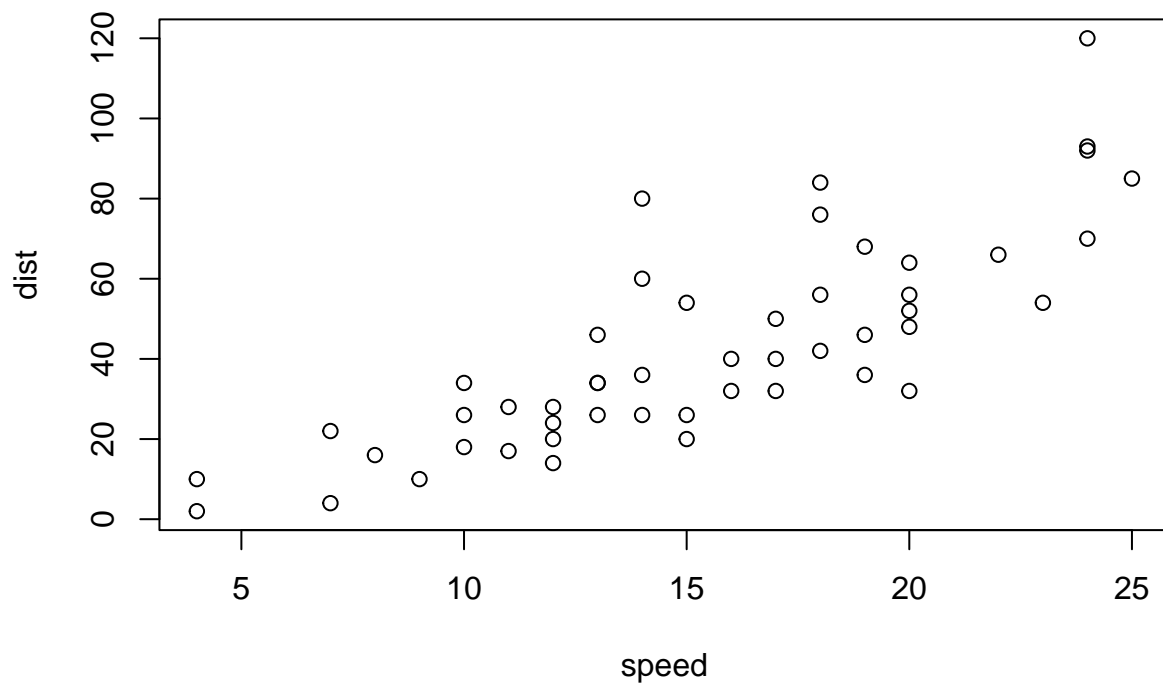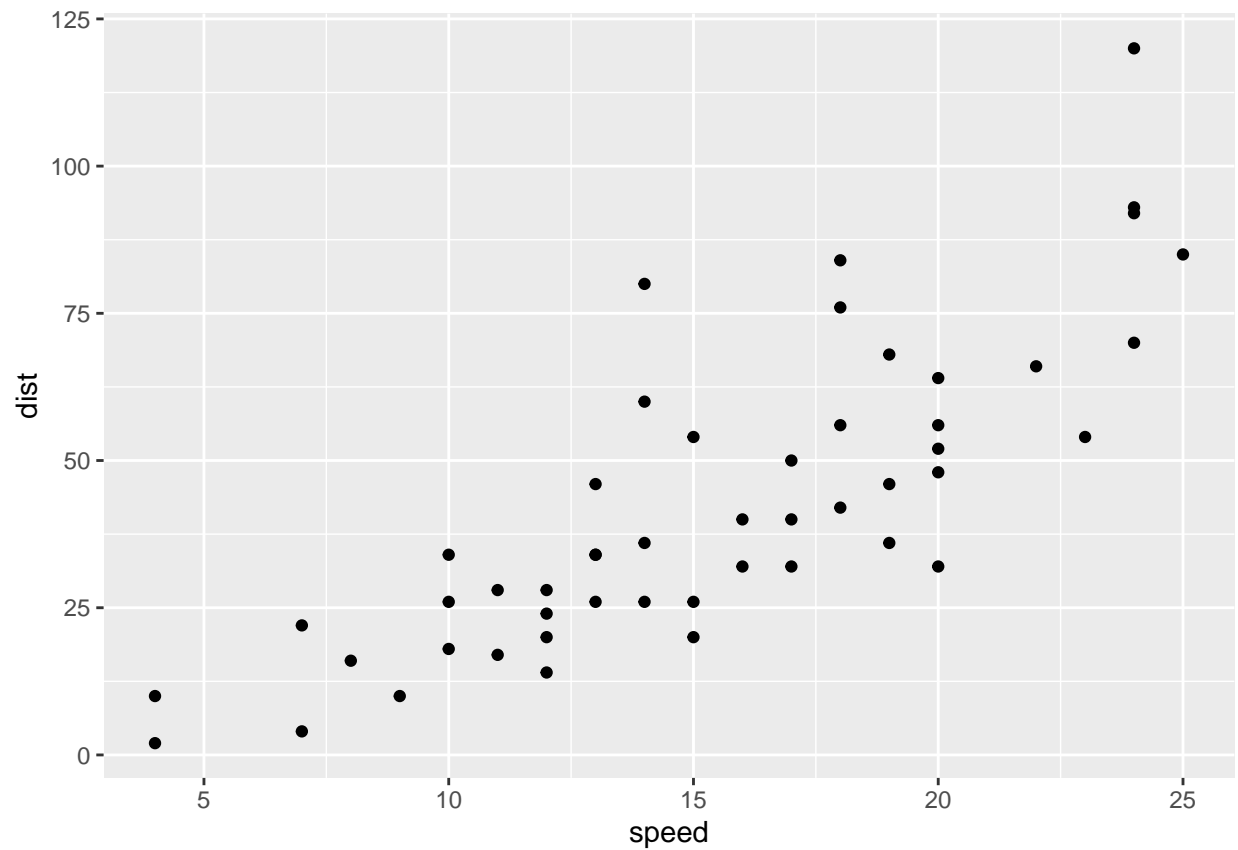# Week 4: Data Visualization Lab

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```
#Week 4 Data visualization Lab

#Install the package ggplot2
#install.packages("ggplot2")

#Any time I want to use this
#package I need to load it
library(ggplot2)

View(cars)

#A quick base R plot- this is not ggplot
plot(cars)
```
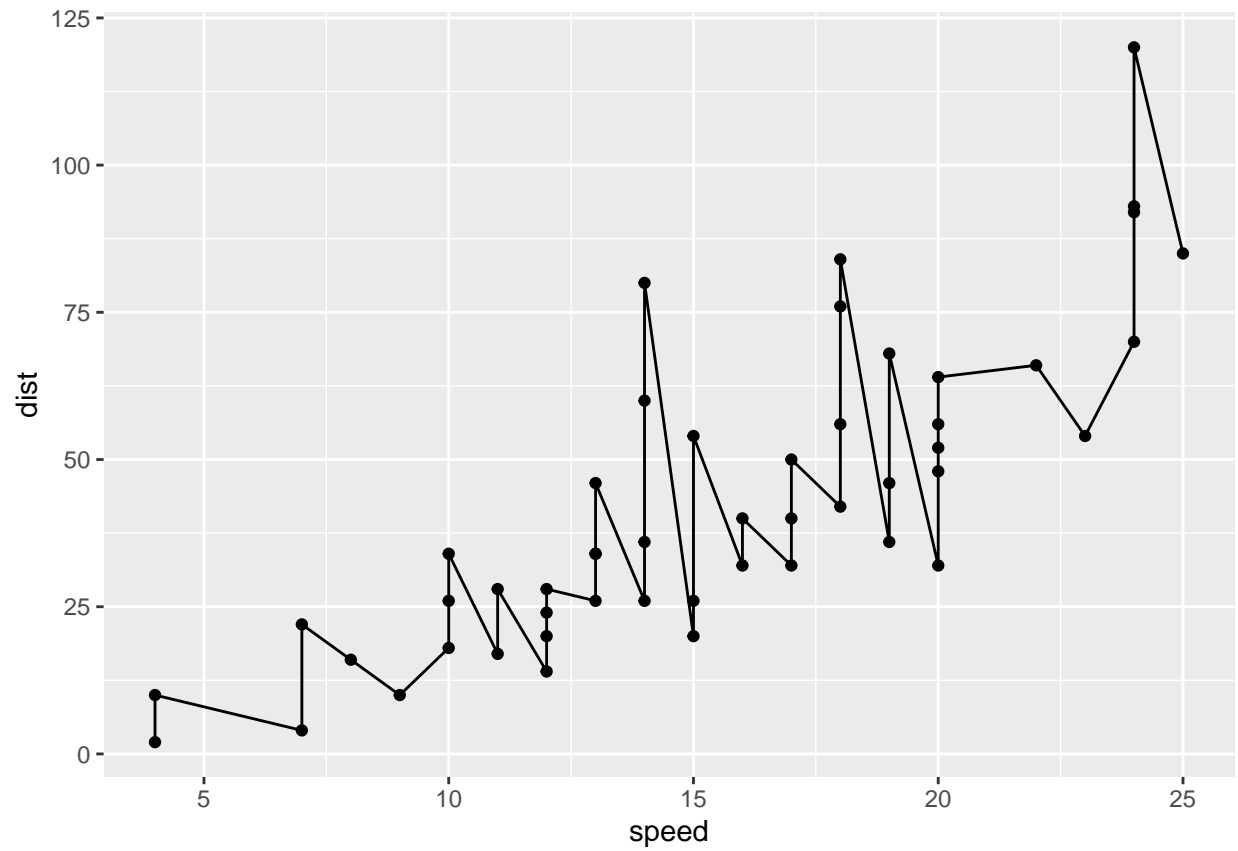
```
#Our first ggplot
#we need data + aes + geoms
ggplot(data=cars)+aes(x=speed, y=dist)+geom_point()
```
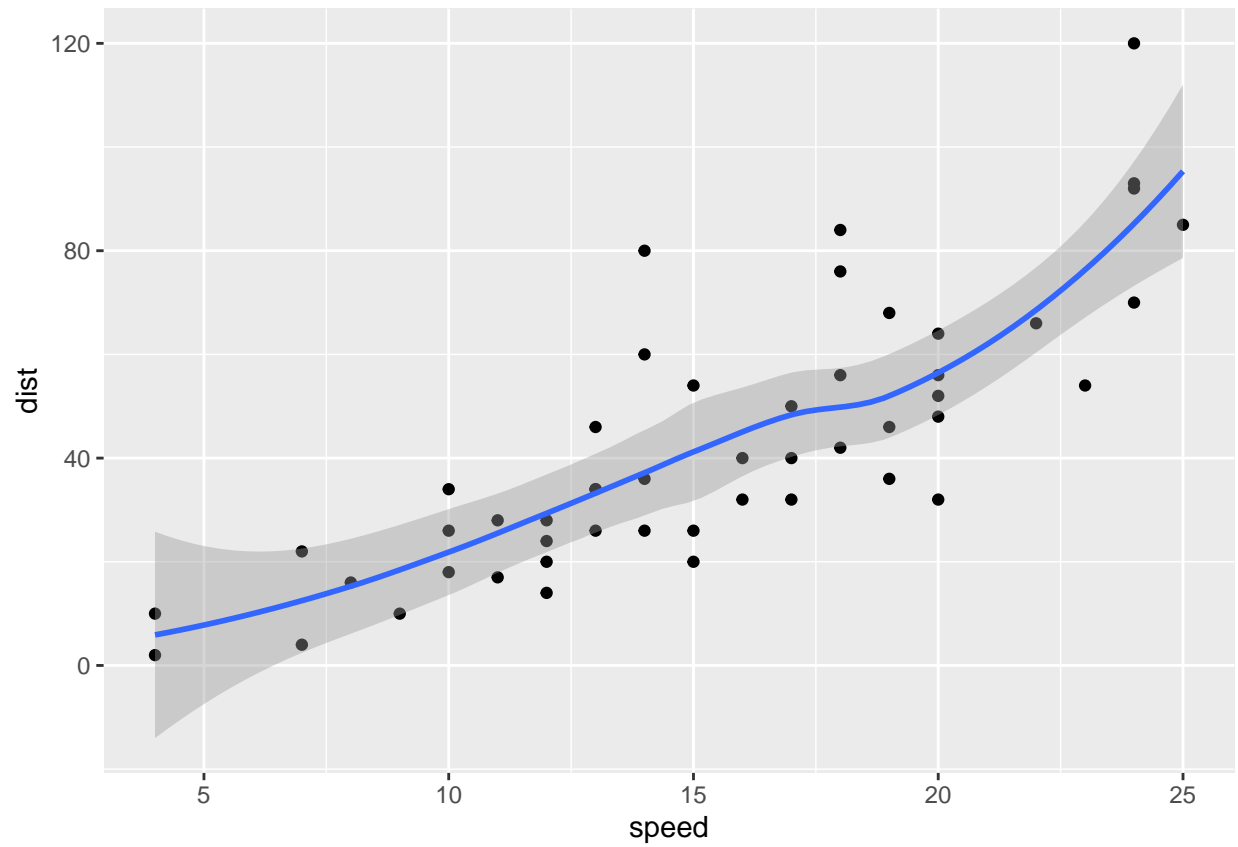


```
p<-ggplot(data=cars)+aes(x=speed, y=dist)+geom_point()

#Add a line geom with geom_line()
p+geom_line()
```
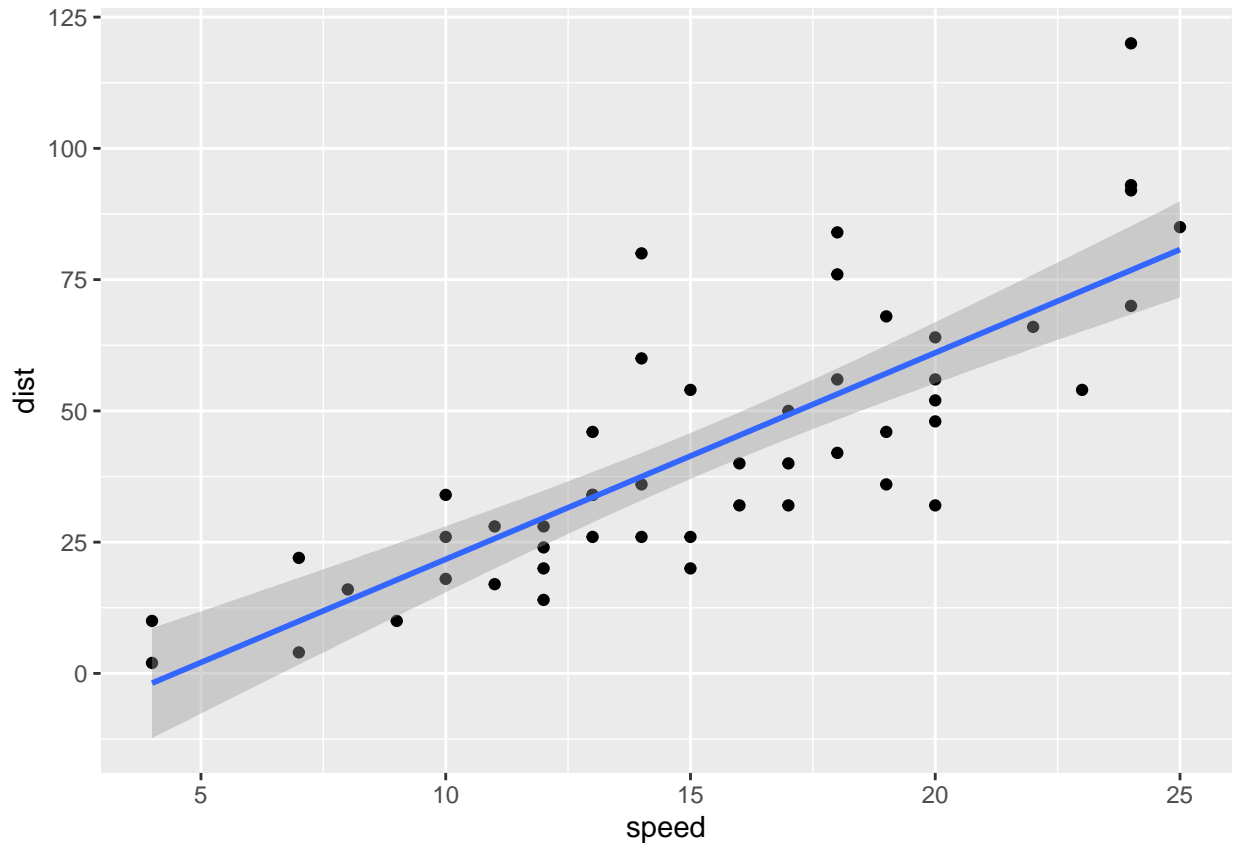
```
#Add a trend line close to the data
p+geom_smooth()
```

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

```
p+geom_smooth(method="lm")
```

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

```
#Read in our drug expression data
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
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 are in this dataset
nrow(genes)
```

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

```
#Q. What are the column names and how many are there
colnames(genes)
```

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

```
ncol(genes)
```

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

```
#Q. How many 'up' regulated genes
table(genes$State)
```

```
##
##       down unchanging         up
##         72       4997        127
```

```
#What fraction of total genes is up-regulated
round( table(genes$State)/nrow(genes)*100,2 )
```
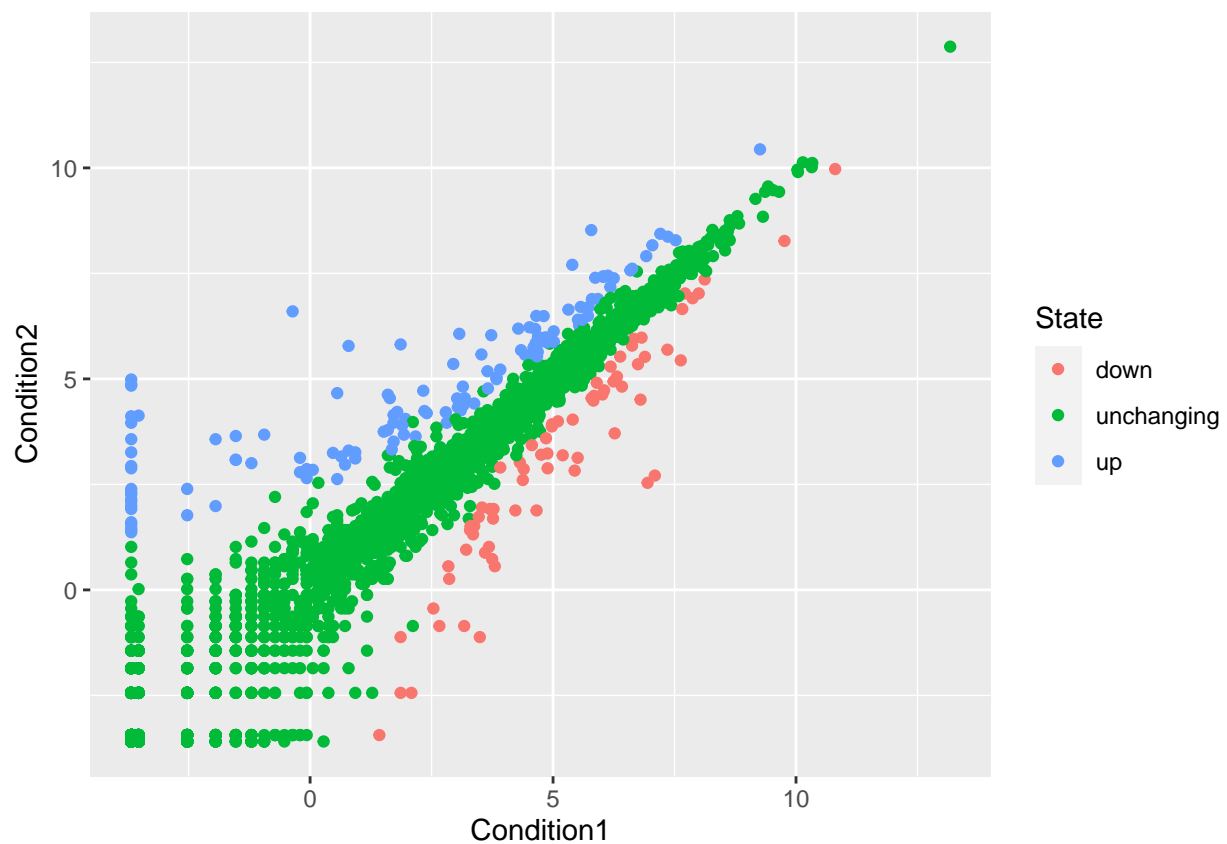
```
##
##       down unchanging         up
##       1.39      96.17       2.44
```

```
#Let's make a first plot attempt
g<-ggplot(data=genes)+aes(x=Condition1, y=Condition2, col=State)+geom_point()

g
```

```
#Add some color
g+scale_color_manual(values=c("blue","gray","red"))+
  labs(title="Gene expression changes",x="Control (no drug)")+
  theme_bw()
```

Gene expression changes