

## Week 5 - Data Visualizaion lab

Galilea Guerrero PID A59010531

Feb. 1, 2022

```
# Week 5 visualization lab
```

```
#View Data
```

```
View(cars)
```

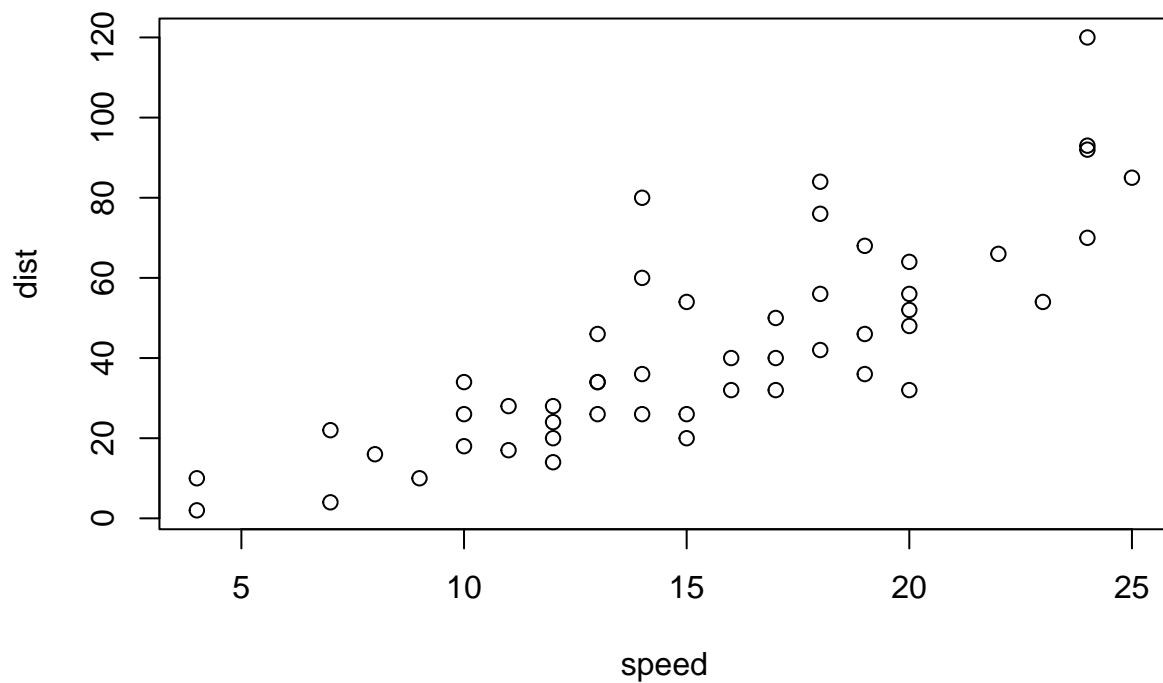
```
# Simple base R plot
```

```
plot(cars)
```

```
#Load package
```

```
library(ggplot2)
```

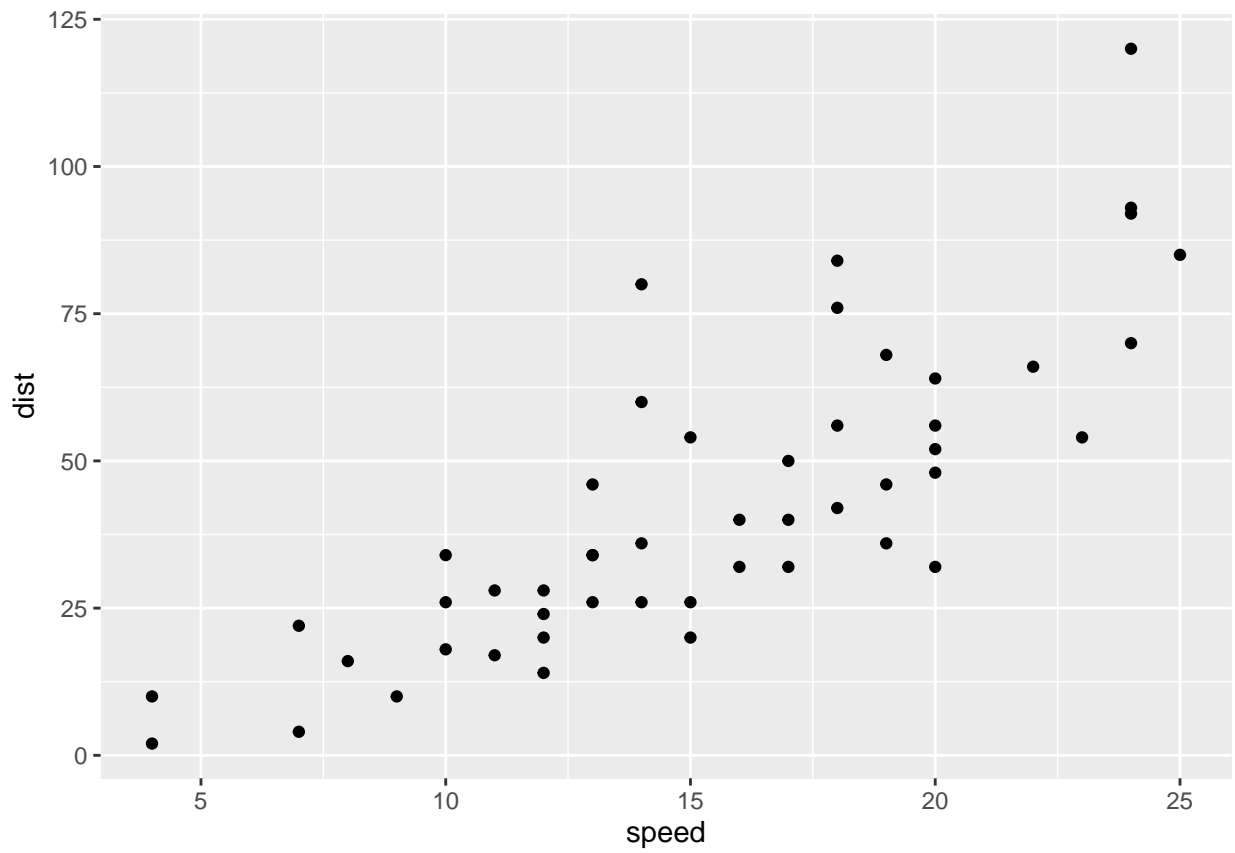
```
## Warning in register(): Can't find generic `scale_type` in package ggplot2 to  
## register S3 method.
```



```
#First ggplot: need data + aes + geom
```

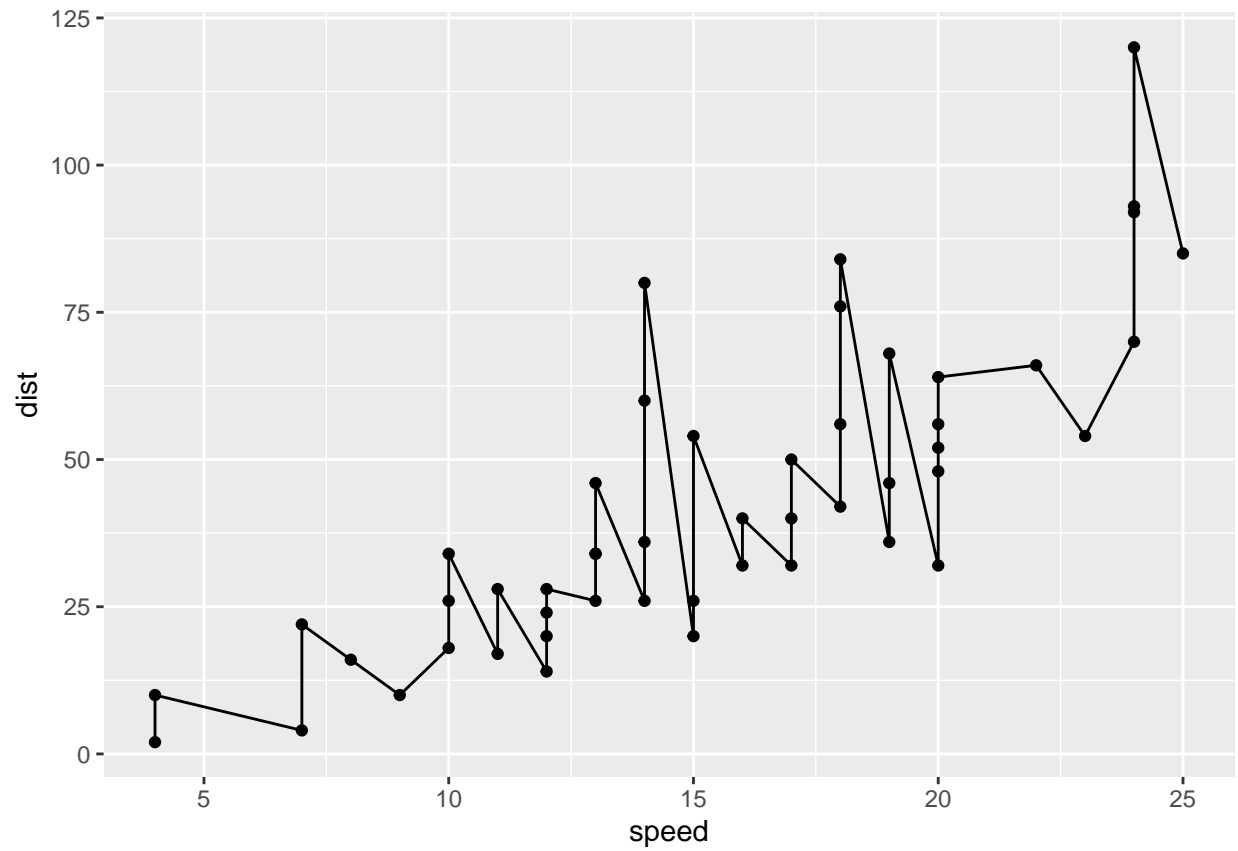
```
p <- ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```

p



```
#line that connects all points
```

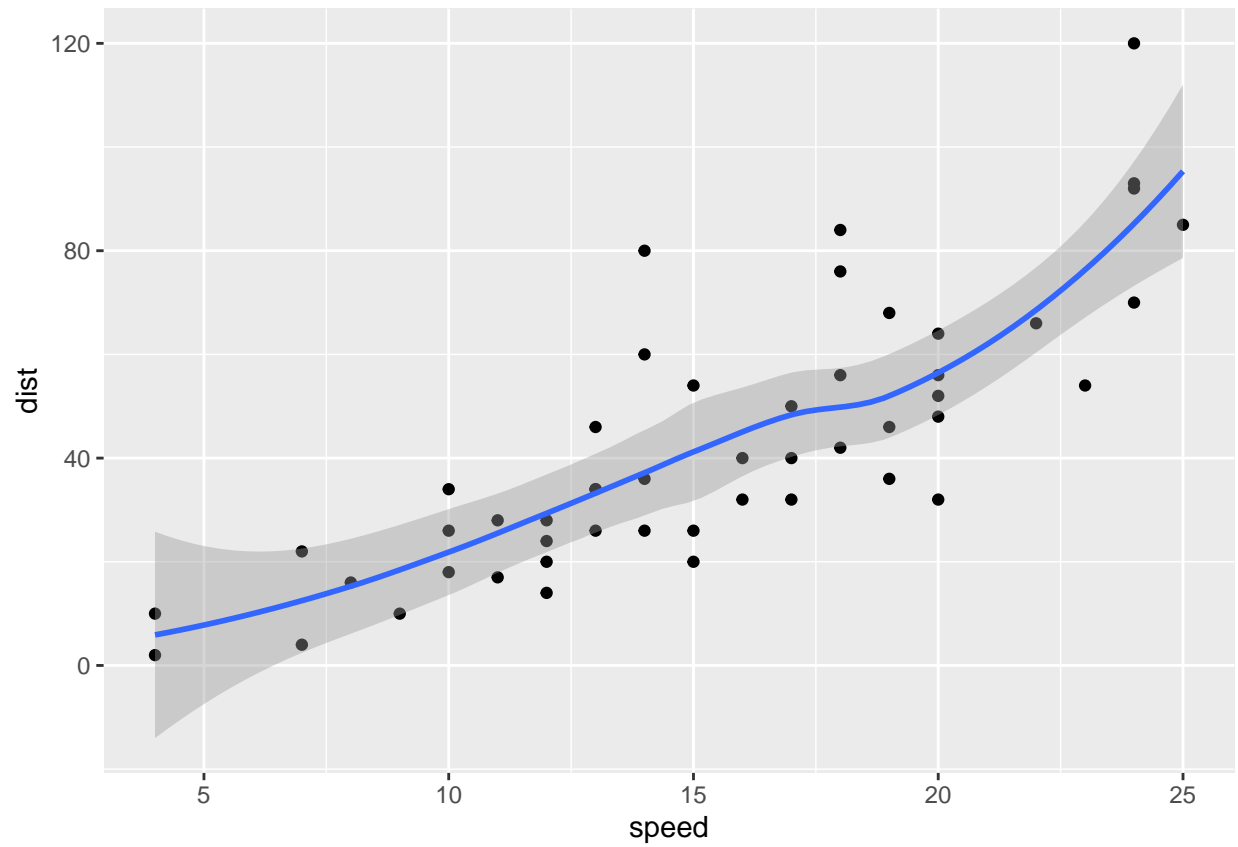
```
p + geom_line()
```



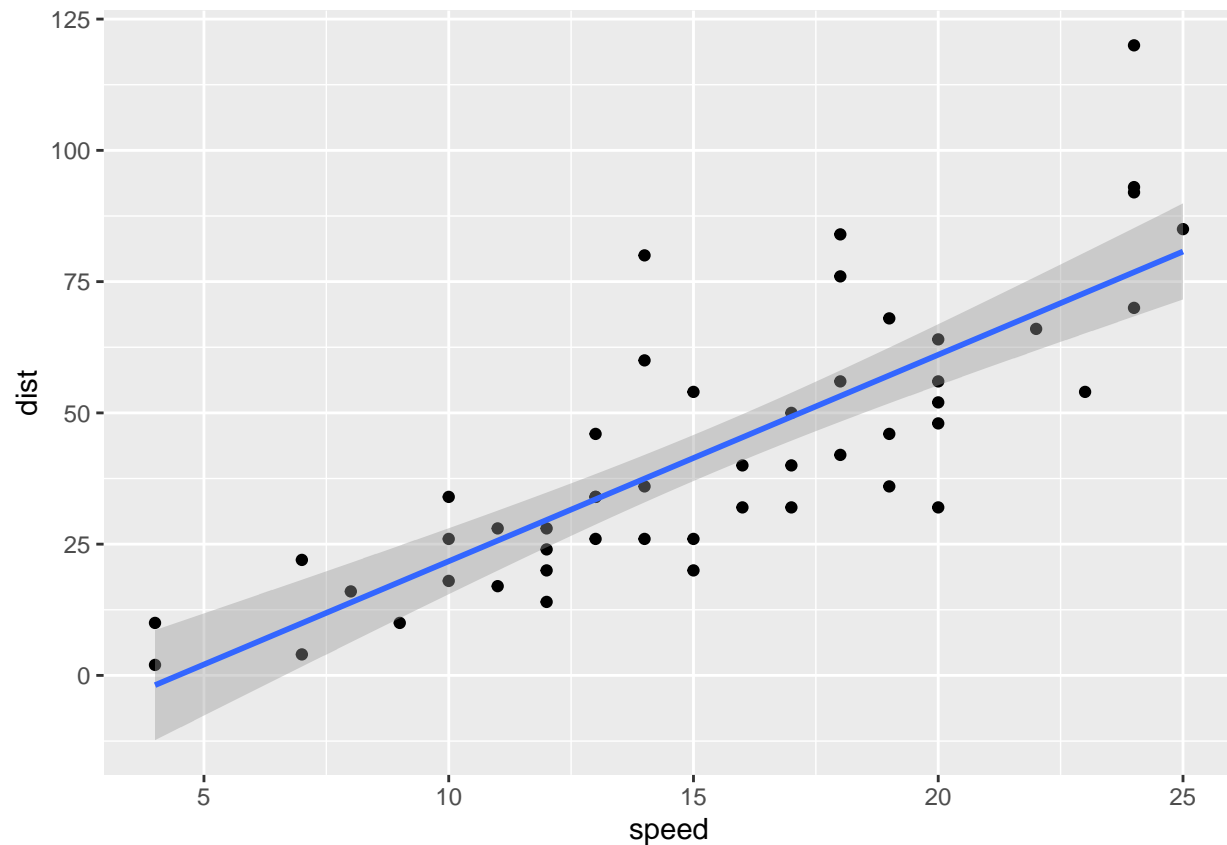
```
#Add a fitted line
```

```
p + geom_smooth()
```

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



```
#Fit a linear model  
p + geom_smooth(method="lm")  
  
## `geom_smooth()` using formula 'y ~ x'
```



```
#Work with RNA-Seq Dataset (Drug vs No Drug treatment)
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
```

```
#Look at first 6 lines
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
```

```
View(genes)
```

```
#How many genes are in the dataset?
nrow(genes)
```

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

```
#number and names of columns
ncol(genes)
```

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

```

colnames(genes)

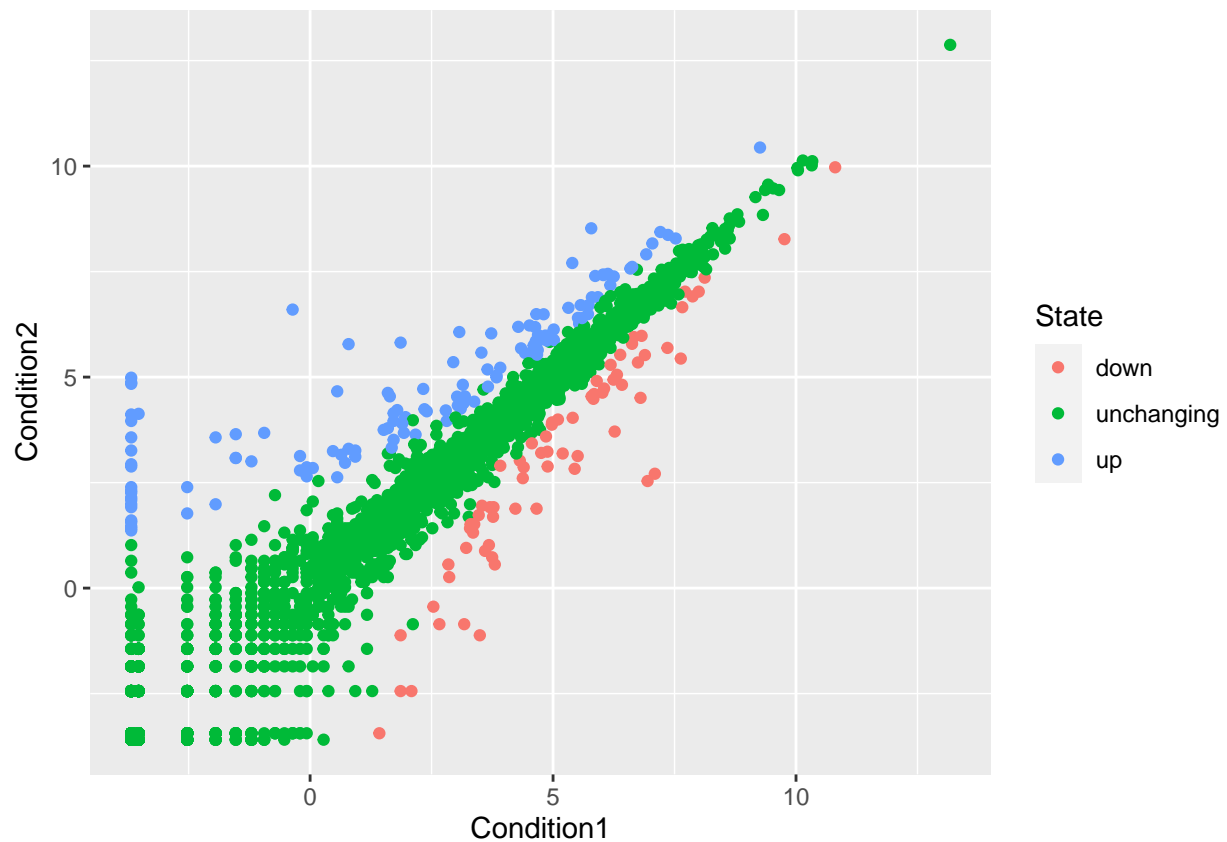
## [1] "Gene"      "Condition1" "Condition2" "State"
#How many upregulated genes are there?
table(genes$State)

##
##      down  unchanged      up
##      72    4997      127
#What fraction of genes are up, down, etc?
round((table(genes$State)/ nrow(genes)) * 100, 2)

##
##      down  unchanged      up
##      1.39    96.17      2.44
#Generate a publication-like plot
g <- ggplot(genes) +
  aes(x=Condition1,
      y=Condition2,
      col=State)+
  geom_point()

g

```



```
# Add more custom layers
g + theme_bw() +
  scale_color_manual(values=c("blue", "grey", "red")) +
  labs(x="Control (no drug)",
       y="Drug treated",
       title="Gene expression changes example plot")
```

