Introduction to R for Biologists

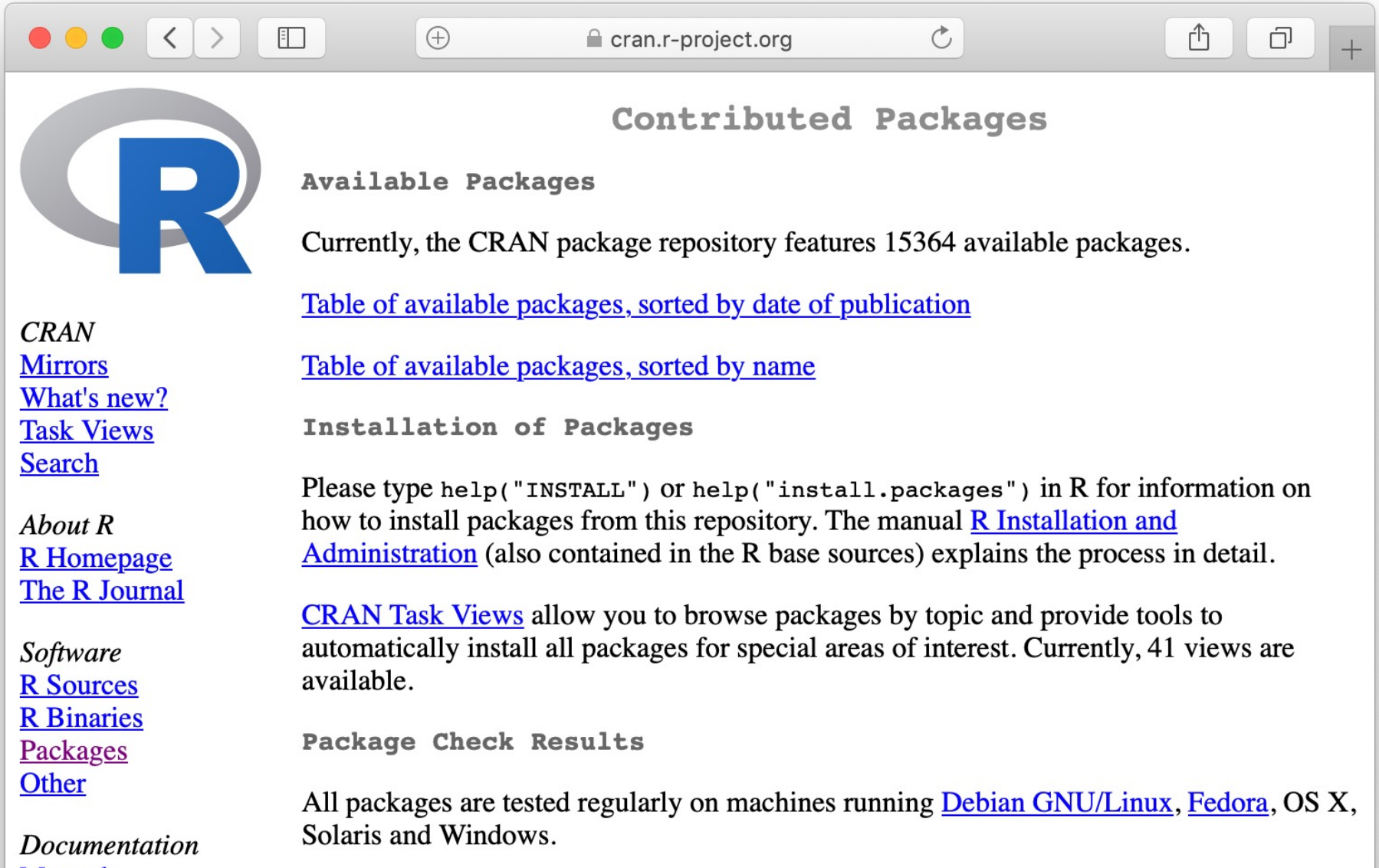
Day 2 – Data visualization with ggplot2

Developed by Rachael Cox

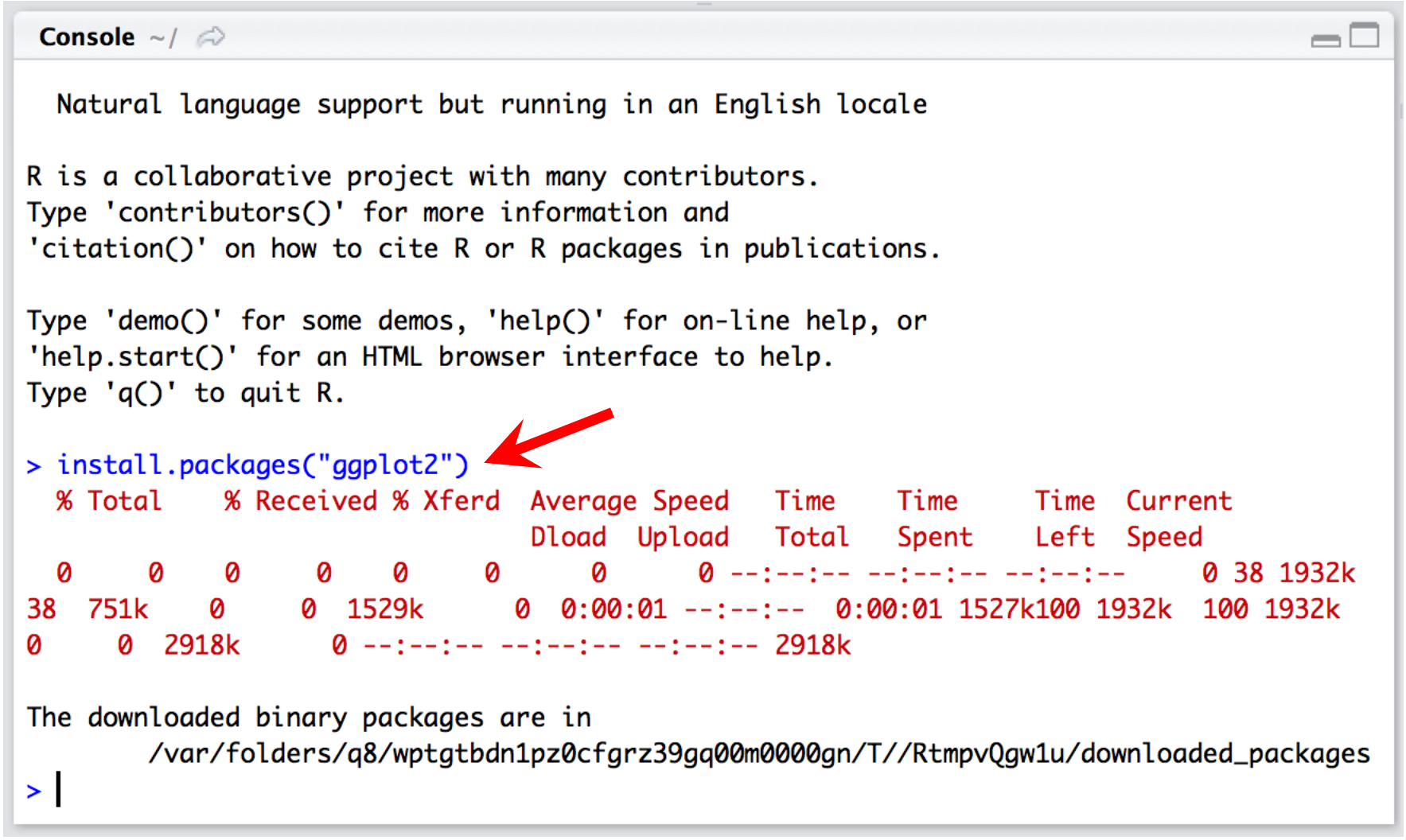
*Several slides have been contributed by or modified from slides by Dr. Claus Wilke

Extending R through packages: There's a package for everything

R packages are available on CRAN (Comprehensive R Archive Network)



You can install packages using `install.packages()` in RStudio



ggplot2: A grammar of graphics

Traditional plotting: You **are** a painter

- Manually place individual graphical elements

ggplot2: You **employ** a painter

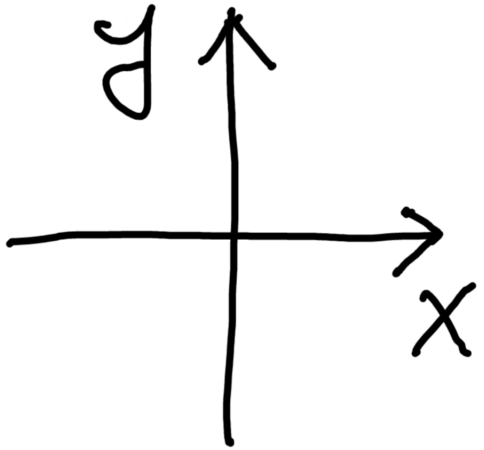
- Describe conceptually how data should be visualized

Most confusing key concept: aesthetic mapping

Maps data values to visual elements of the plot

A few examples of aesthetics

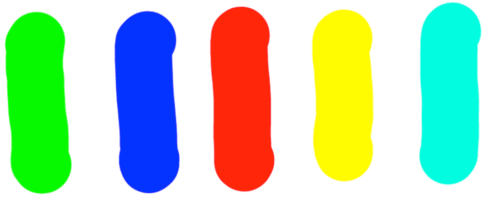
position



shape

size

color



Where there's a figure, there's a geom_ for that!

- Example website LINK

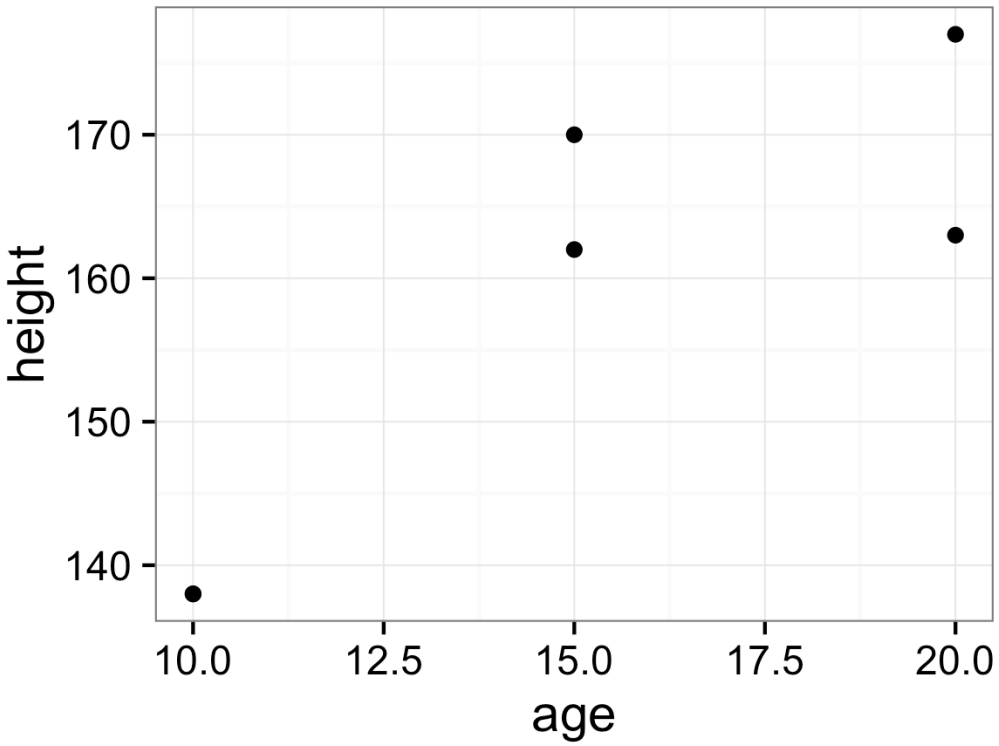
Let's go over a simple example: mean height and weight of boys/girls ages 10-20

age (yrs)	height (cm)	weight (kg)	sex
10	138	32	M
15	170	56	M
20	177	71	M
10	138	33	F
15	162	52	F
20	163	53	F

Data from: http://www.cdc.gov/growthcharts/

Map age to x, height to y, visualize using points

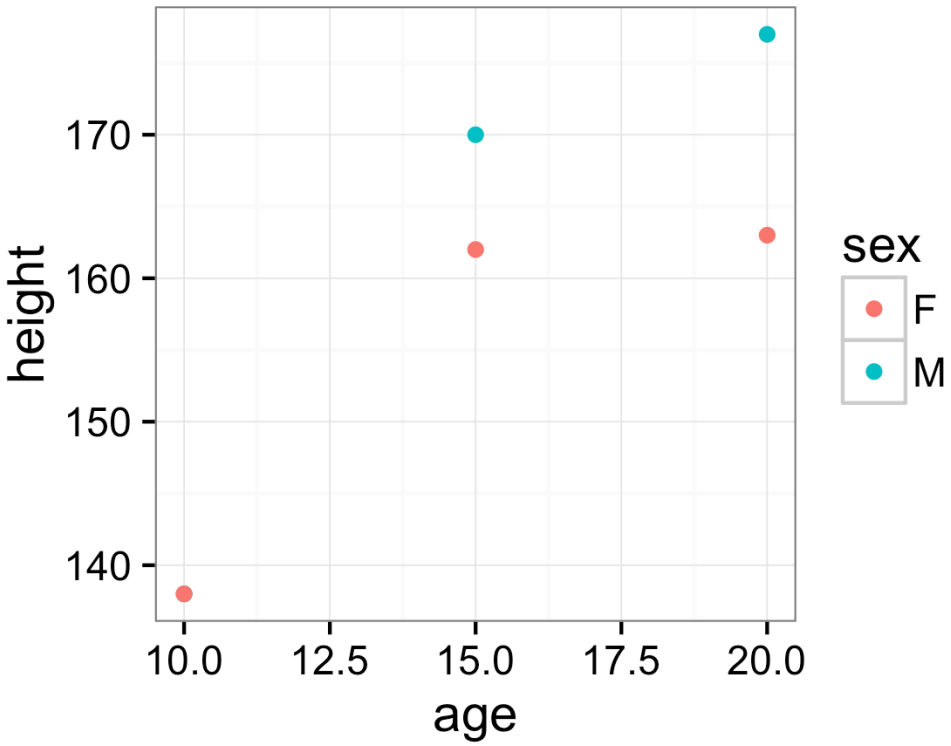
```
ggplot(data, aes(x=age, y=height)) +
                                    geom_point()
```



Let's color the points by sex

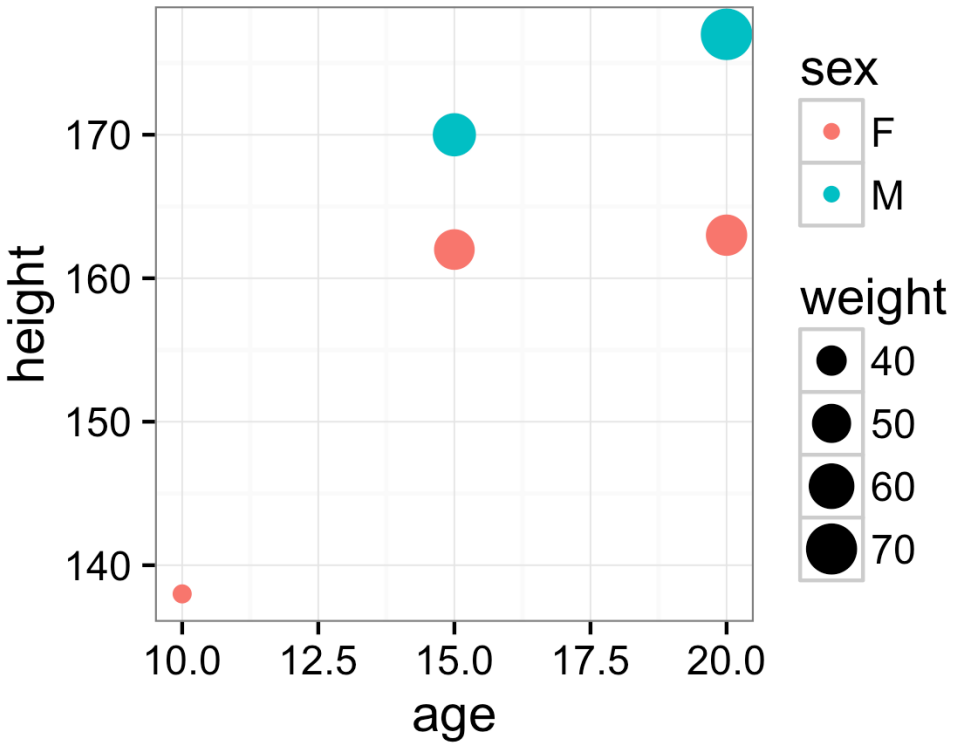
```
ggplot(data, aes(x=age, y=height,
                 color=sex)) + geom_point()
```

★ NOTE: "color" aesthetic is for coloring points & lines;
"fill" aesthetic is for coloring bars & distributions



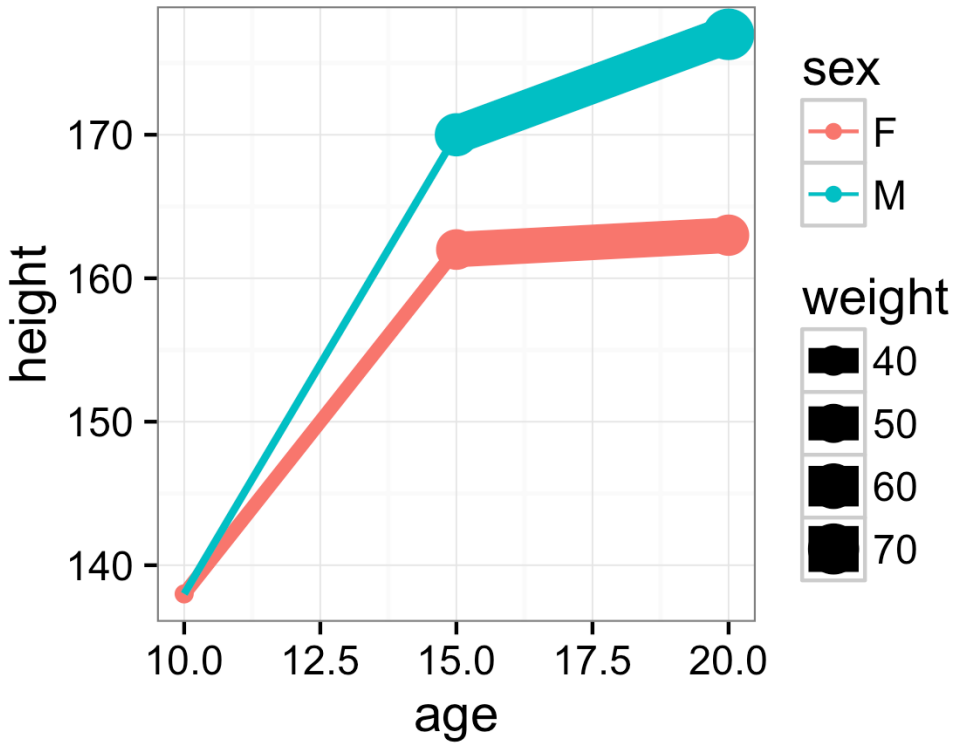
And change point size by weight

```
ggplot(data, aes(x=age, y=height,
       color=sex, size=weight)) + geom_point()
```



And connect the points with lines

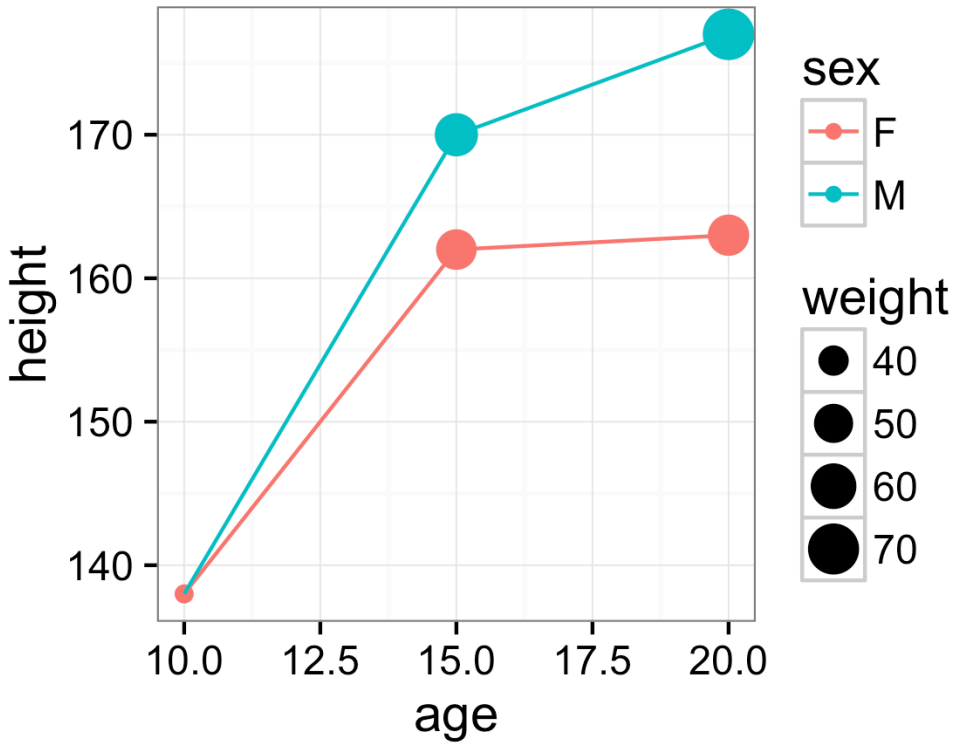
```
ggplot(data, aes(x=age, y=height,
       color=sex, size=weight)) +
                    geom_point() + geom_line()
```



Oops!

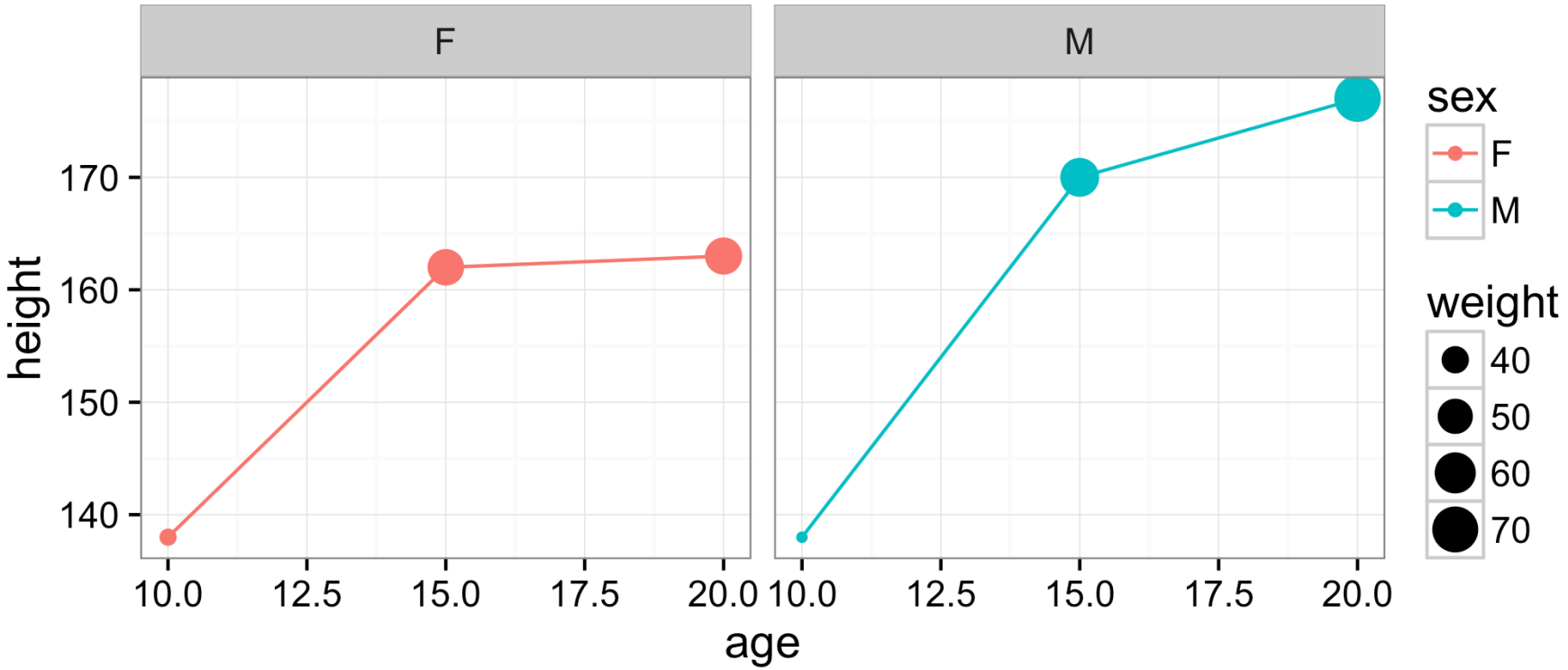
The weight-to-size mapping should only be applied to points

```
ggplot(data, aes(x=age, y=height,
 color=sex)) + geom_point(aes(size=weight)) +
                                    geom_line()
```



We can also make side-by-side plots (called facets)

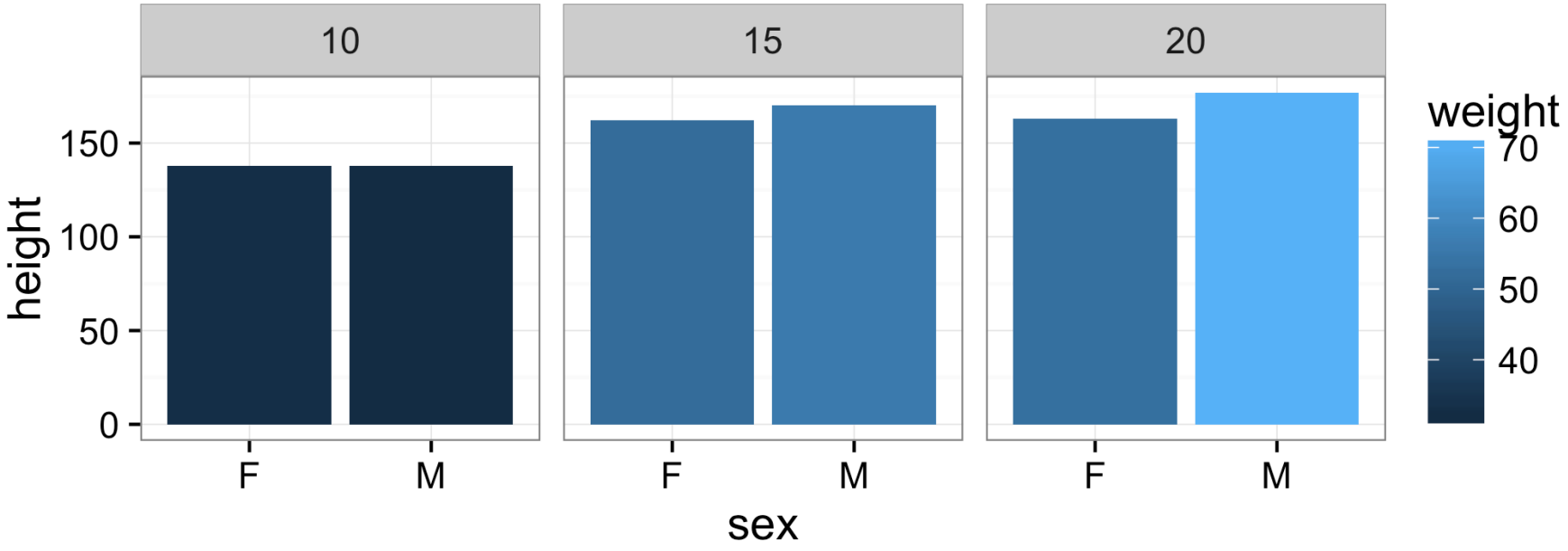
```
ggplot(data, aes(x=age, y=height,
 color=sex)) + geom_point(aes(size=weight)) +
                  geom_line() + facet_wrap(~sex)
```



Now let's facet by age, color by weight, and use bars (columns) to plot height

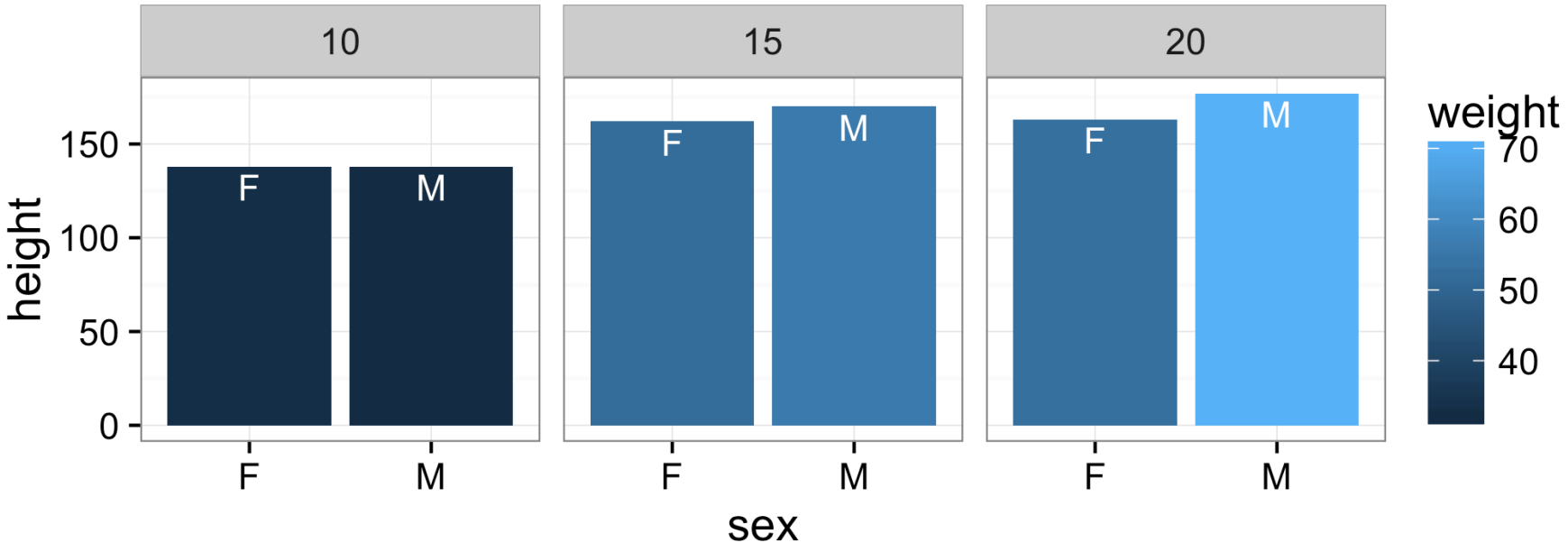
```
ggplot(data, aes(x=sex, y=height, fill=weight)) +
 geom_col() + facet_wrap(~age)
```

NOTE: "fill" ★ aesthetic is for coloring bars & distributions



Let's plot the sex also at the top of the bar

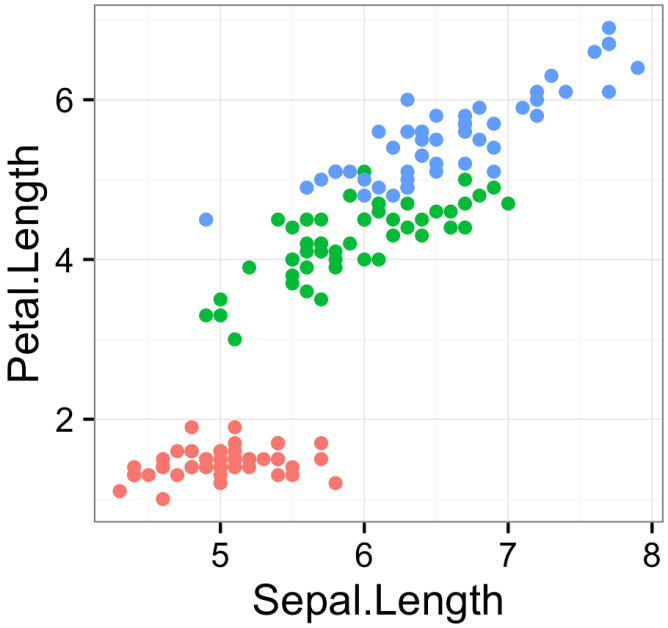
```
ggplot(data, aes(x=sex, y=height, fill=weight)) +
 geom_col() +
 geom_text(aes(label=sex), vjust=1.3, color='white') +
                                        facet_wrap(~age)
```



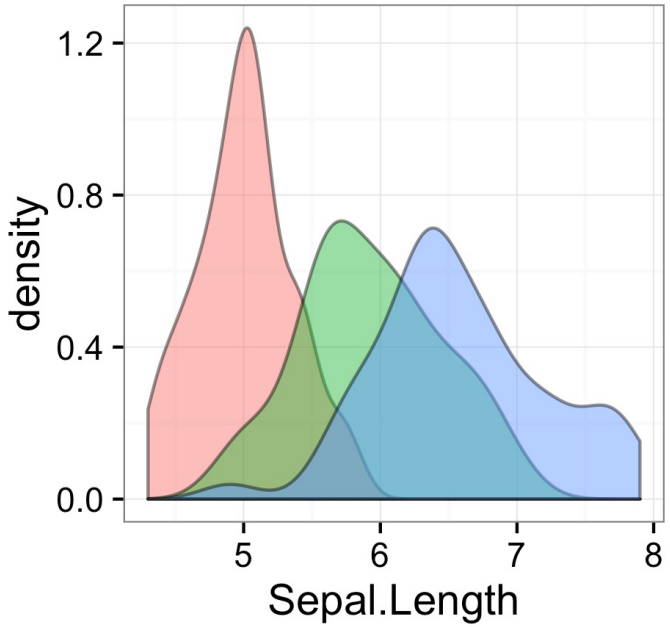
All the geoms with all their options are described on the ggplot2 web page

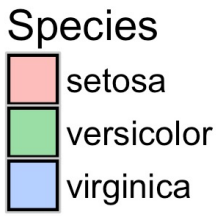
https://ggplot2.tidyverse.org/reference/

We often need to do statistical transformations before plotting

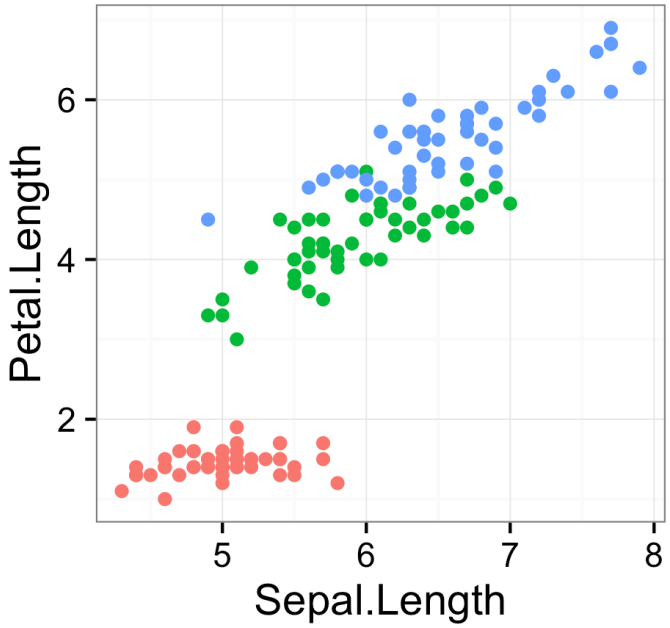


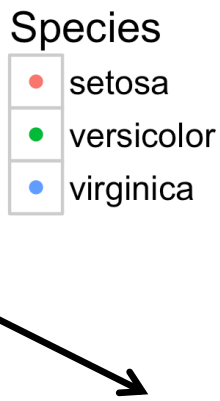
density of data points



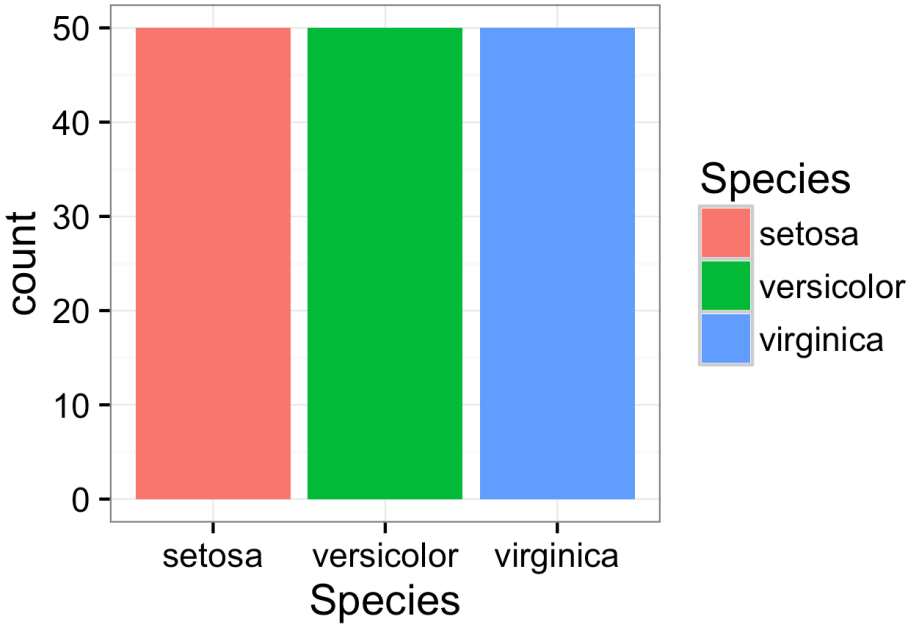


We often need to do statistical transformations before plotting

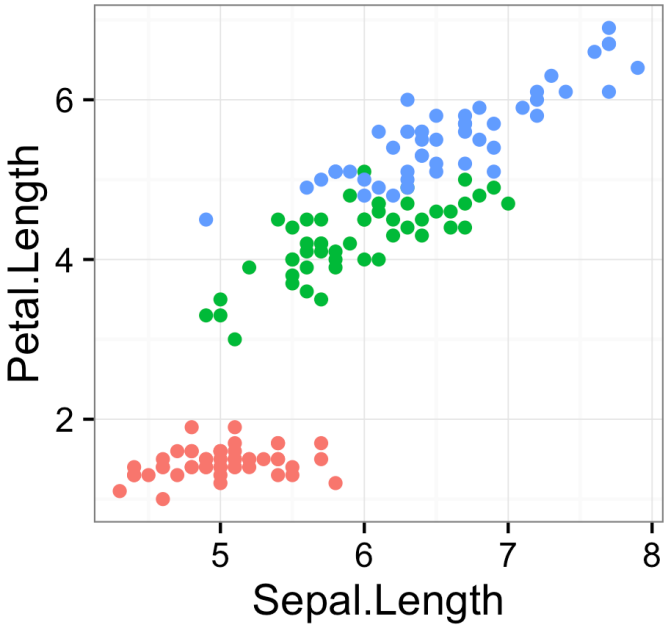




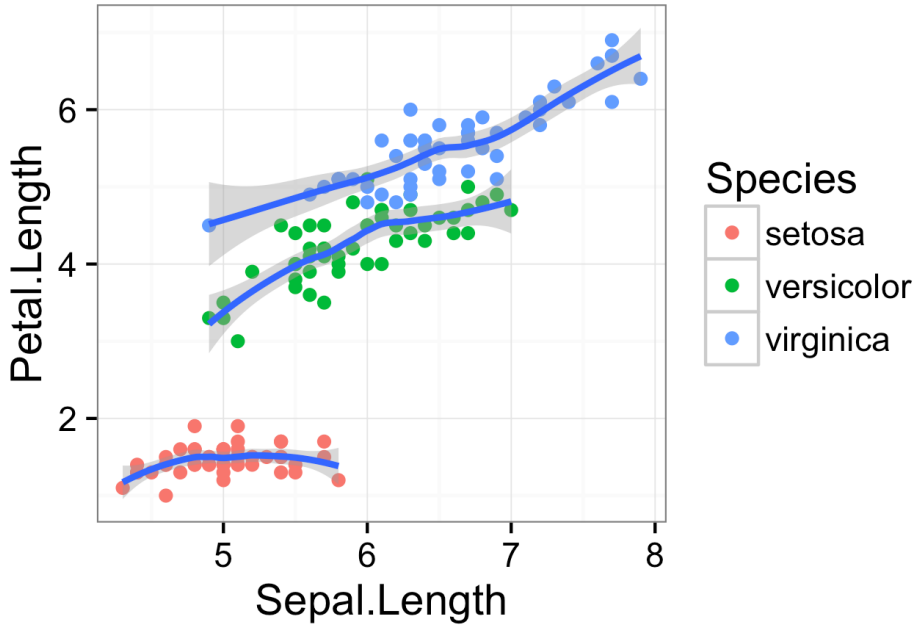
count of number of different types



We often need to do statistical transformations before plotting

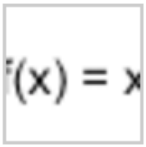


statistical smoothing/ trend lines



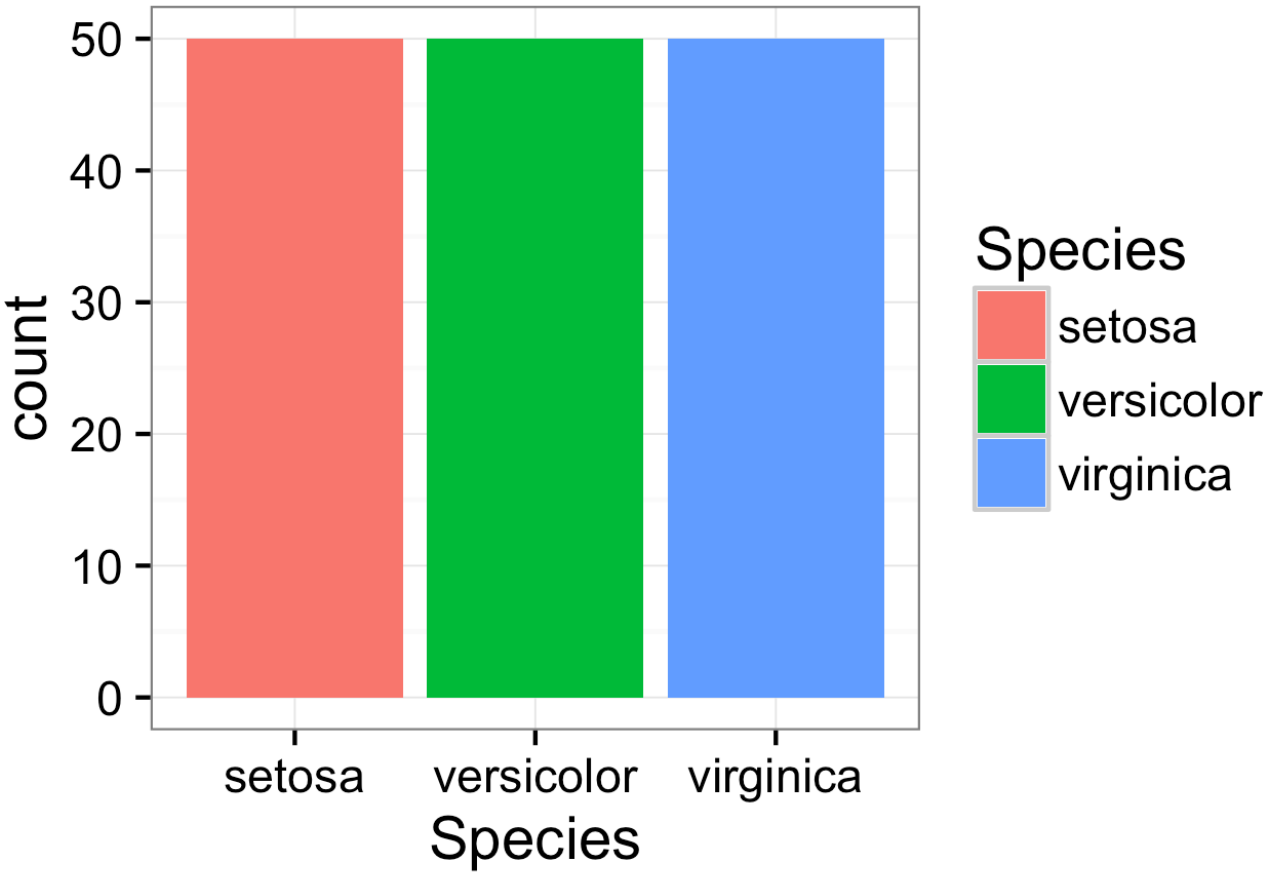
In ggplot2, these transformations are done with stats

- `stat_ecdf`
  Empirical Cumulative Density Function
- `stat_ellipse`
  Plot data ellipses.
- `stat_function`
  Superimpose a function.
- `stat_identity`
  Identity statistic.
- `stat_qq` (geom_qq)
  Calculation for quantile-quantile plot.
- `stat_summary_2d` (stat_summary2d, stat_summary_hex)
  Bin and summarise in 2d (rectangle & hexagons)
- `stat_unique`
  Remove duplicates.



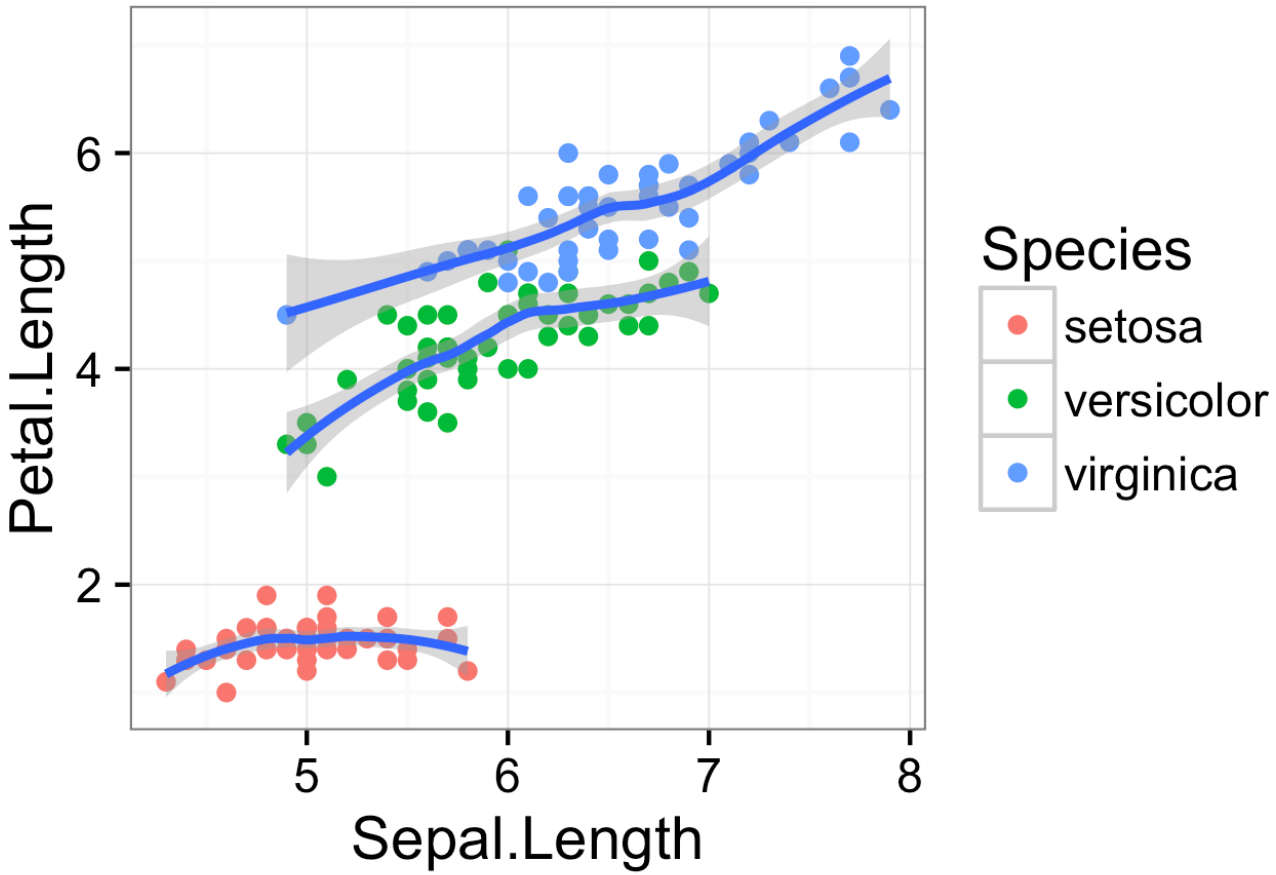
In most cases we just need to call the appropriate geom and it calls a stat

```
ggplot(iris, aes(x=Species, fill=Species)) +
                                    geom_bar()
```



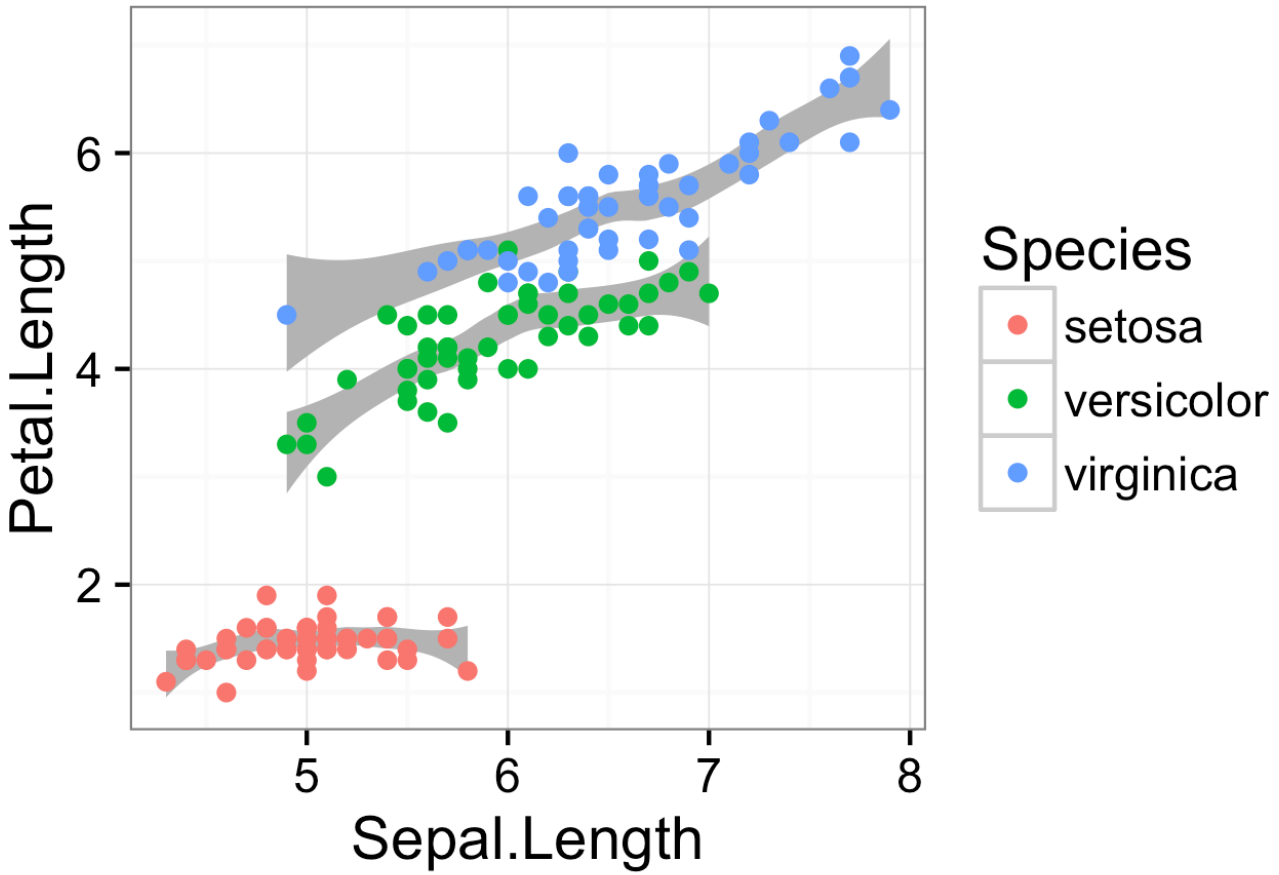
In most cases we just need to call the appropriate geom and it calls a stat

```
ggplot(iris, aes(x=Sepal.Length, y=Petal.Length)) +
                    geom_point(aes(color=Species)) +
                    geom_smooth(aes(group=Species))
```



However, sometimes it can be helpful to call the stat directly

```
ggplot(iris, aes(x=Sepal.Length, y=Petal.Length)) +
stat_smooth(aes(group=Species), geom="ribbon", fill='gray70') +
                                    geom_point(aes(color=Species))
```

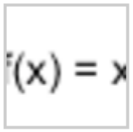


Scales define how to map data onto aesthetics

- `scale_colour_grey` (scale_color_grey, scale_fill_grey)
  Sequential grey colour scale.

- `scale_colour_hue` (scale_color_discrete, scale_color_hue, scale_colour_discrete, scale_fill_discrete, scale_fill_hue)
  Qualitative colour scale with evenly spaced hues.

- `scale_identity` (scale_alpha_identity, scale_color_identity, scale_colour_identity, scale_fill_identity, scale_linetype_identity, scale_shape_identity, scale_size_identity)
  Use values without scaling.



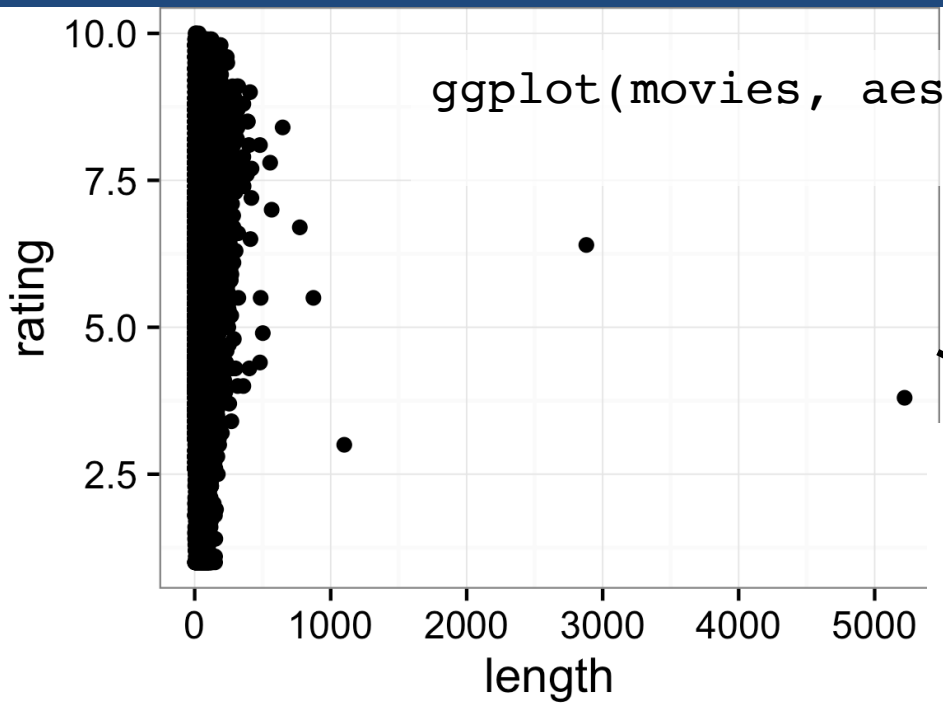
- `scale_manual` (scale_alpha_manual, scale_color_manual, scale_colour_manual, scale_fill_manual, scale_linetype_manual, scale_shape_manual, scale_size_manual)
  Create your own discrete scale.

- `scale_linetype` (scale_linetype_continuous, scale_linetype_discrete)
  Scale for line patterns.

- `scale_shape` (scale_shape_continuous, scale_shape_discrete)
  Scale for shapes, aka glyphs.

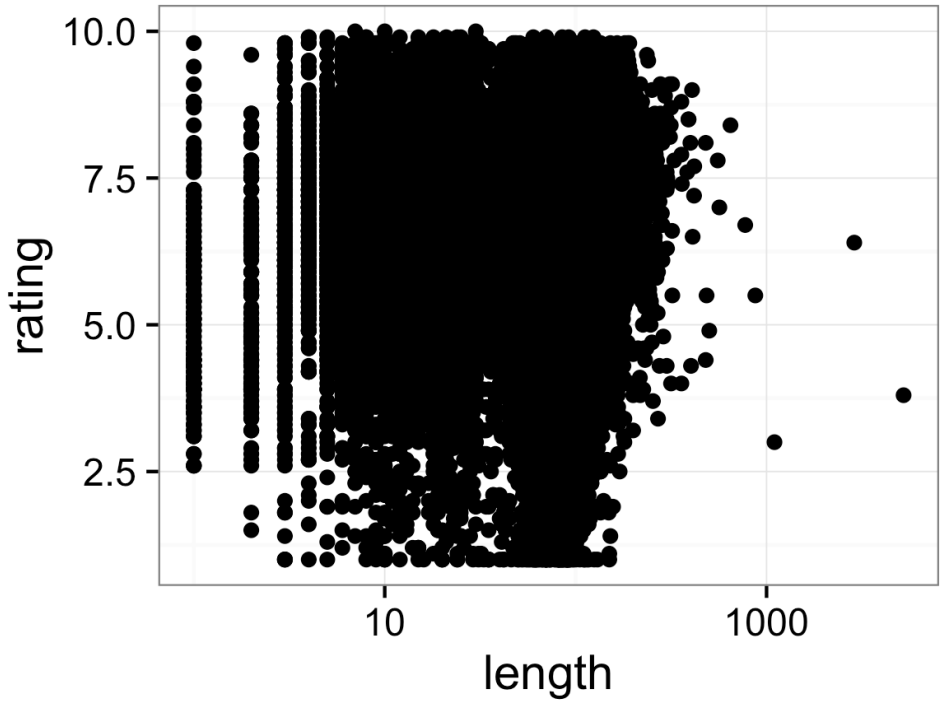
- `scale_size` (scale_radius, scale_size_area, scale_size_continuous, scale_size_discrete)

Example 1: Change scaling of x axis

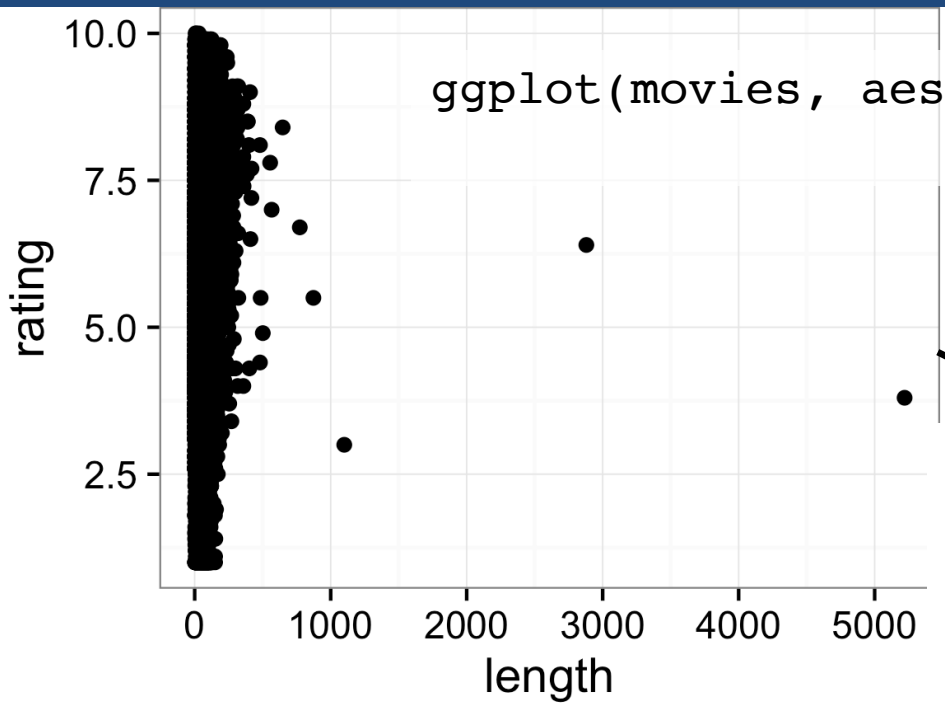



```
ggplot(movies, aes(x=length, y=rating)) +
                                    geom_point()
```

```
+ scale_x_log10()
```

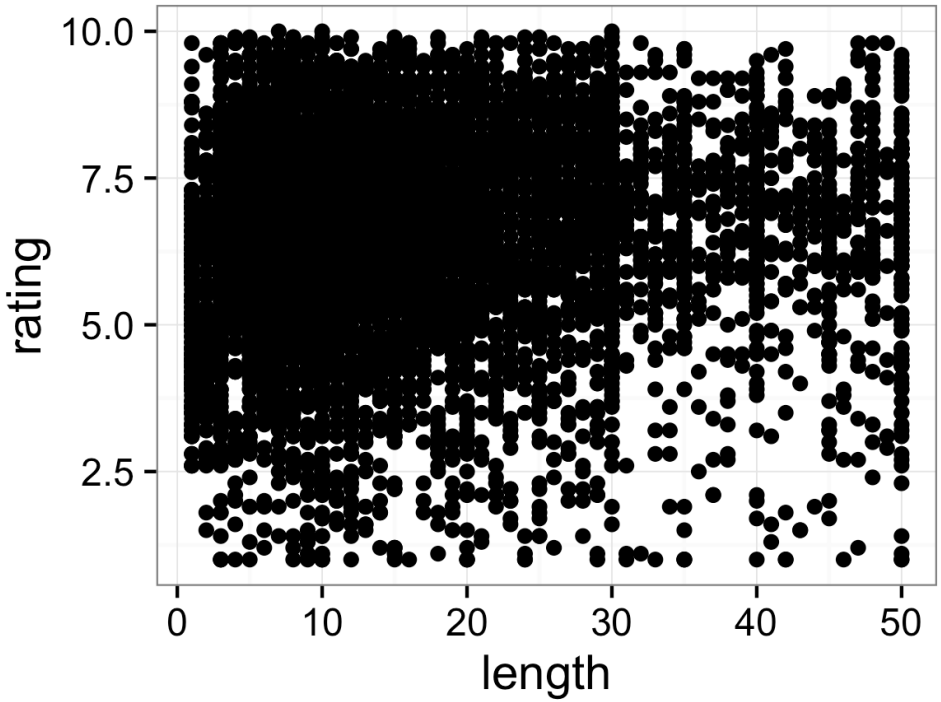


Example 1: Change scaling of x axis

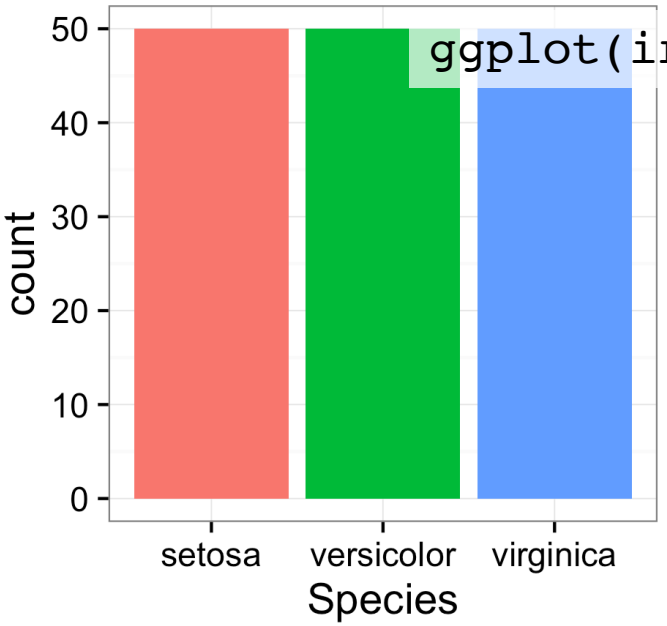



```
ggplot(movies, aes(x=length, y=rating)) +
                                    geom_point()
```

```
+ xlim(1, 50)
```

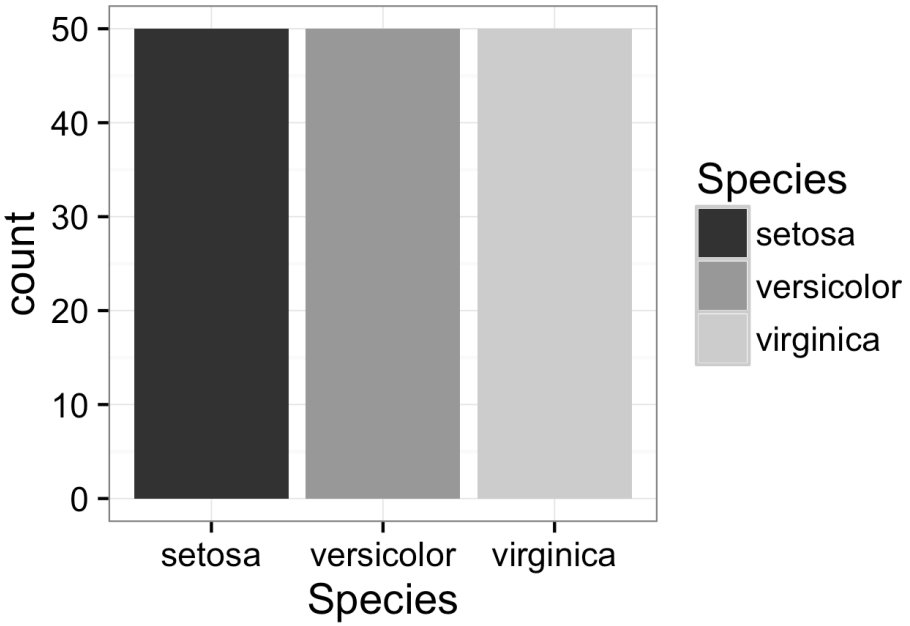


Example 2: Change color scaling




```
ggplot(iris, aes(x=Species, fill=Species)) +
                                        geom_bar()
```


```
+ scale_fill_grey()
```



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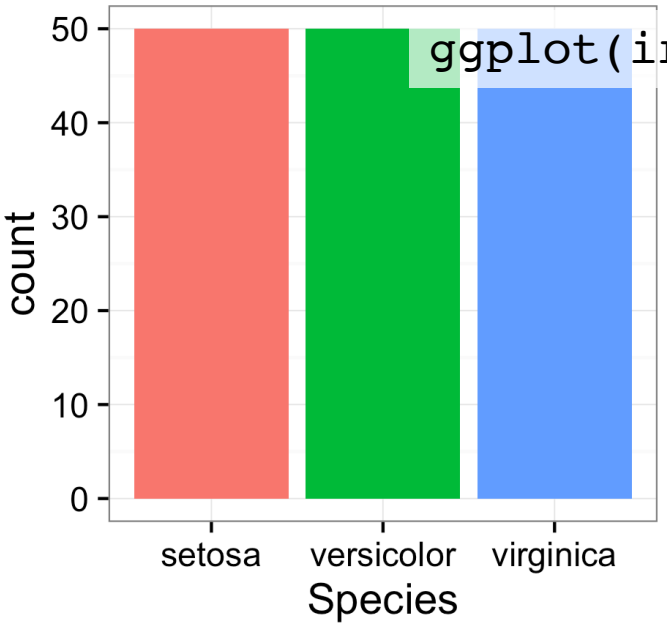
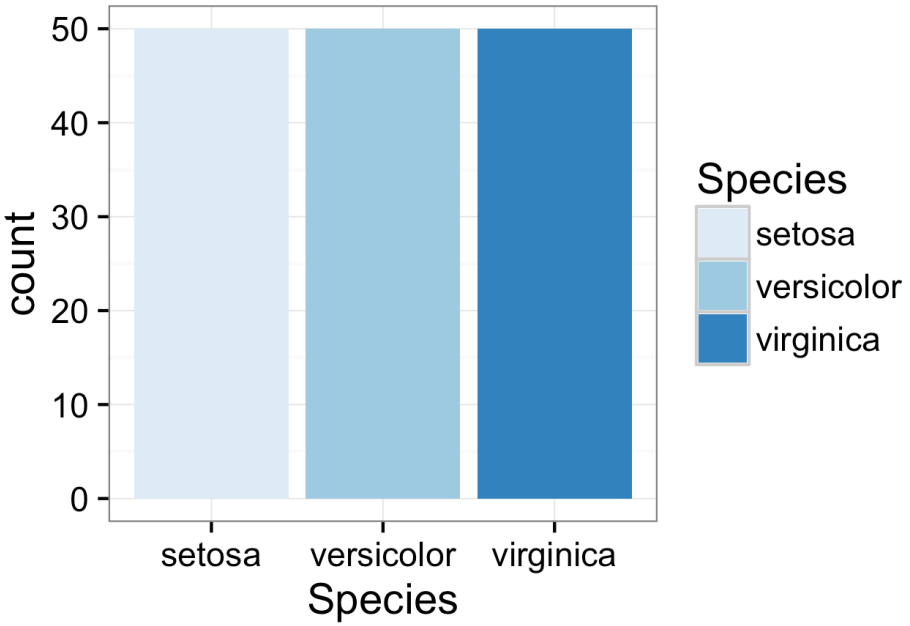



```
ggplot(iris, aes(x=Species, fill=Species)) +
                                        geom_bar()
```


```
+ scale_fill_brewer()
```



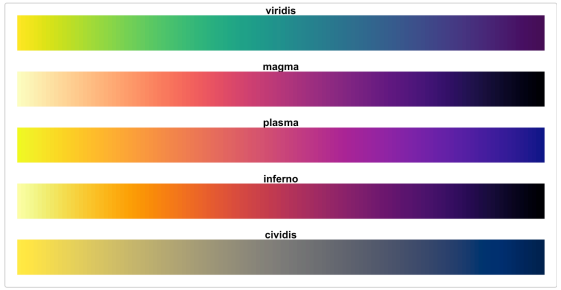
Some color scaling options in ggplot2

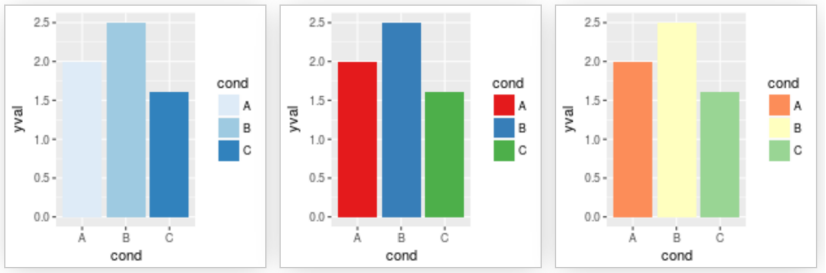
- `scale_color_gradient()`, `scale_fill_gradient()`
- `scale_color_discrete()`, `scale_fill_discrete()`

- `scale_color_brewer()`, `scale_fill_brewer()`
- `scale_color_distiller()`, `scale_fill_distiller()`

- `scale_color_colorblind()`, `scale_fill_colorblind()`

- `scale_color_manual()`, `scale_fill_manual()`





```
palette_pretty <- c("#0072B2","#E69F00","#009E24","#FF0000", "#979797","#5530AA")
palette_bgy <- c("#FFFFCC","#A1DAB4","#41B6C4","#2C7FB8","#253494")
palette_wine <- c("#bcb37b", "#9e934d", "#8f8023", "#790000", "#5b0b0b")
palette_cb <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442",
  "#0072B2", "#D55E00", "#CC79A7", "#999999")
```

Themes control non-data display

The `labs()` function lets you change the title, x- and y-axis labels, and color/legend labels:

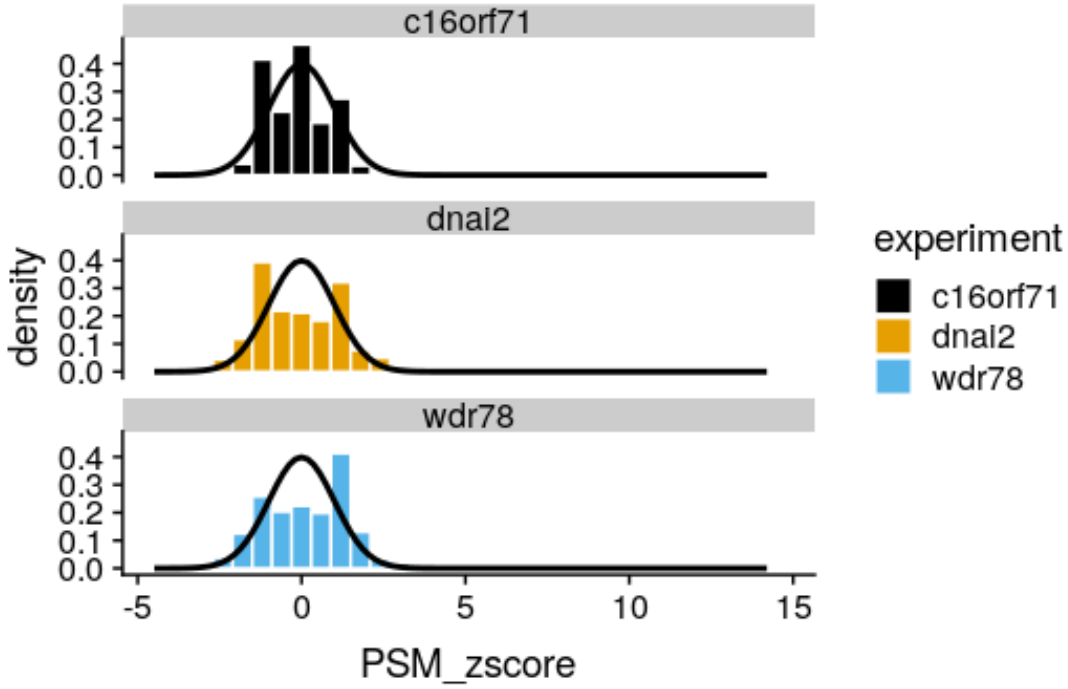
https://ggplot2.tidyverse.org/reference/labs.html

Adding `theme()` layers allow you to customize fonts, sizes, and positions of titles, labels, background, gridlines and legends:

https://ggplot2.tidyverse.org/reference/theme.html

Putting it all together, example 1

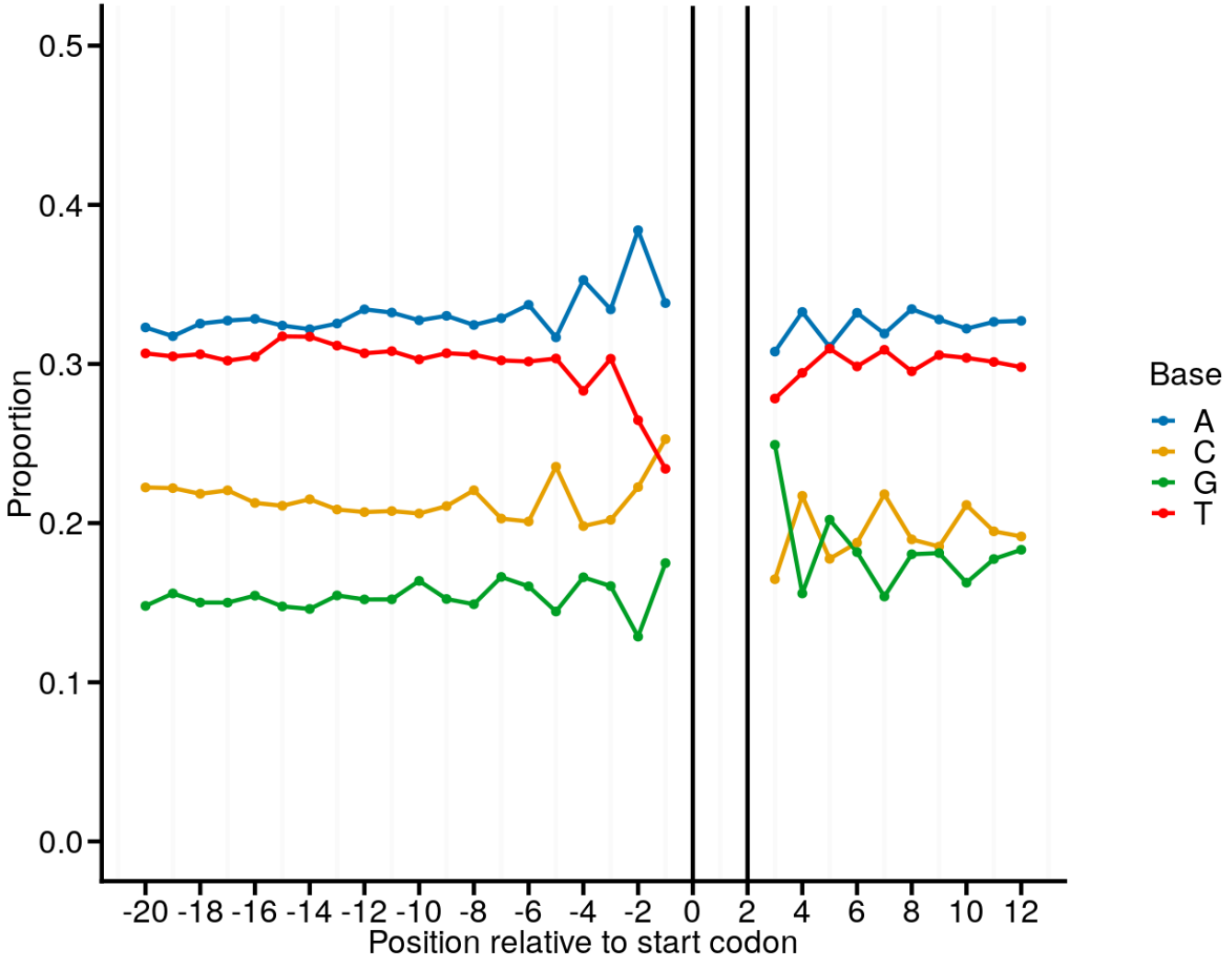
```
ggplot(apms_df, aes(x = PSM_zscore, fill = experiment)) +
    geom_histogram(binwidth = 0.6, color = "white") +
    facet_wrap(~experiment, ncol = 1) +
    stat_function(aes(group = experiment), fun = dnorm, n = 101,
                  args = list(mean = 0, sd = 1), size = 1) +
    scale_fill_colorblind()
```



Putting it all together, example 2

```
seq_plot <- seq_df %>%
    ggplot(aes(x = pos, y = prop, group = Base, color = Base)) +
        geom_line() +
        geom_point(size = 0.5) +
        scale_x_continuous(breaks = seq(-20, 13, 2),
                           labels = seq(-20, 13, 2)) +
        scale_color_manual(values = palette_pretty) +
        geom_vline(xintercept = 0) +
        geom_vline(xintercept = 2)  +
        background_grid(major = "only_minor", minor = "x") +
        ylim(0,0.5) +
        ylab("Proportion") +
        xlab("Position relative to start codon")
```

Putting it all together, example 2



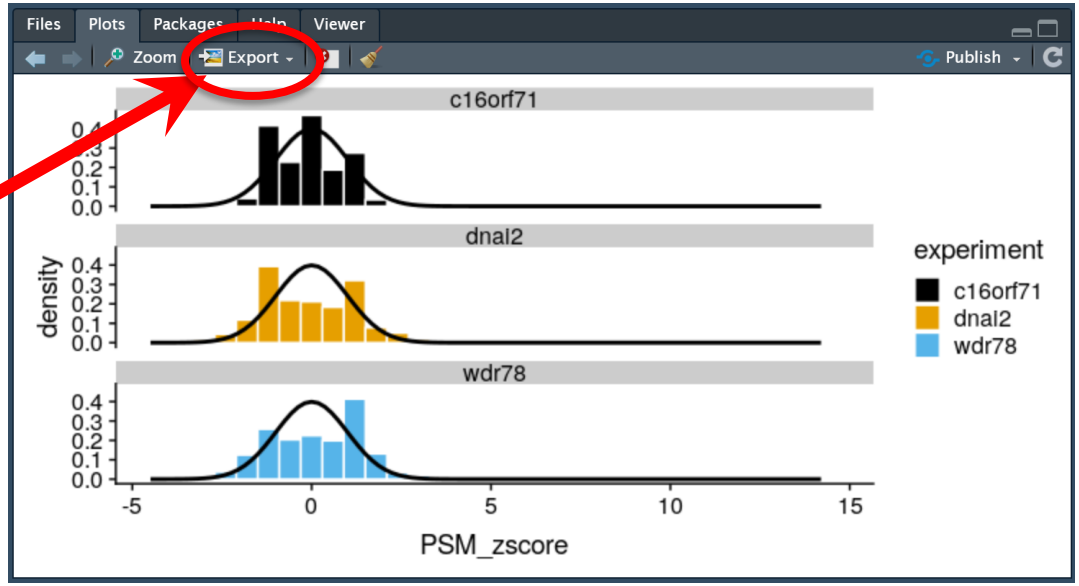
Saving plots

With code:

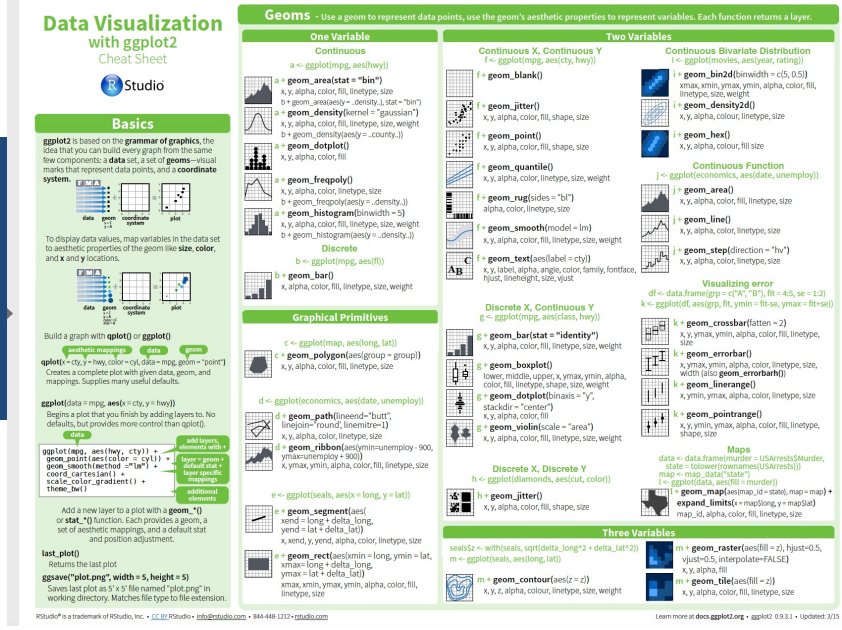
```
seq_plot %>% ggsave("relative_start_plot.png", .,device =
"png", width = 4.5, height = 3.5,  units = "in")

seq_plot %>% ggsave("relative_start_plot.pdf", ., device =
"pdf", width = 4.5, height = 3.5, units = "in")
```

In RStudio; to make plots appear in the bottom-right window:

- Tools > Global Options > R Markdown > Uncheck “Show output inline”



Demonstration Time!



Checkout the “ggplot cheatsheet” in the Day 2 folder for code examples