

Class05.R

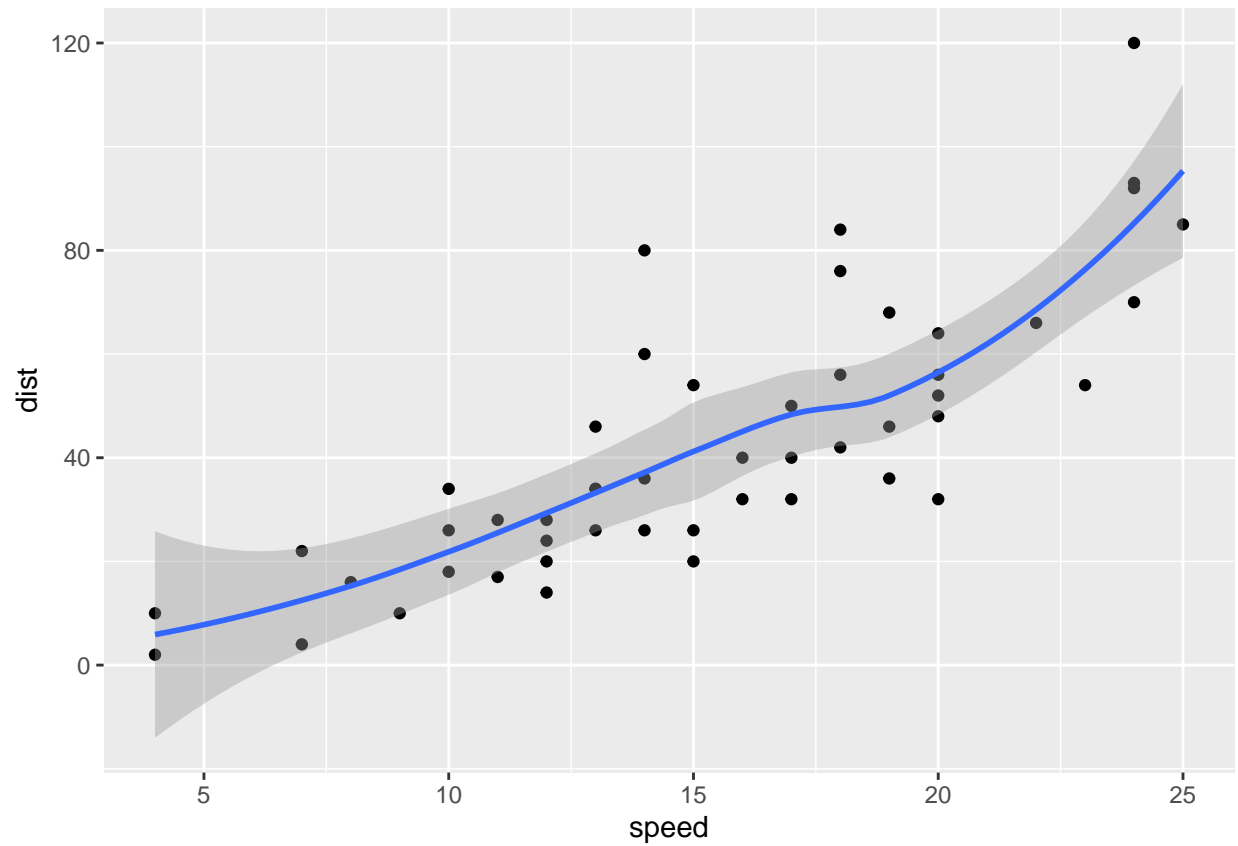
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```
#Class 05 Data visualization  
  
# lets start with a scatterplot  
# Before we use it we need to load it up!  
  
library(ggplot2)  
ggplot(cars)
```

```
# Every ggplot has a data + aes + geoms  
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()+  
  geom_smooth()
```

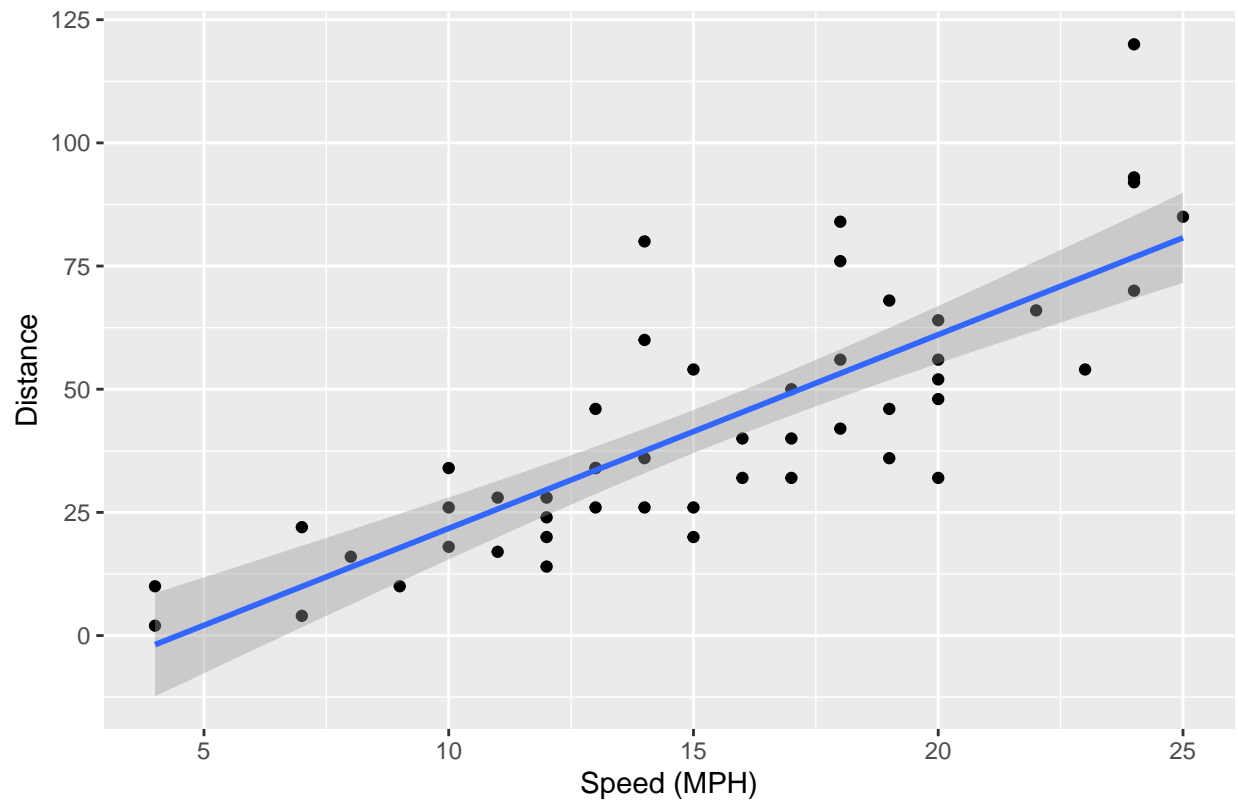
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



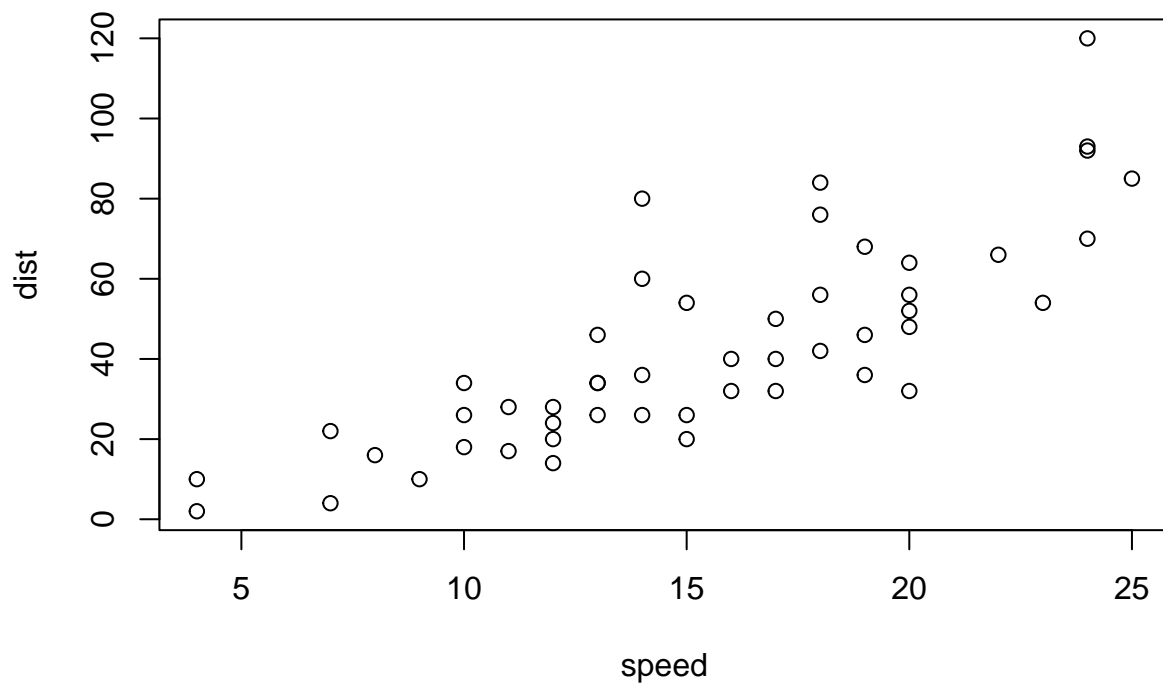
```
#Change to a linear model  
p <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()+  
  geom_smooth(method = "lm")  
  
p+labs(title = "My nice plot", x="Speed (MPH)", y="Distance")
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

My nice plot



```
#Base graphics is shorter  
plot(cars)
```



```
#Genes graph practice
genes <- read.delim("https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt")
head(genes)
```

```
##      Gene Condition1 Condition2      State
## 1    A4GNT -3.6808610 -3.4401355  unchanging
## 2    AAAS  4.5479580  4.3864126  unchanging
## 3    AASDH  3.7190695  3.4787276  unchanging
## 4    AATF  5.0784720  5.0151916  unchanging
## 5    AATK  0.4711421  0.5598642  unchanging
## 6 AB015752.4 -3.6808610 -3.5921390  unchanging
```

```
# Q. How many genes
nrow(genes)
```

```
## [1] 5196
```

```
colnames(genes)
```

```
## [1] "Gene"      "Condition1" "Condition2" "State"
```

```
ncol(genes)
```

```
## [1] 4
```

```
# Q. how to access State col
table(genes$State)
```

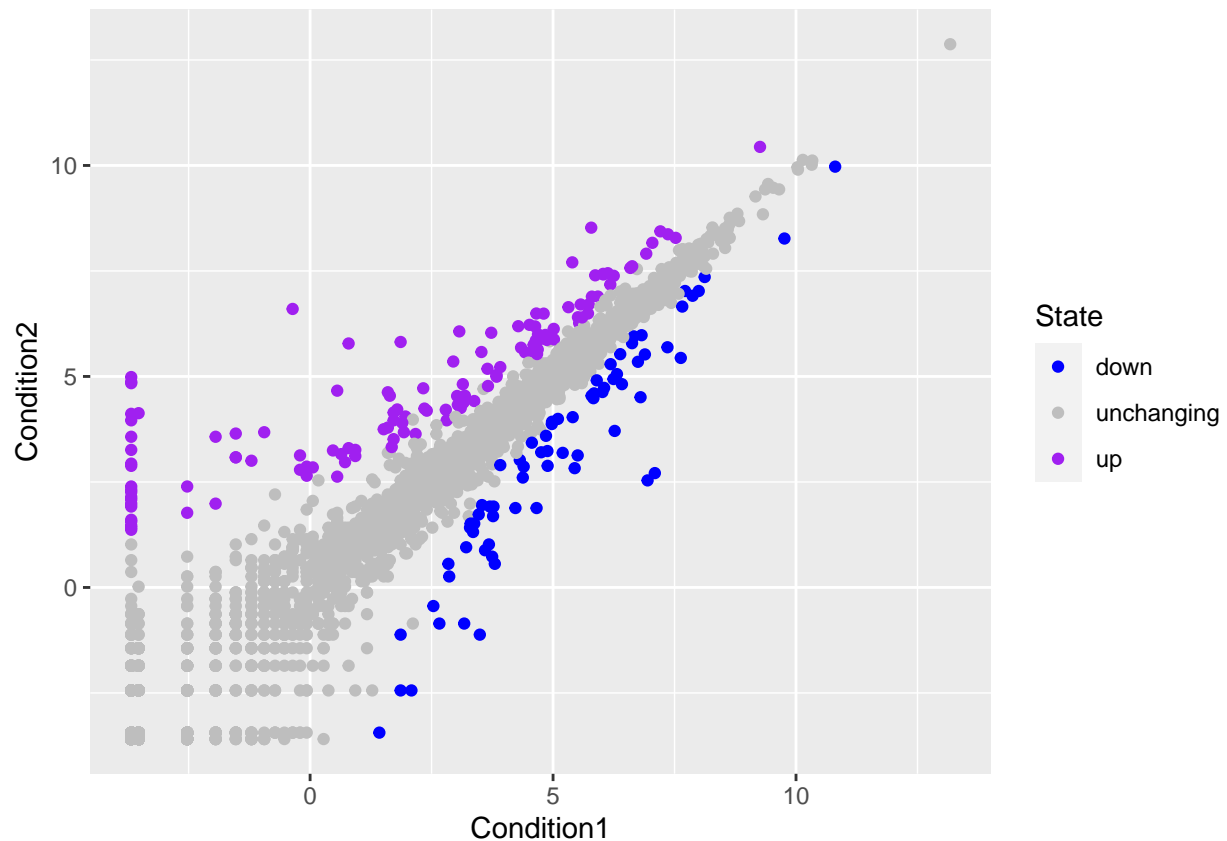
```
##
##      down  unchanged      up
##      72      4997      127
```

```
# What % up/down (rounded)
round(table(genes$State)/nrow(genes)*100,2)
```

```
##
##      down  unchanged      up
##      1.39      96.17      2.44
```

```
# Genes plot
g <- ggplot(genes) + aes(x= Condition1, y=Condition2, col=State) + geom_point()

# Changing the colors
g + scale_colour_manual(values=c("blue","gray","purple"))
```



```
labs(title= "Gene Expression Changes Upon Drug Treatment",
      x="Control (no drug)", y="Dog Treatment")
```

```
## $x
## [1] "Control (no drug)"
##
## $y
## [1] "Drug Treatment"
##
## $title
## [1] "Gene Expression Changes Upon Drug Treatment"
##
## attr(,"class")
## [1] "labels"
```

```
# Add titles
```

```
g + scale_colour_manual(values=c("blue","gray","purple")) + labs(title= "Gene Expression Changes Upon D
```

