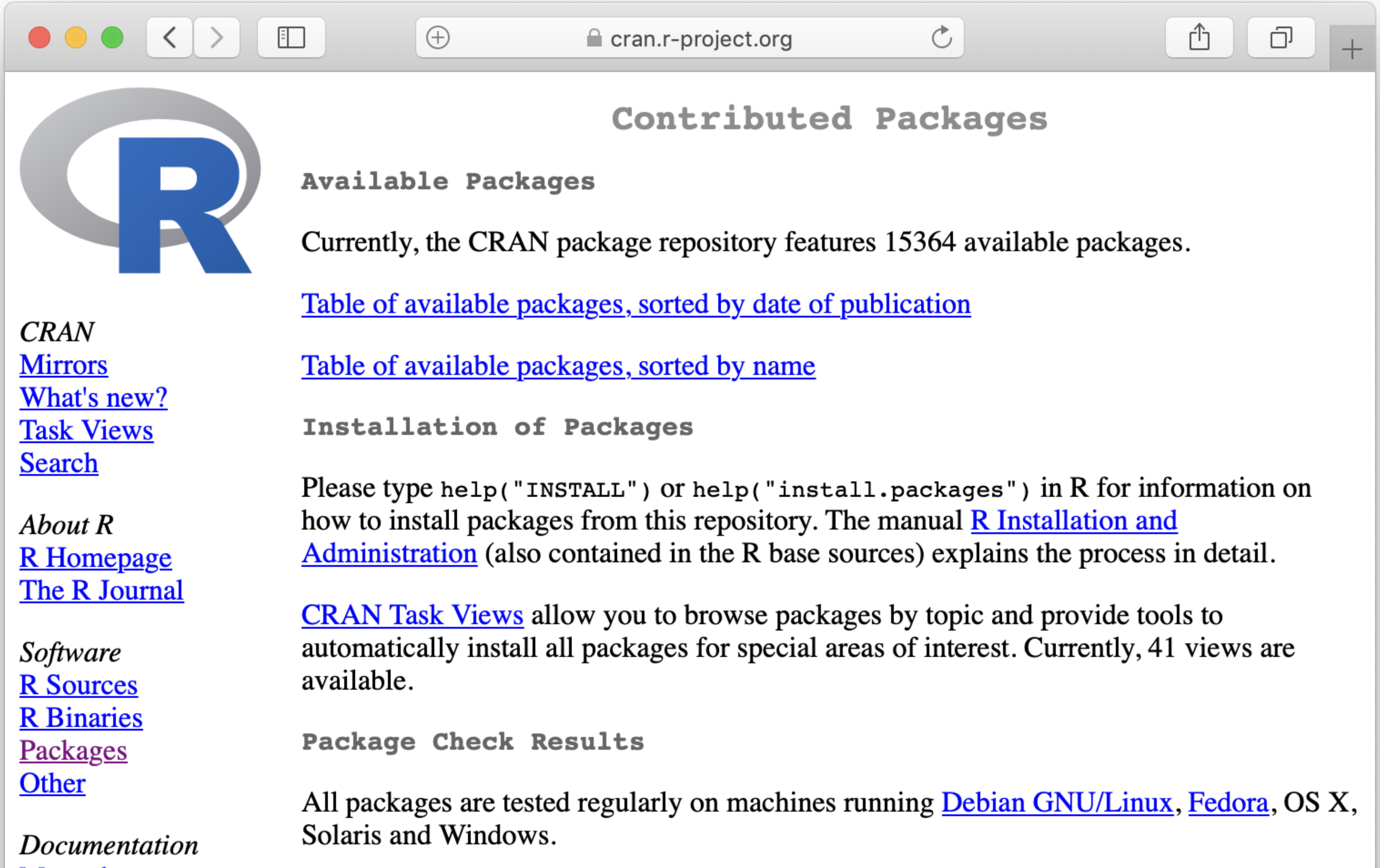
Practical Approaches to Bioanalysis in R

Day 2 – Data visualization with ggplot2

*Many of these slides have been contributed by or modified from slides contributed by Dr. Claus Wilke

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

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



Contributed Packages

Available Packages

Currently, the CRAN package repository features 15364 available packages.

Table of available packages, sorted by date of publication

Table of available packages, sorted by name

Installation of Packages

Please type `help("INSTALL")` or `help("install.packages")` in R for information on how to install packages from this repository. The manual R Installation and Administration (also contained in the R base sources) explains the process in detail.

CRAN Task Views allow you to browse packages by topic and provide tools to automatically install all packages for special areas of interest. Currently, 41 views are available.

Package Check Results

All packages are tested regularly on machines running Debian GNU/Linux, Fedora, OS X, Solaris and Windows.

CRAN
Mirrors
What's new?
Task Views
Search

About R
R Homepage
The R Journal

Software
R Sources
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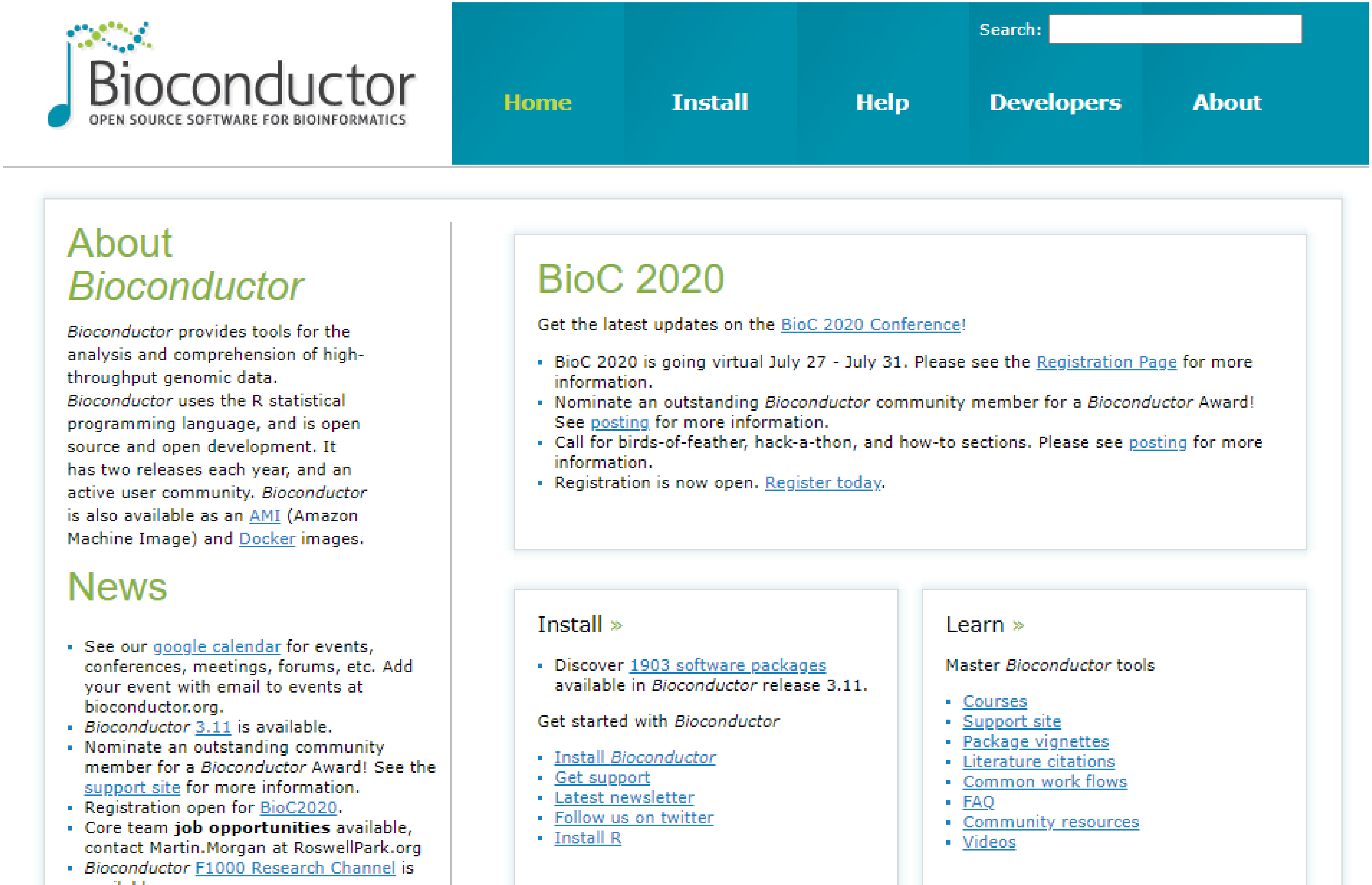
Packages
Other

Documentation

Bio-specific R packages are available on Bioconductor



About *Bioconductor*

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. *Bioconductor* uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community. *Bioconductor* is also available as an AMI (Amazon Machine Image) and Docker images.

News

- See our google calendar for events, conferences, meetings, forums, etc. Add your event with email to events at bioconductor.org.
- *Bioconductor* 3.11 is available.
- Nominate an outstanding community member for a *Bioconductor* Award! See the support site for more information.
- Registration open for BioC2020.
- Core team **job opportunities** available, contact Martin.Morgan at RoswellPark.org
- *Bioconductor* F1000 Research Channel is

BioC 2020

Get the latest updates on the BioC 2020 Conference!

- BioC 2020 is going virtual July 27 - July 31. Please see the Registration Page for more information.
- Nominate an outstanding *Bioconductor* community member for a *Bioconductor* Award! See posting for more information.
- Call for birds-of-feather, hack-a-thon, and how-to sections. Please see posting for more information.
- Registration is now open. Register today.

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- Discover 1903 software packages available in *Bioconductor* release 3.11.

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- Common work flows
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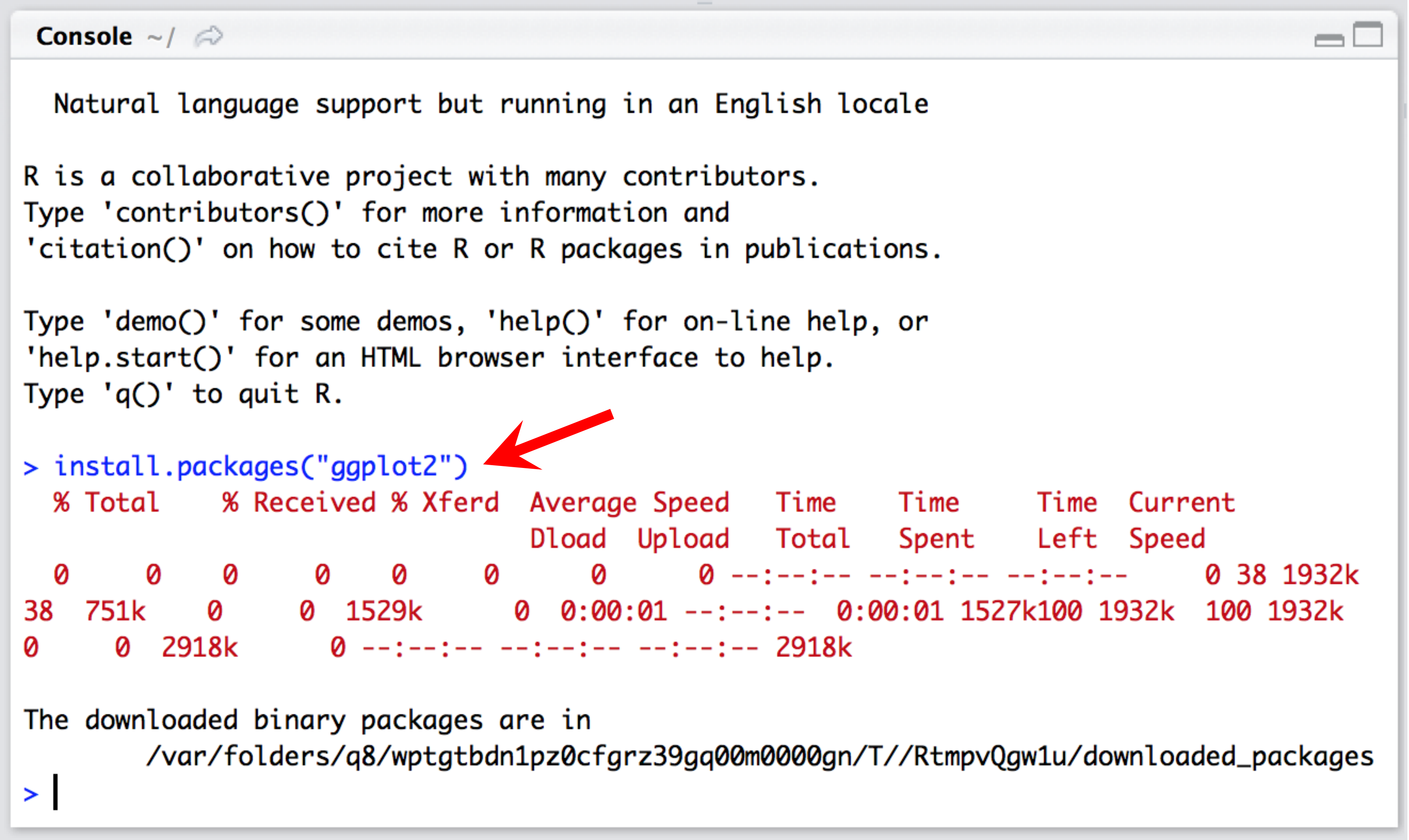
You can install packages using `install.packages()` in RStudio



```
  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> install.packages("ggplot2")
  % Total    % Received % Xferd  Average Speed   Time    Time     Time  Current
                                 Dload  Upload   Total   Spent    Left  Speed
  0     0    0     0    0     0      0      0 --:--:-- --:--:-- --:--:--     0 38 1932k
38  751k    0     0  1529k      0  0:00:01 --:--:--  0:00:01 1527k100 1932k  100 1932k
0     0  2918k      0 --:--:-- --:--:-- --:--:-- 2918k

The downloaded binary packages are in
        /var/folders/q8/wptgtbdn1pz0cfgrz39gq00m0000gn/T//RtmpvQgw1u/downloaded_packages
> 
```

ggplot2: A grammar of graphics

Traditional plotting: You **are** a painter

- Manually place individual graphical elements

ggplot2: You **employ** a painter

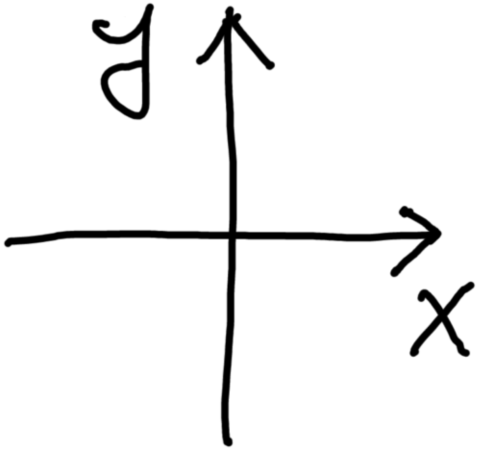
- Describe conceptually how data should be visualized

Most confusing key concept: aesthetic mapping

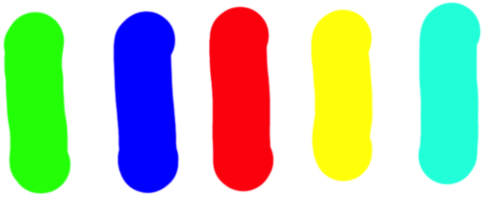
Maps data values to visual elements of the plot

A few examples of aesthetics

position



color



shape

size

angle

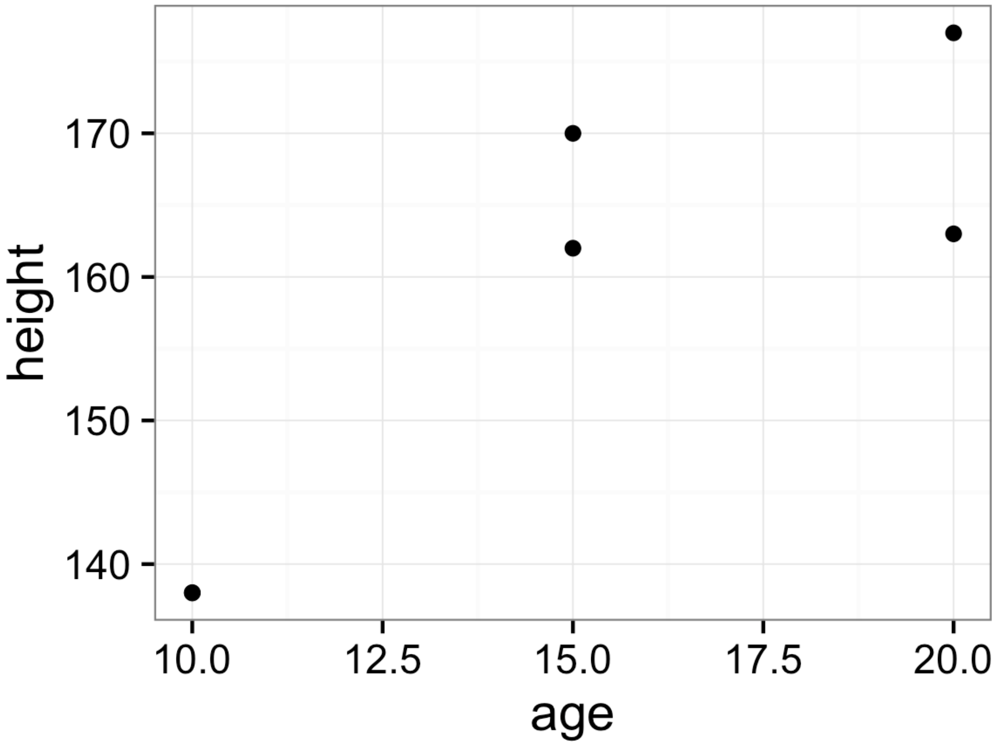
Let’s go over a simple example: mean height and weight of boys/girls ages 10-20

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()
```

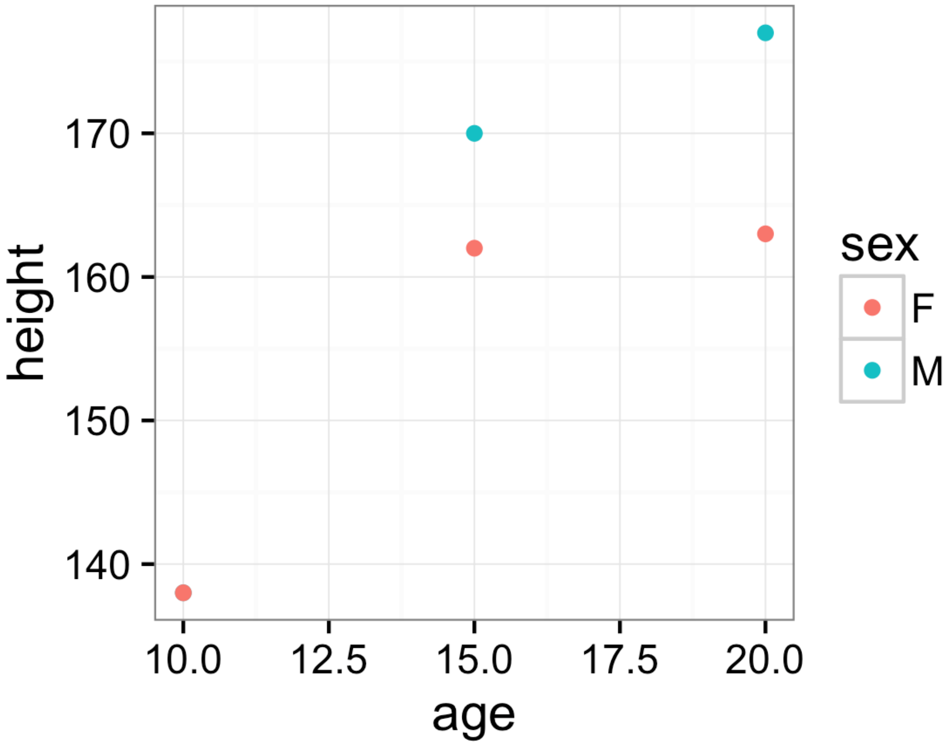


Let’s color the points by sex

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

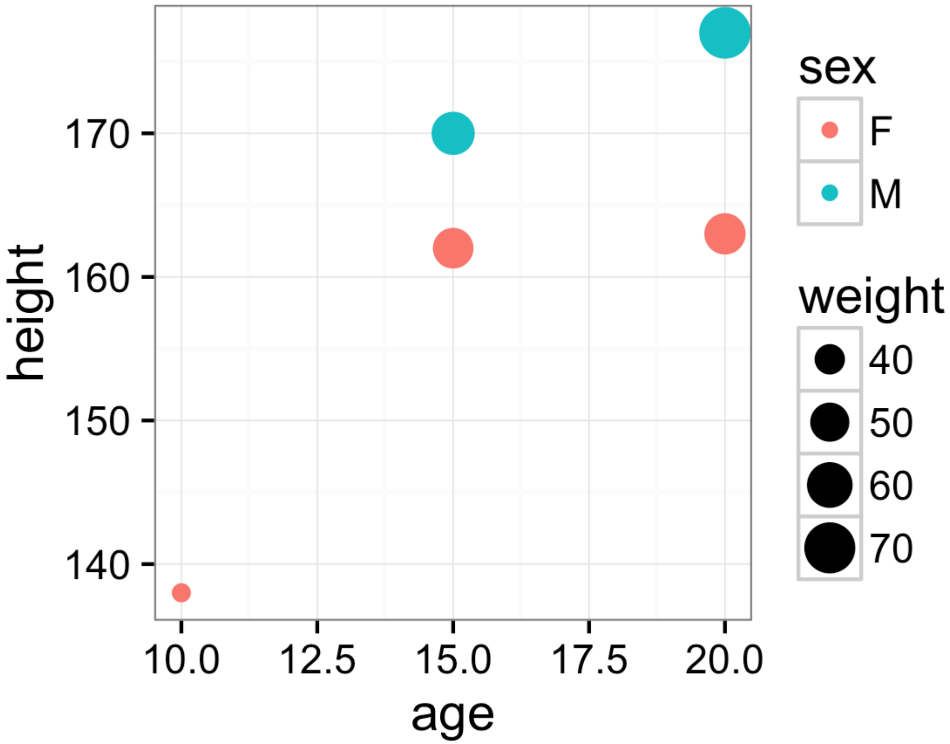
★ NOTE: “color” aesthetic is for coloring points & lines;

“fill” aesthetic is for coloring bars & distributions



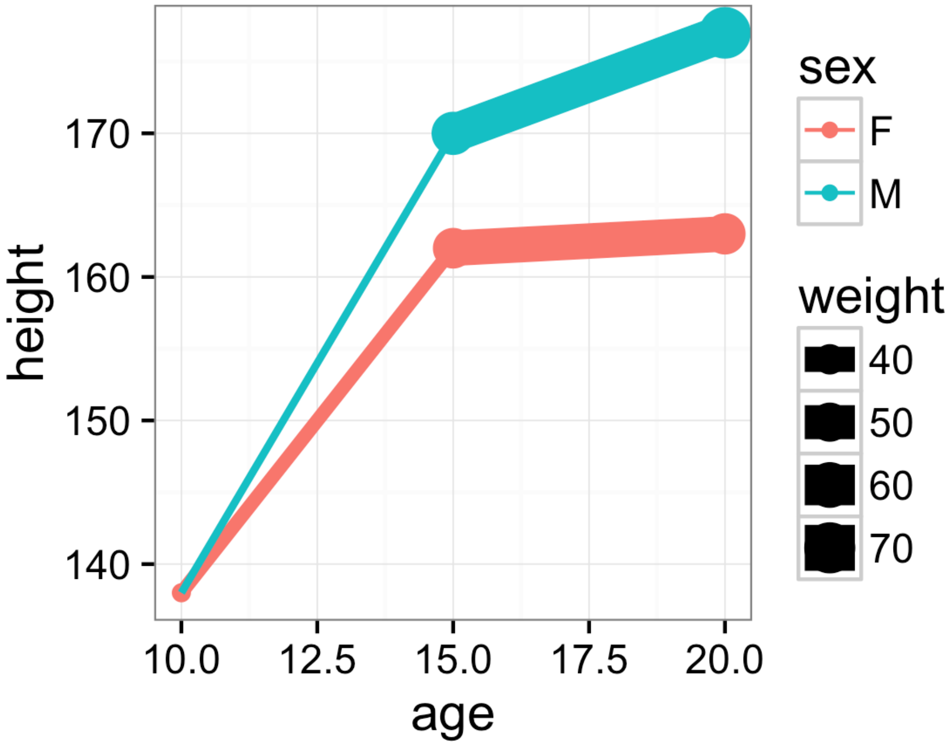
And change point size by weight

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



And connect the points with lines

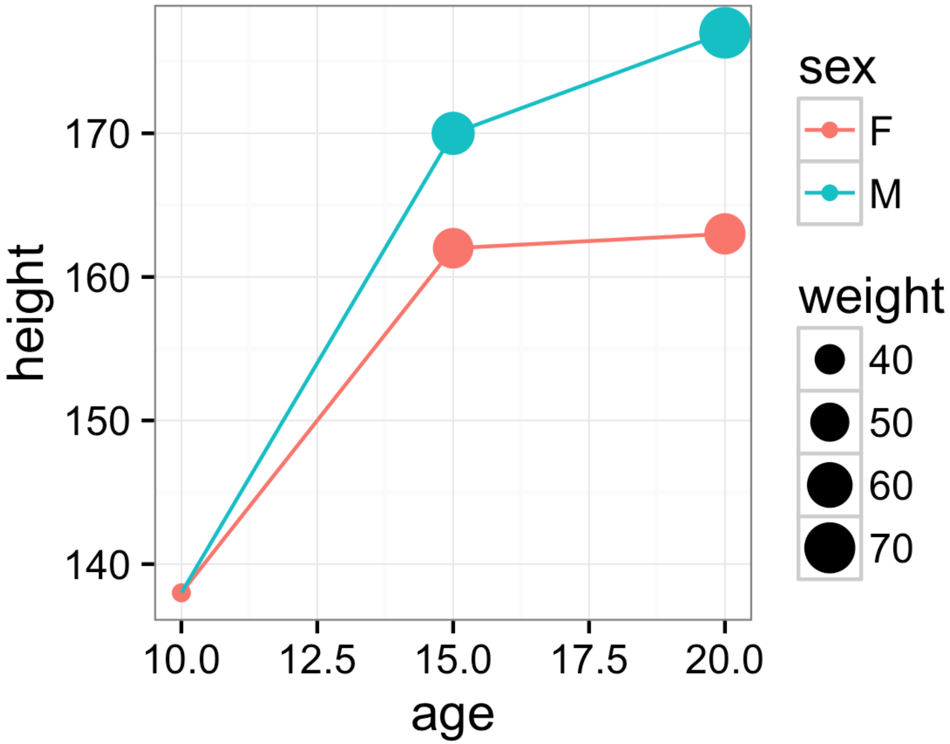
```
ggplot(data, aes(x=age, y=height,
        color=sex, size=weight)) +
                geom_point() + geom_line()
```



Oops!

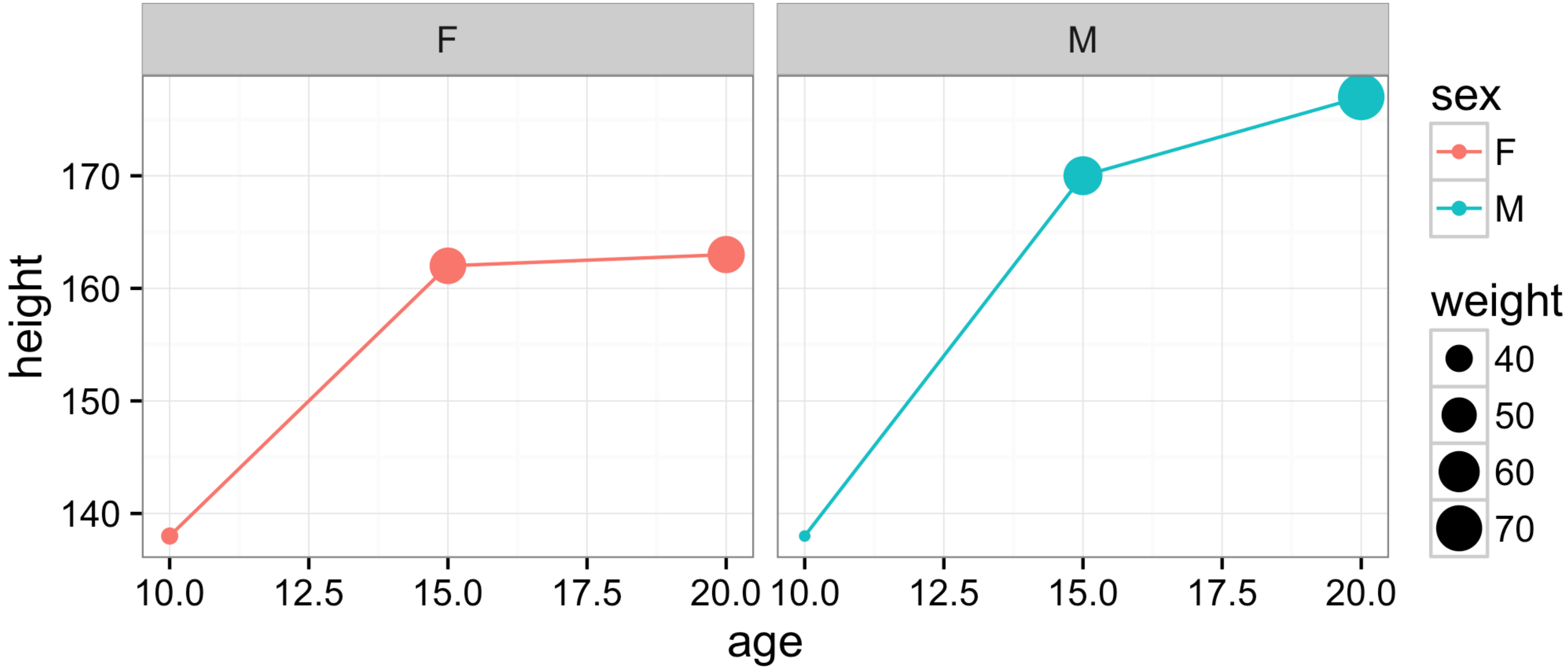
The weight-to-size mapping should only be applied to points

```
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)

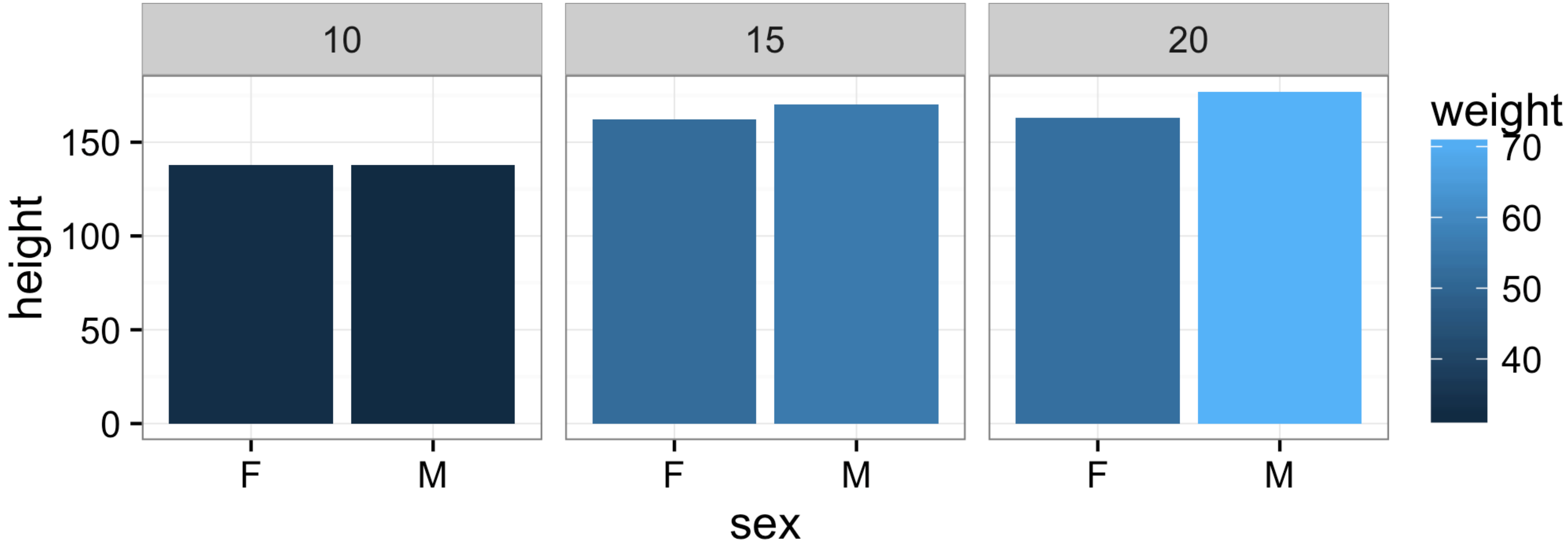
```
ggplot(data, aes(x=age, y=height,
 color=sex)) + geom_point(aes(size=weight)) +
               geom_line() + facet_wrap(~sex)
```



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

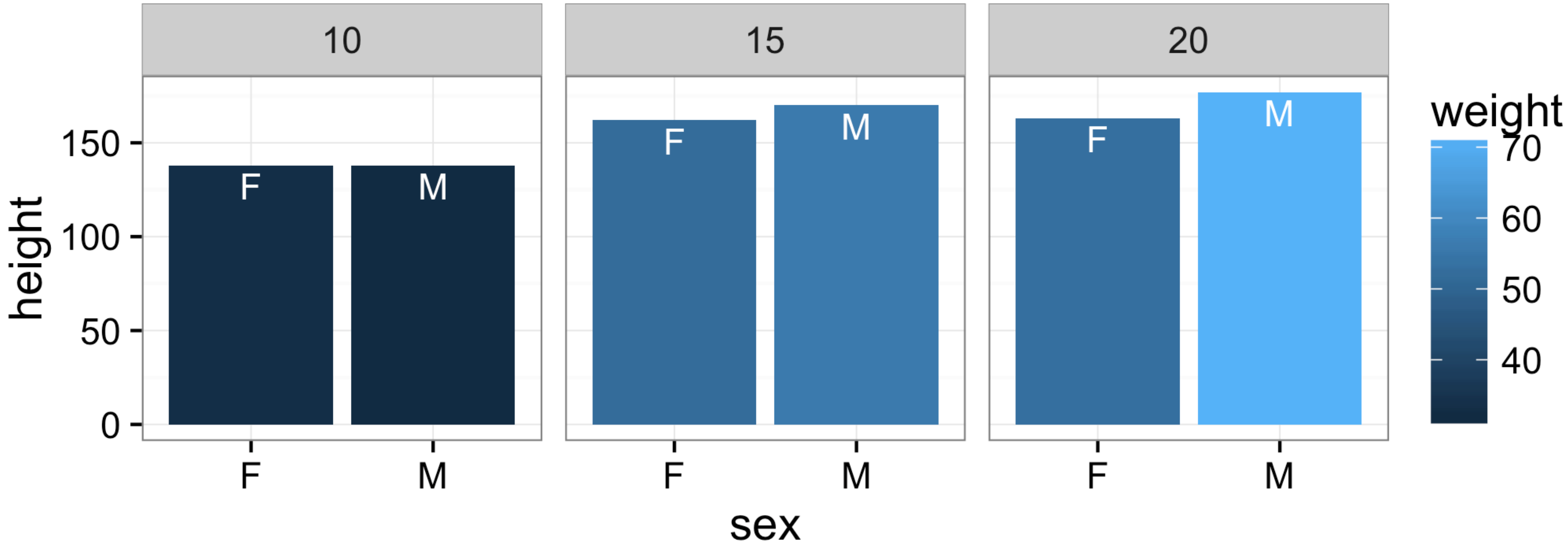
```
ggplot(data, aes(x=sex, y=height, fill=weight)) +
 geom_col() + facet_wrap(~age)
```

<u>NOTE:</u> "fill" ★ aesthetic is for coloring bars & distributions



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

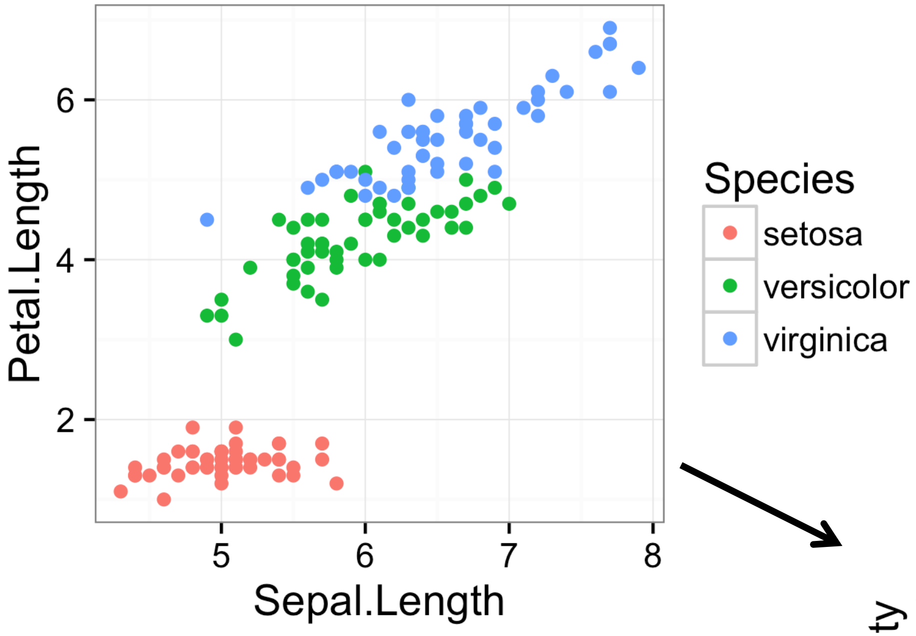
```
ggplot(data, aes(x=sex, y=height, fill=weight)) +
 geom_col() +
 geom_text(aes(label=sex), vjust=1.3, color='white') +
                                       facet_wrap(~age)
```



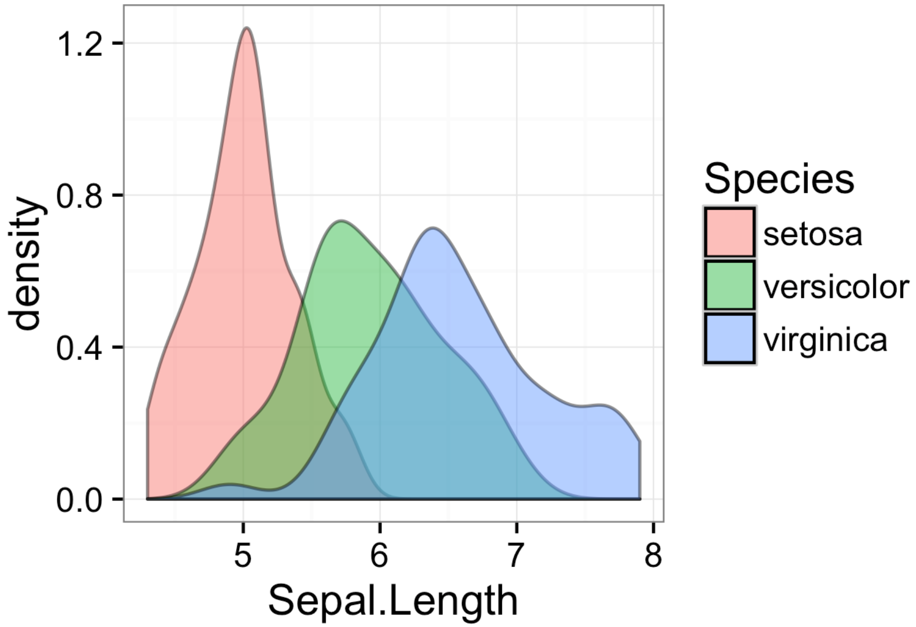
All the geoms with all their options are described on the ggplot2 web page

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

We often need to do statistical transformations before plotting



density of
data points



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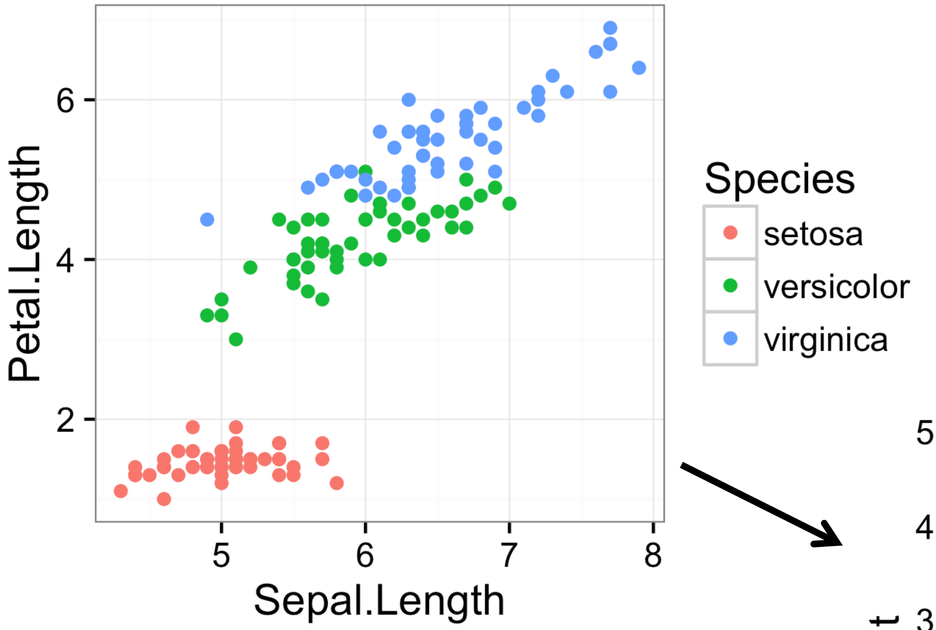
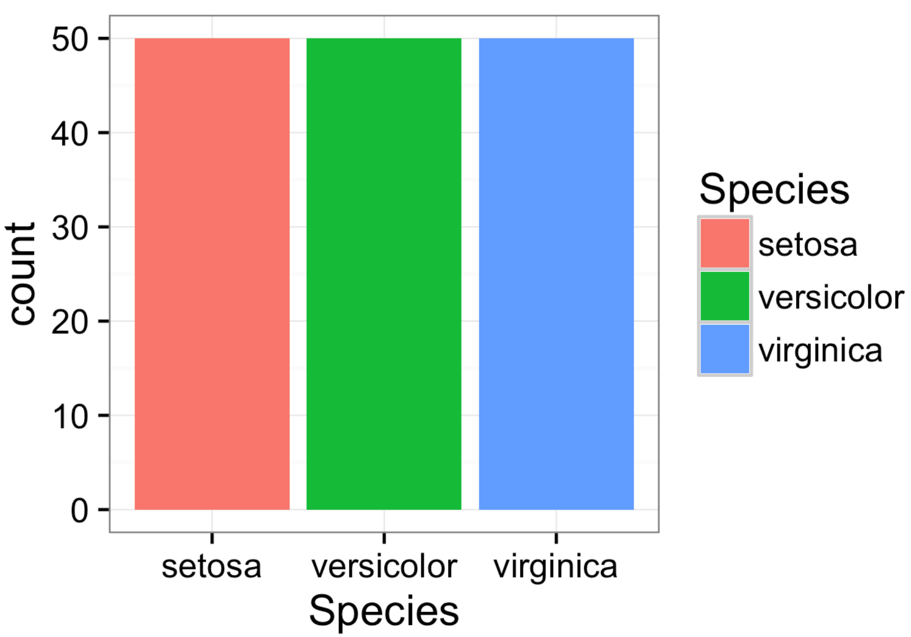
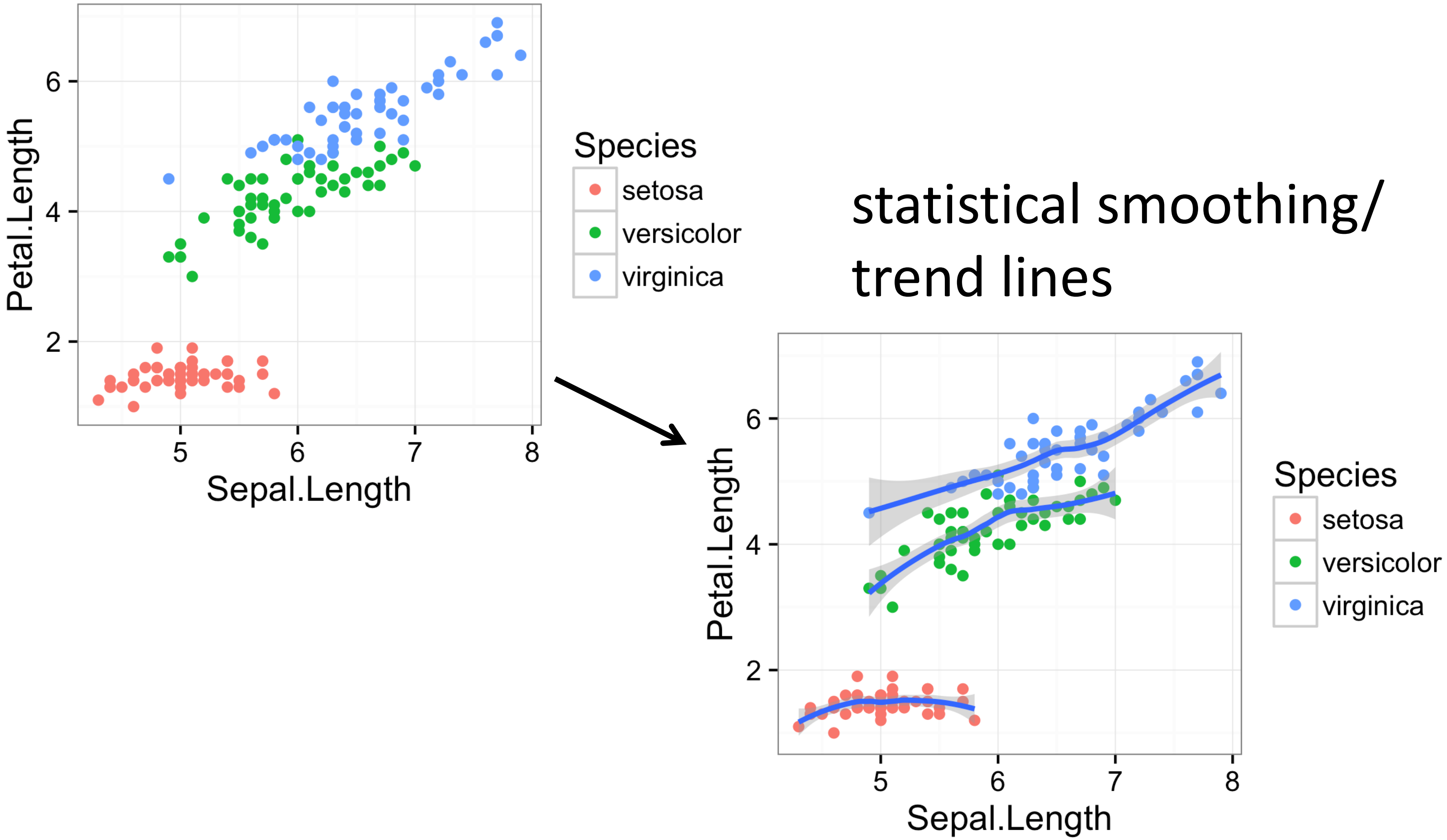


count of number of different types

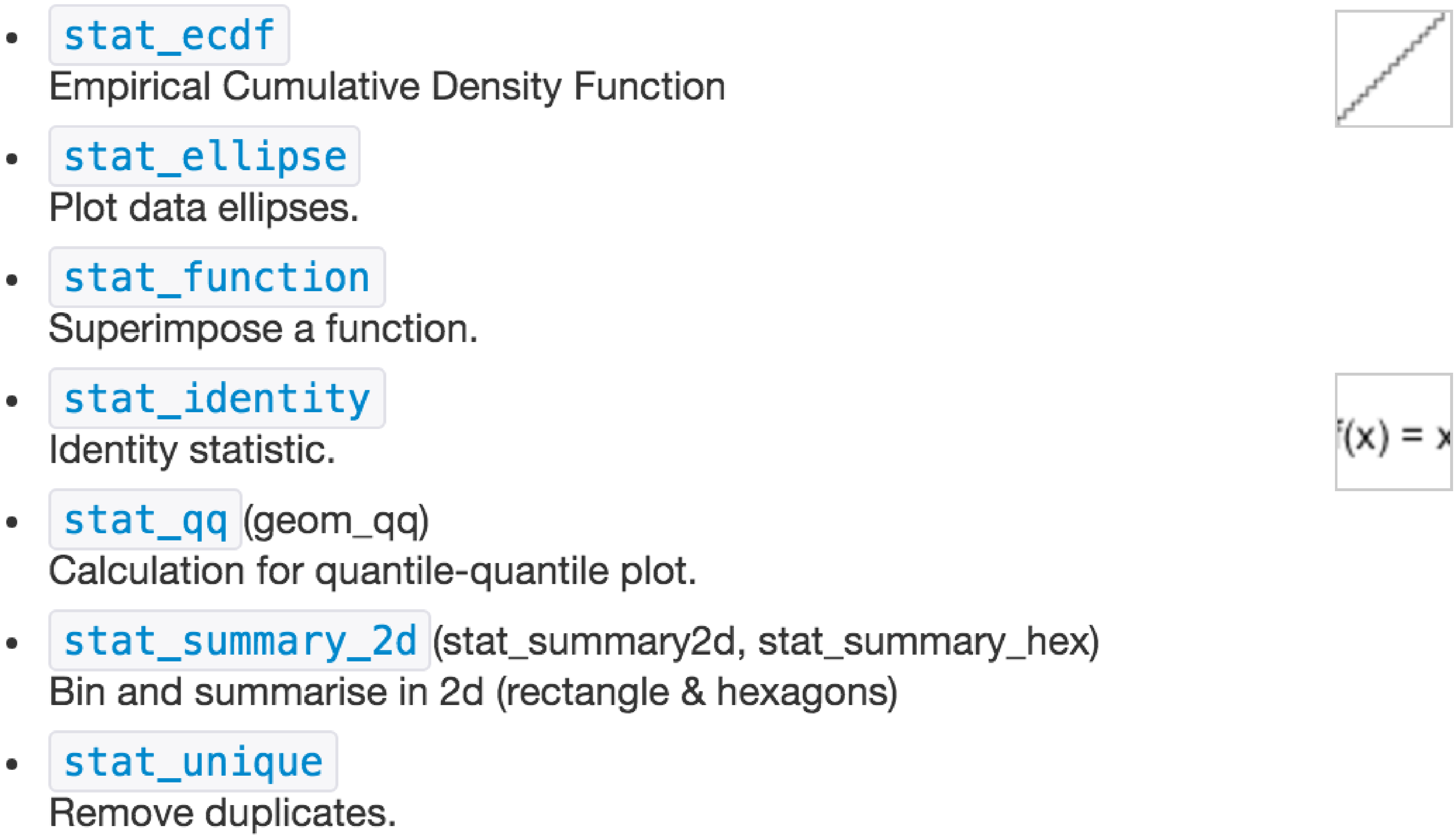


We often need to do statistical transformations before plotting



statistical smoothing/ trend lines

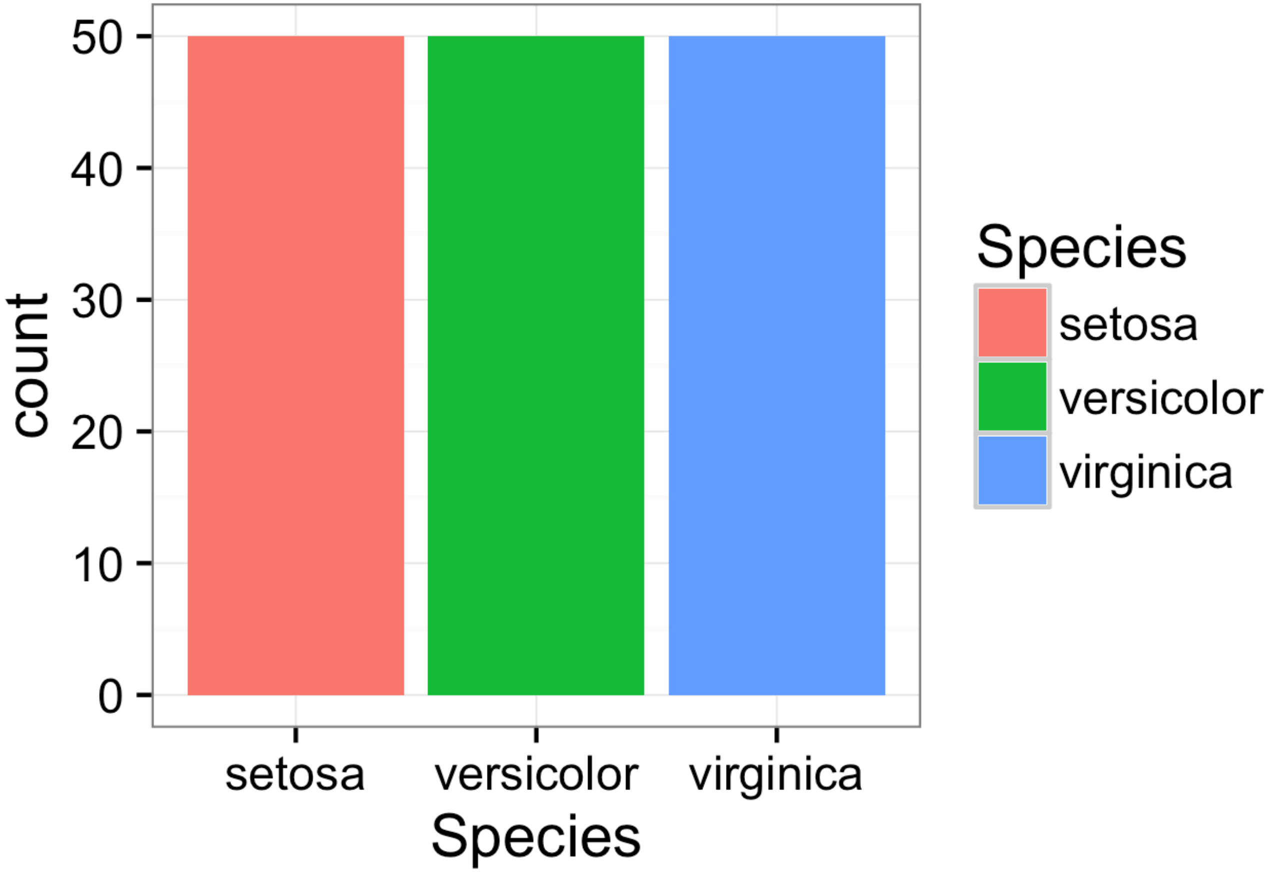
In ggplot2, these transformations are done with stats



- `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.

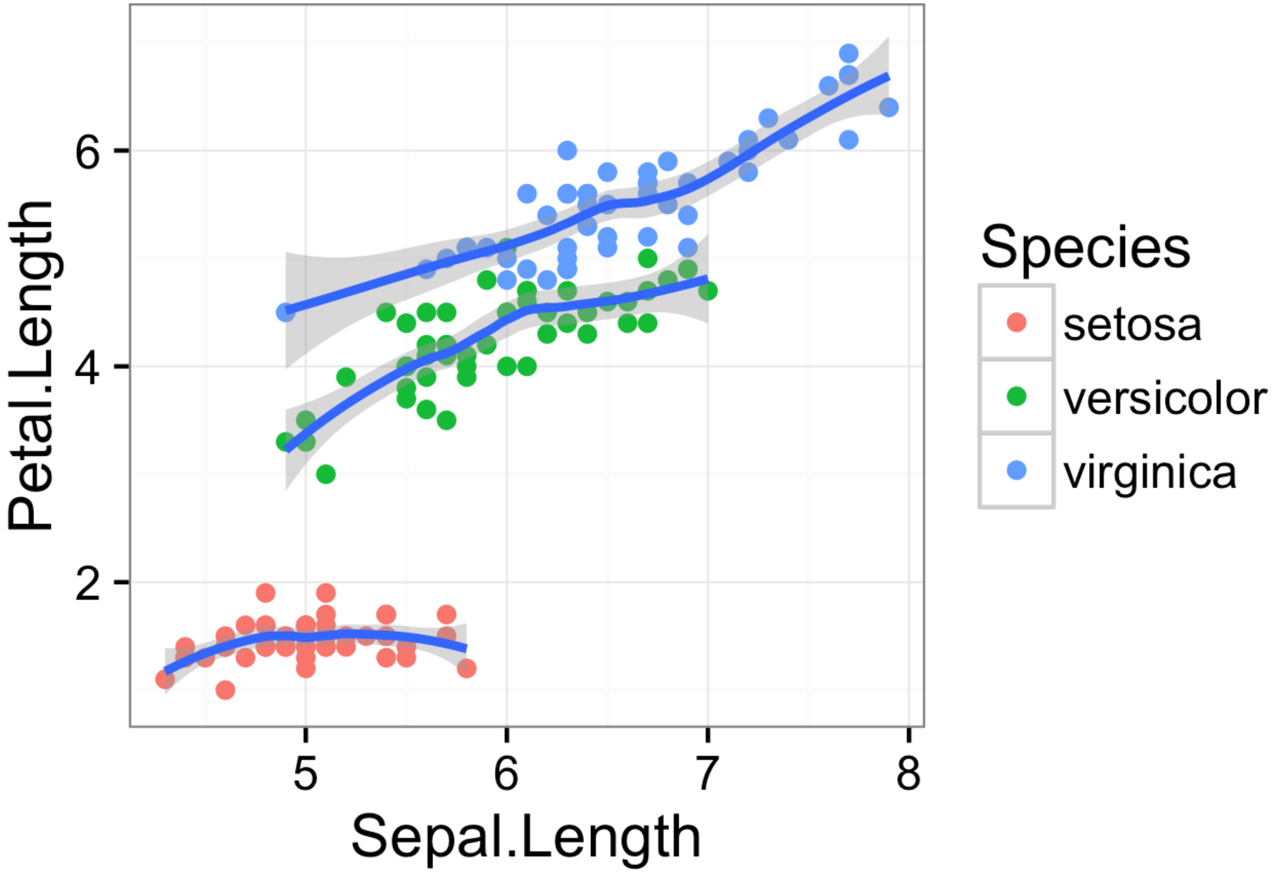
In most cases we just need to call the appropriate geom and it calls a stat

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



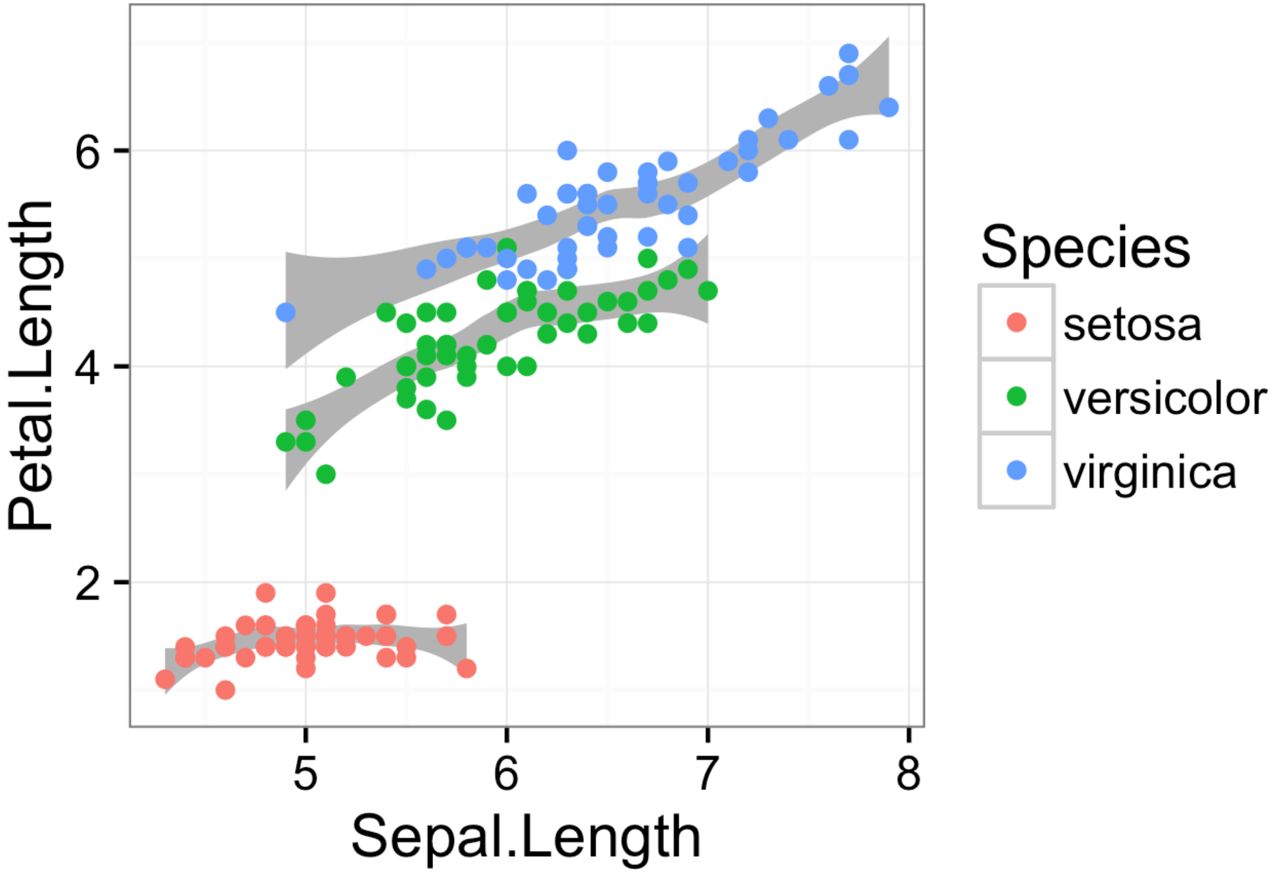
In most cases we just need to call the appropriate geom and it calls a stat

```
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))
```

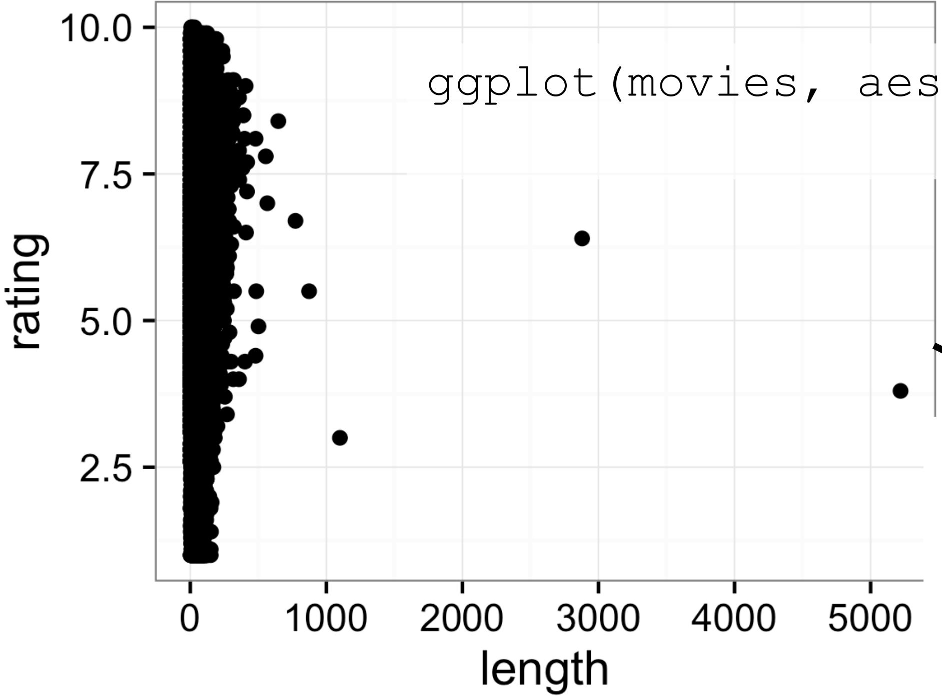


Scales define how to map data onto aesthetics

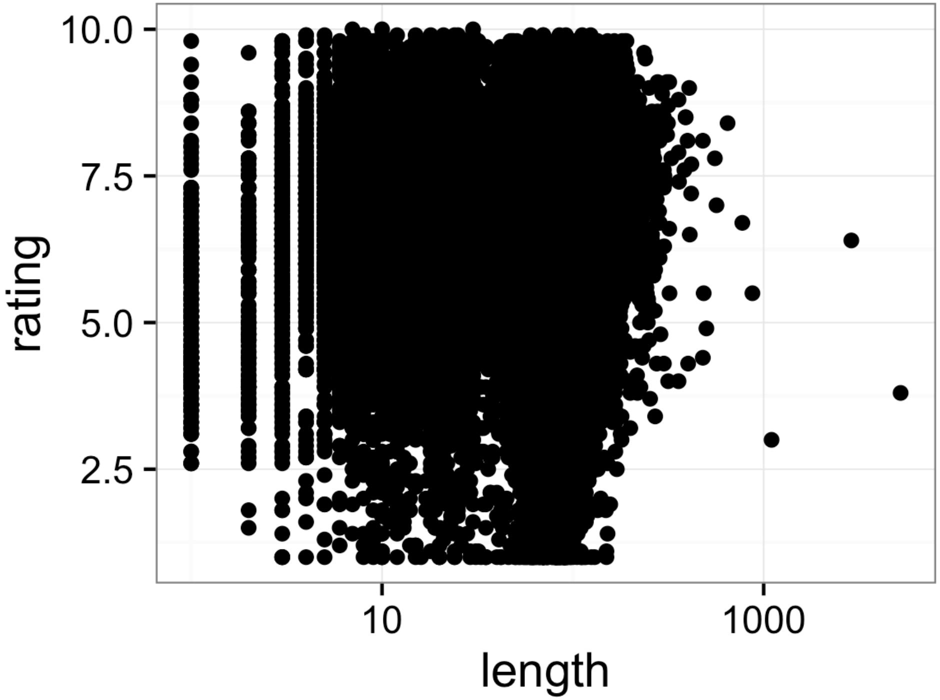
- `scale_colour_grey` (scale_color_grey, scale_fill_grey)
  Sequential grey colour scale.
- `scale_colour_hue` (scale_color_discrete, scale_color_hue, scale_colour_discrete, scale_fill_discrete, scale_fill_hue)
  Qualitative colour scale with evenly spaced hues.
- `scale_identity` (scale_alpha_identity, 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

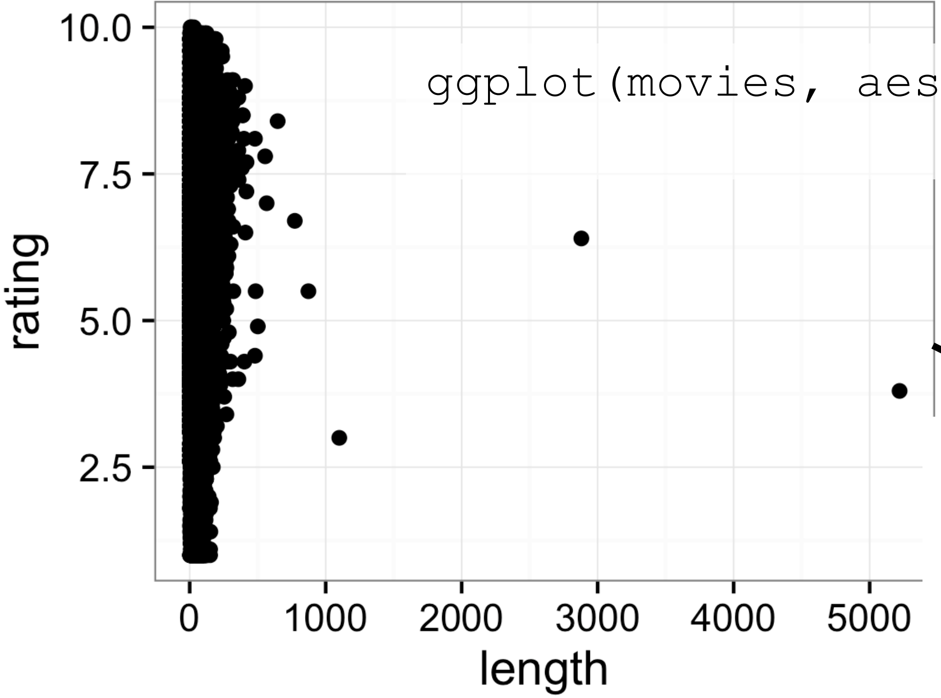
```
ggplot(movies, aes(x=length, y=rating)) +
                                geom_point()
```



```
+ scale_x_log10()
```

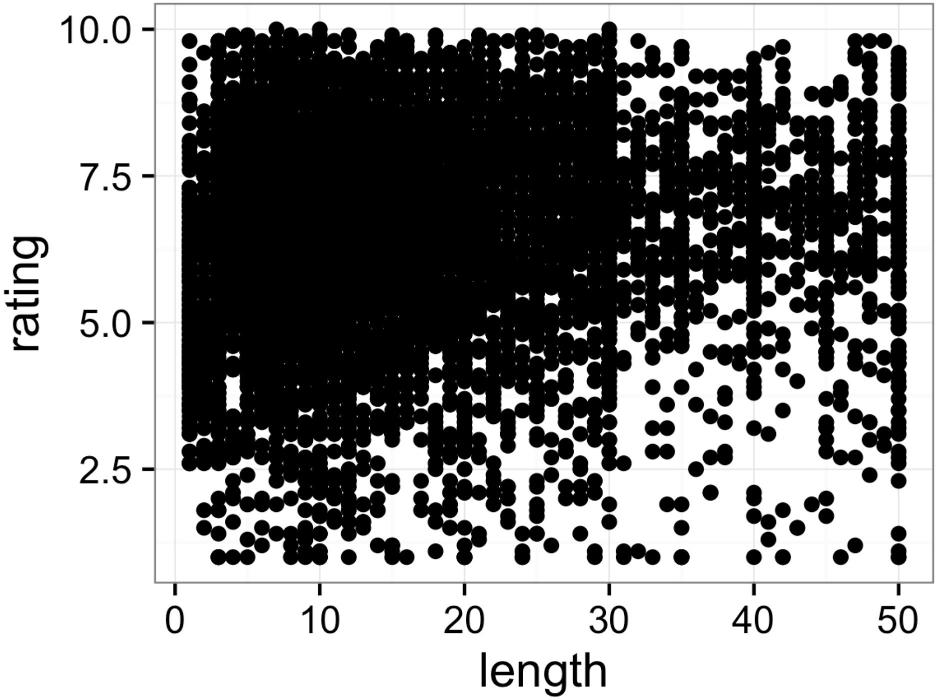


Example 1: Change scaling of x axis



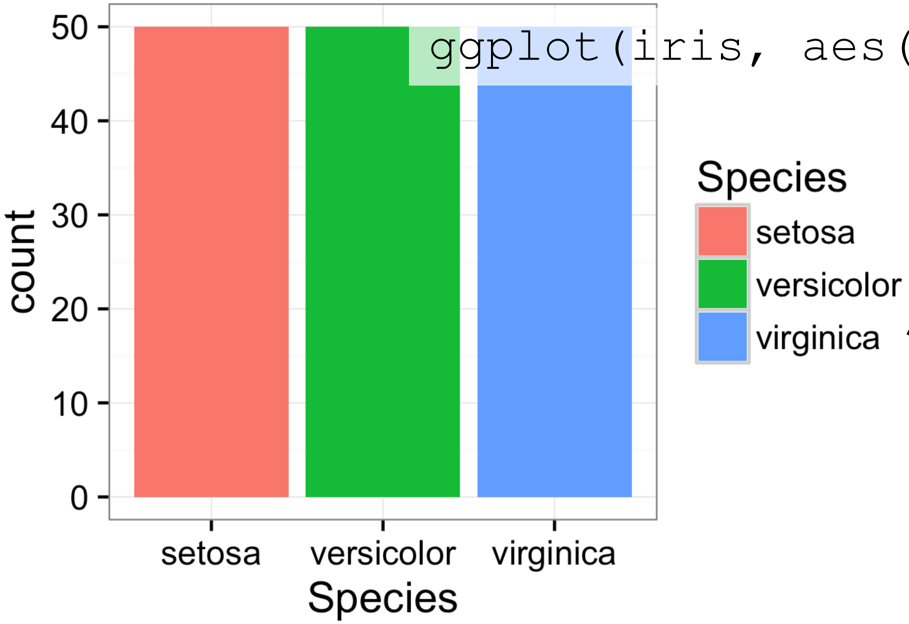
```
ggplot(movies, aes(x=length, y=rating)) +
                                 geom_point()
```

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

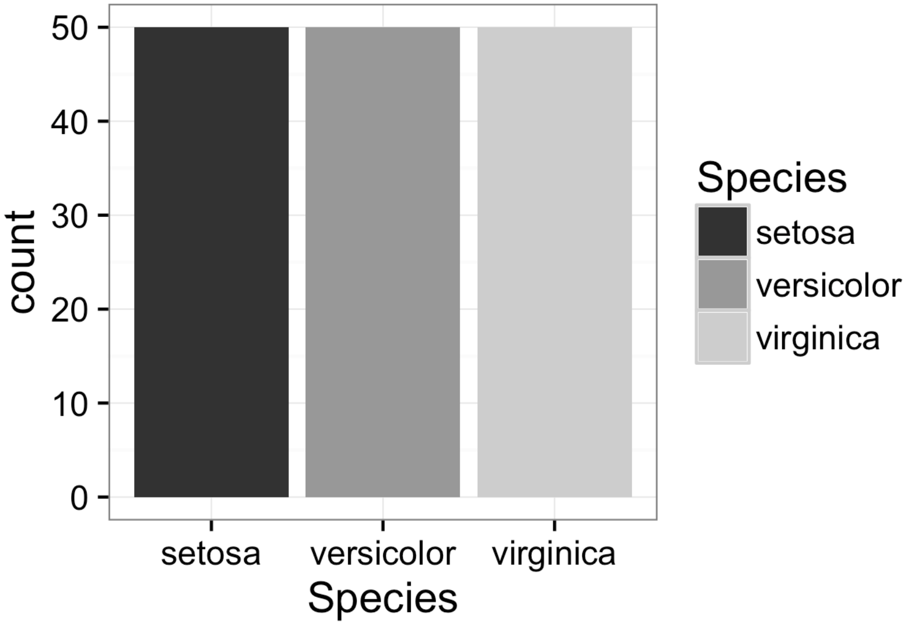


Example 2: Change color scaling

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

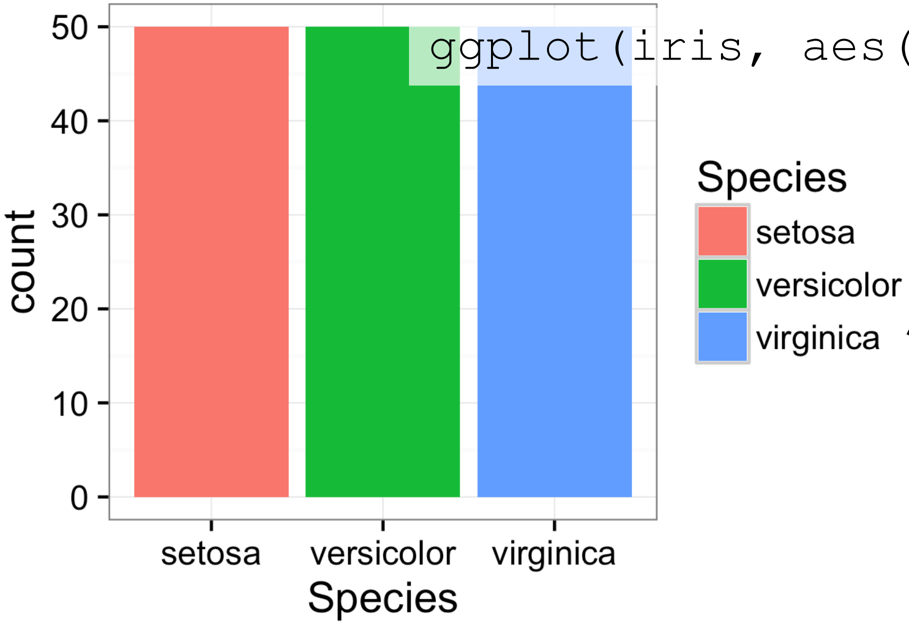


```
+ scale_fill_grey()
```

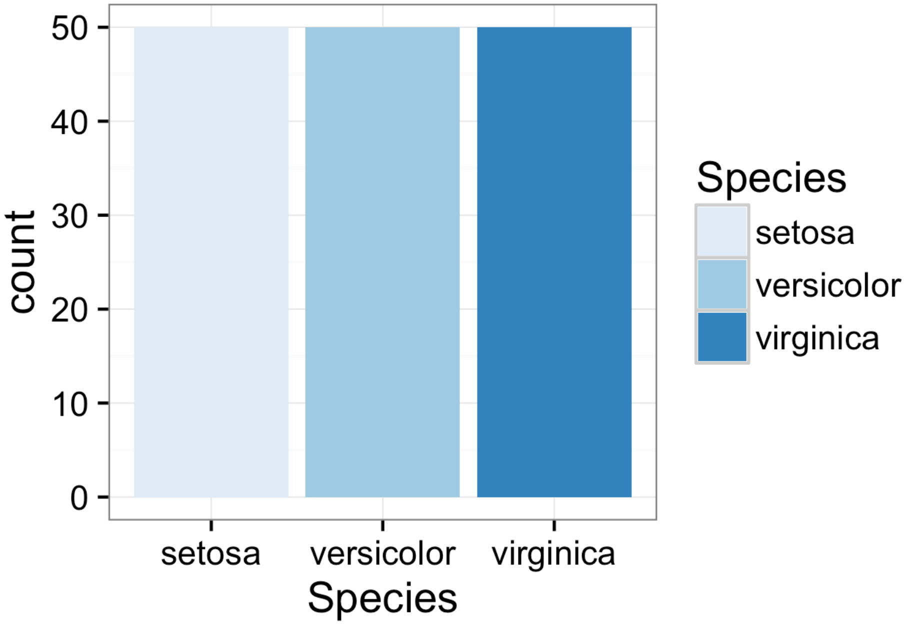


Example 2: Change color scaling

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

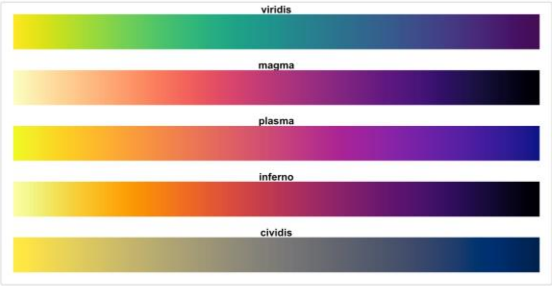


```
+ scale_fill_brewer()
```

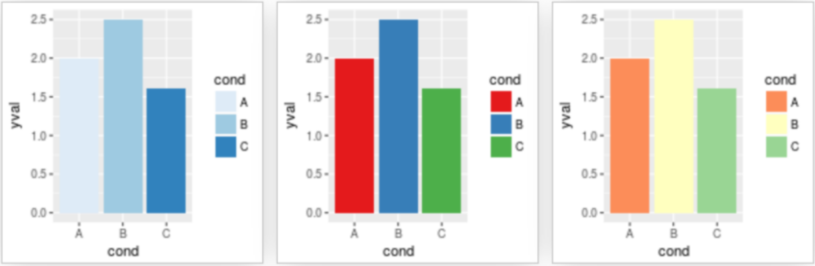


Some color scaling options in ggplot2

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

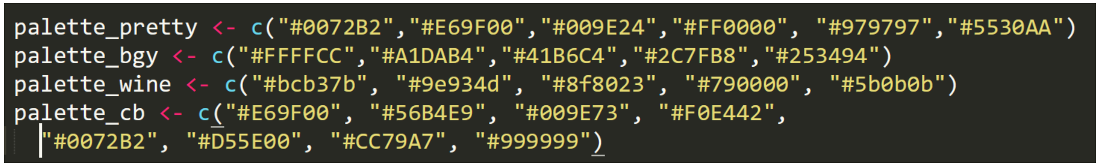


- `scale_color_brewer()`, `scale_fill_brewer()`
- `scale_color_distiller()`, `scale_fill_distiller()`



- `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:

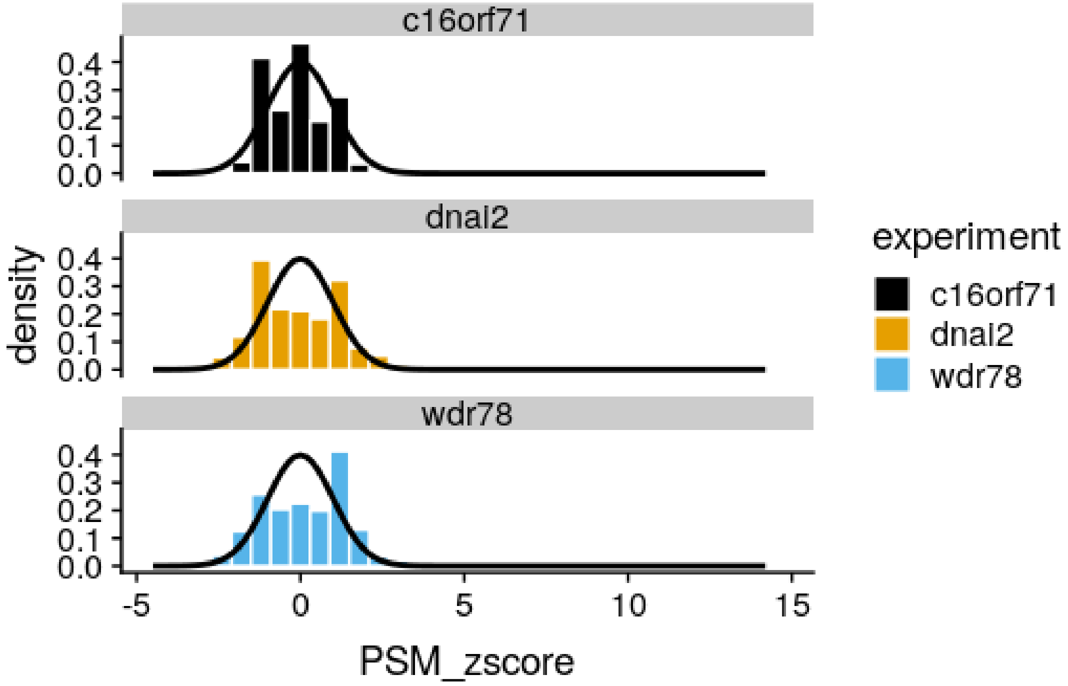
https://ggplot2.tidyverse.org/reference/labs.html

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

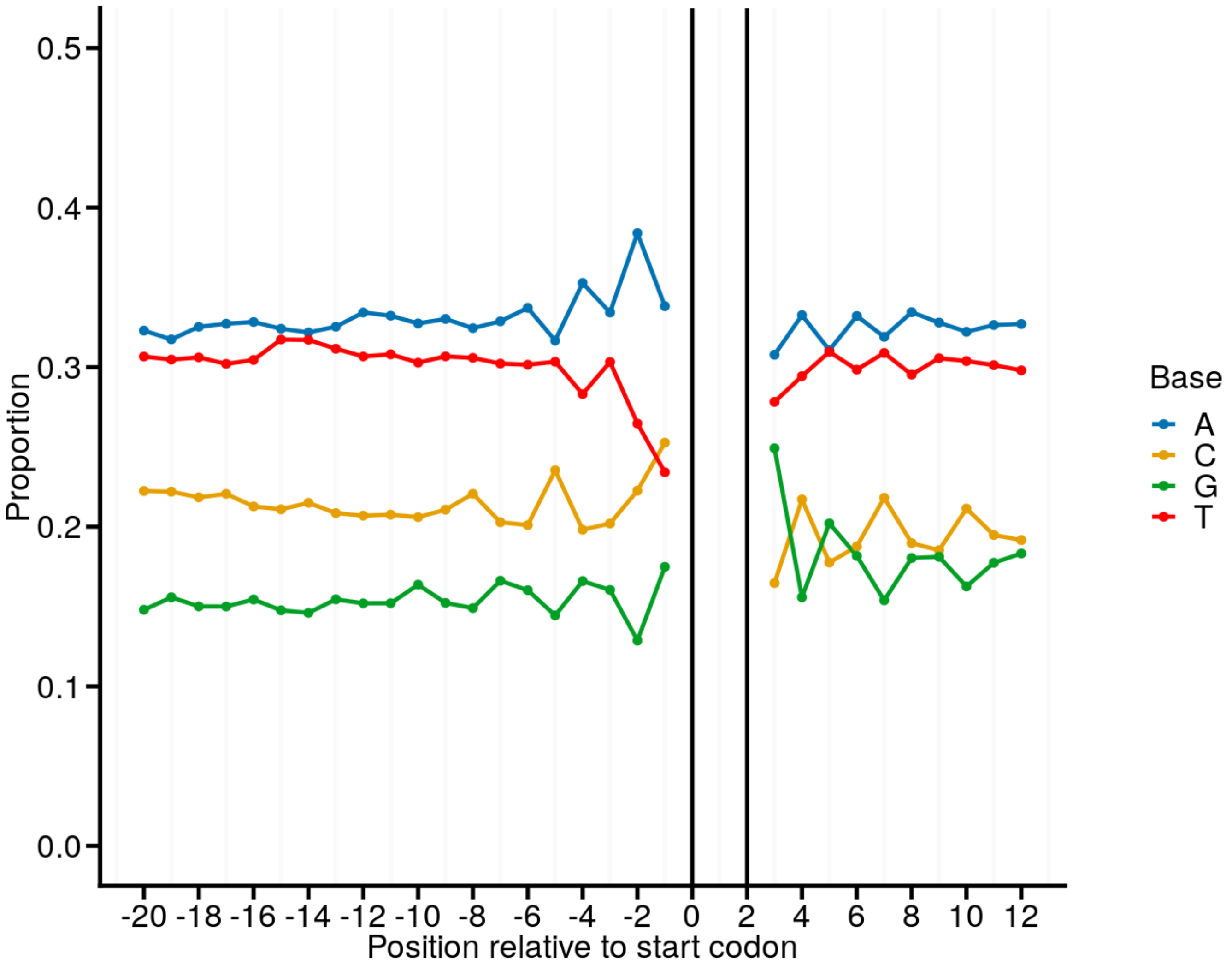
```
ggplot(combined_exp, aes(x = PSM_zscore, fill = experiment)) +
   geom_histogram(binwidth = 0.6, color = "white") +
   facet_wrap(~experiment, ncol = 1) +
   stat_function(aes(group = experiment), fun = dnorm, n = 101,
                 args = list(mean = 0, sd = 1), size = 1) +
   scale_fill_colorblind()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



Putting it all together, example 2

```
final_plot <- final_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:

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

final_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”