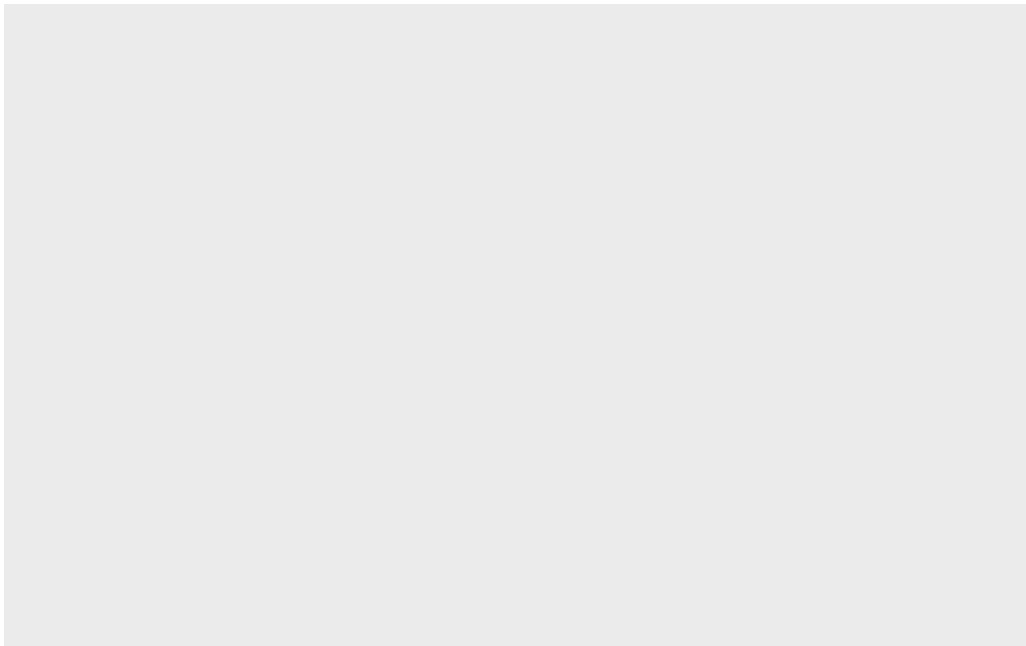


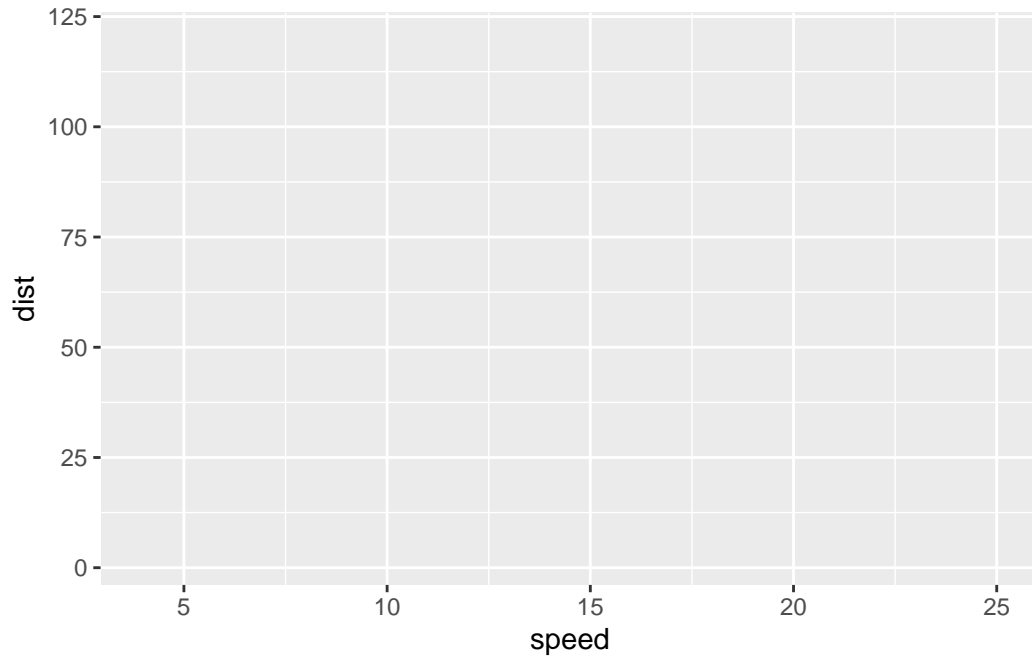
Lab Class 5

Adelaida Estrada-Cardenas

```
#install.packages("ggplot2")  
library(ggplot2)  
ggplot(cars)
```



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

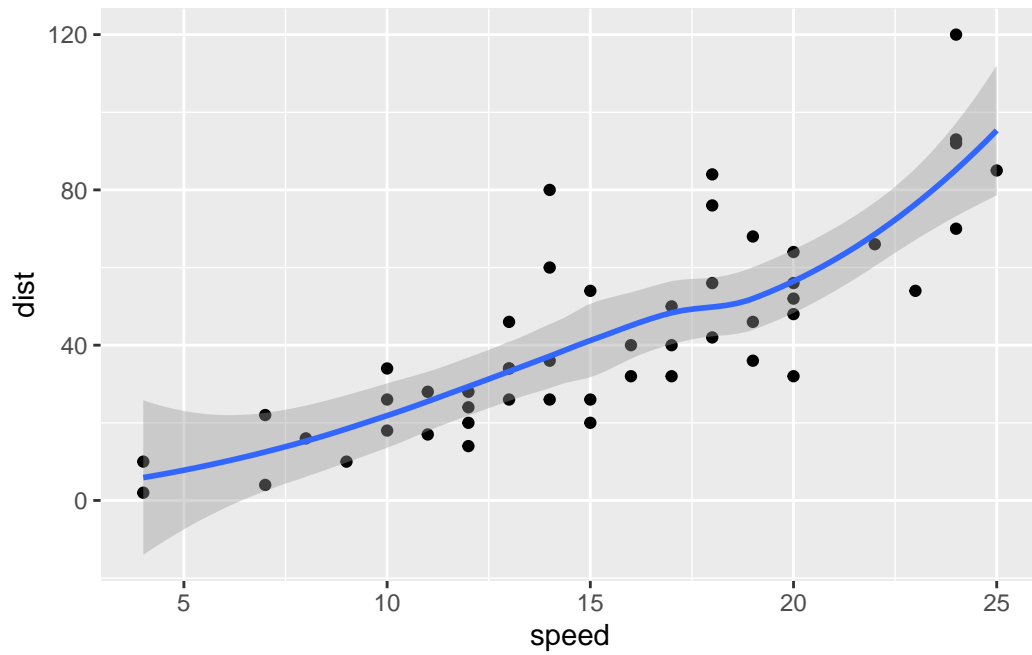


```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```



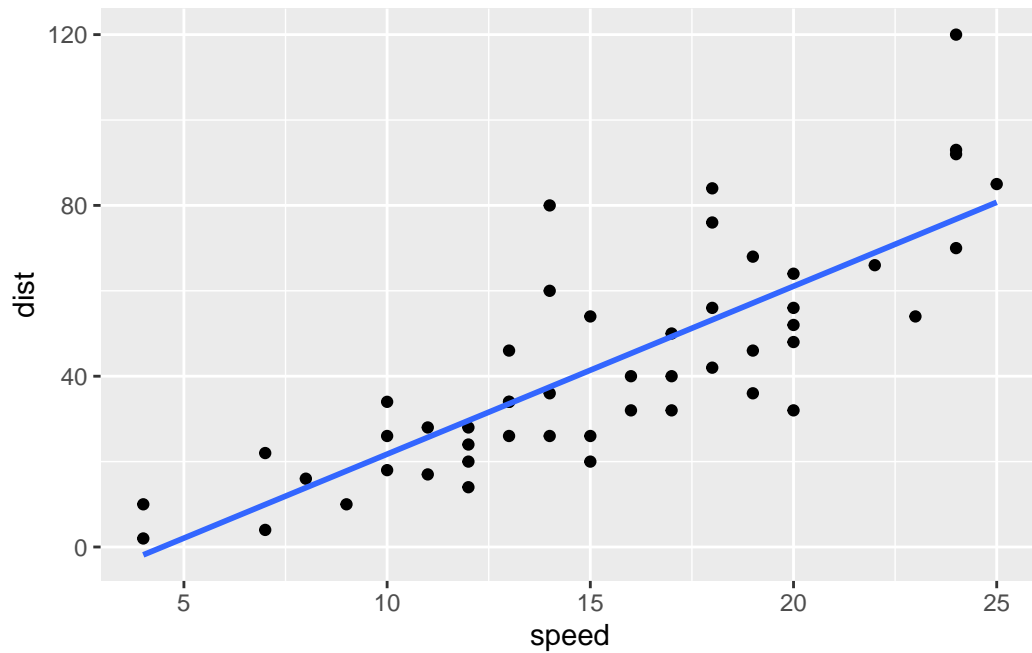
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth()
```

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



```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(method="lm", se=FALSE)
```

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

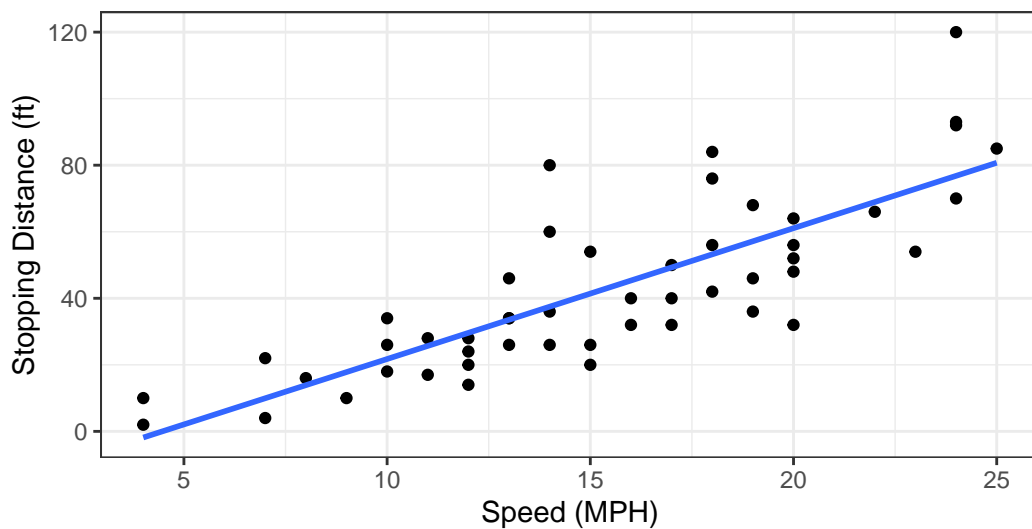


```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  labs(title="Speed and Stopping Distances of Cars",  
        x="Speed (MPH)",  
        y="Stopping Distance (ft)",  
        subtitle = "Your informative subtitle text here",  
        caption="Dataset: 'cars'") +  
  geom_smooth(method="lm", se=FALSE) +  
  theme_bw()
```

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

Speed and Stopping Distances of Cars

Your informative subtitle text here



Dataset: 'cars'

```
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

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

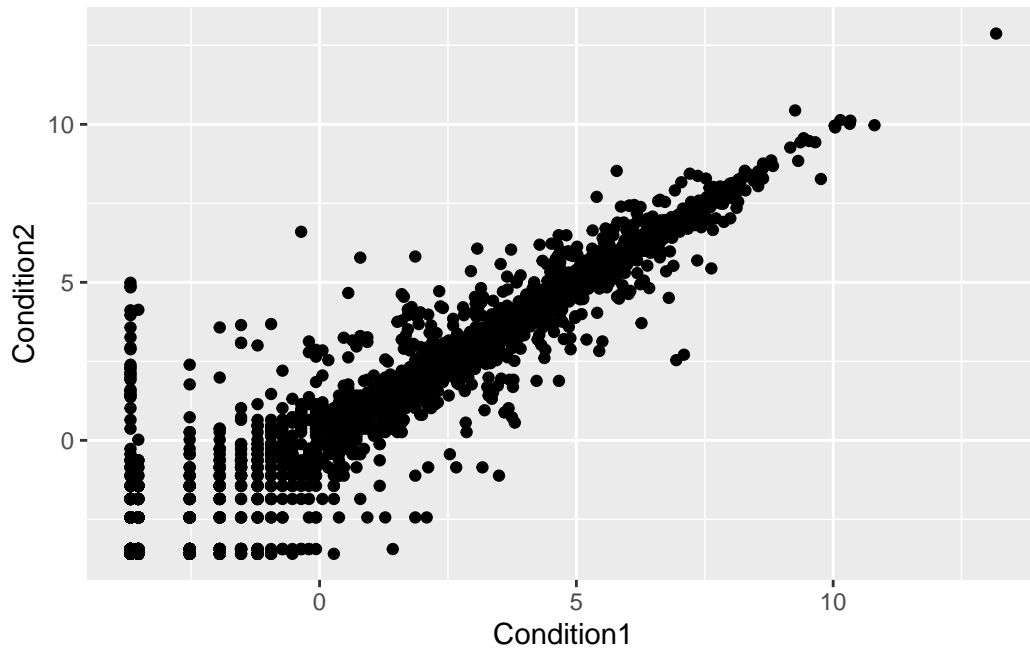
```
table(genes[,4])
```

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

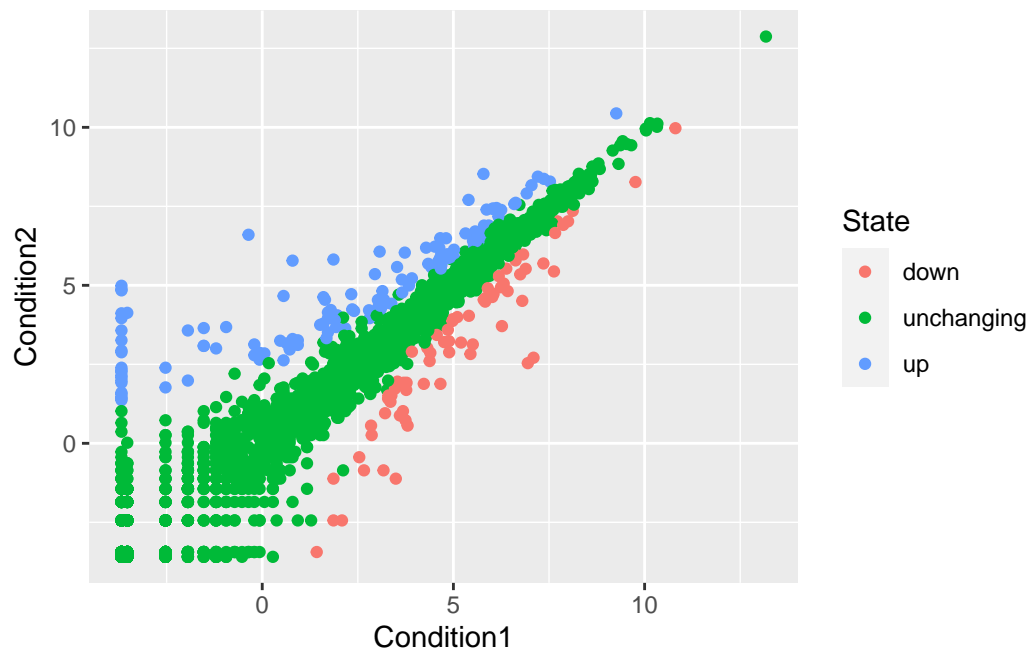
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

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

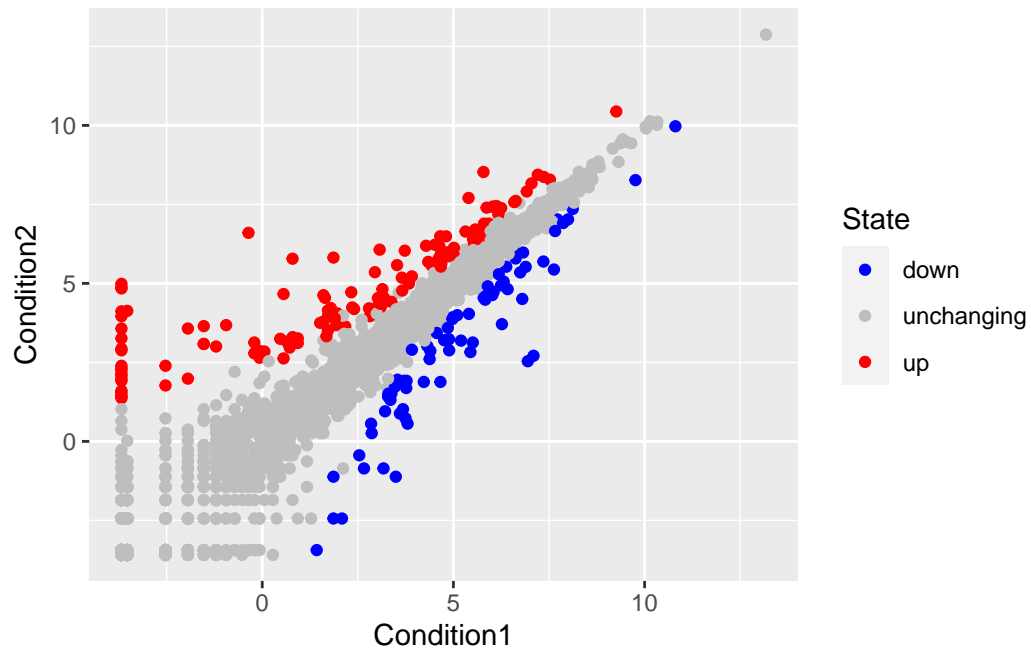
```
ggplot(genes) +  
  aes(x=Condition1, y=Condition2) +  
  geom_point()
```



```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p
```



```
p + scale_colour_manual( values=c("blue","gray","red") )
```

```
p + scale_colour_manual(values=c("blue","gray","red")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment

