

class05.R

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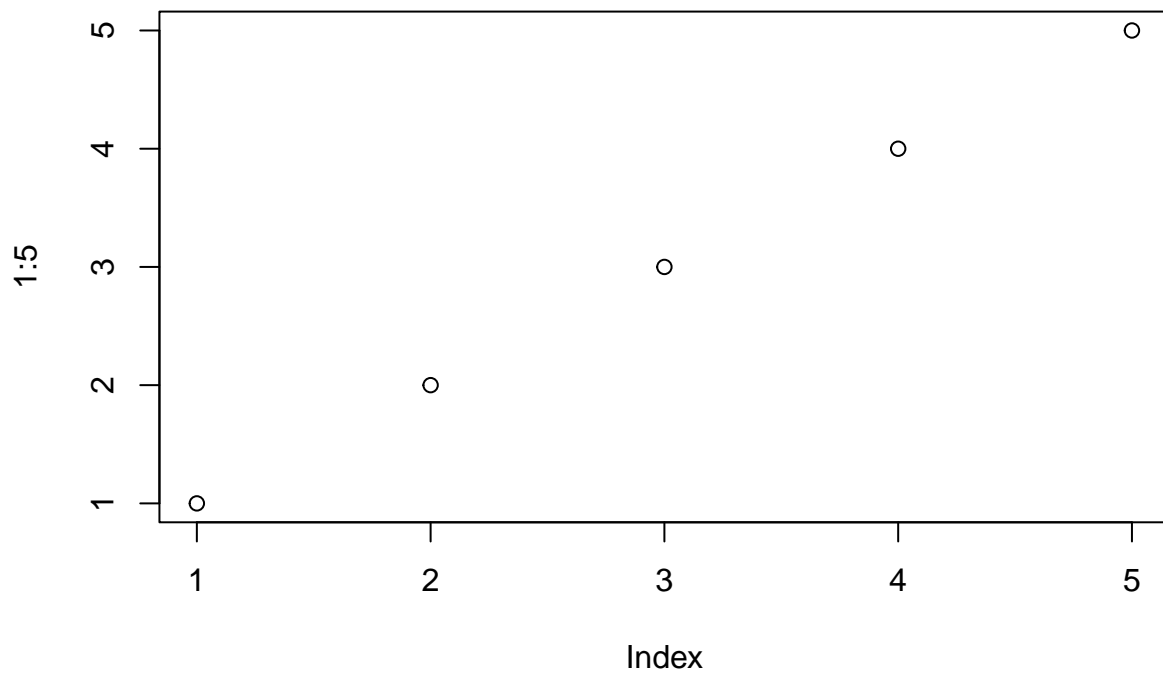
```
# Class 5 Data Visualization
```

```
plot(1:5)
```

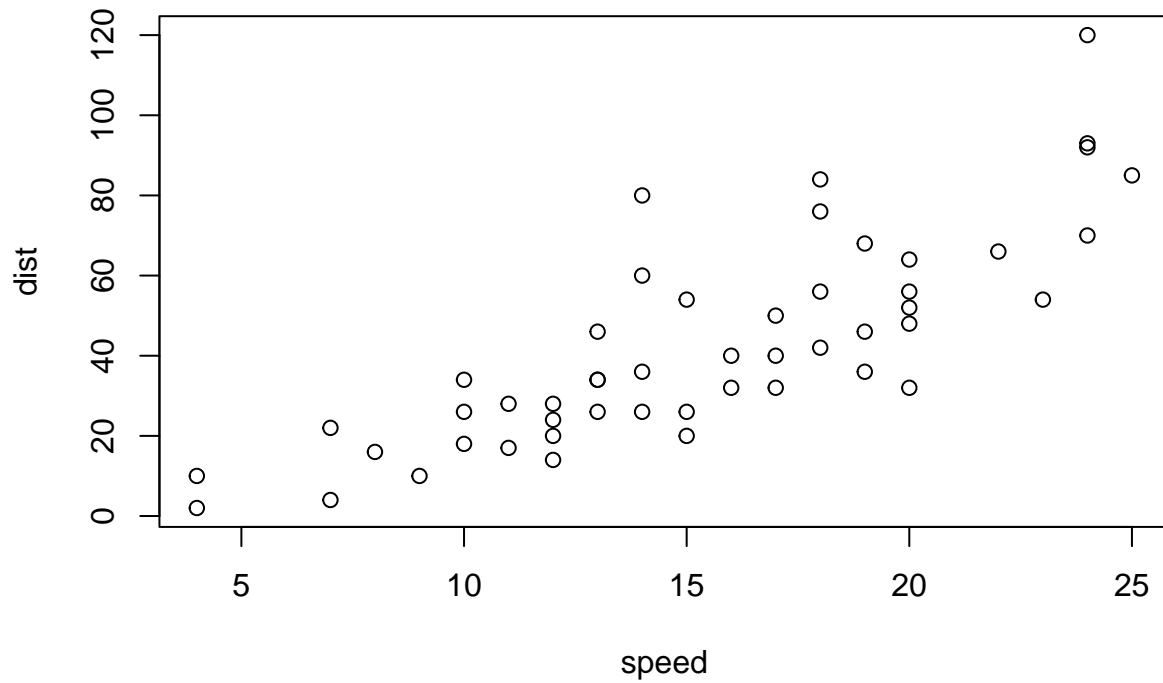
```
# That was base R plot - quick and not nice!  
# We will use an add on package called ggplot2
```

```
library(ggplot2)
```

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

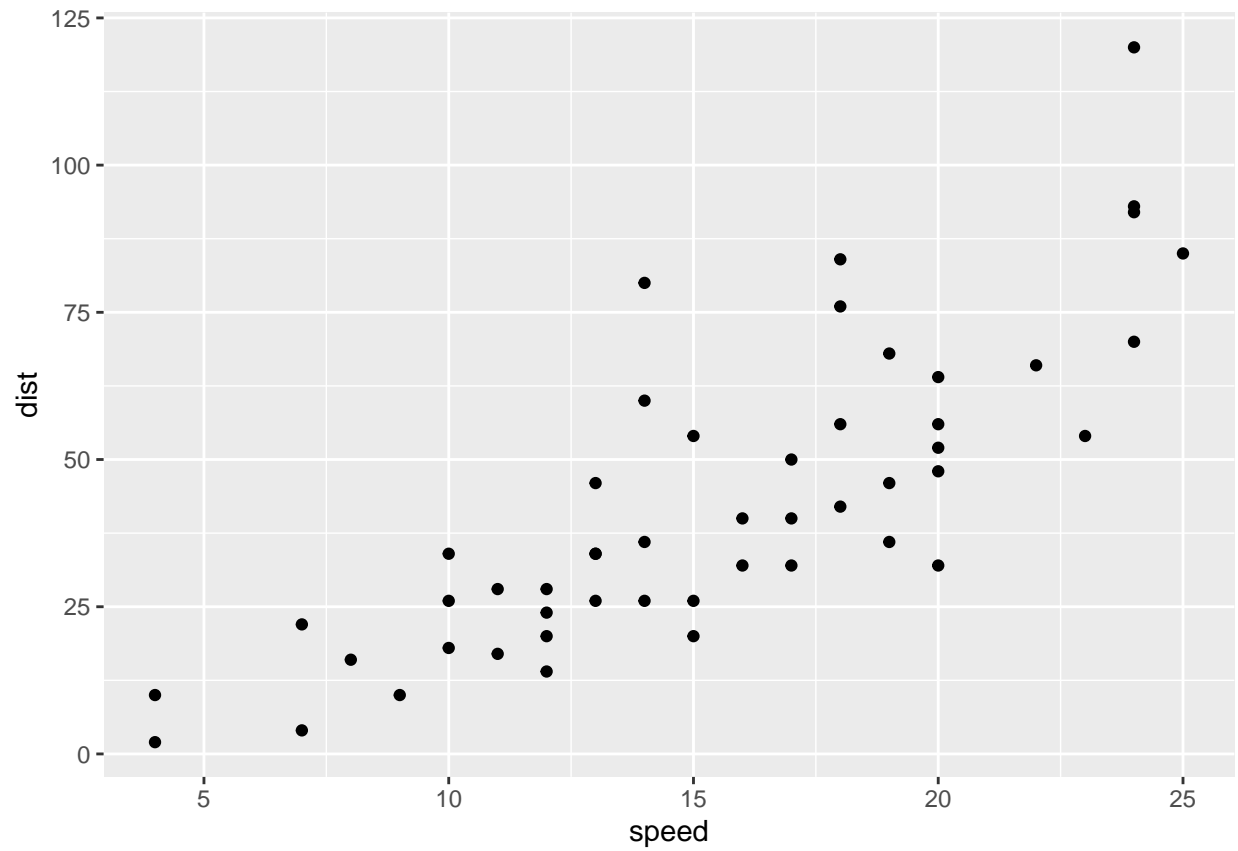


```
plot(cars)
```

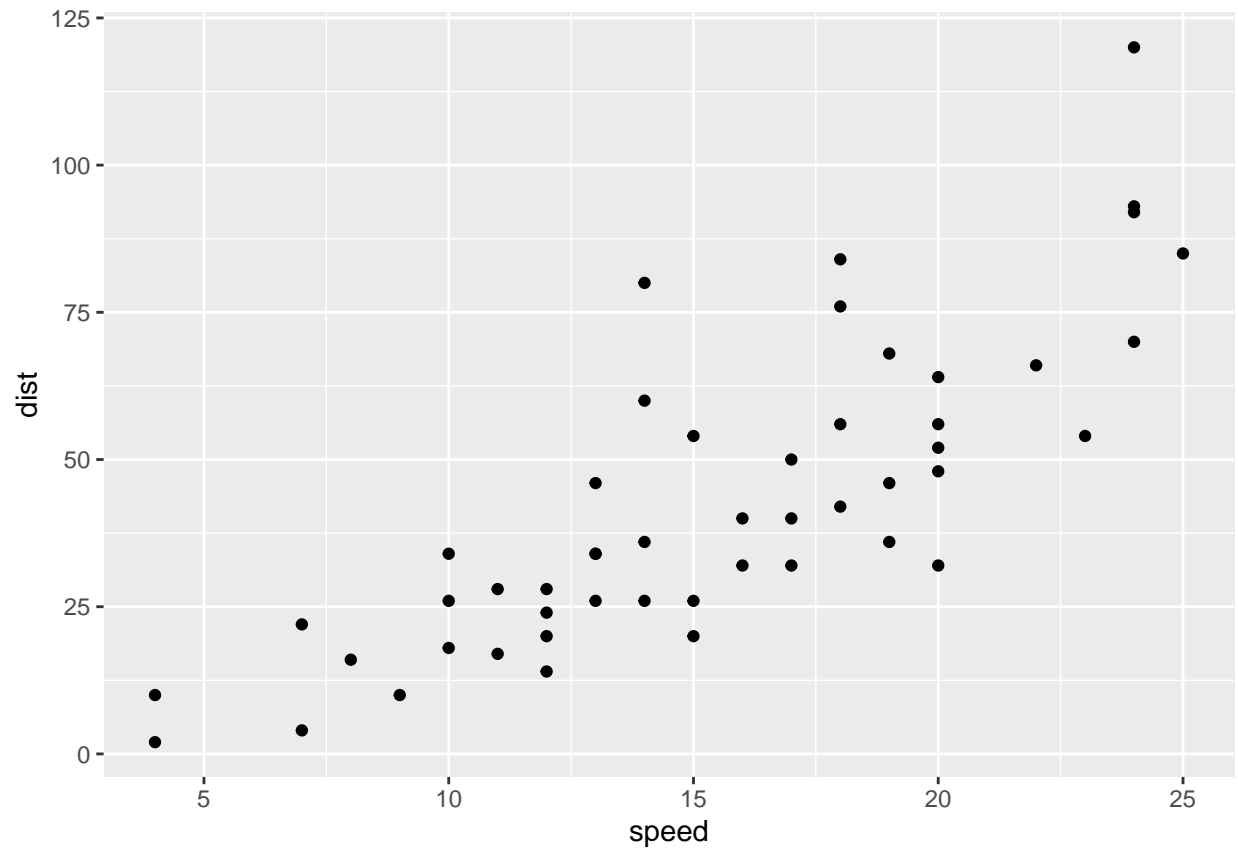


#Every ggplot has at least 3 layers: data + aes + geoms

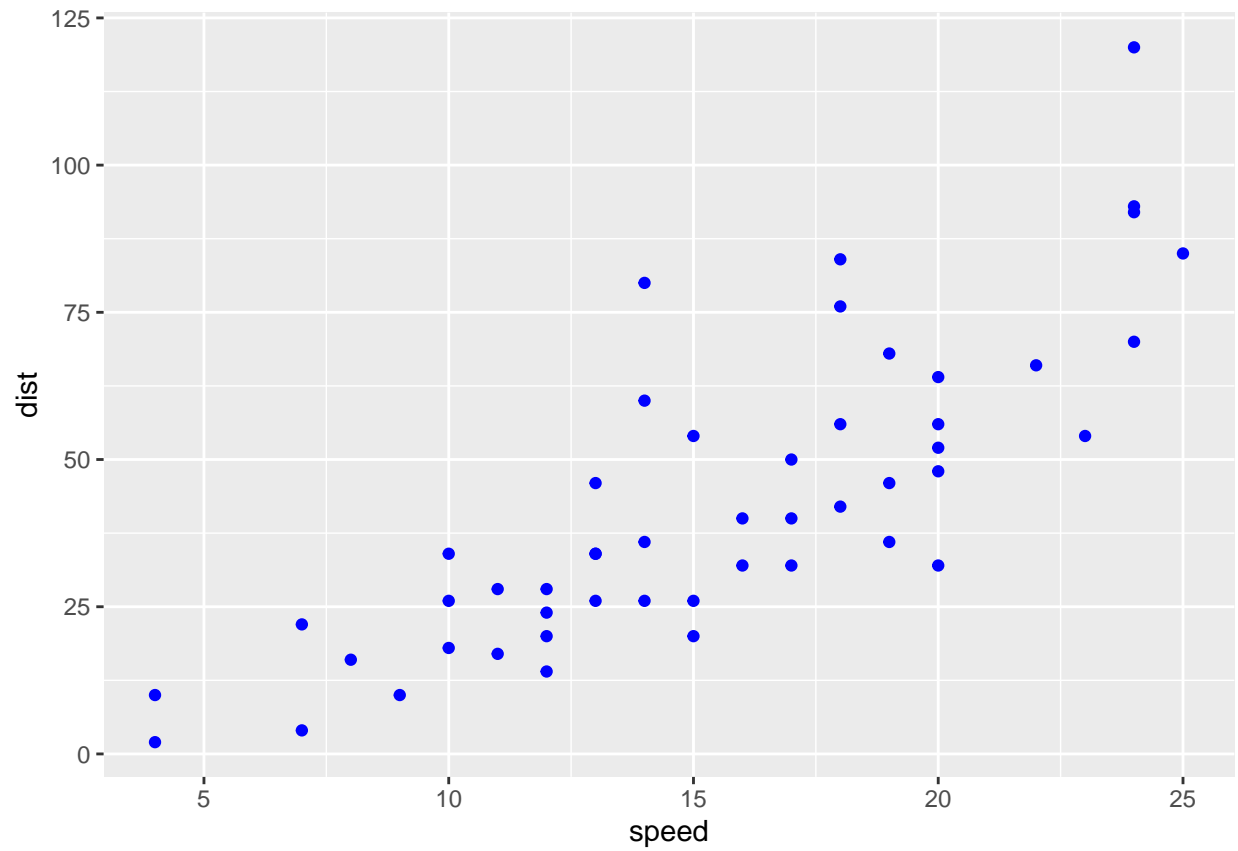
```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```



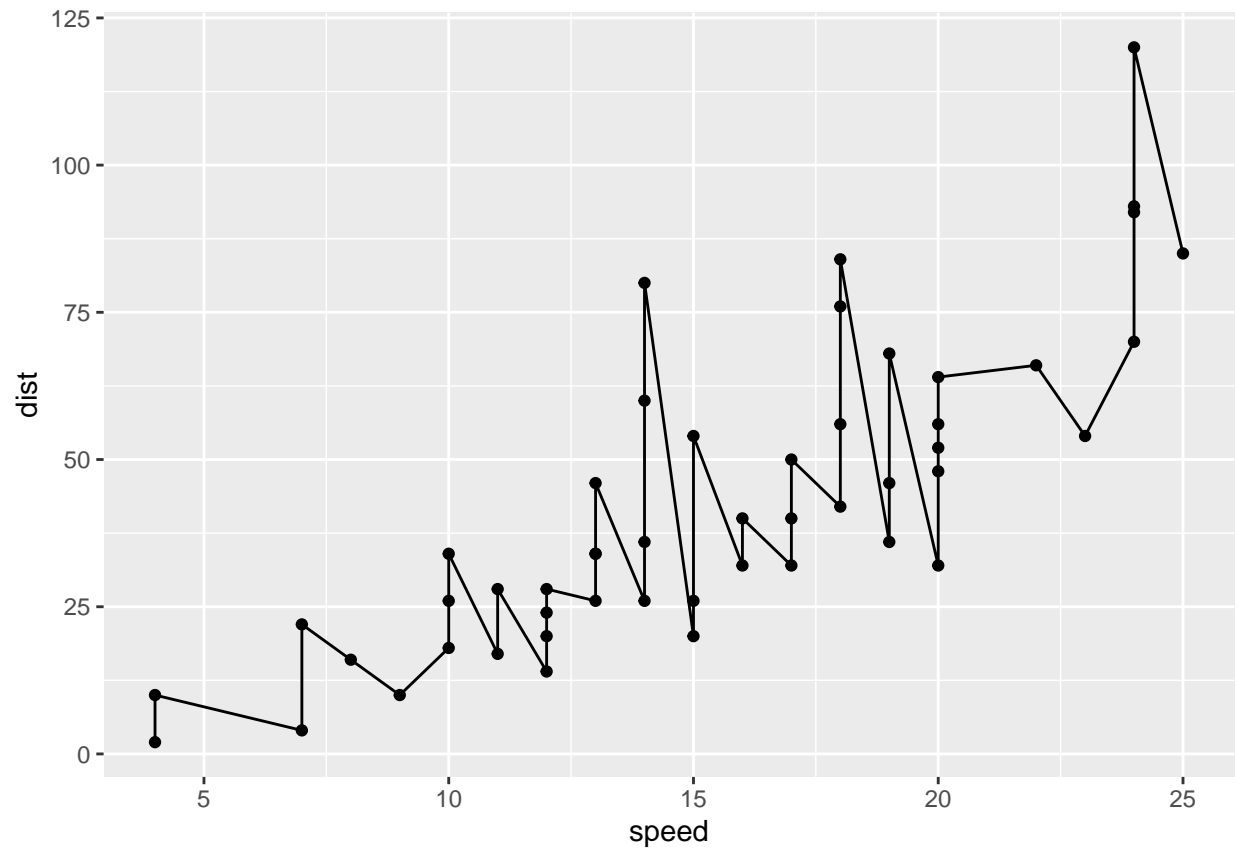
```
ggplot(cars, aes(speed, dist)) + geom_point()
```



```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point(col="blue")
```

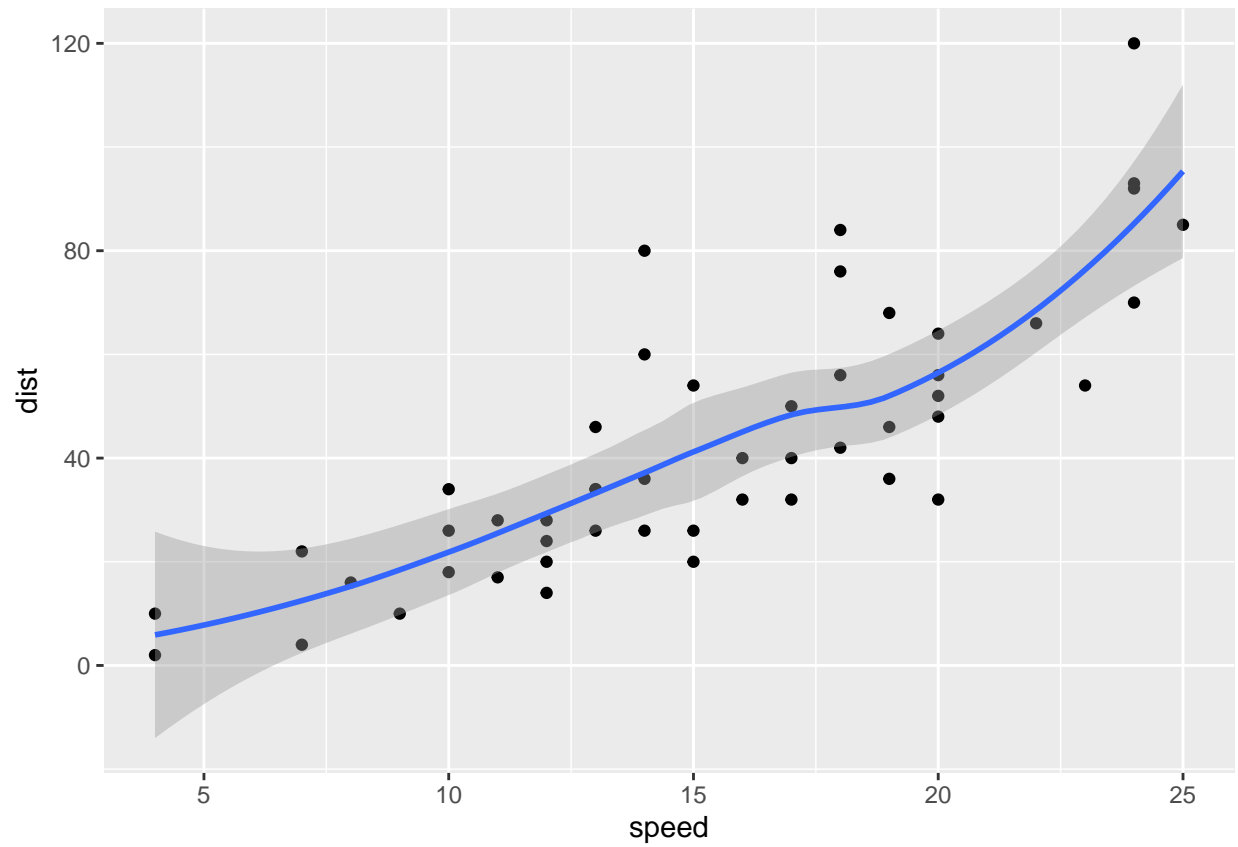


```
p <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()  
  
p + geom_line()
```



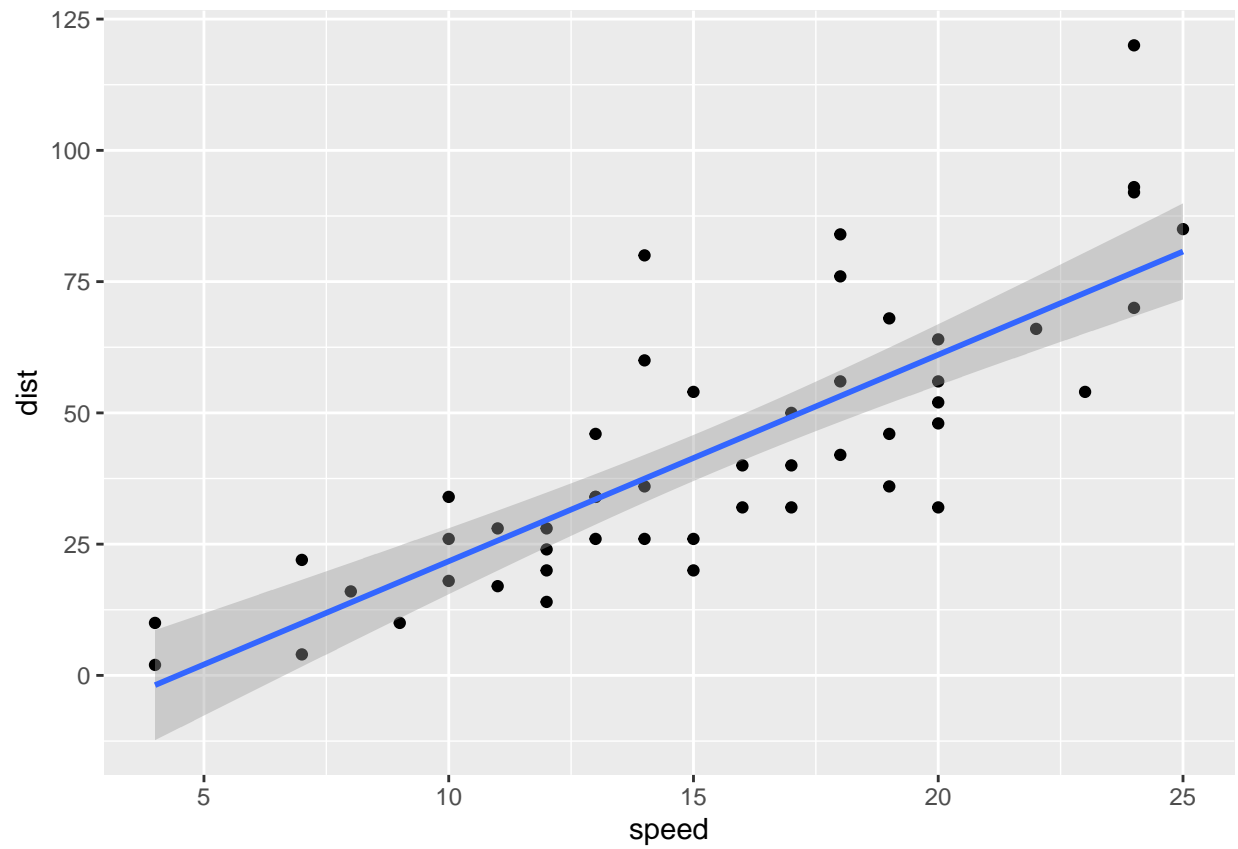
```
p + geom_smooth()
```

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

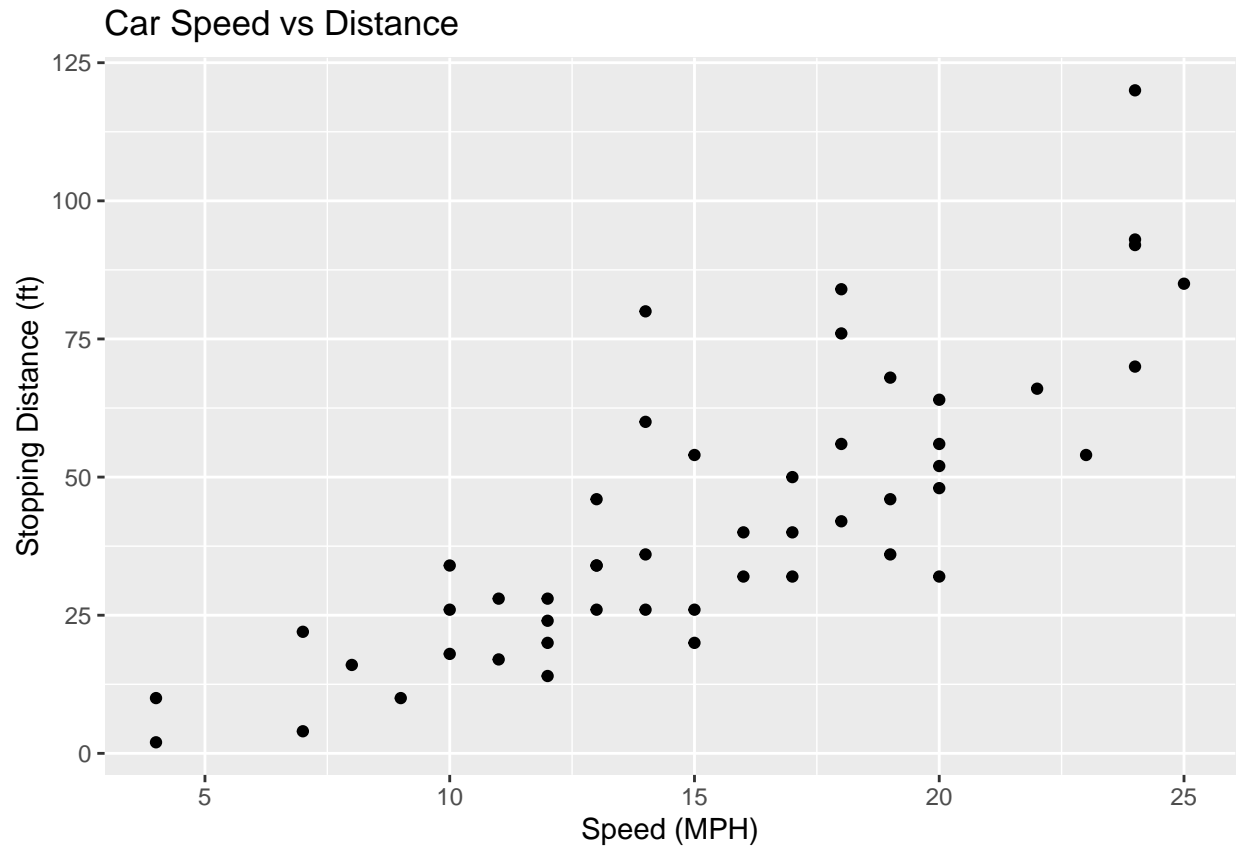


```
p + geom_smooth(method="lm")
```

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



```
p + labs(title = "Car Speed vs Distance") +  
  xlab("Speed (MPH)") +  
  ylab("Stopping Distance (ft)")
```

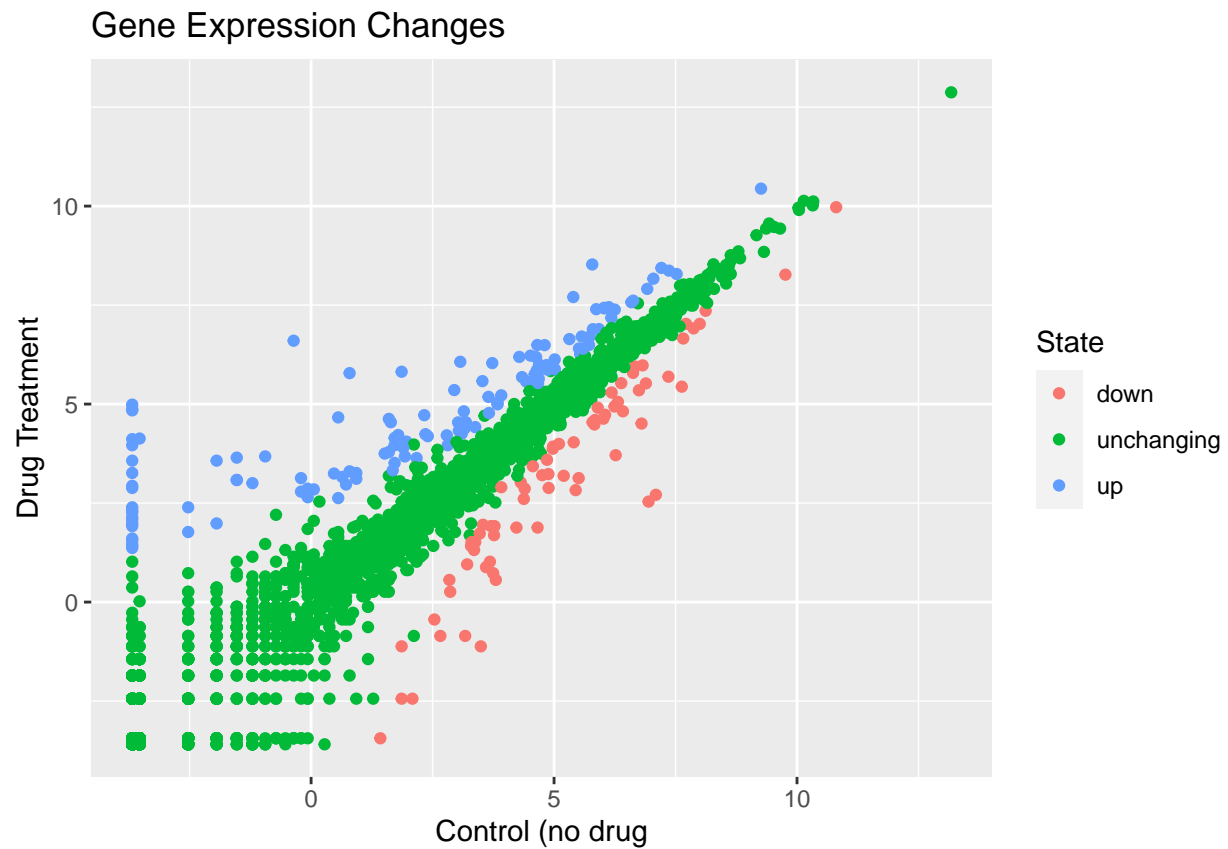



#RNA-Seq plot

```
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
```

```
ggplot(data = genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  labs(title = "Gene Expression Changes") +
  xlab("Control (no drug)") +
  ylab("Drug Treatment")
```



```
nrow(genes)
```

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

```
ncol(genes)
```

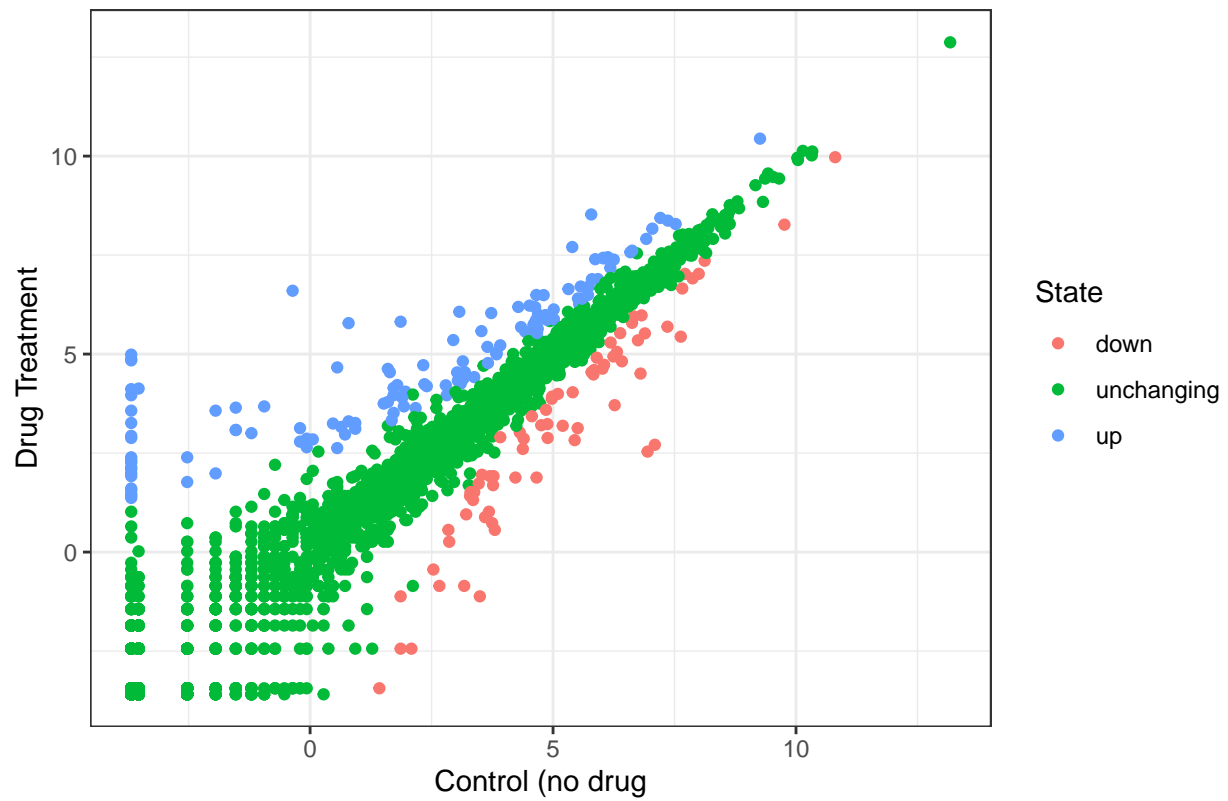
```
## [1] 4
```

```
colnames(genes)
```

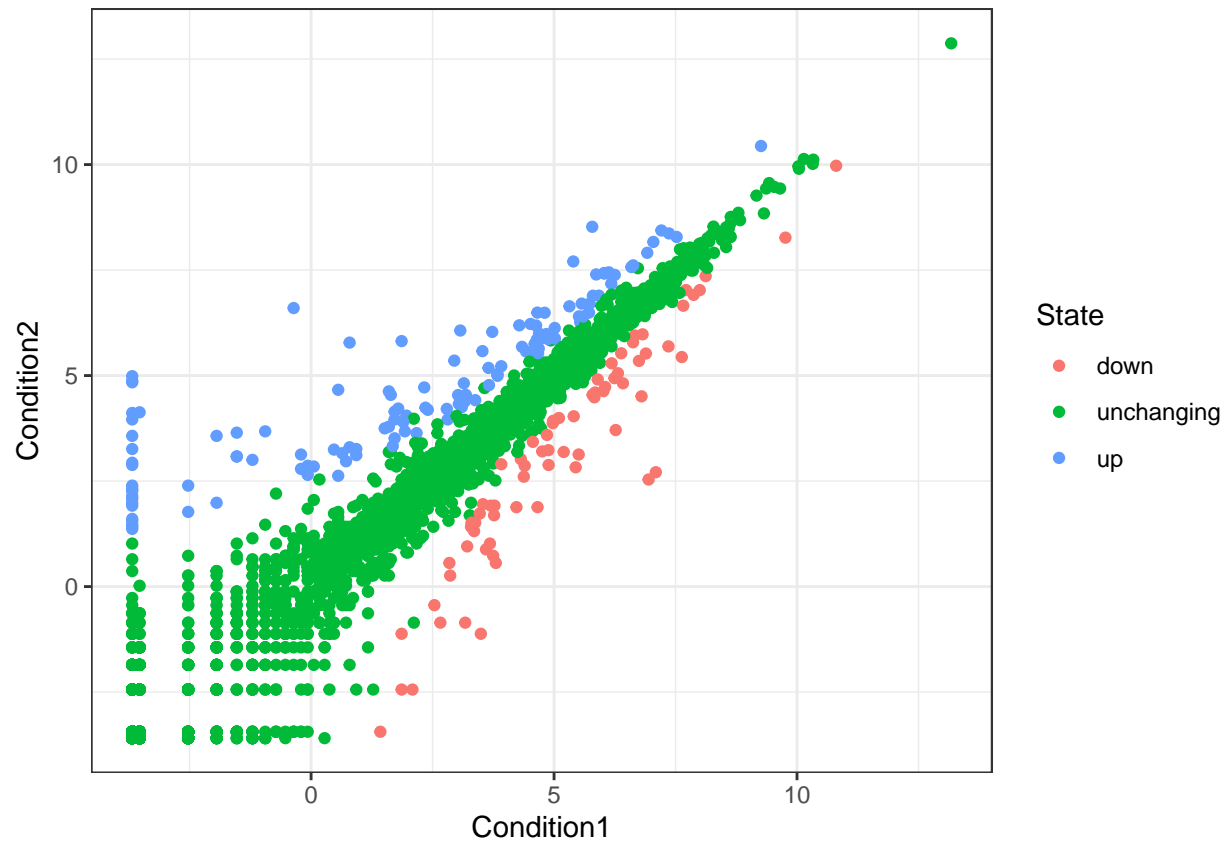
```
## [1] "Gene"          "Condition1" "Condition2" "State"
```

```
ggplot(data = genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  theme_bw() +
  labs(title = "Gene Expression Changes") +
  xlab("Control (no drug)") +
  ylab("Drug Treatment")
```

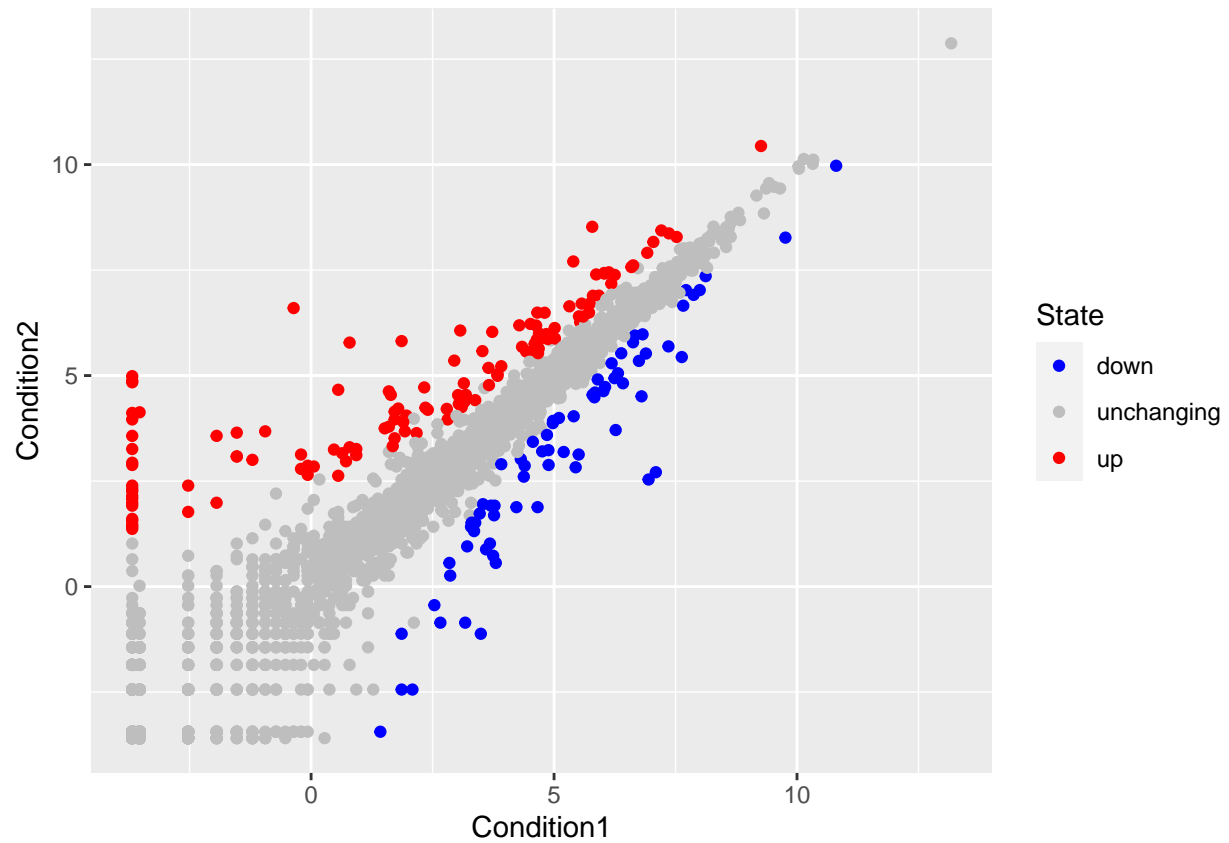
Gene Expression Changes



```
ggplot(data = genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point() +  
  theme_bw()
```



```
p <- ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()  
  
p + scale_colour_manual( values=c("blue", "gray", "red"))
```



```
ggplot(data = genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  scale_colour_manual( values=c("blue", "gray", "red")) +
  labs(title = "Gene Expression Changes") +
  xlab("Control (no drug)") +
  ylab("Drug Treatment")
```

Gene Expression Changes

