# Data Visualization Using R & ggplot2

Naupaka Zimmerman (@naupakaz)
Andrew Tredennick (@ATredennick)

Hat tip to Karthik Ram (@_inundata) for original slides

February 22, 2015

# Some housekeeping

Install some packages

```
install.packages("ggplot2", dependencies = TRUE)
install.packages("plyr")
install.packages("ggthemes")
install.packages("reshape2")
```

# Section 1

## Why ggplot2?

# Why ggplot2?

- More elegant & compact code than with base graphics
- More aesthetically pleasing defaults than lattice
- Very powerful for exploratory data analysis

# Why ggplot2?

- 'gg' is for 'grammar of graphics' (term by Lee Wilkinson)
- A set of terms that defines the basic components of a plot
- Used to produce figures using coherant, consistant syntax

# Why ggplot2?

- Supports a continuum of expertise:
- Easy to get started, plenty of power for complex figures

Section 2

# The Grammar

# Some terminology

- **data**
  - Must be a data.frame
  - Gets pulled into the ggplot() object

# The iris dataset

```
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

# plyr and reshape are key for using R

These two packages are the swiss army knives of R.

- plyr
  1. ddply (data frame to data frame ply)
     - 1.1 split
     - 1.2 apply
     - 1.3 combine
  2. llply (list to list ply)
  3. join

# plyr

```
iris[1:2, ]

##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa

# Note the use of the . function to allow Species to be used
# without quoting
ddply(iris, .(Species), summarize,
      mean.Sep.Wid = mean(Sepal.Width, na.rm = TRUE))

##      Species mean.Sep.Wid
## 1     setosa        3.428
## 2 versicolor        2.770
## 3  virginica        2.974
```

# plyr and reshape are key for using R

These two packages are the swiss army knives of R.

- reshape
  1. melt
  2. dcast (data frame output)
  3. acast (vector/matrix/array output)

# reshape2

```
iris[1:2, ]

##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa

df  <- melt(iris, id.vars = "Species")
df[1:2, ]

##   Species     variable value
## 1  setosa Sepal.Length   5.1
## 2  setosa Sepal.Length   4.9
```

# reshape2

```
df[1:2, ]

##   Species     variable value
## 1  setosa Sepal.Length   5.1
## 2  setosa Sepal.Length   4.9

dcast(df, Species ~ variable, mean)

##      Species Sepal.Length Sepal.Width Petal.Length
## 1     setosa        5.006       3.428        1.462
## 2 versicolor        5.936       2.770        4.260
## 3  virginica        6.588       2.974        5.552
##   Petal.Width
## 1       0.246
## 2       1.326
## 3       2.026
```

Section 3

# Aesthetics

# Some terminology

- data
- **aes**thetics

- **How your data are represented visually**
  - *a.k.a. mapping*
- which data on the x
- which data on the y
- but also: color, size, shape, transparency

# Let's try an example

```
myplot <- ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width))
summary(myplot)

## data: Sepal.Length, Sepal.Width, Petal.Length,
##   Petal.Width, Species [150x5]
## mapping:  x = Sepal.Length, y = Sepal.Width
## faceting: facet_null()
```

# Section 4

## Geoms

# Some terminology

- data
- aesthetics
- **geom**etry

- **The geometric objects in the plot**
- points, lines, polygons, etc
- shortcut functions: geom_point(), geom_bar(), geom_line()

# Basic structure

```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width))
    + geom_point()

myplot <- ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width))
myplot + geom_point()
```

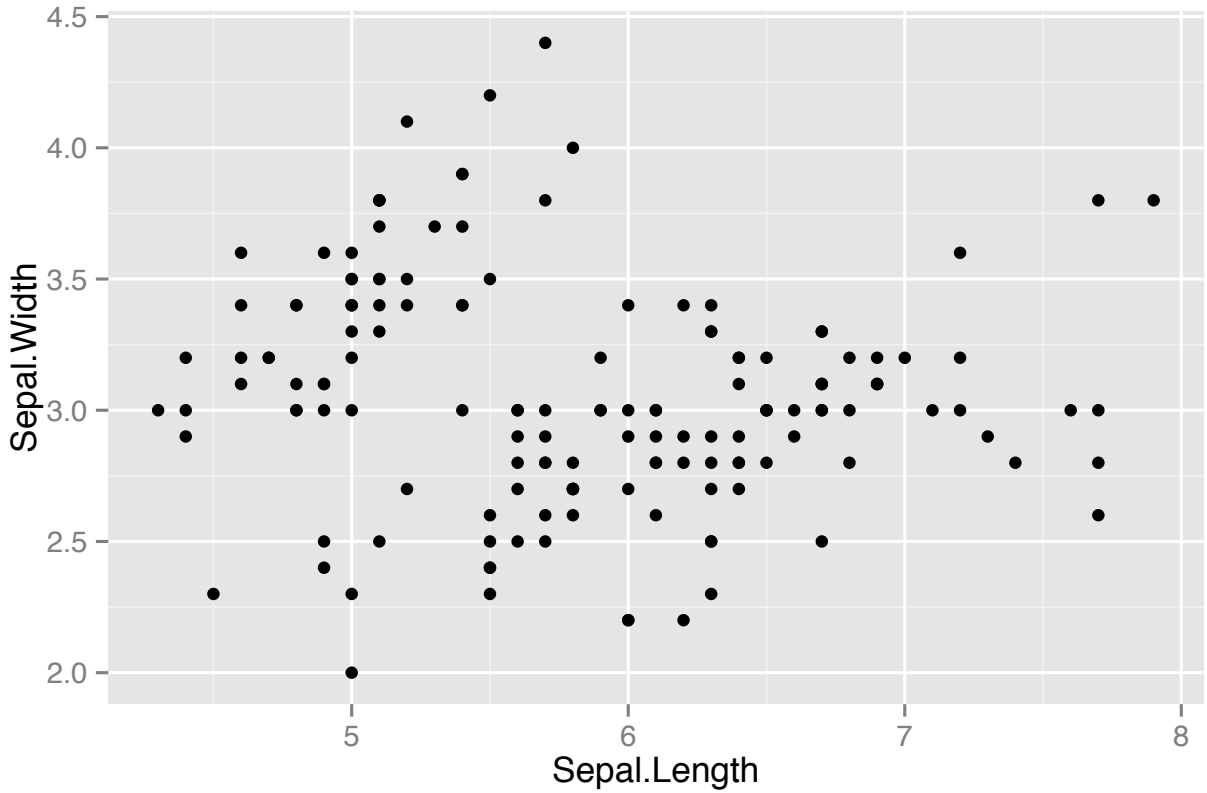
- Specify the data and variables inside the ggplot function.
- Anything else that goes in here becomes a global setting.
- Then add layers: geometric objects, statistical models, and facets.

# Quick note

- Never use `qplot` - short for quick plot.
- You'll end up unlearning and relearning a good bit.

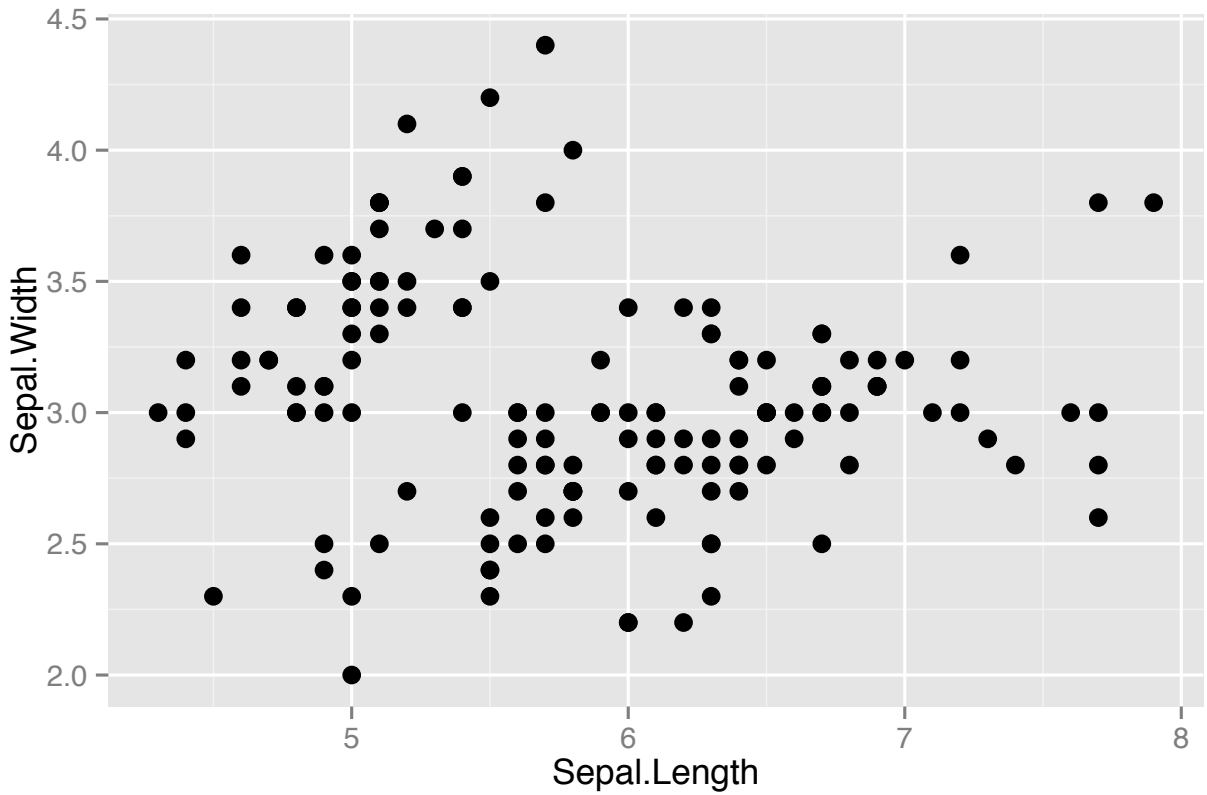
# Let's try an example

```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width)) +
    geom_point()
```



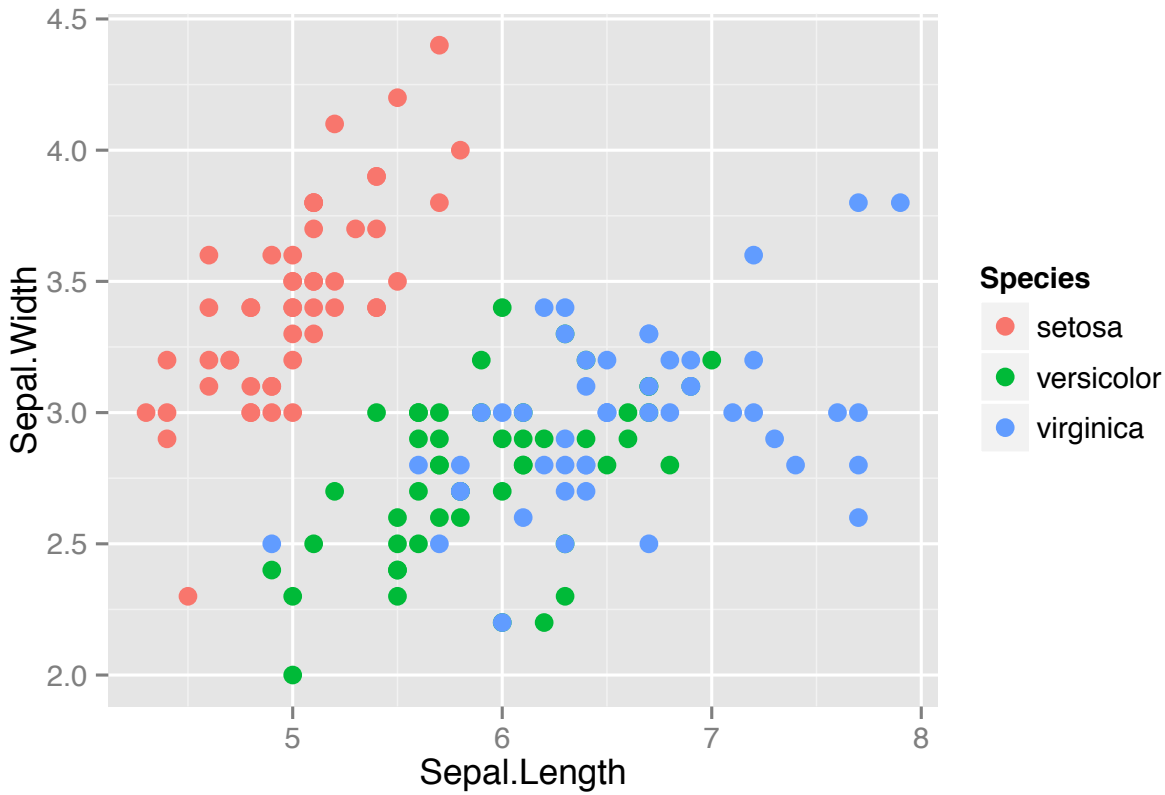
# Changing the aesthetics of a geom: Increase the size of points

```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width)) +
    geom_point(size = 3)
```



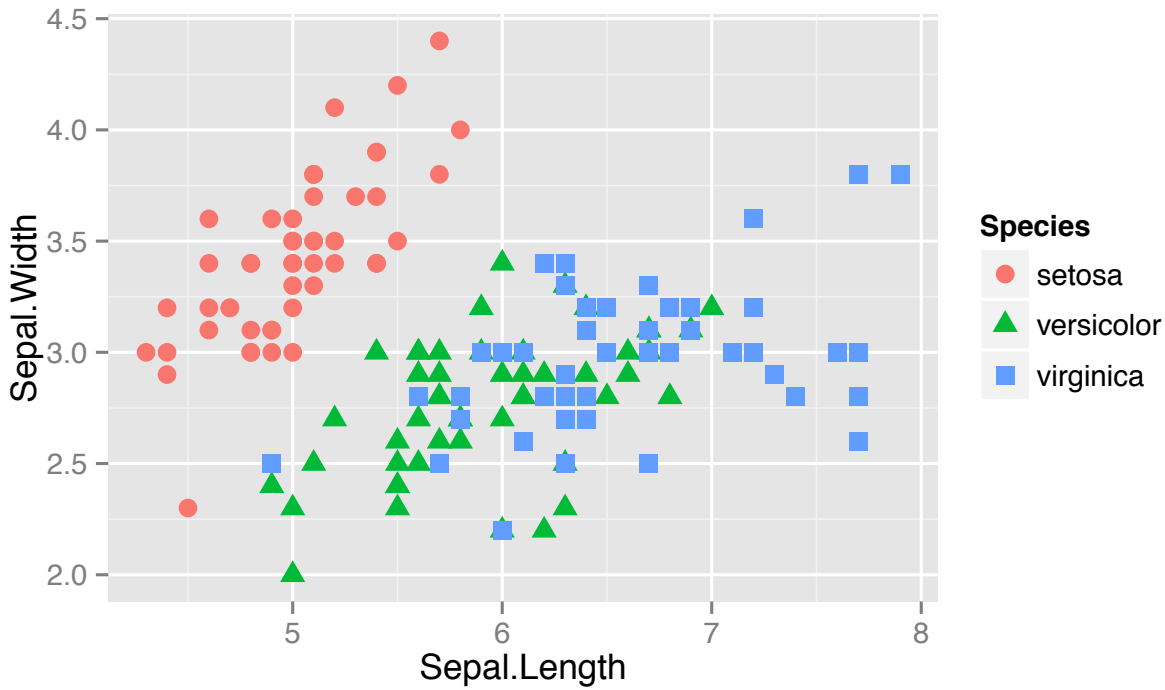
# Changing the aesthetics of a geom: Add some color

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point(size = 3)
```



# Changing the aesthetics of a geom: Differentiate points by shape

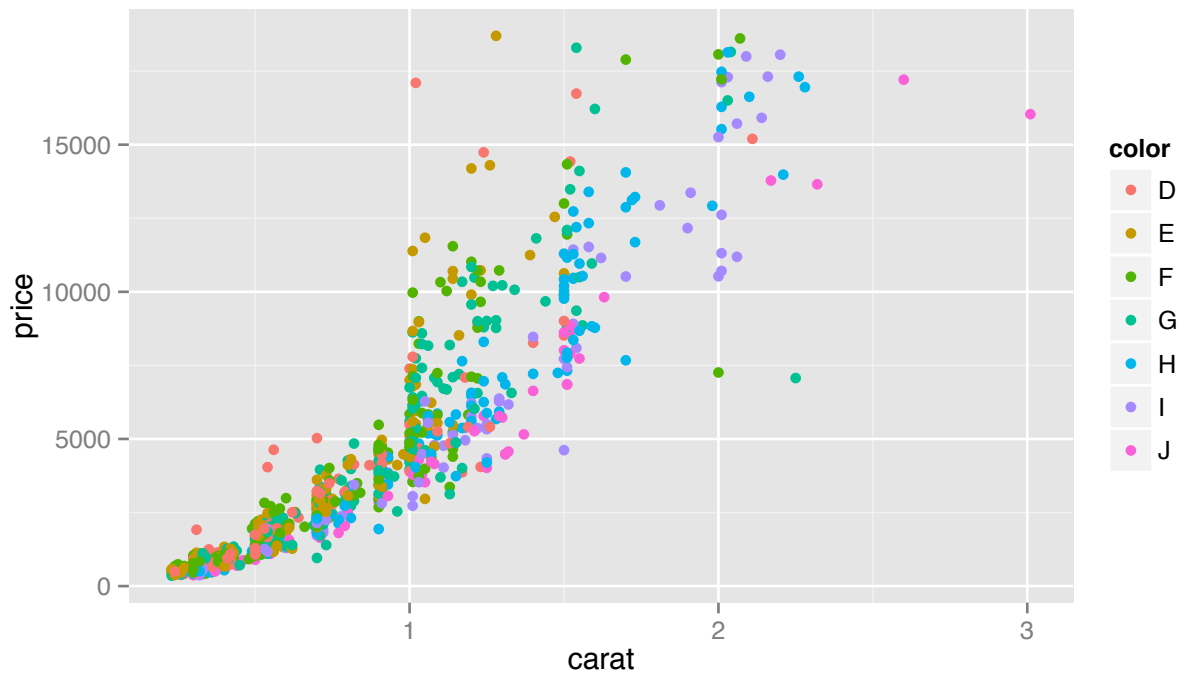
```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point(aes(shape = Species), size = 3)
# Why aes(shape = Species)?
```



# Exercise 1

```
# Make a small sample of the diamonds dataset
d2 <- diamonds[sample(1:dim(diamonds)[1], 1000), ]
```

Then generate this plot below.



# Section 5

## Stats

# Some terminology

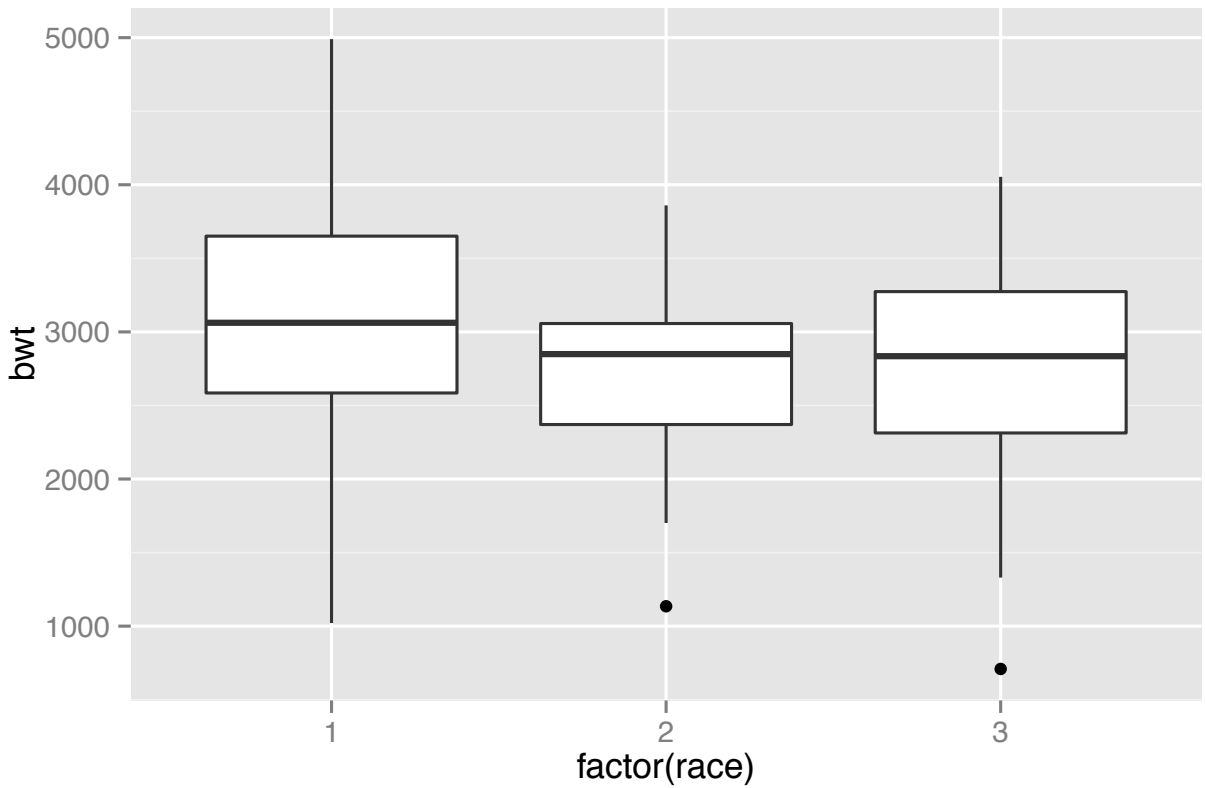
- data
- aesthetics
- geometry
- **stat**s

- **Statistical transformations and data summary**
- All geoms have associated default stats, and vice versa
- e.g. binning for a histogram or fitting a linear model

# Built-in stat example: Boxplots

See ?geom_boxplot for list of options

```
library(MASS)
ggplot(birthwt, aes(factor(race), bwt)) + geom_boxplot()
```



# Built-in stat example: Boxplots

```
myplot <- ggplot(birthwt, aes(factor(race), bwt)) + geom_boxplot()
summary(myplot)

## data: low, age, lwt, race, smoke, ptl, ht, ui, ftv,
##   bwt [189x10]
## mapping:  x = factor(race), y = bwt
## faceting: facet_null()
## -----------------------------------
## geom_boxplot: outlier.colour = black, outlier.shape = 16, outlier.size =
## stat_boxplot:
## position_dodge: (width = NULL, height = NULL)
```

Section 6

# Facets

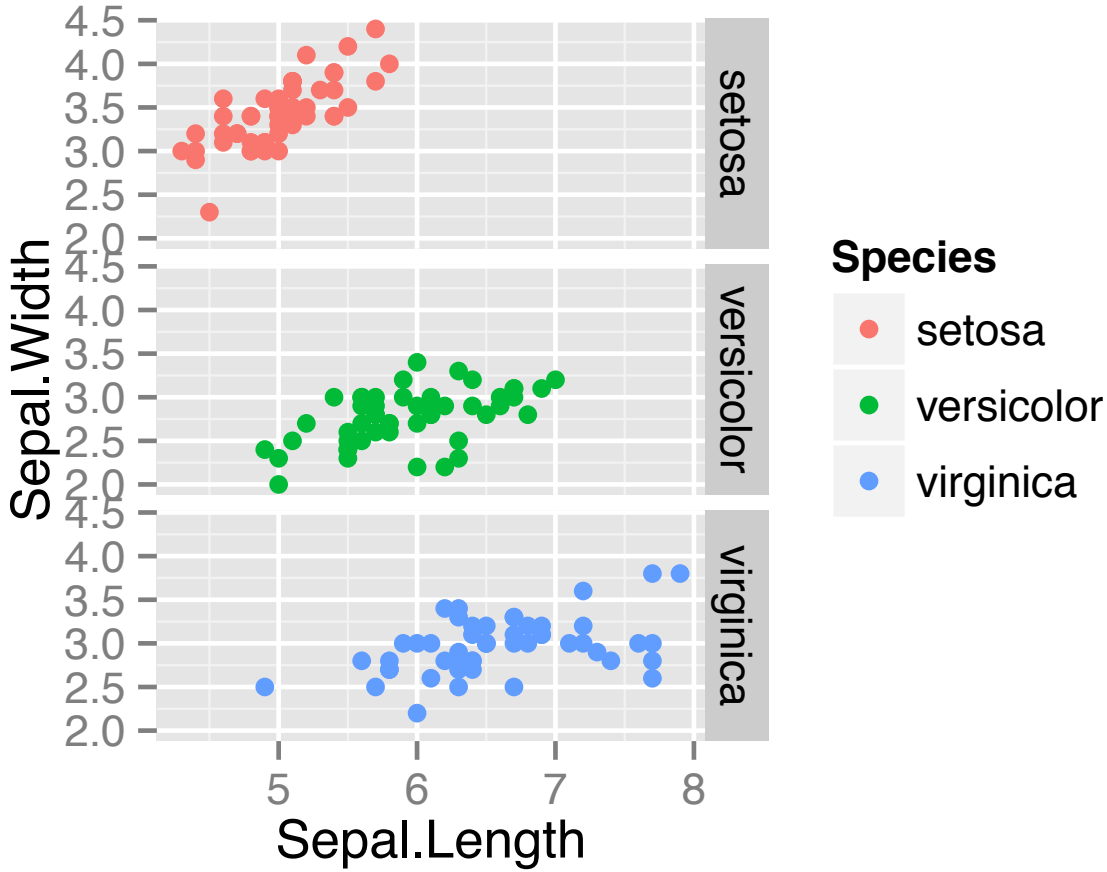
# Some terminology

- data
- aesthetics
- geometry
- stats
- **facet**s

- **Subsetting data to make lattice plots**
- Really powerful

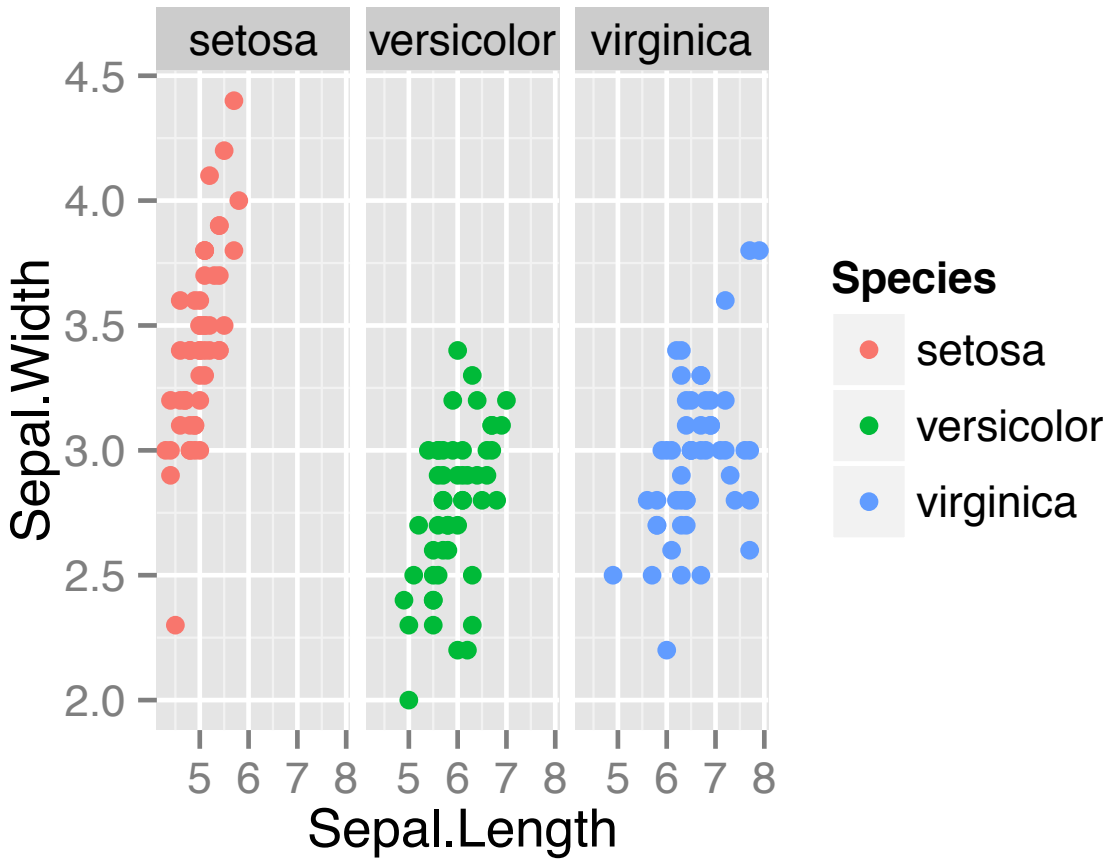
# Faceting: single column, multiple rows

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point() +
    facet_grid(Species ~ .)
```



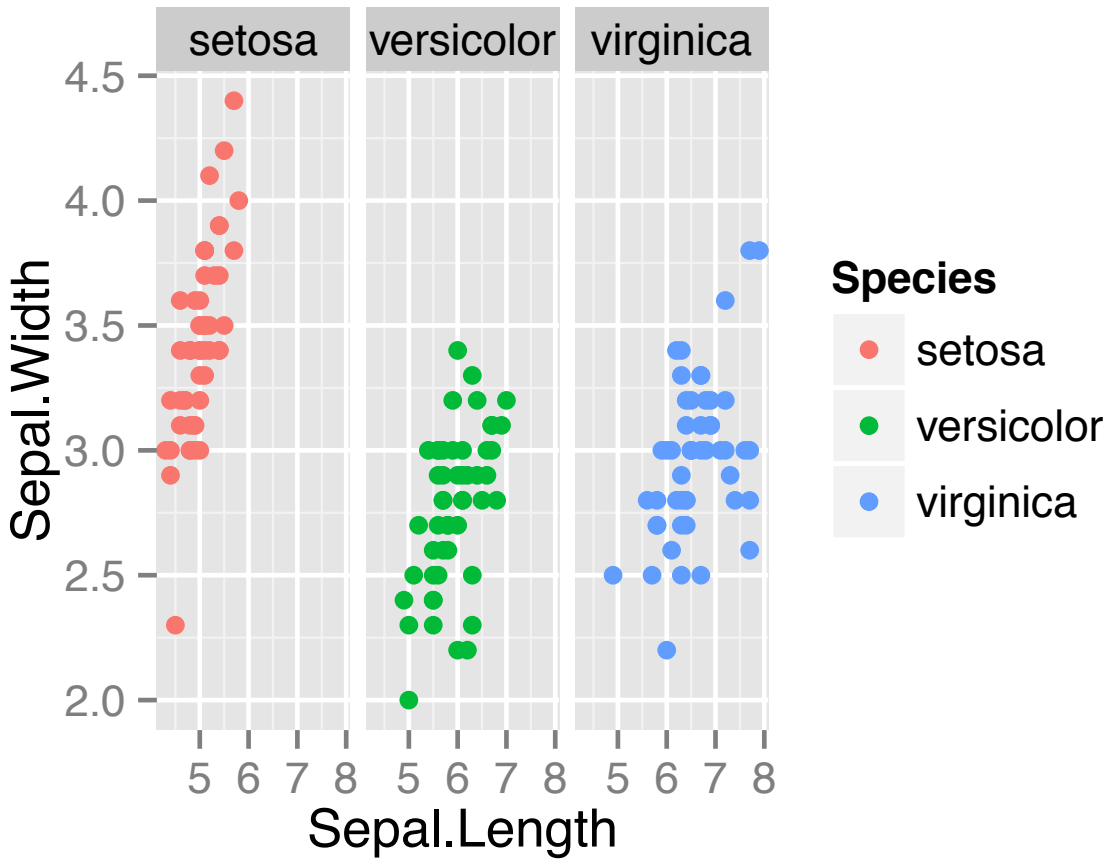
# Faceting: single row, multiple columns

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point() +
    facet_grid(. ~ Species)
```



# or just wrap your facets

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point() +
    facet_wrap( ~ Species) # notice lack of .
```



Section 7

# Scales

# Some terminology

- data
- aesthetics
- geometry
- stats
- facets
- **scales**

- **Control the mapping from data to aesthetics**
- Often used for adjusting color mapping

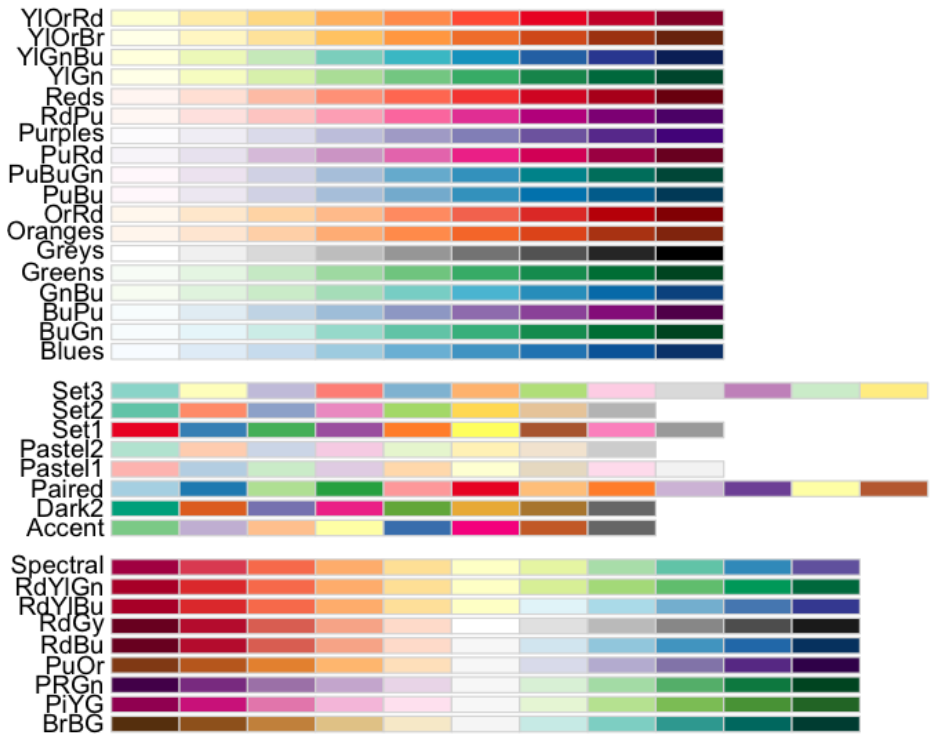
# Colors

```
aes(color = variable) # mapping
color = "black" # setting

# Or add it as a scale
scale_fill_manual(values = c("color1", "color2"))
```

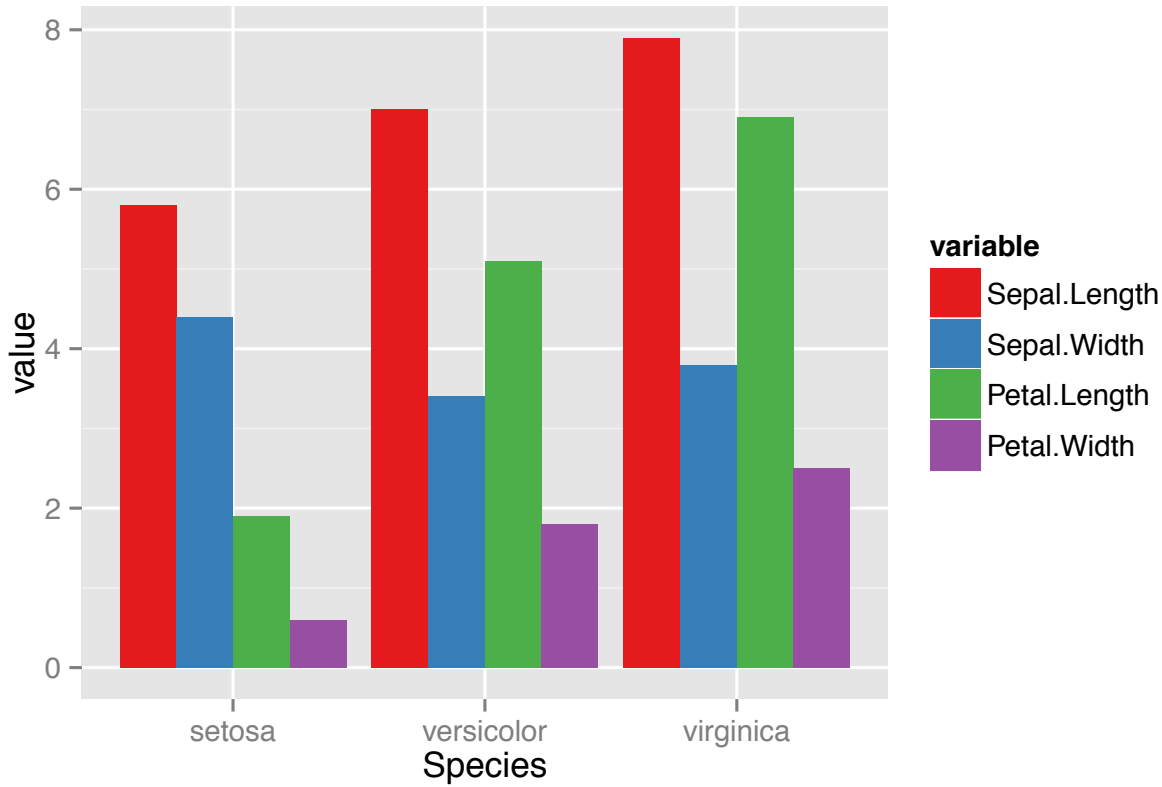
# The RColorBrewer package

```
library(RColorBrewer)
display.brewer.all()
```



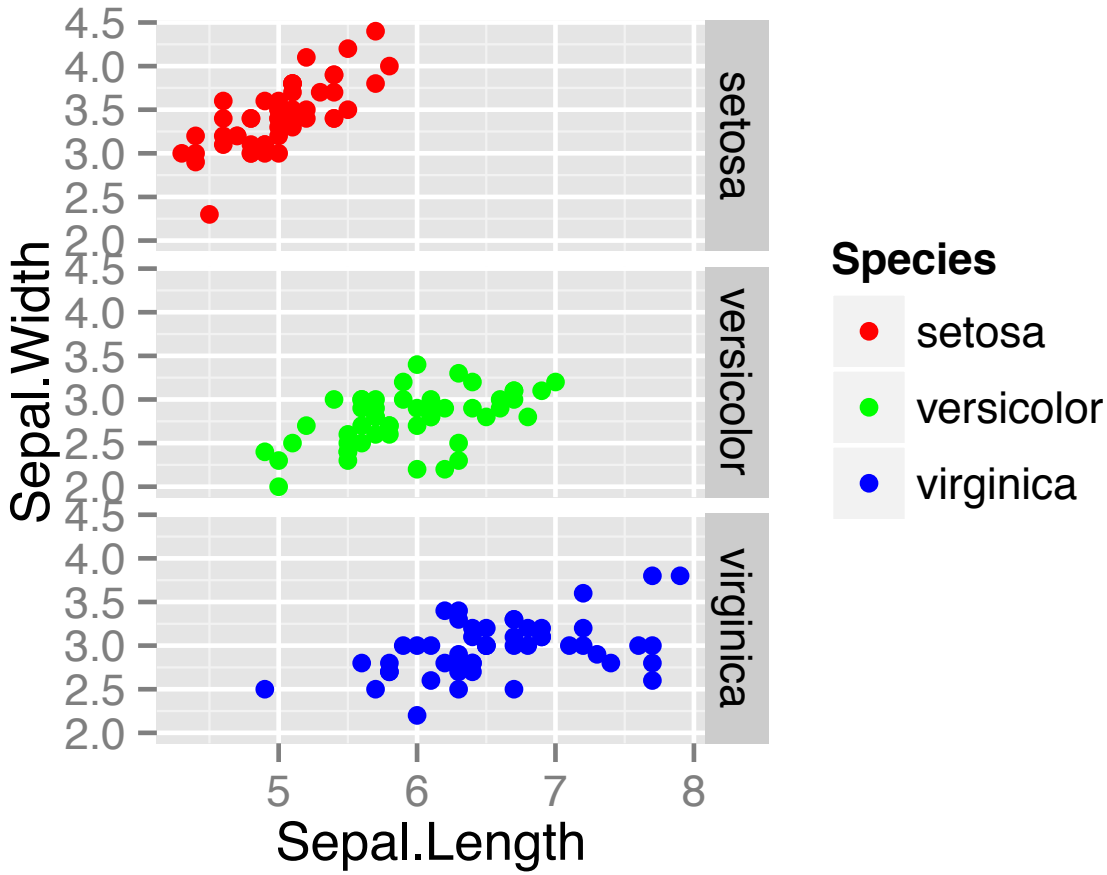
# Using a color brewer palette

```
df  <- melt(iris, id.vars = "Species")
ggplot(df, aes(Species, value, fill = variable)) +
    geom_bar(stat = "identity", position = "dodge") +
    scale_fill_brewer(palette = "Set1")
```



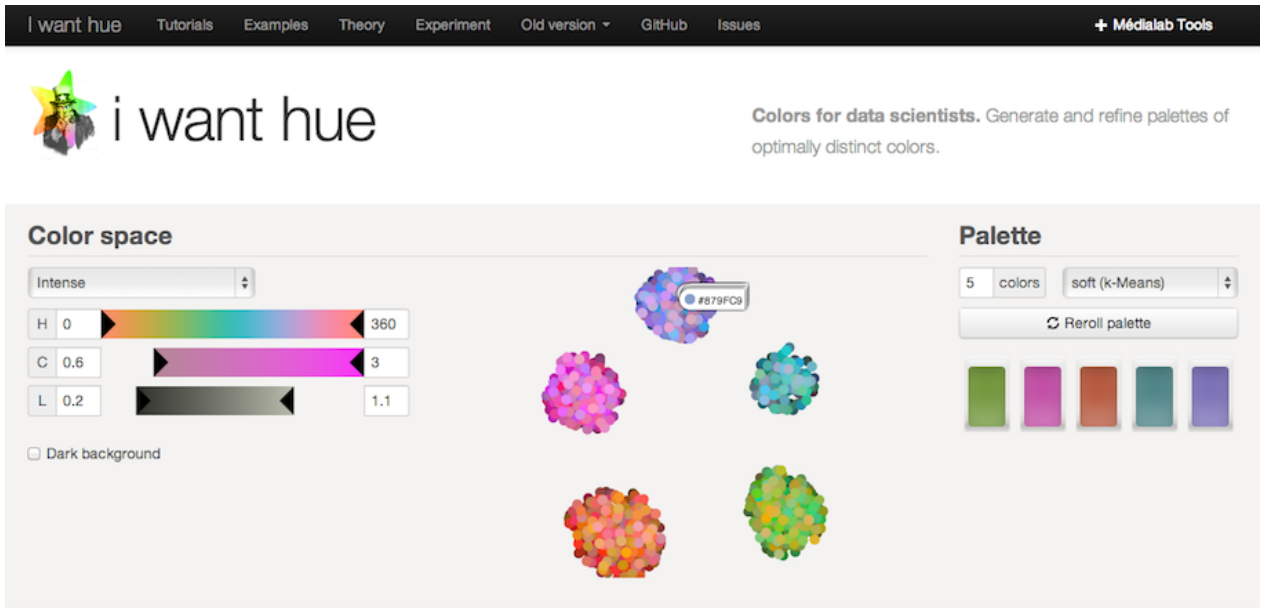
# Manual color scale

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point() +
    facet_grid(Species ~ .) +
    scale_color_manual(values = c("red", "green", "blue"))
```



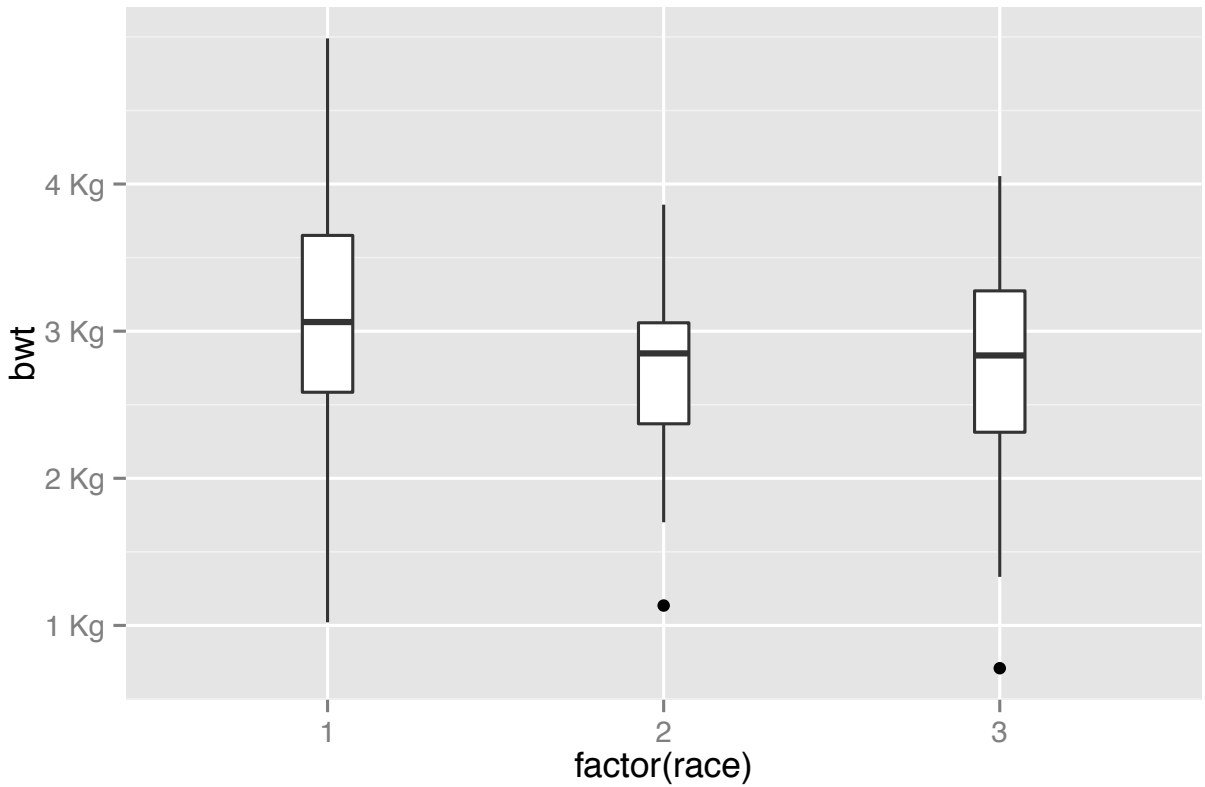
# Refer to a color chart for beautful visualizations

http://tools.medialab.sciences-po.fr/iwanthue/



# Adding a continuous scale to an axis

```
library(MASS)
ggplot(birthwt, aes(factor(race), bwt)) +
    geom_boxplot(width = .2) +
    scale_y_continuous(labels = (paste0(1:4, " Kg")),
        breaks = seq(1000, 4000, by = 1000))
```



# Commonly used scales

```
scale_fill_discrete(); scale_colour_discrete()
scale_fill_hue(); scale_color_hue()
scale_fill_manual();  scale_color_manual()
scale_fill_brewer(); scale_color_brewer()
scale_linetype(); scale_shape_manual()
```

Section 8

# Coordinates

# Some terminology

- **data**
- **aesthetics**
- **geometry**
- **stats**
- **facets**
- **scales**
- **coord**inates

- Not going to cover this in detail
- e.g. polar coordinate plots

# Section 9

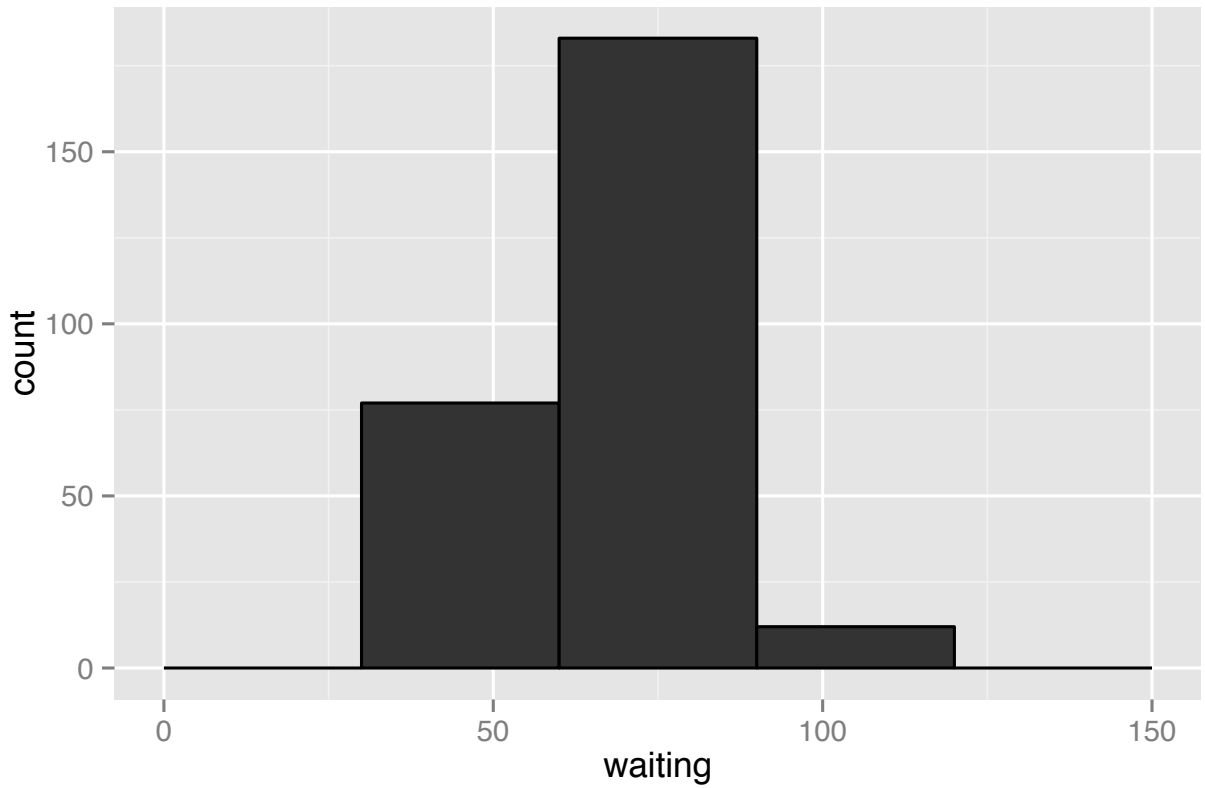
## Putting it all together with more examples

Section 10

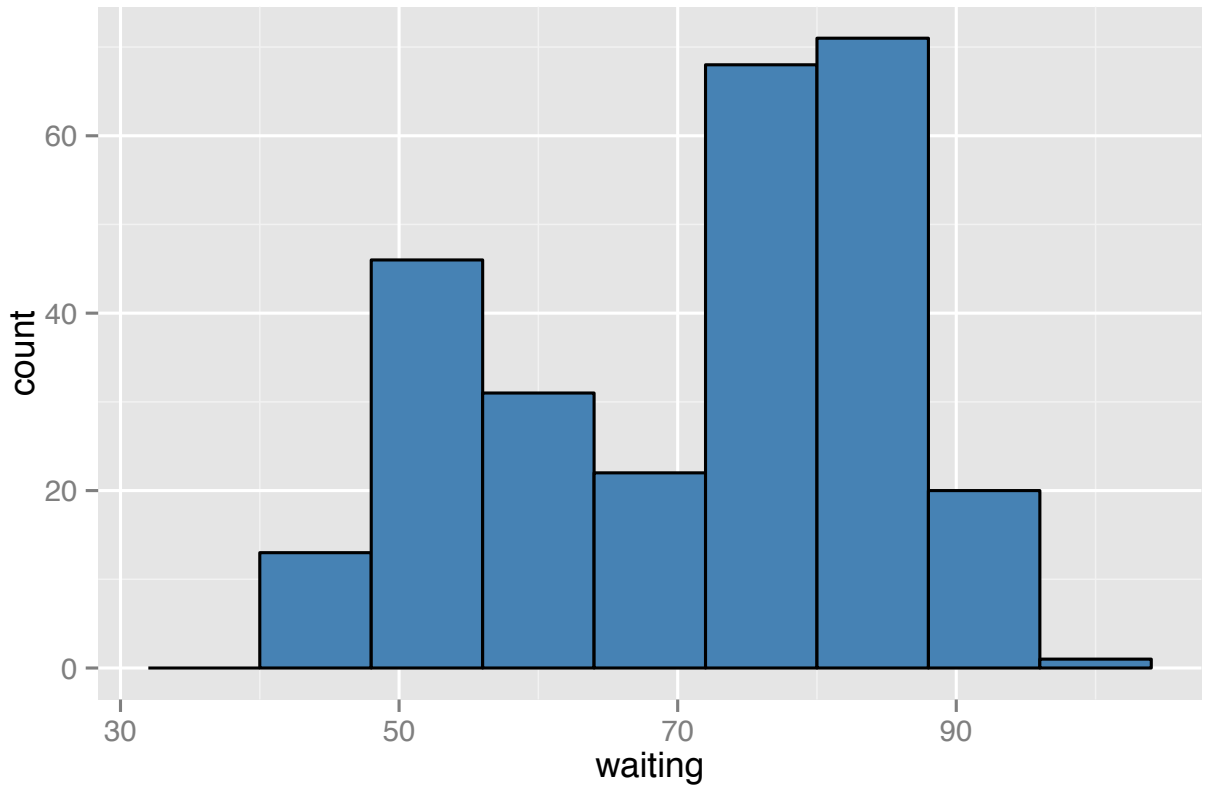
# Histograms

See ?geom_histogram for list of options

```
h <- ggplot(faithful, aes(x = waiting))
h + geom_histogram(binwidth = 30, colour = "black")
```



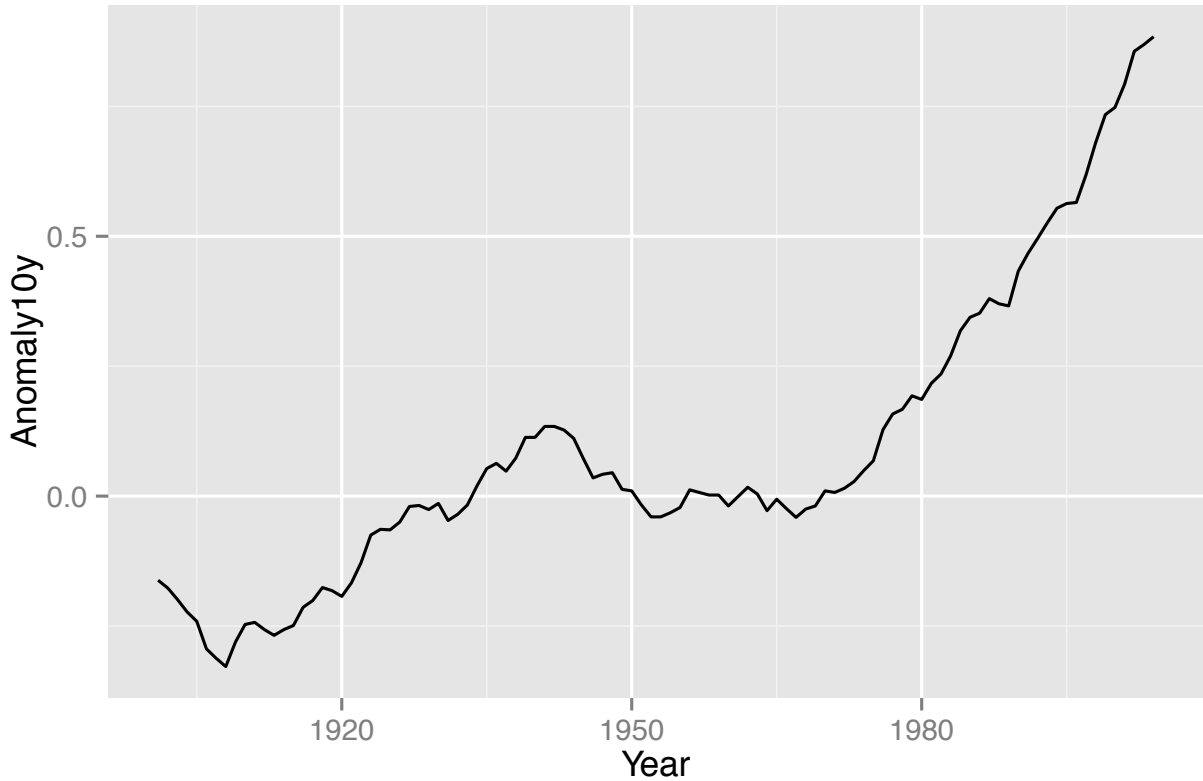
```
h <- ggplot(faithful, aes(x = waiting))
h + geom_histogram(binwidth = 8, fill = "steelblue",
colour = "black")
```



Section 11

# Line plots

```r
climate <- read.csv("data/climate.csv", header = T)
ggplot(climate, aes(Year, Anomaly10y)) +
    geom_line()
```

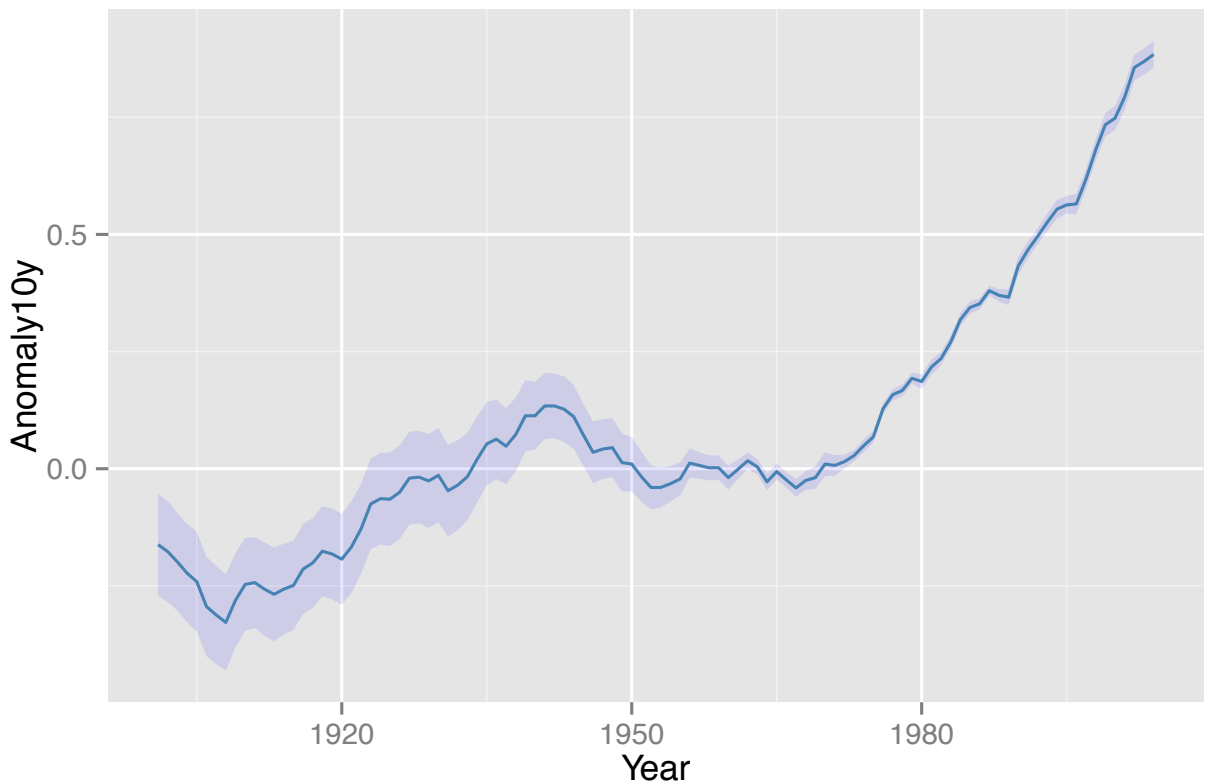



```r
climate <- read.csv(text =

RCurl::getURL(https://raw.github.com/karthikram/ggplot-lecture/master/climate.csv))
```

# We can also plot confidence regions

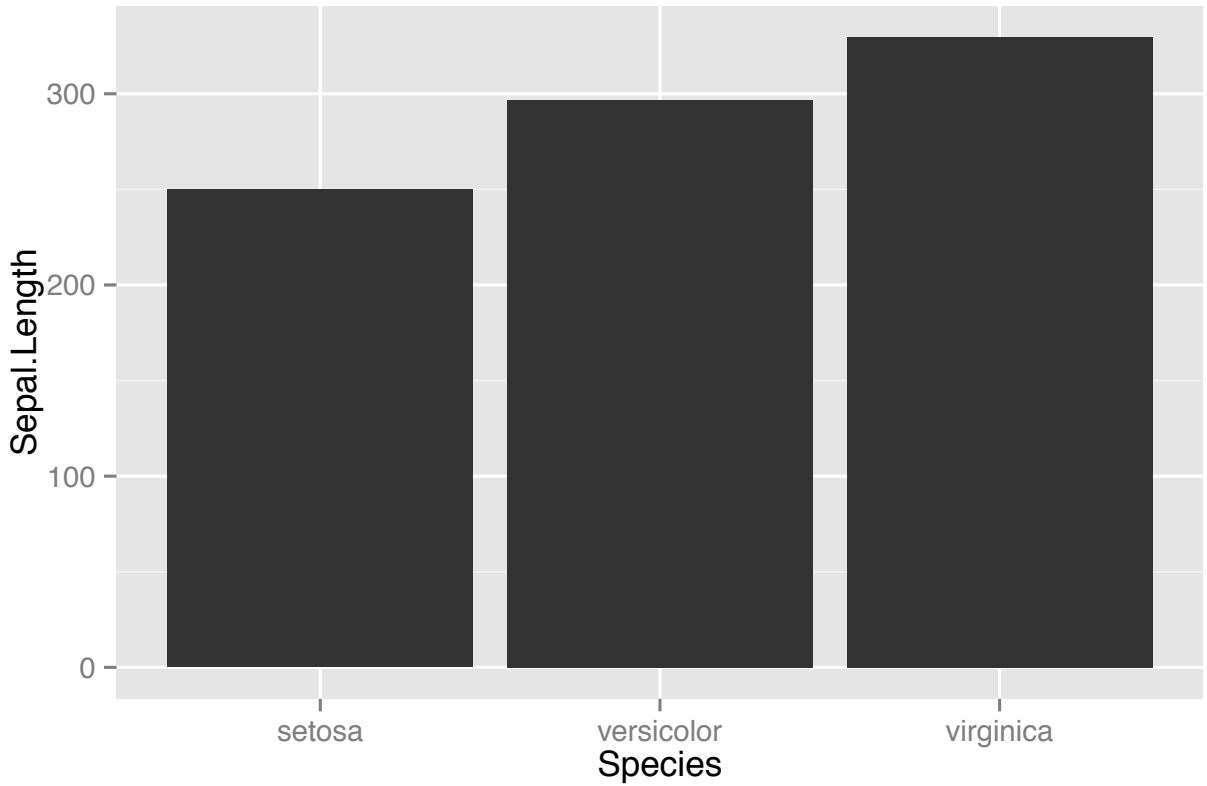
```
climate <- read.csv("data/climate.csv", header = T)
ggplot(climate, aes(Year, Anomaly10y)) +
    geom_ribbon(aes(ymin = Anomaly10y - Unc10y,
        ymax = Anomaly10y + Unc10y),
        fill = "blue", alpha = .1) +
    geom_line(color = "steelblue")
```



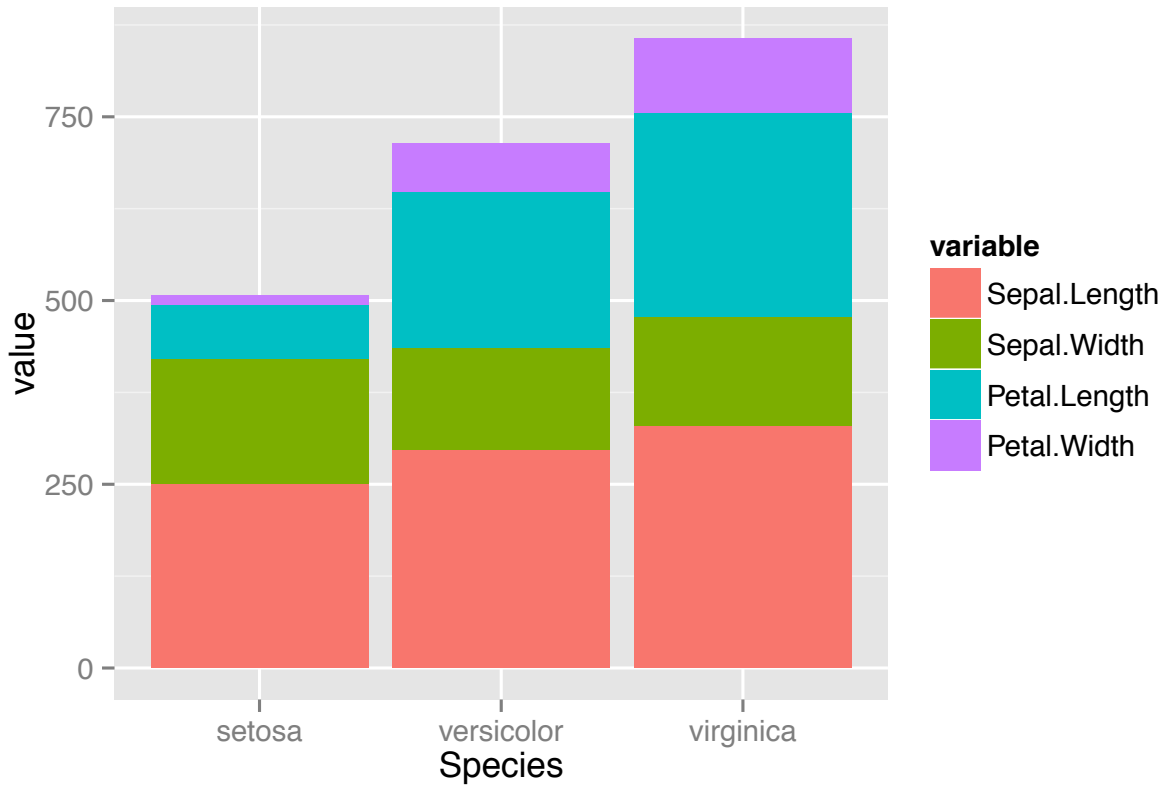
Section 12

# Bar plots

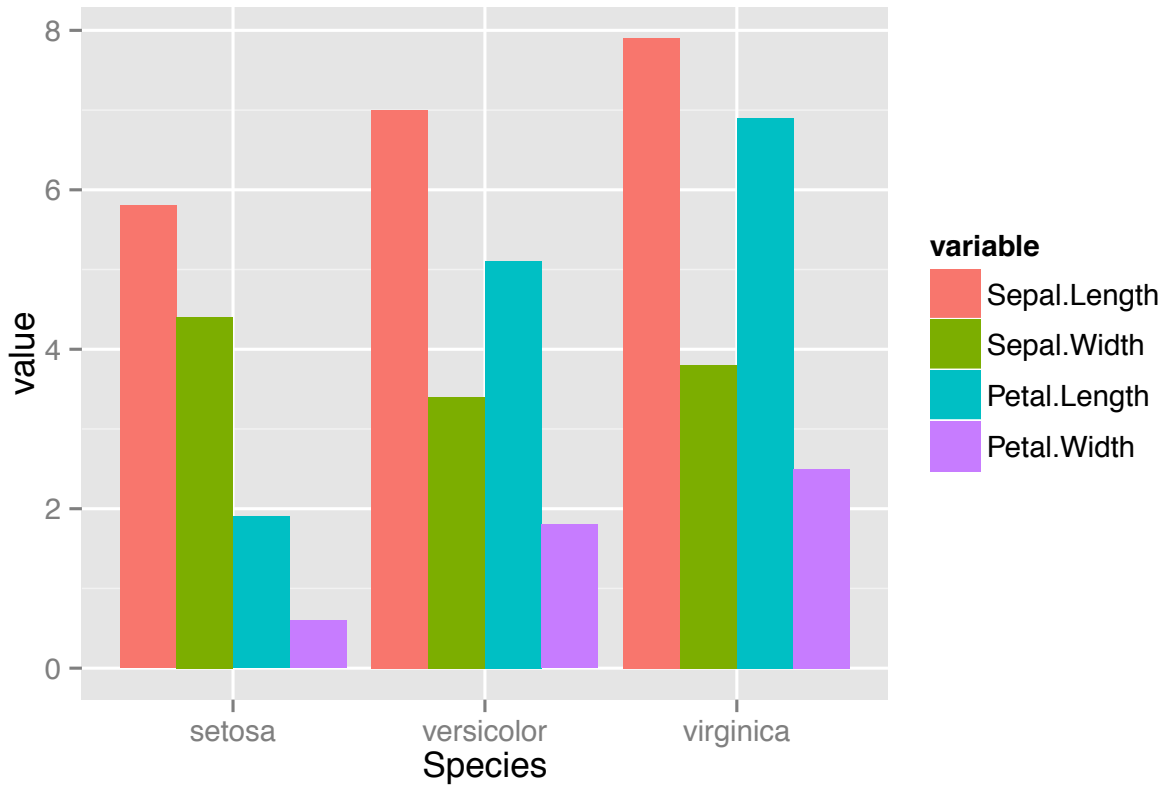
```
ggplot(iris, aes(Species, Sepal.Length)) +
geom_bar(stat = "identity")
```



```
df  <- melt(iris, id.vars = "Species")
ggplot(df, aes(Species, value, fill = variable)) +
    geom_bar(stat = "identity")
```

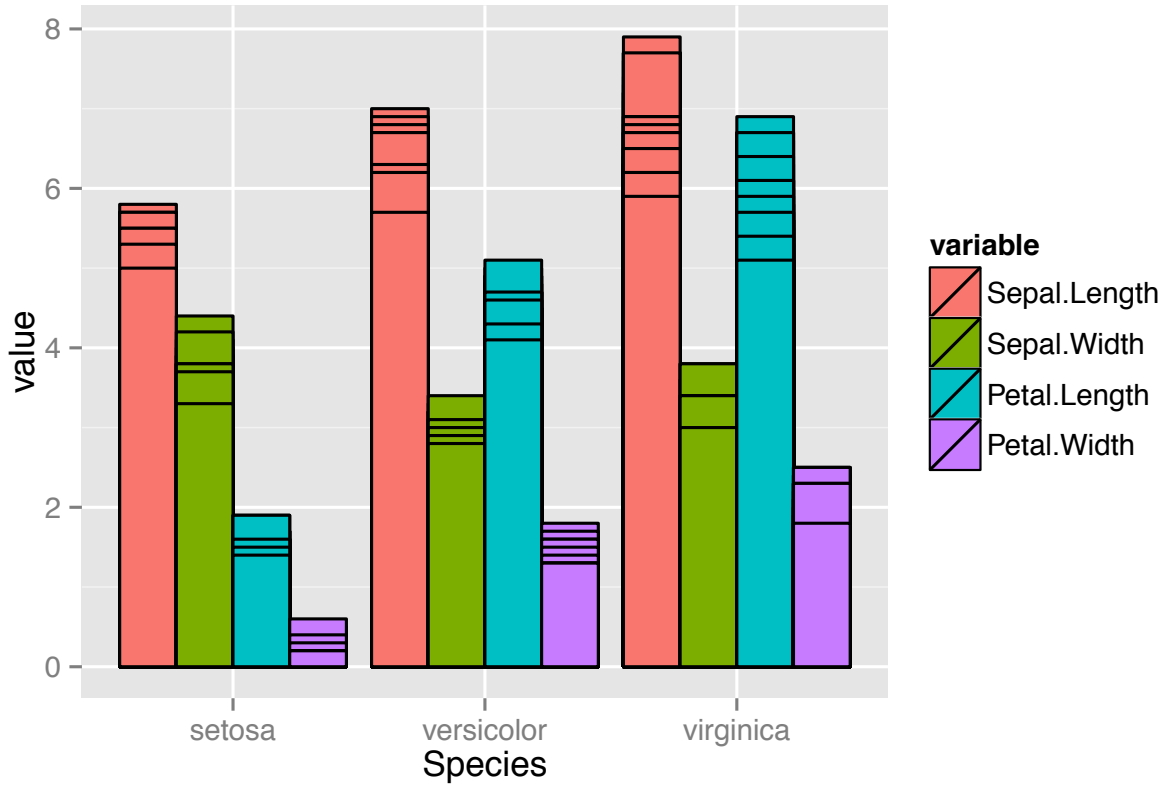


```
ggplot(df, aes(Species, value, fill = variable)) +
    geom_bar(stat = "identity", position = "dodge")
```



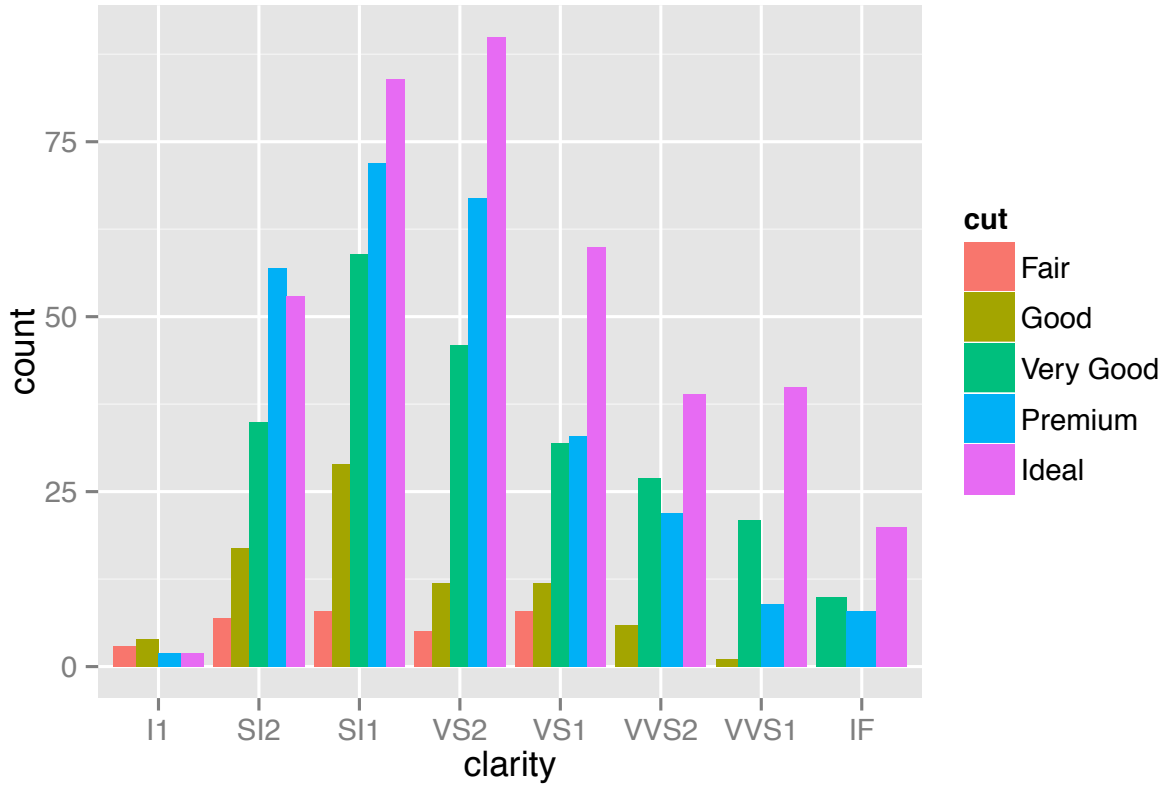

What's going on with the y axis?

```
ggplot(df, aes(Species, value, fill = variable)) +
    geom_bar(stat = "identity", position="dodge", color="black")
```



# Exercise 3

Using the d2 dataset you created earlier, generate this plot below. Take a quick look at the data first to see if it needs to be binned.

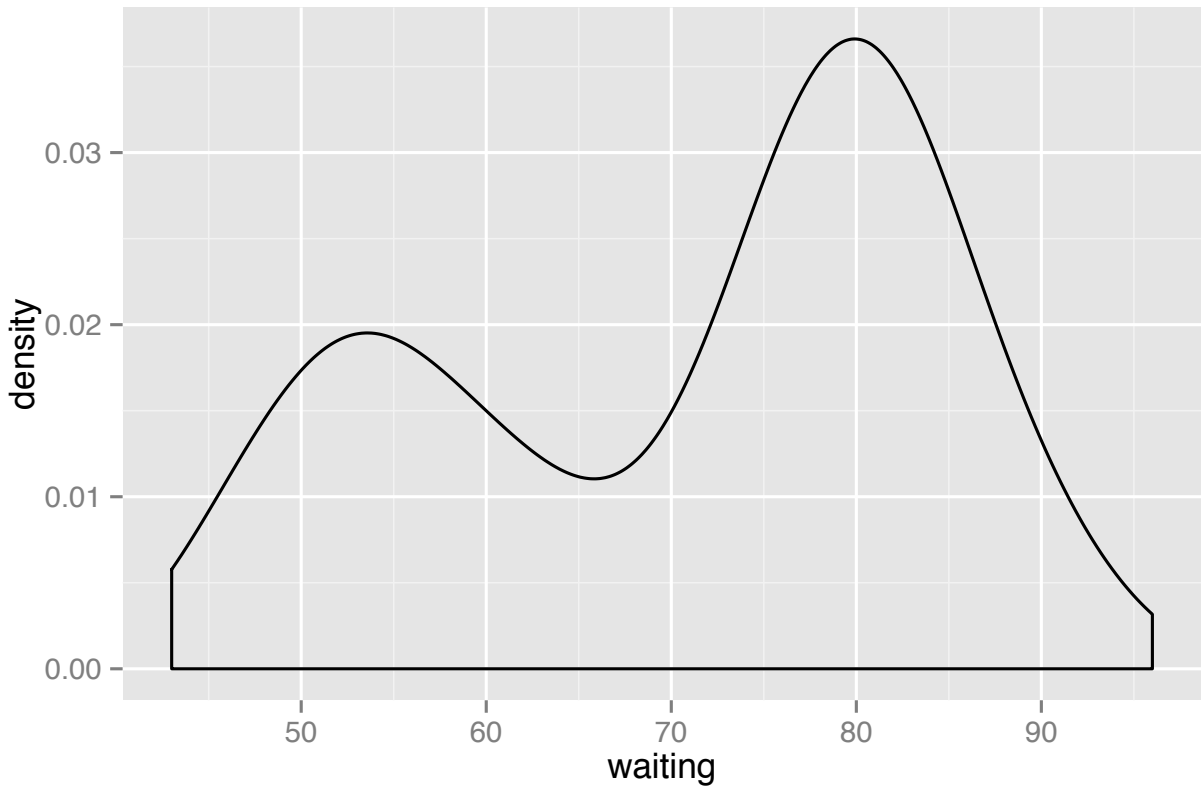


Section 13

# Density Plots

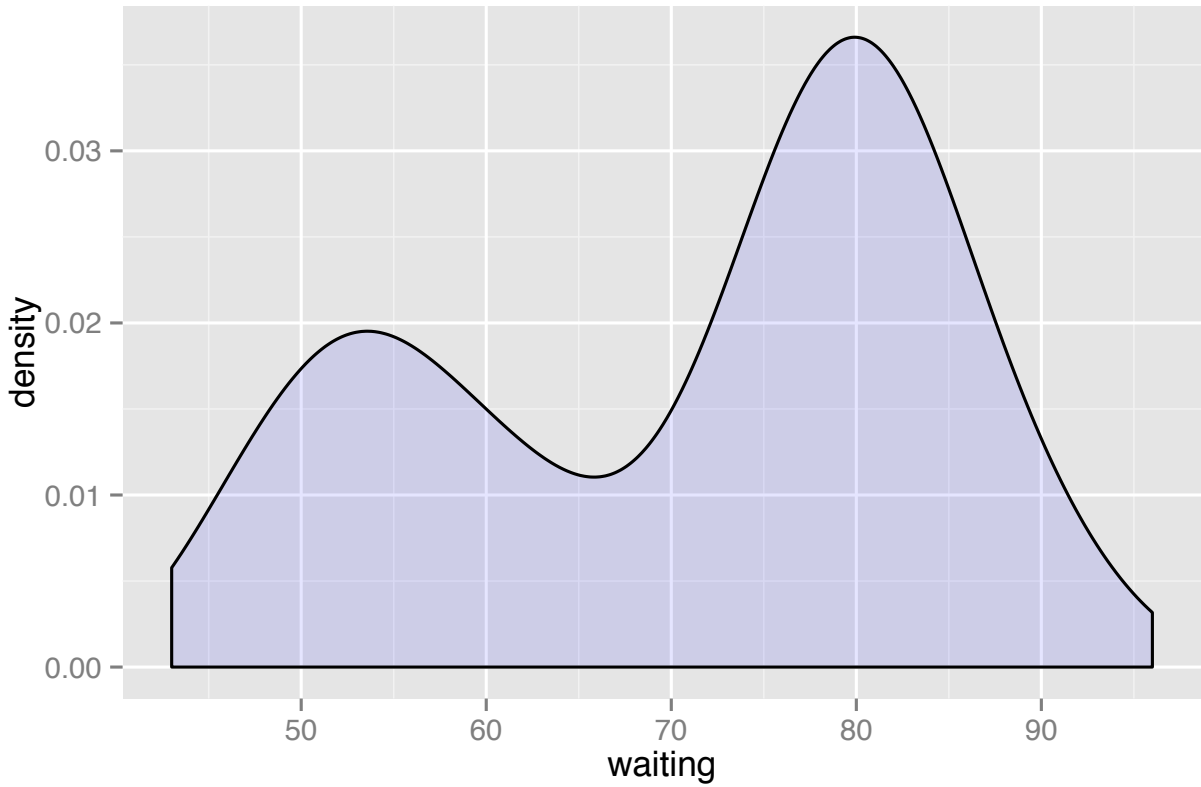
# Density plots

```
ggplot(faithful, aes(waiting)) + geom_density()
```

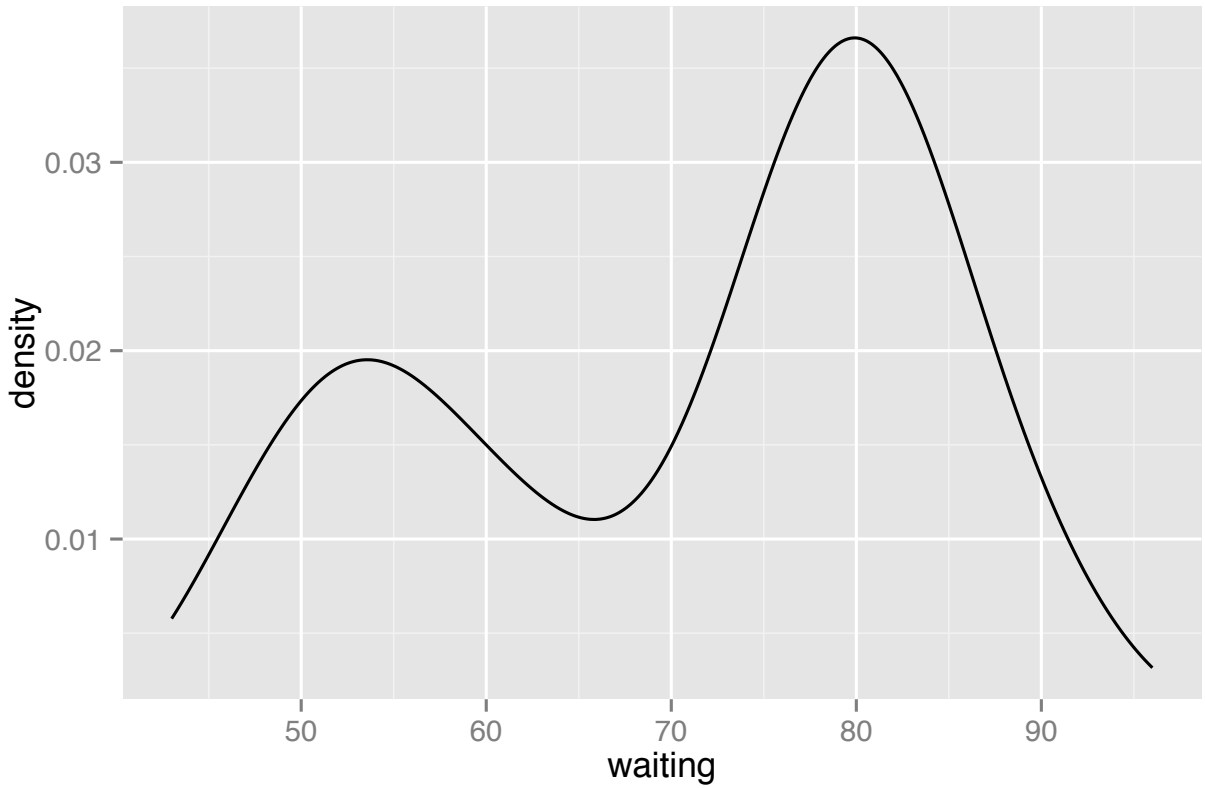


# Density plots

```
ggplot(faithful, aes(waiting)) +
    geom_density(fill = "blue", alpha = 0.1)
```



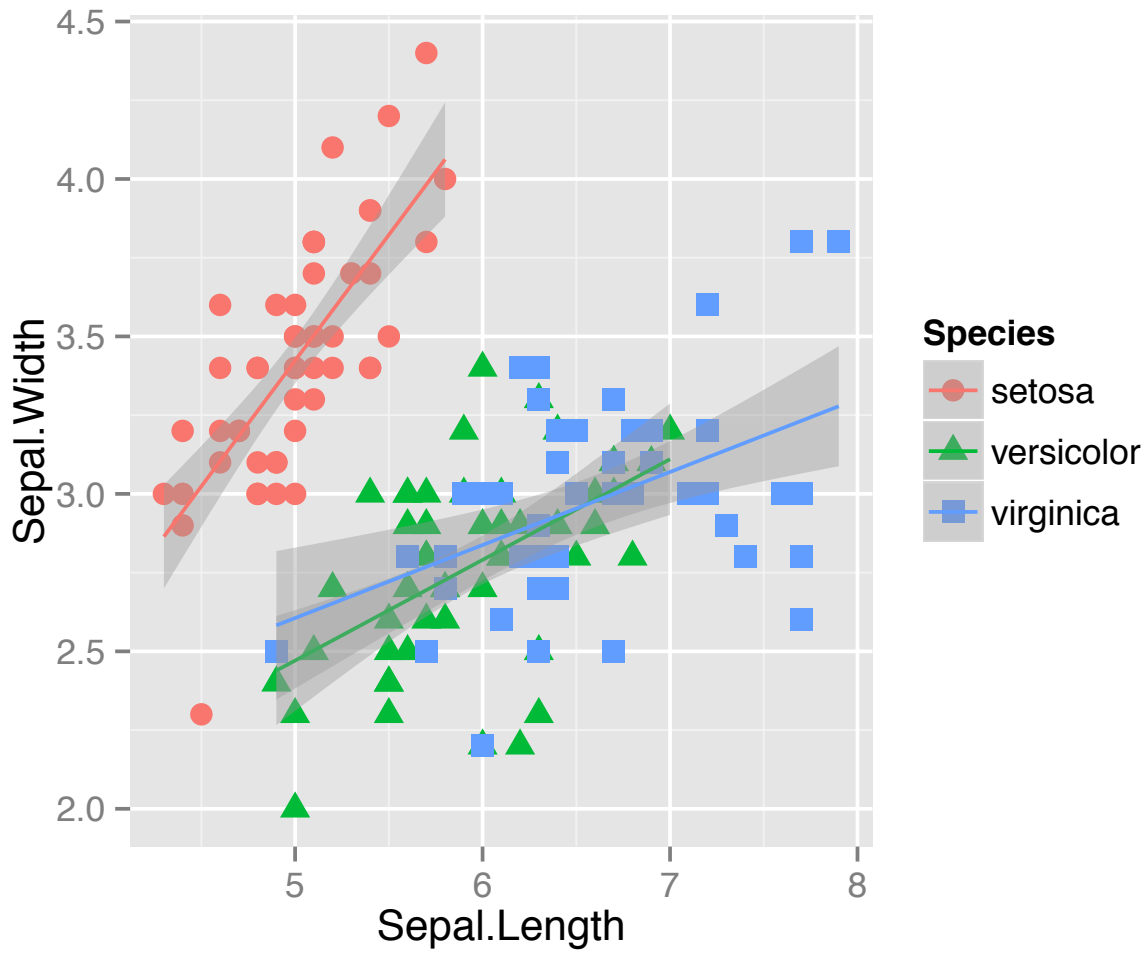
```
ggplot(faithful, aes(waiting)) +
    geom_line(stat = "density")
```



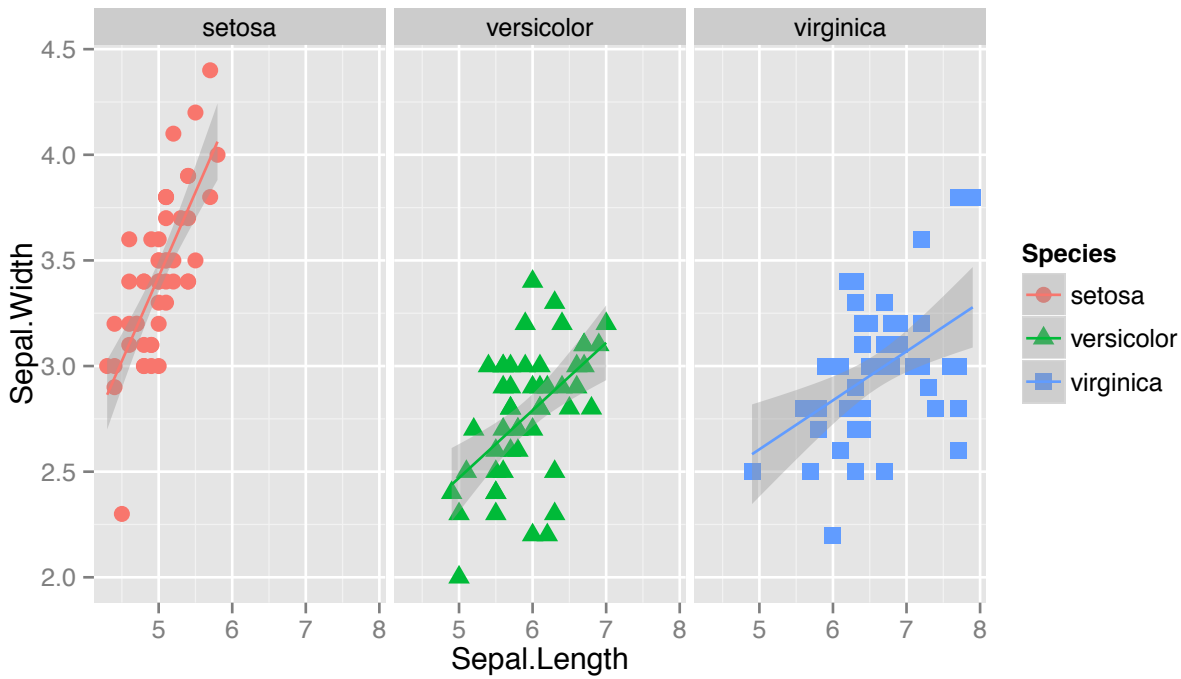
# Section 14

# Adding smoothers

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point(aes(shape = Species), size = 3) +
    geom_smooth(method = "lm")
```



```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point(aes(shape = Species), size = 3) +
    geom_smooth(method = "lm") +
    facet_grid(. ~ Species)
```



# Section 15

## Themes

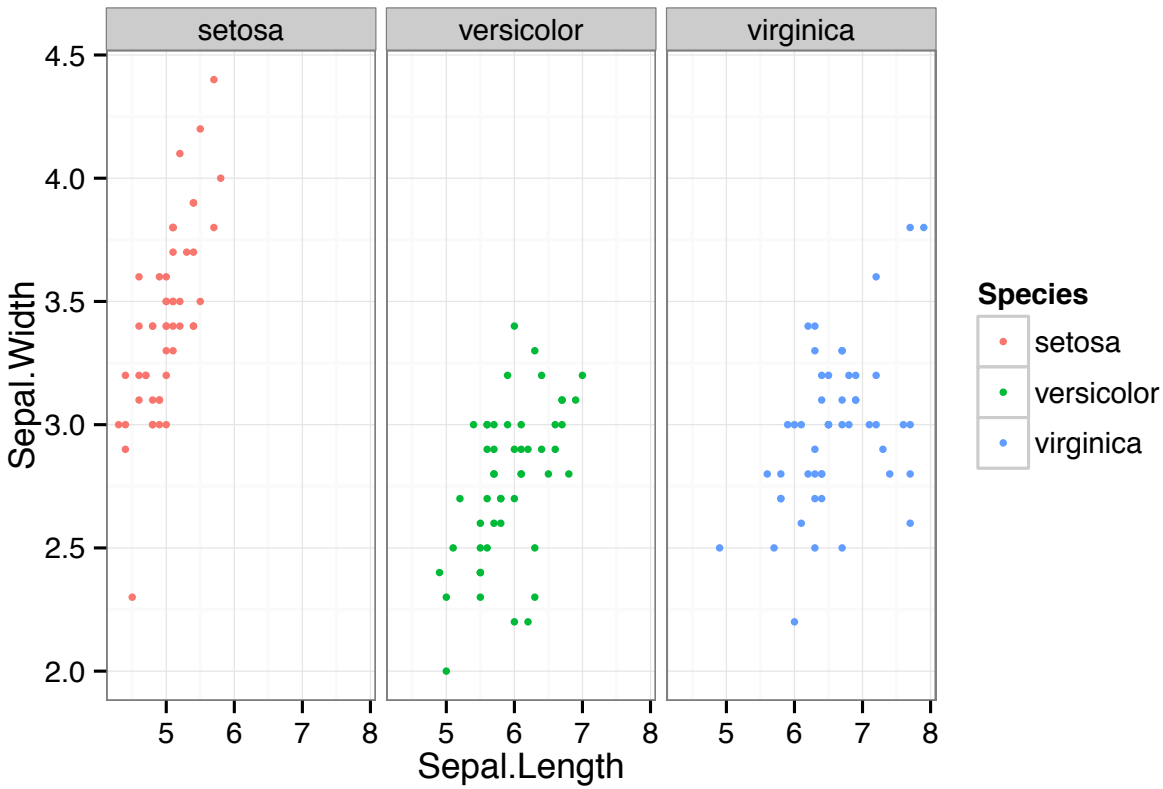
# Adding themes

Themes are a great way to define custom plots.

```
+ theme()
# see ?theme() for more options
```

# A more basic theme

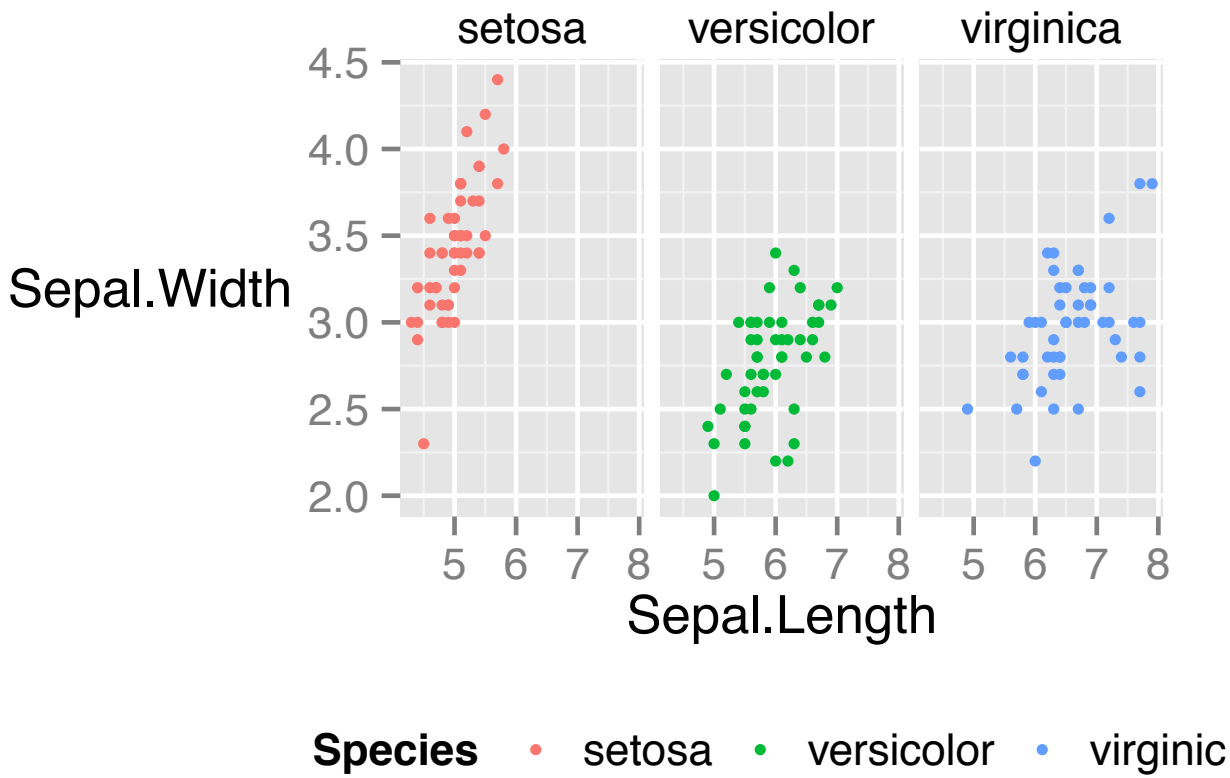
```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point(size = 1.2, shape = 16) +
    facet_wrap( ~ Species) +
    theme_bw()
```



# A themed plot

```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
    geom_point(size = 1.2, shape = 16) +
    facet_wrap( ~ Species) +
    theme(legend.key = element_rect(fill = NA),
        legend.position = "bottom",
        strip.background = element_rect(fill = NA),
        axis.title.y = element_text(angle = 0))
```

# A themed plot



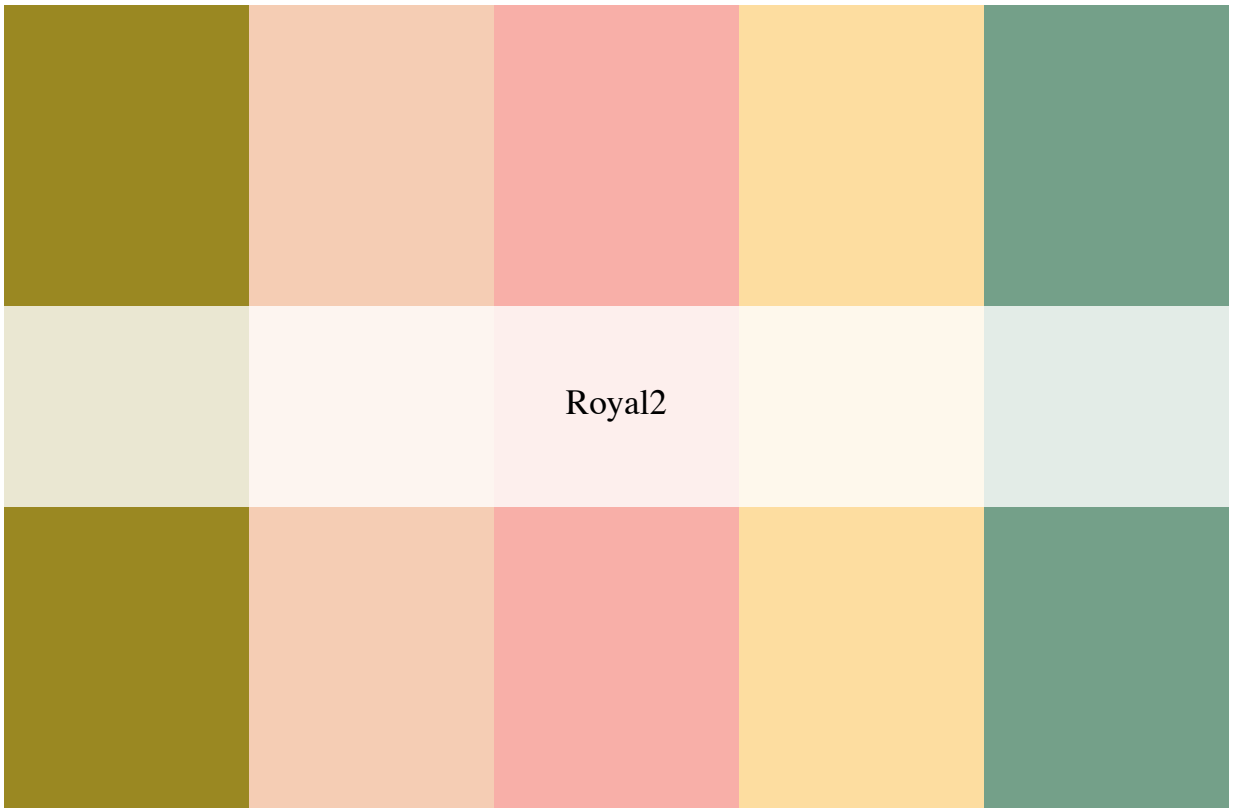
# ggthemes library

```
install.packages(ggthemes)
library(ggthemes)
# Then add one of these themes to your plot
 + theme_stata()
 + theme_excel()
 + theme_wsj()
 + theme_solarized()
```

# Fan of Wes Anderson movies?

# Yup, that's a thing

```
# install.packages(wesanderson)
library("wesanderson")
# display a palette
wes_palette("Royal2", 5)
```



# Section 16

## Create functions to automate your plotting

# Write functions for day to day plots

```
my_custom_plot <- function(df, title = "", ...) {
    ggplot(df, ...) +
    ggtitle(title) +
    whatever_geoms() +
    theme(...)
}
```

Then just call your function to generate a plot. It's a lot easier to fix one function that do it over and over for many plots

```
plot1 <- my_custom_plot(dataset1, title = "Figure 1")
```

Section 17

# Publication quality figures

- If the plot is on your screen

```
ggsave(~/path/to/figure/filename.png)
```

- If your plot is assigned to an object

```
ggsave(plot1, file = "~/path/to/figure/filename.png")
```

- Specify a size

```
ggsave(file = "/path/to/figure/filename.png", width = 6,
height =4)
```

- or any format (pdf, png, eps, svg, jpg)

```
ggsave(file = "/path/to/figure/filename.eps")
ggsave(file = "/path/to/figure/filename.jpg")
ggsave(file = "/path/to/figure/filename.pdf")
```

# Further help

- You've just scratched the surface with ggplot2.
- Practice
- Read the docs (either locally in `R` or at `http://docs.ggplot2.org/current/`)
- Work together