ggplot2

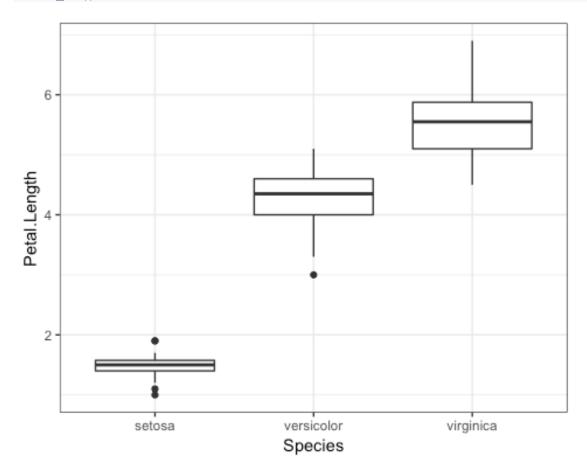
Fonti Kar

20/09/2018

Slide 6 - An example

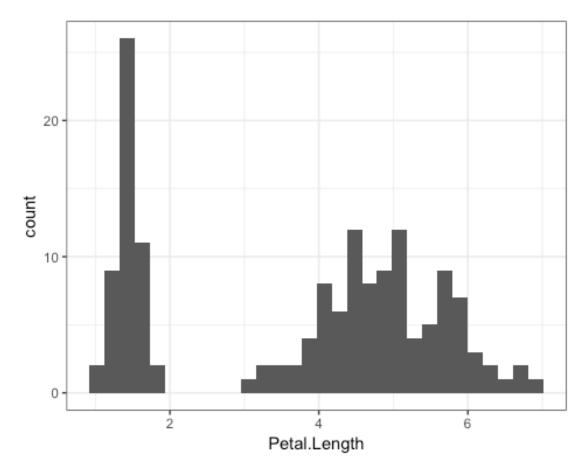
```
library(ggplot2)

ggplot(iris, aes(x = Species, y = Petal.Length)) + geom_boxplot() +
theme_bw()
```

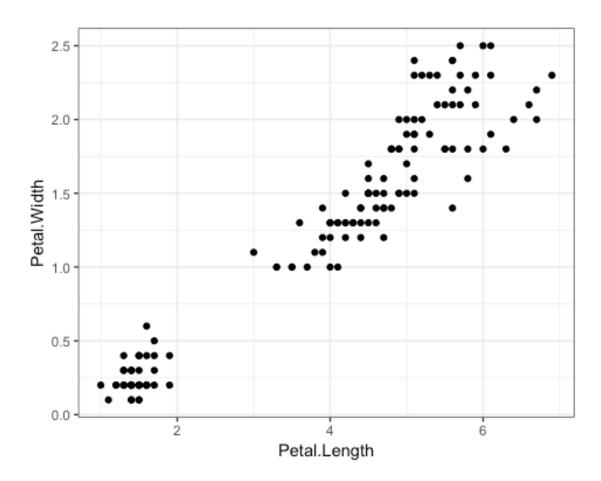


Slide 7, 8 - Some other key plots

```
ggplot(iris, aes(x = Petal.Length)) + geom_histogram() + theme_bw()
```

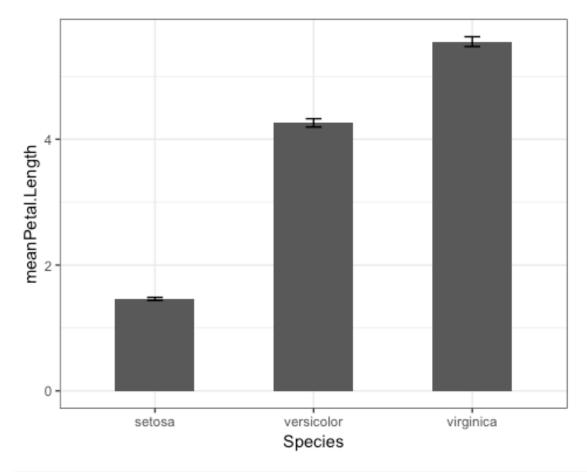


```
ggplot(iris, aes(x = Petal.Length, y = Petal.Width)) + geom_point() +
theme_bw()
```



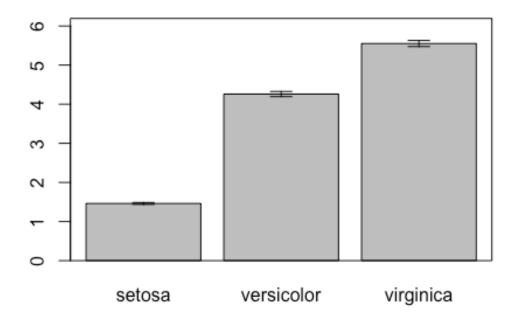
Slide 11 - 14 Data wrangling and barplots with base and ggplot2

```
library(dplyr)
iris.barplot <- iris %>% group by(Species) %>% summarise(meanPetal.Length =
mean(Petal.Length), stderPetal.Length =
sd(Petal.Length)/sqrt(length(Petal.Length)), lowerErr = (meanPetal.Length -
stderPetal.Length), upperErr = (meanPetal.Length + stderPetal.Length))
iris.barplot
## # A tibble: 3 x 5
                meanPetal.Length stderPetal.Length lowerErr upperErr
##
     Species
     <fct>
                           <dbl>
                                              <dbl>
                                                       <dbl>
                                                                <dbl>
##
## 1 setosa
                            1.46
                                             0.0246
                                                        1.44
                                                                 1.49
## 2 versicolor
                            4.26
                                             0.0665
                                                       4.19
                                                                 4.33
## 3 virginica
                            5.55
                                             0.0780
                                                        5.47
                                                                 5.63
ggplot(iris.barplot, aes(x = Species, y = meanPetal.Length)) + geom_col(width
= 0.5) + geom_errorbar(aes(ymin = lowerErr, ymax = upperErr), width = 0.1) +
theme bw()
```



```
#Base R
meanPetal.length <- tapply(iris$Petal.Length, iris$Species, mean)
nPetal.length <- tapply(iris$Petal.Length, iris$Species, length)
sePetal.length <- tapply(iris$Petal.Length,
iris$Species,sd)/sqrt(nPetal.length)

xx <-
barplot(meanPetal.length,ylim=c(0,max(meanPetal.length+sePetal.length)*1.1))
#we add error bars using the function arrows()
#by setting code=3, we get arrow heads on both ends
#by setting angle=90, the arrow heads become flat
arrows(xx,meanPetal.length-sePetal.length,xx,meanPetal.length+sePetal.length,
angle=90,code=3, length = 0.1)
#adds box to outside of figure
box()</pre>
```

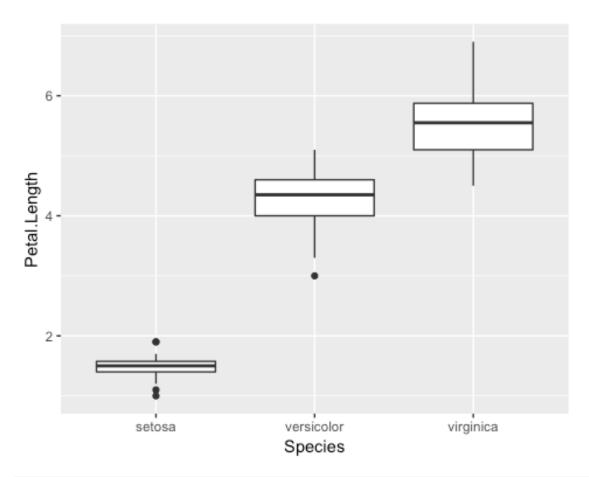


Slide 16 Themes

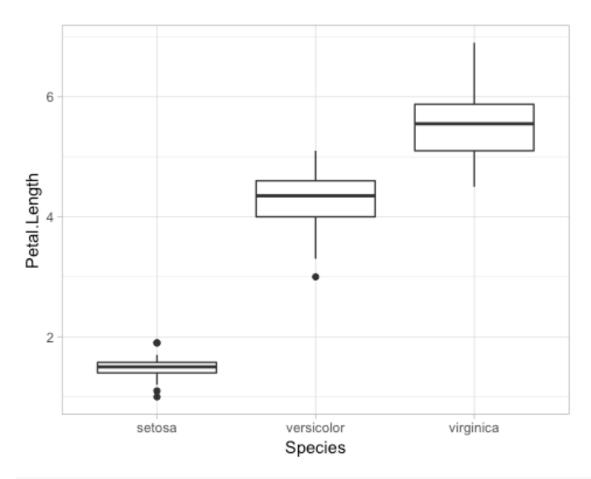
```
irisboxplot <- ggplot(iris, aes(x = Species, y = Petal.Length)) +
geom_boxplot()
irisboxplot + theme_classic()</pre>
```



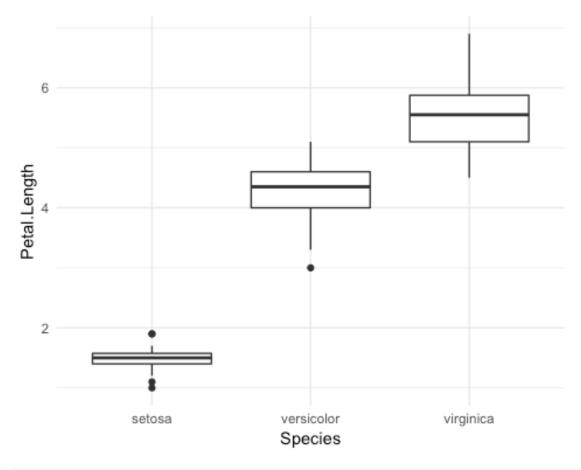
irisboxplot + theme_gray()



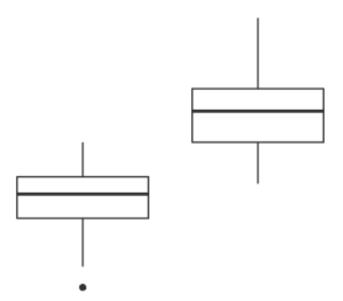
irisboxplot + theme_light()

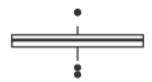


irisboxplot + theme_minimal()

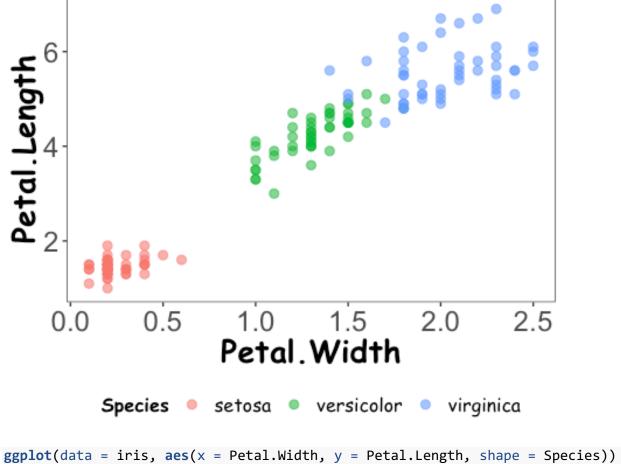


irisboxplot + theme_void()

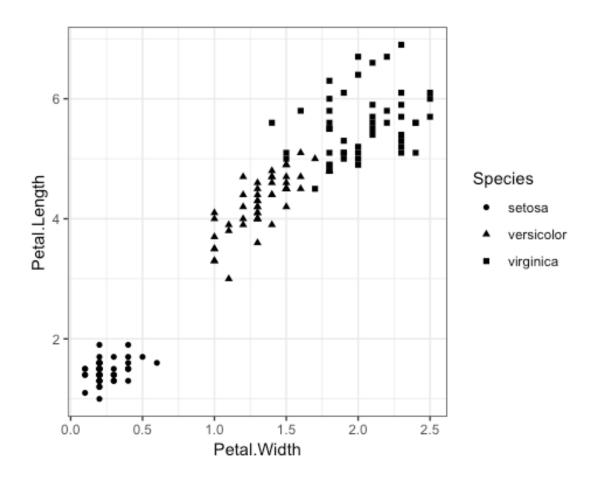




Slide 17 - 19 Customising your plot but less is more!

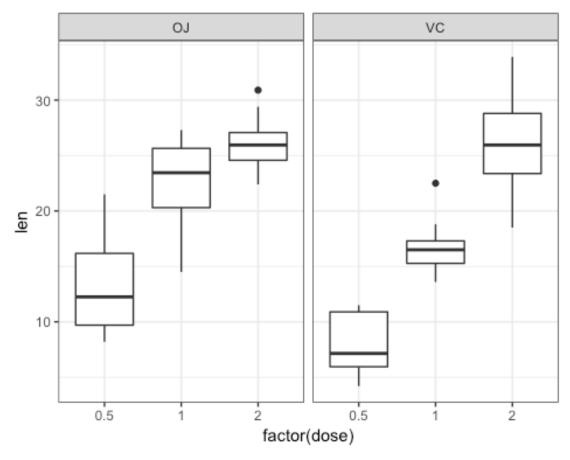


```
ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length, shape = Species))
+ geom_point() +
theme_bw()
```



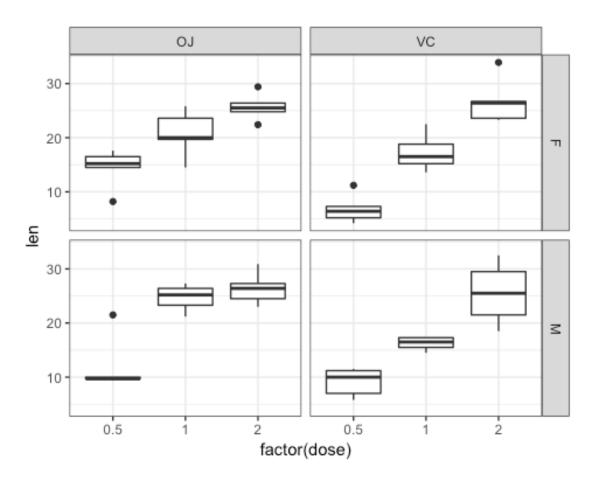
Slide 20 -21 Facets

```
Toothplot <- ggplot(data = ToothGrowth, aes(x = factor(dose), y = len)) +
   geom_boxplot() +
   theme_bw()
Toothplot + facet_wrap(~supp)</pre>
```



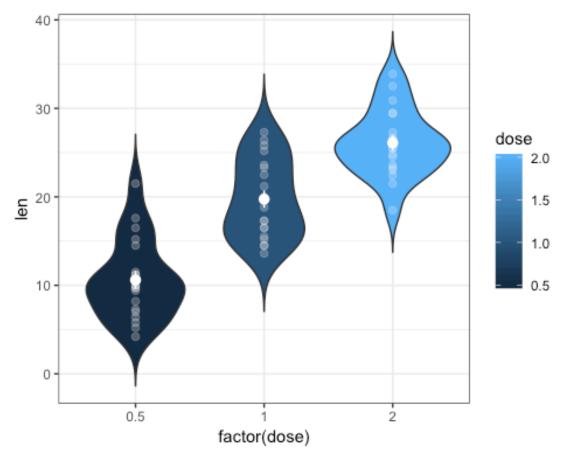
```
ToothGrowth$Sex <- rep(c("F", "M"), 2, 30) #Creating some fake sex data

ggplot(data = ToothGrowth, aes(x = factor(dose), y = len)) +
   geom_boxplot() +
   facet_grid(Sex ~supp) +
   theme_bw()</pre>
```

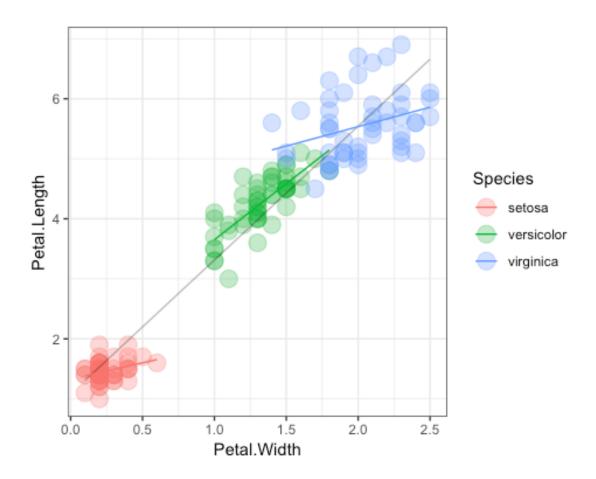


Slide 22 - 23 Built in functions

```
ggplot(data = ToothGrowth,
aes(x = factor(dose), y = len, fill = dose)) +
  geom_violin(trim = F) +
  geom_point(col = "white", size = 2, alpha = 0.2) +
  stat_summary(fun.data = "mean_se", col = "white") +
  theme_bw()
```



```
ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +
   geom_point(aes(color = Species), size = 5, alpha = 0.3) +
   geom_line(stat="smooth", method = "lm", alpha = 0.3) +
   geom_line(aes(group = Species, colour = Species), stat="smooth", method =
"lm", lwd = 0.5) +
   theme_bw()
```

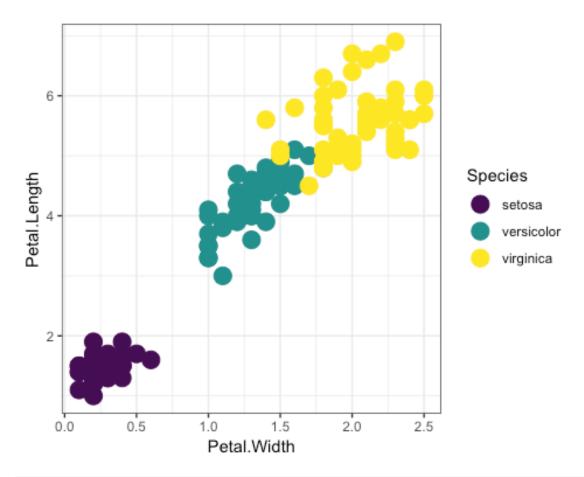


Slide 26 -27 Working with palettes

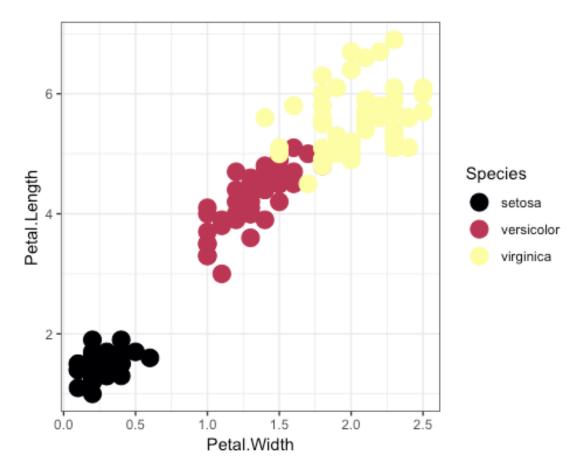
```
library(viridis)

irisplot <- ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length, color
= Species)) +
    geom_point(size = 5) +
    theme_bw()

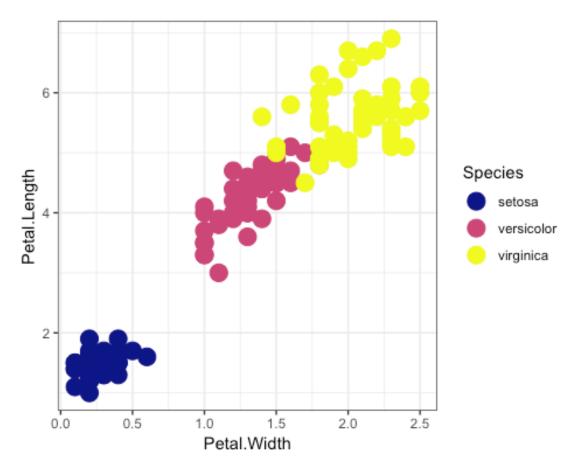
irisplot + scale_color_viridis(discrete = T)</pre>
```



irisplot + scale_color_viridis(discrete = T, option = "B")



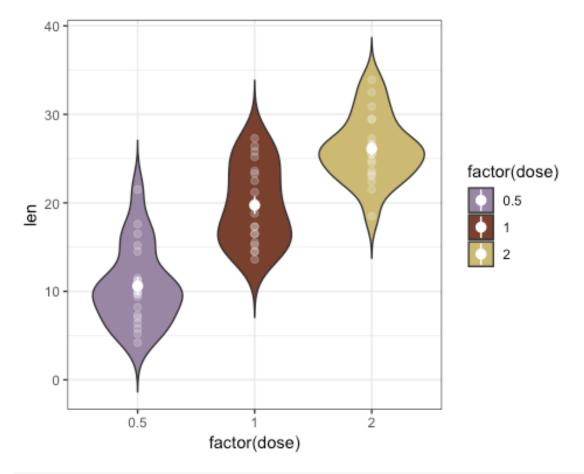
irisplot + scale_color_viridis(discrete = T, option = "C")



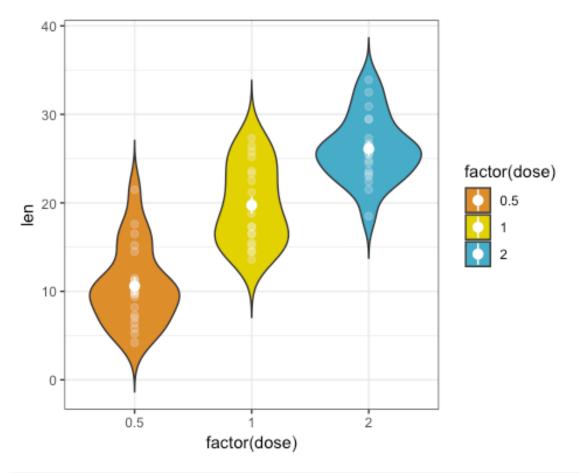
```
devtools::install_github("karthik/wesanderson")
library(wesanderson)

toothplot <- ggplot(data = ToothGrowth, aes(x = factor(dose), y = len, fill = factor(dose))) +
    geom_violin(trim = F) +
    geom_point(col = "white", size = 2, alpha = 0.2) +
    stat_summary(fun.data = "mean_se", col = "white") +
    theme_bw()

toothplot + scale_fill_manual(values = wes_palette("IsleofDogs1"))</pre>
```



toothplot + scale_fill_manual(values = wes_palette("FantasticFox1"))



toothplot + scale_fill_manual(values = wes_palette("Cavalcanti1"))

