

# Data Visualization Using R & ggplot2

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# Some housekeeping

Install some packages

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

# 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 coherent, consistent 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. dply (data frame to data frame ply)

- 1.1 split

- 1.2 apply

- 1.3 combine

- 2. lply (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**
- ▶ **aesthetics**
- ▶ **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**
- ▶ **geometry**
- ▶ **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()
```

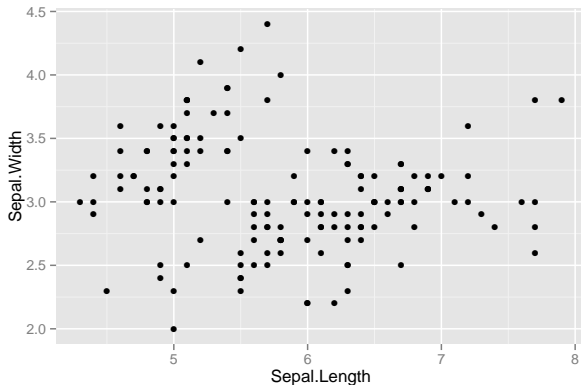
- ▶ Specify the data and variables inside the ggplot function.
- ▶ Anything else that goes in here becomes a global setting.
- ▶ Then add layers: geometric objects, statistical models, and facets.

## Quick note

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

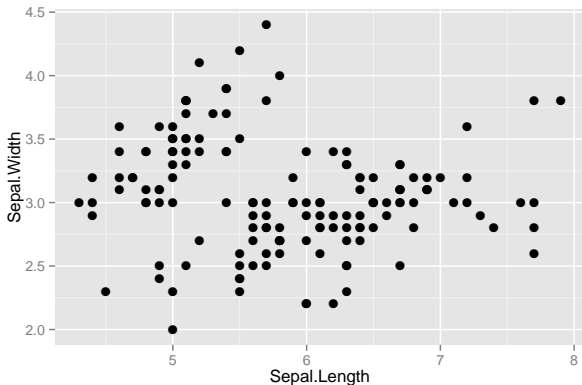
## Let's try an example

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



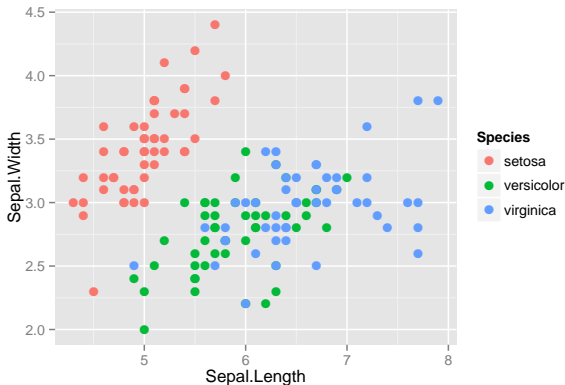
## Changing the aesthetics of a geom: Increase the size of points

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



## Changing the aesthetics of a geom: Add some color

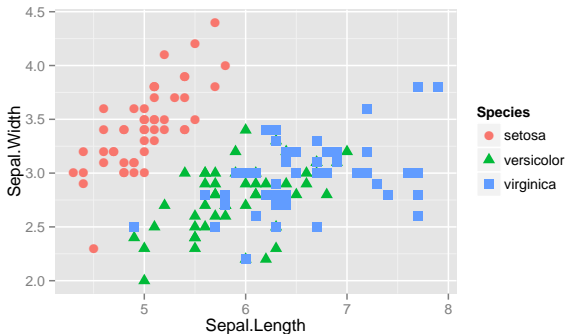
```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +  
geom_point(size = 3)
```





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

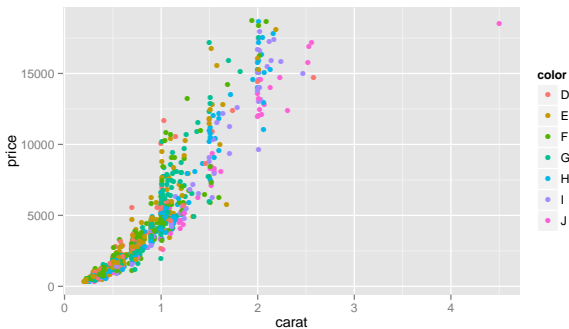
```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +  
geom_point(aes(shape = Species), size = 3)  
# Why aes(shape = Species)?
```



# 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

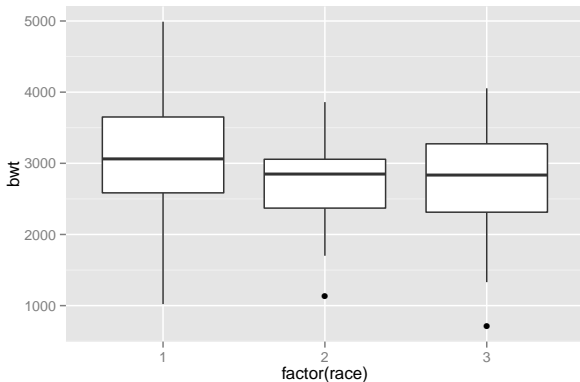
## Some terminology

- ▶ **data**
- ▶ **aesthetics**
- ▶ **geometry**
- ▶ **stats**
- ▶ **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 = 2
## stat_boxplot:
## position_dodge: (width = NULL, height = NULL)
```

## Section 6

### Facets

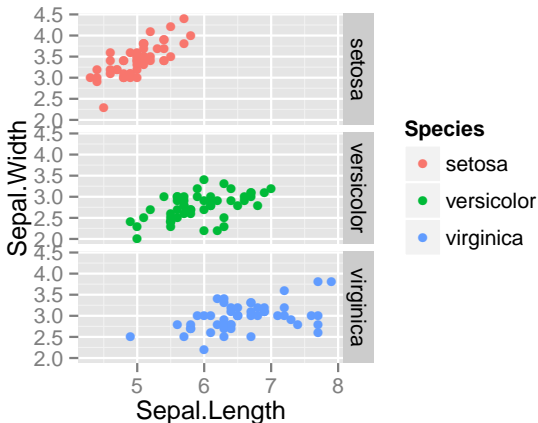
## Some terminology

- ▶ data
  - ▶ aesthetics
  - ▶ geometry
  - ▶ stats
  - ▶ facets
- ▶ **Subsetting data to make lattice plots**
  - ▶ Really powerful



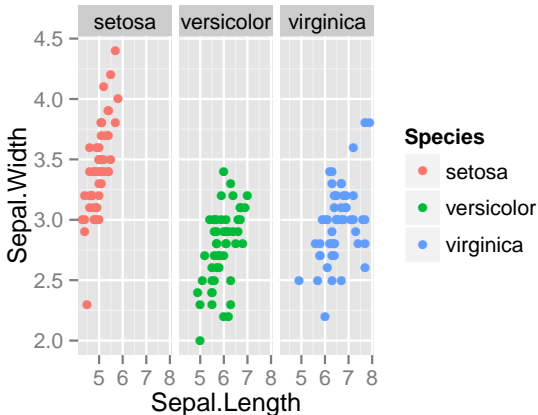
## Faceting: single column, multiple rows

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



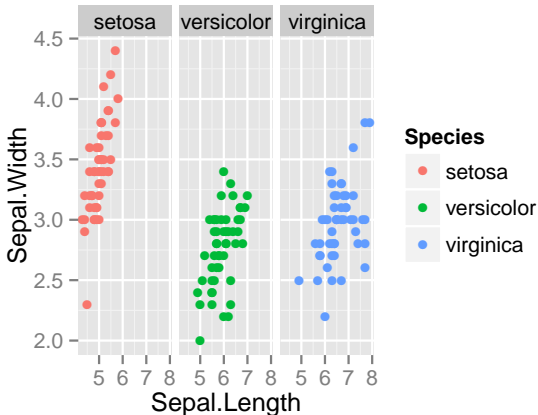
## Faceting: single row, multiple columns

```
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

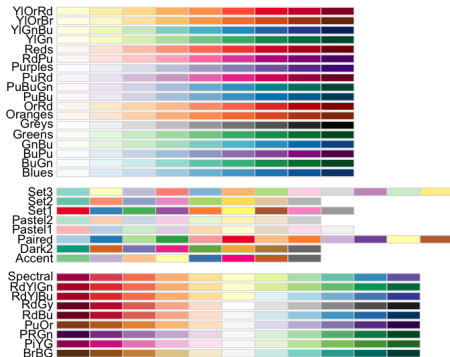
- ▶ data
  - ▶ aesthetics
  - ▶ geometry
  - ▶ stats
  - ▶ facets
  - ▶ scales
- ▶ **Control the mapping from data to aesthetics**
  - ▶ Often used for adjusting color mapping

# Colors

```
aes(color = variable) # mapping  
color = "black" # setting  
  
# Or add it as a scale  
scale_fill_manual(values = c("color1", "color2"))
```

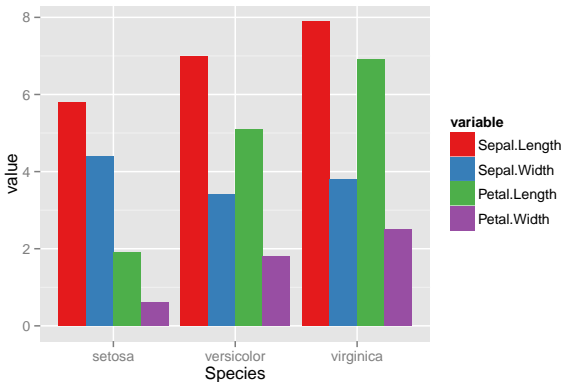
# The RColorBrewer package

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



## Using a color brewer palette

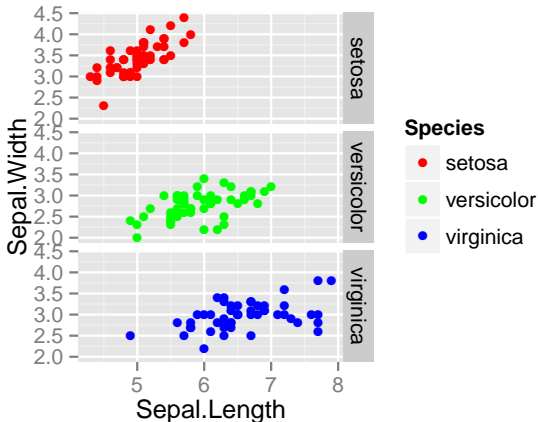
```
df <- melt(iris, id.vars = "Species")
ggplot(df, aes(Species, value, fill = variable)) +
  geom_bar(stat = "identity", position = "dodge") +
  scale_fill_brewer(palette = "Set1")
```





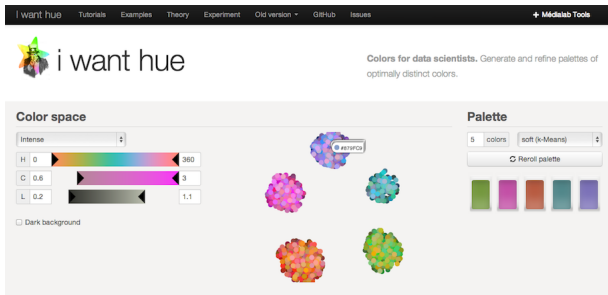
## Manual color scale

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



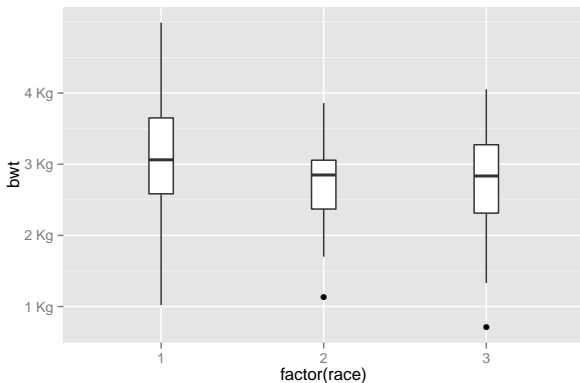
# Refer to a color chart for beautiful visualizations

<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**
  - ▶ **coordinates**
- ▶ Not going to cover this in detail
  - ▶ e.g. polar coordinate plots

## Section 9

Putting it all together with more examples

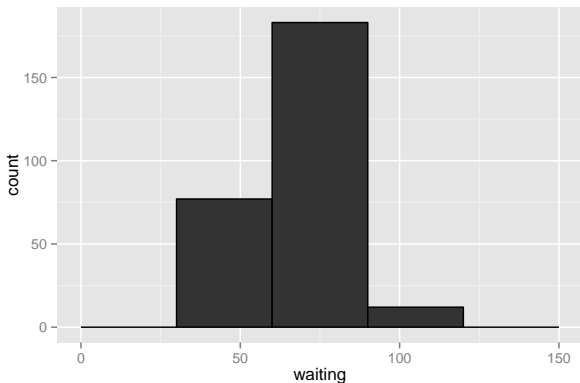
## Section 10

# Histograms

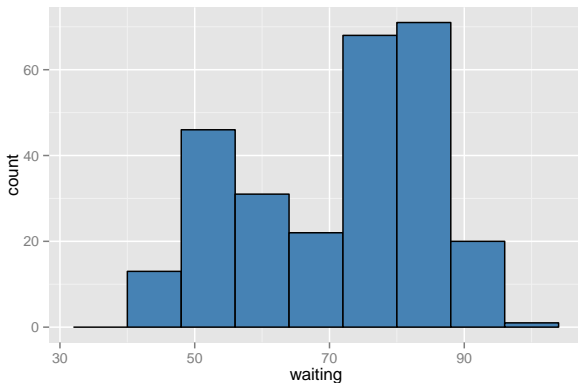


See `?geom_histogram` for list of options

```
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")
```

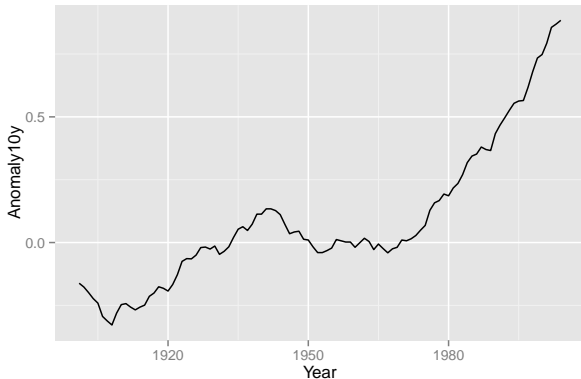


# Section 11

## Line plots

## ## Error: cannot change working directory

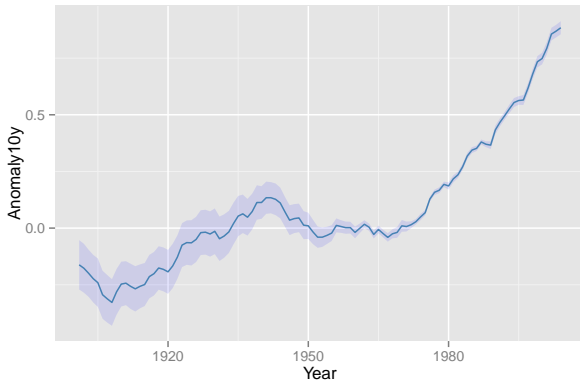
```
climate <- read.csv("data/climate.csv", header = T)
ggplot(climate, aes(Year, Anomaly10y)) +
  geom_line()
```



```
climate <- read.csv(text =
  RCurl::getURL('https://raw.githubusercontent.com/karthikram/ggplot-lecture/master/climate.csv'))
```

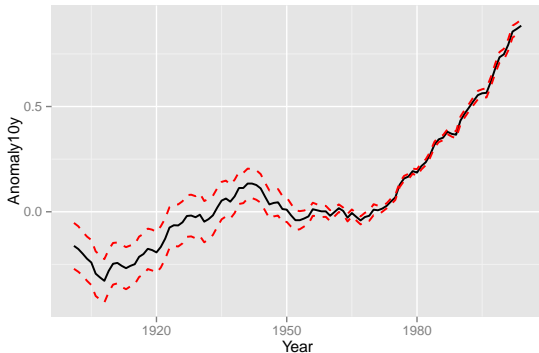
## We can also plot confidence regions

```
ggplot(climate, aes(Year, Anomaly10y)) +  
  geom_ribbon(aes(ymin = Anomaly10y - Unc10y,  
ymax = Anomaly10y + Unc10y),  
fill = "blue", alpha = .1) +  
  geom_line(color = "steelblue")
```



## Exercise 2

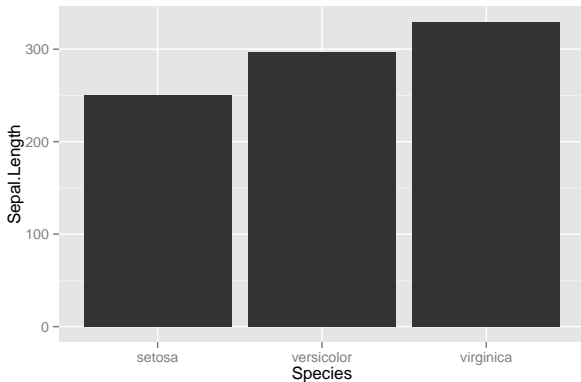
- Modify the previous plot and change it such that there are three lines instead of one with a confidence band.



## Section 12

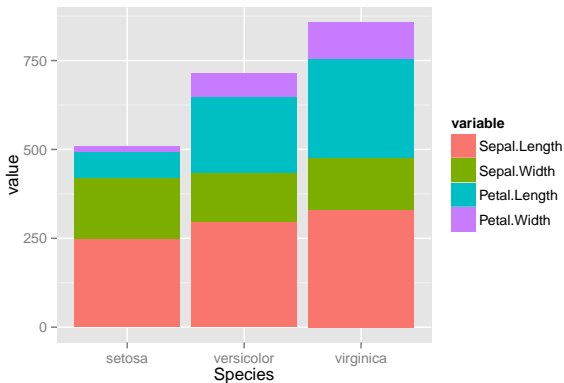
### Bar plots

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

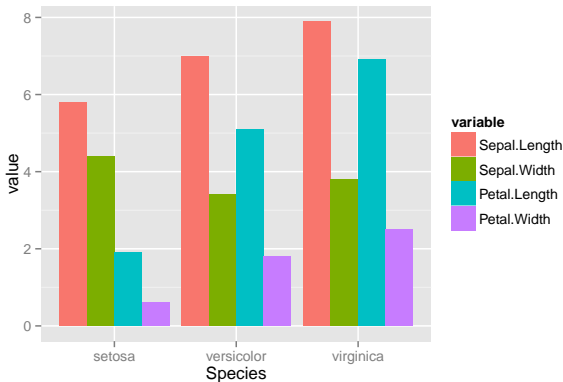




```
df <- melt(iris, id.vars = "Species")
ggplot(df, aes(Species, value, fill = variable)) +
  geom_bar(stat = "identity")
```

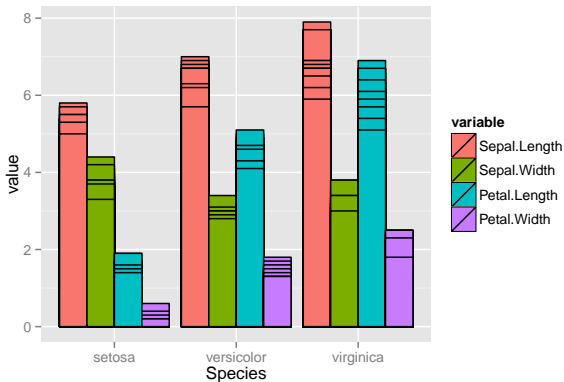


```
ggplot(df, aes(Species, value, fill = variable)) +  
geom_bar(stat = "identity", position = "dodge")
```



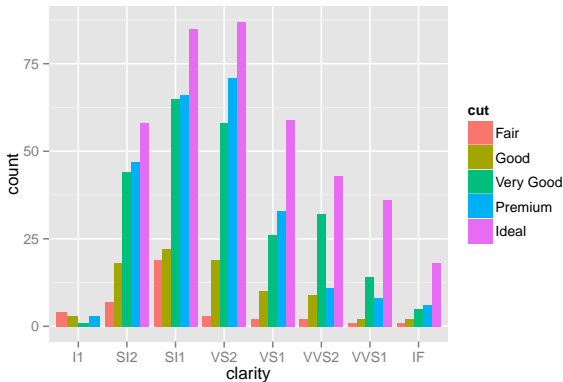
What's going on with the y axis?

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



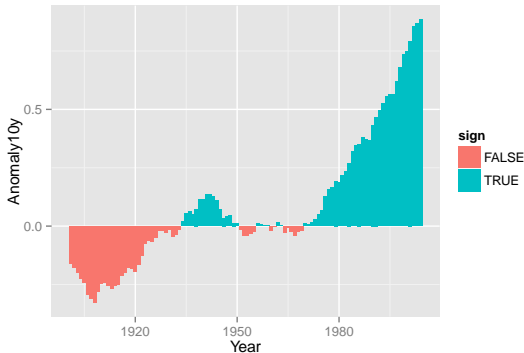
## Exercise 3

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.



## Exercise 4

- ▶ Using the climate dataset, create a new variable called `sign`. Make it logical (true/false) based on the sign of `Anomaly10y`.
- ▶ Plot a bar plot and use `sign` variable as the fill.

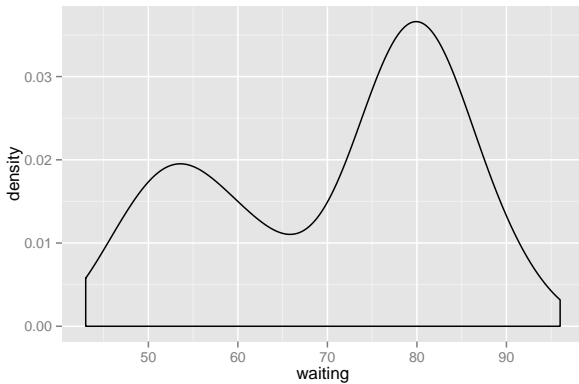


## Section 13

### Density Plots

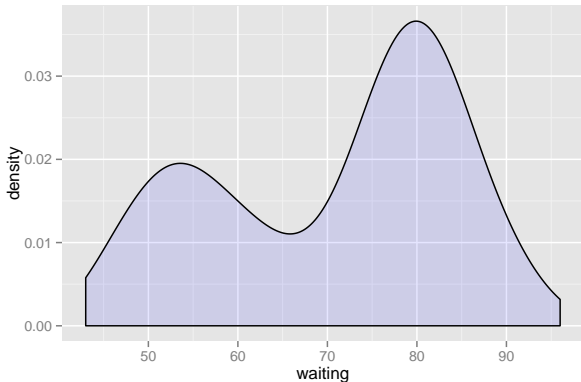
# Density plots

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



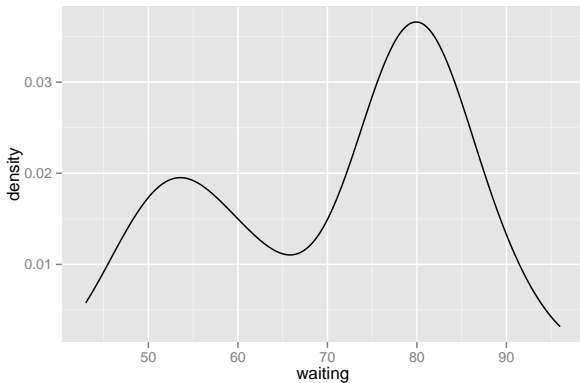
# Density plots

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





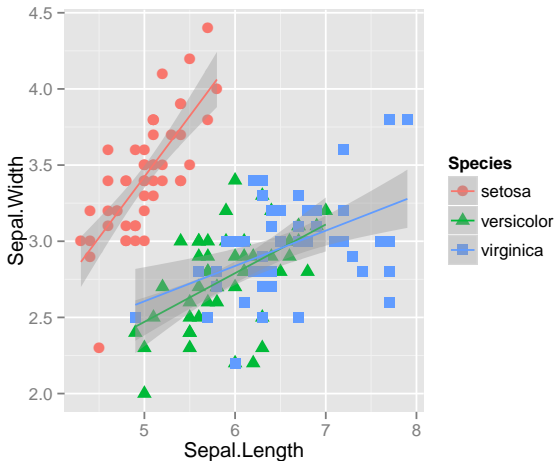
```
ggplot(faithful, aes(waiting)) +  
geom_line(stat = "density")
```



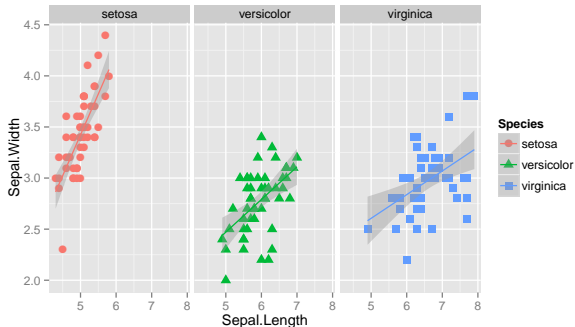
## Section 14

### 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

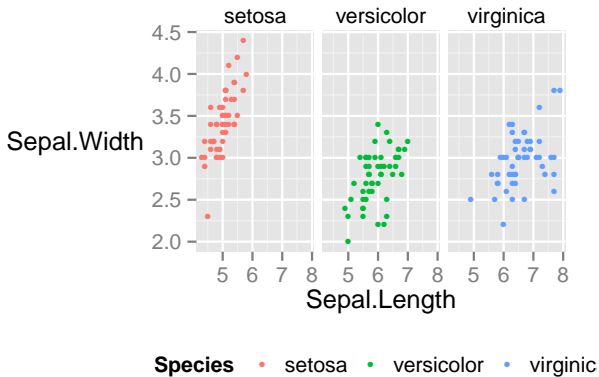
Themes are a great way to define custom plots.

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

## A 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))
```

## Adding themes





# ggthemes library

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

## 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

