

# Data Visualization with R & ggplot2

Karthik Ram

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github.com/karthikram/ggplot-lecture

https://speakerdeck.com/karthik/

The screenshot shows the GitHub repository page for `karthikram/ggplot-lecture`. The repository is public and has 0 pull requests, 0 issues, 0 stars, and 0 forks. The main content area shows the repository name and a description: "My lecture on ggplot at Cal (spring 2013) — Read more". Below the description, there are buttons for "Clone in Mac", "ZIP" (highlighted with a red box), "HTTP", "SSH", "Git Read-Only", and a text field containing the repository URL: `git@github.com:karthikram/ggplot-lecture.git` (also highlighted with a red box). To the right of the text field is a button for "Read+Write access". Below the cloning options, there is a dropdown menu for the branch (currently set to "master") and tabs for "Files", "Commits", and "Branches" (with 1 branch). The "Files" tab is selected, showing a file named "cropped slide image" with a commit message "Added new beamer theme and some images [karthikram]" and a commit hash "f171851480". The repository has 16 commits.

# Some housekeeping

Install some packages (make sure you also have recent copies of reshape2 and plyr)

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

# Base graphics

- Ugly, laborious, and verbose
- There are better ways to describe statistical visualizations.

# Why ggplot2?

- Follows a grammar, just like any language.
- It defines basic components that make up a sentence. In this case, the grammar defines components in a plot.
- Grammar of graphics originally coined by Lee Wilkinson

# Why ggplot2?

- Supports a continuum of expertise.
- Get started right away but with practice you can effortlessly build complex, publication quality figures.

# Section 1

## Basics

## Some terminology

- **ggplot** - The main function where you specify the dataset and variables to plot
- **geoms** - geometric objects
  - `geom_point()`, `geom_bar()`, `geom_density()`, `geom_line()`, `geom_area()`
- **aes** - aesthetics
  - shape, transparency (`alpha`), color, fill, linetype.
- **scales** Define how your data will be plotted
  - *continuous*, *discrete*, *log*



## Section 2

### Assembling your first ggplot

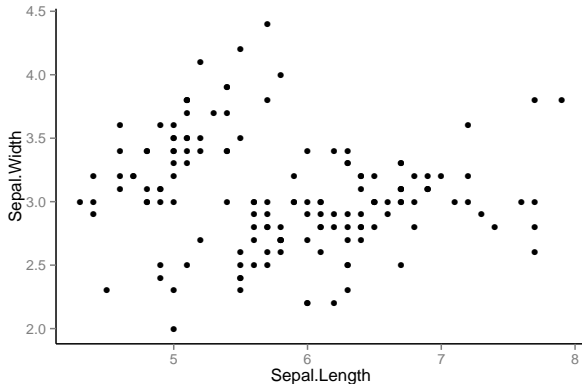
# The iris dataset

```
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

## Let's try an example

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



# 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()
```

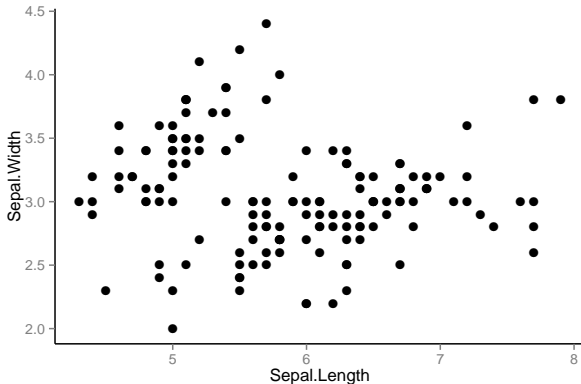
- Specify the data and variables inside the ggplot function.
- Anything else that goes in here becomes a global setting.
- Then add layers of geometric objects, statistical models, and panels.

## Quick note

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

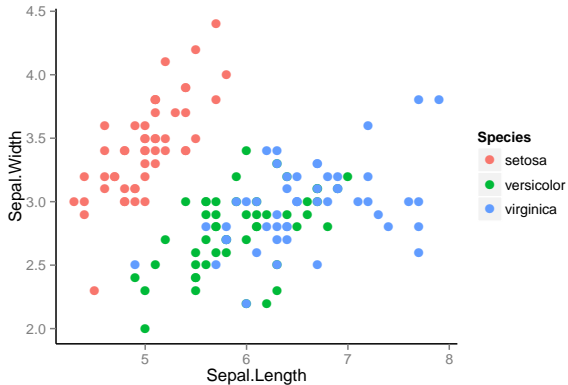
## Increase the size of points

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



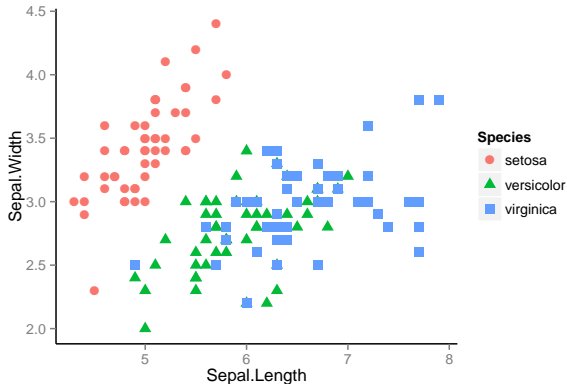
## Add some color

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



# Differentiate points by shape

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

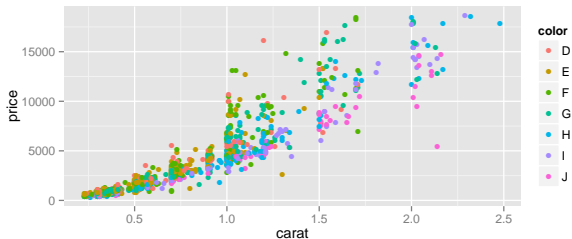




# Exercise 1

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

Then generate this plot below.

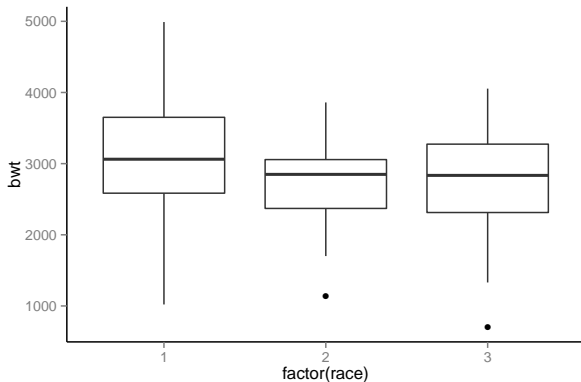


## Section 3

### Box plots

See ?geom\_boxplot for list of options

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

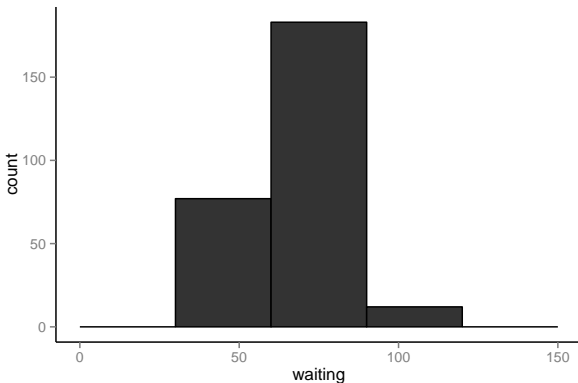


## Section 4

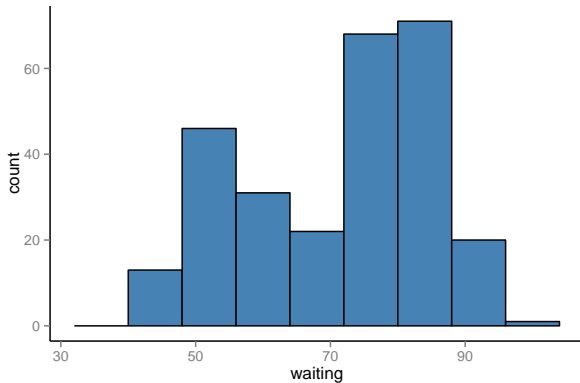
# Histograms

See ?geom\_histogram for list of options

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



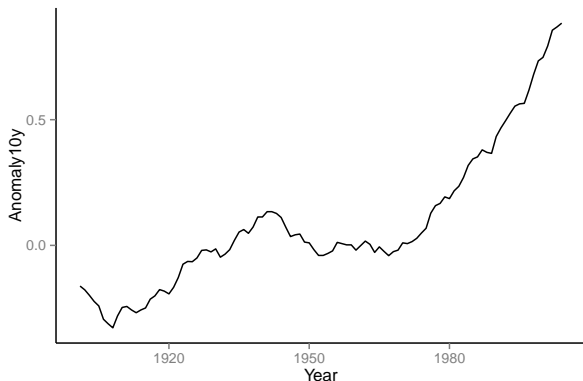
```
h <- ggplot(faithful, aes(x = waiting))  
h + geom_histogram(binwidth = 8, fill = "steelblue",  
colour = "black")
```



# Section 5

## Line plots

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

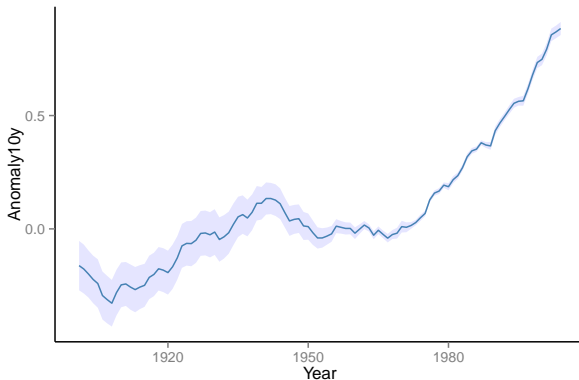


```
climate <- read.csv(text =
  RCurl::getURL(https://raw.githubusercontent.com/karthikram/ggplot-lecture/master/climate.csv))
```



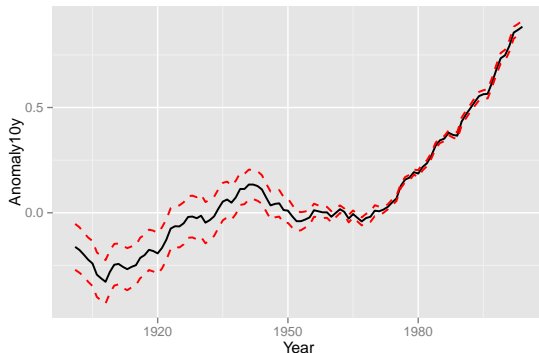
## We can also plot confidence regions

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



## Exercise 2

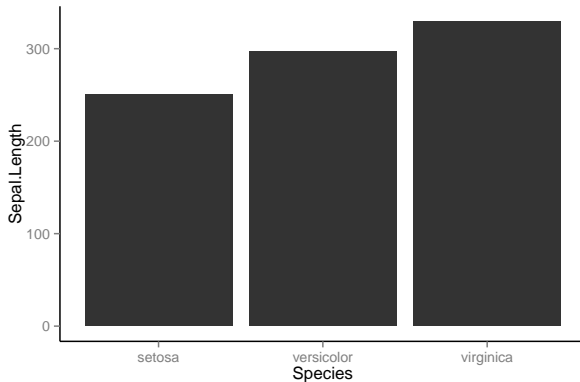
- Modify the previous plot and change it such that there are three lines instead of one with a confidence band.



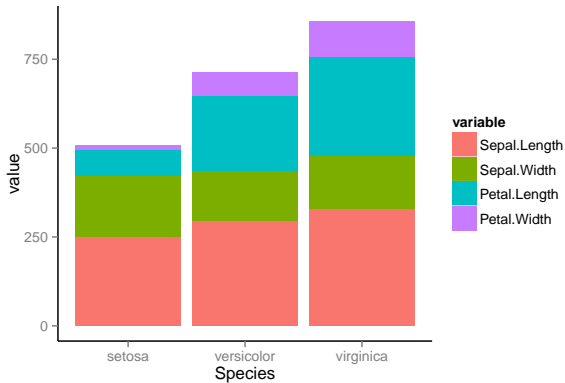
## Section 6

### 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")
```



## Section 7

plyr and reshape are key for using R

# plyr and reshape

These two packages are the swiss army knives of R.

- plyr
  - ① dply
  - ② lply
  - ③ join
- reshape.
  - ① melt
  - ② dcast
  - ③ acast

```
iris[1:2, ]
```

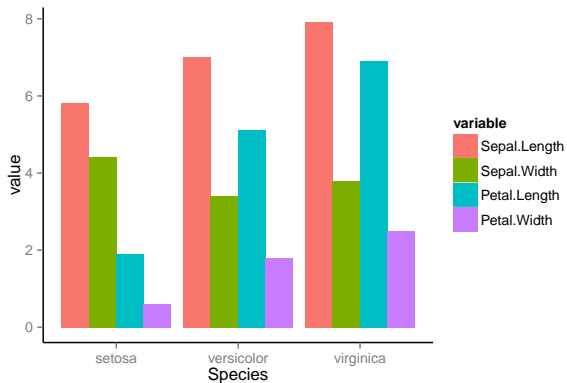
```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1          3.5          1.4          0.2  setosa
## 2          4.9          3.0          1.4          0.2  setosa
```

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

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

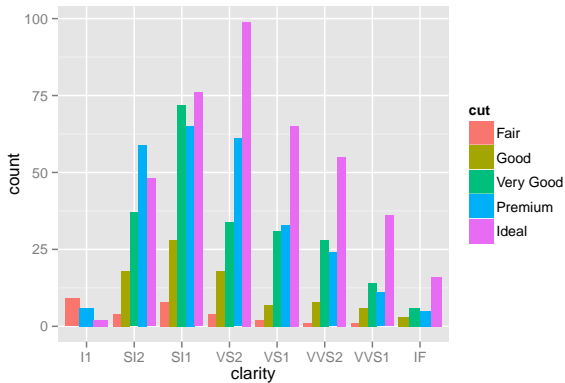


```
ggplot(df, aes(Species, value, fill = variable)) +  
geom_bar(stat = "identity", position = "dodge")
```



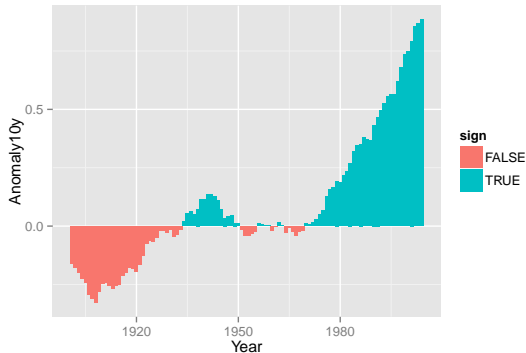
## Exercise 3

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.

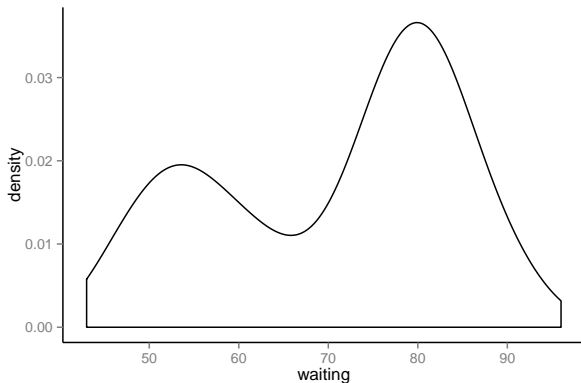


# Section 8

## Density Plots

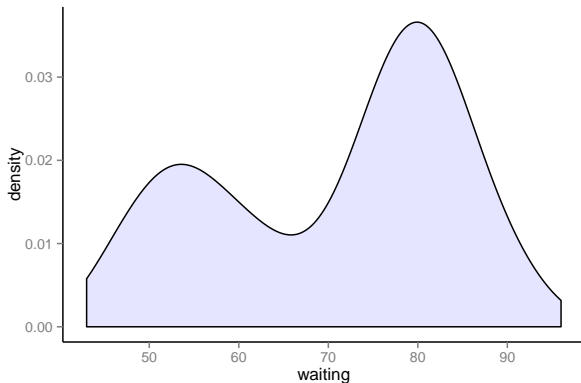
# Density plots

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

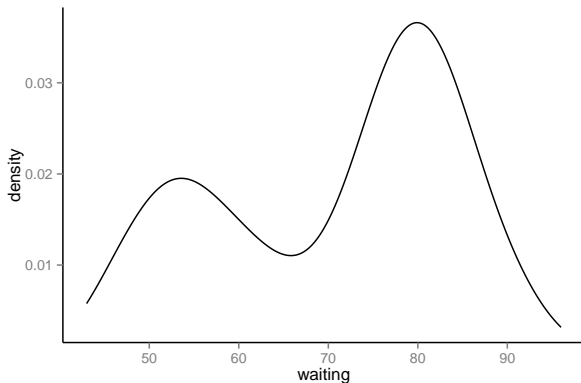


# Density plots

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



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



## Section 9

# Mapping Variables to colors

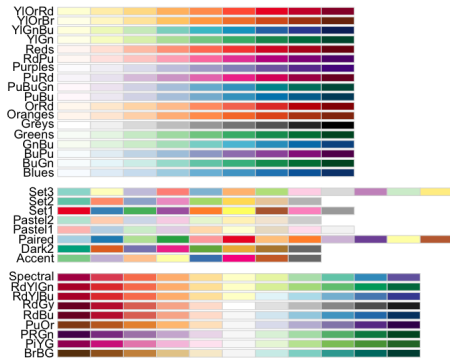


# Colors

```
# Map all points to one color
aes(color = "black")
# Or map the points to a variable
aes(color = variable)
# Then add a scale for the colors. Below we manually
# define colors but there are other ways (see next slide)
scale_fill_manual(values = c("color1", "color2"))
```

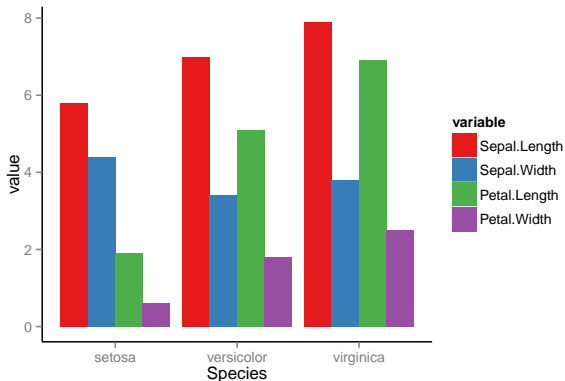
# The RColorBrewer package

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



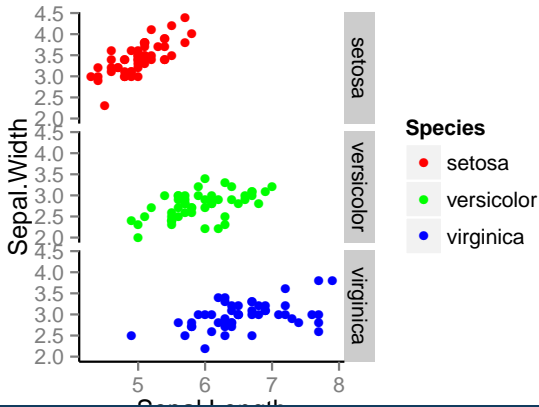
## Using a color brewer palette

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



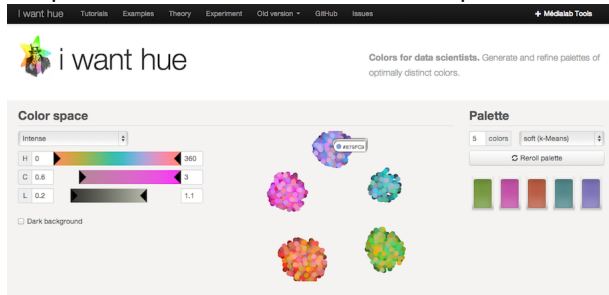
# Manual color scale

```
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/>

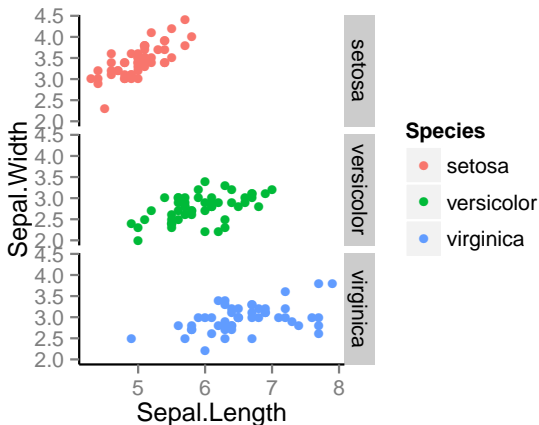


## Section 10

# Faceting

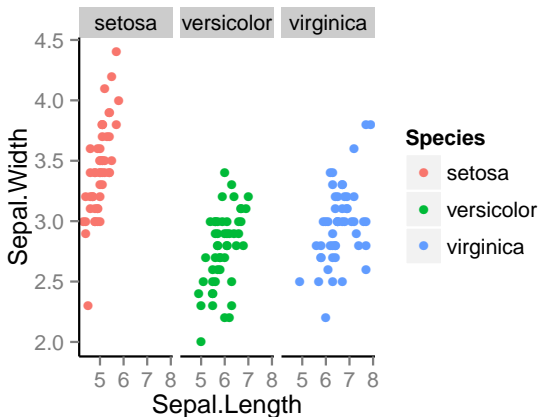
## Faceting along columns

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



and along rows

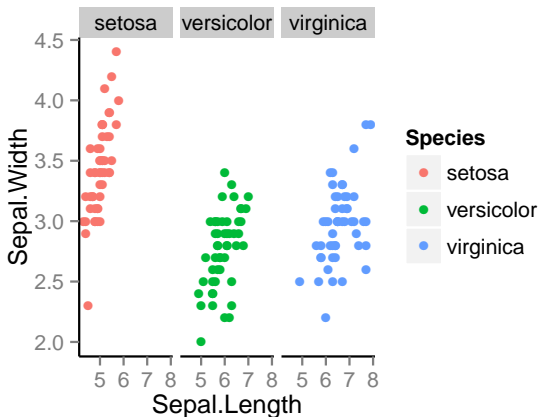
```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +  
geom_point() +  
facet_grid(. ~ Species)
```





or just wrap your panels

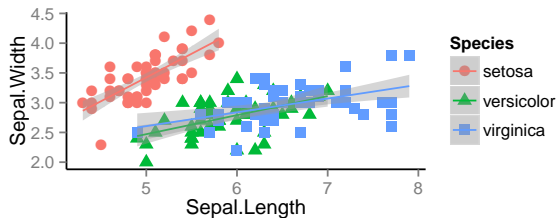
```
ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +  
geom_point() +  
facet_wrap(~ Species)
```



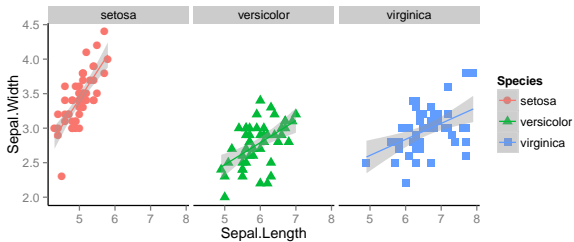
## Section 11

### 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 12

### Themes

# Adding themes

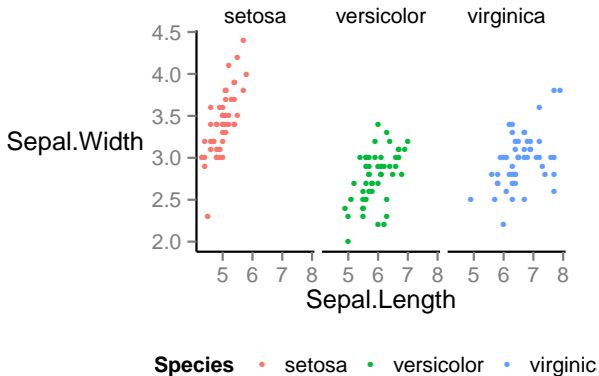
Themes are a great way to define custom plots.

```
+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_wsaj()  
+theme_solarized()
```

## Section 13

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 14

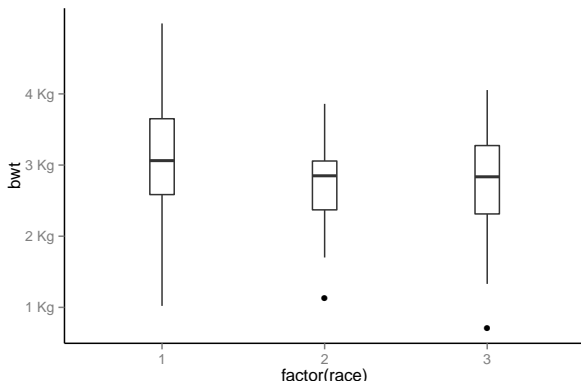
### Scales

# 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()
```

## Adding a continuous scale

```
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))
```

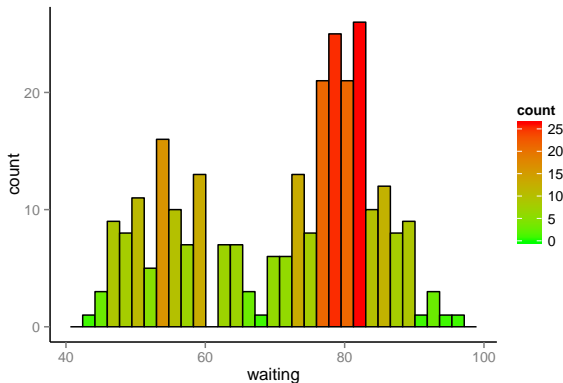


## Another continuous scale with custom labels

```
# Assign the plot to an object
dd <- ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
  geom_point(size = 4, shape = 16) +
  facet_grid(. ~Species)
# Now add a scale
dd +
  scale_y_continuous(breaks = seq(2, 8, by = 1),
    labels = paste0(2:8, " cm"))
```

# gradients

```
h + geom_histogram( aes(fill = ..count..), color="black") +  
  scale_fill_gradient(low="green", high="red")
```





## Section 15

### 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

