characters.",
    caption = "Error bars represent \u00B1 1 SE of the mean.",
    x = "Species",
    y = "Mean Height (in cm)"
  ) +
  theme_bw()
```

Putting it Together



Recap

We've learned...

- How and when to use **different types of plots** using `ggplot2`.
- How to set options within different **geoms** for our plots.
- How to differentiate between groups using **fill** and **facets**.
- How to **save plots** for use in your reports.
- How to **chain functions together** to make a summary, and then plot it!