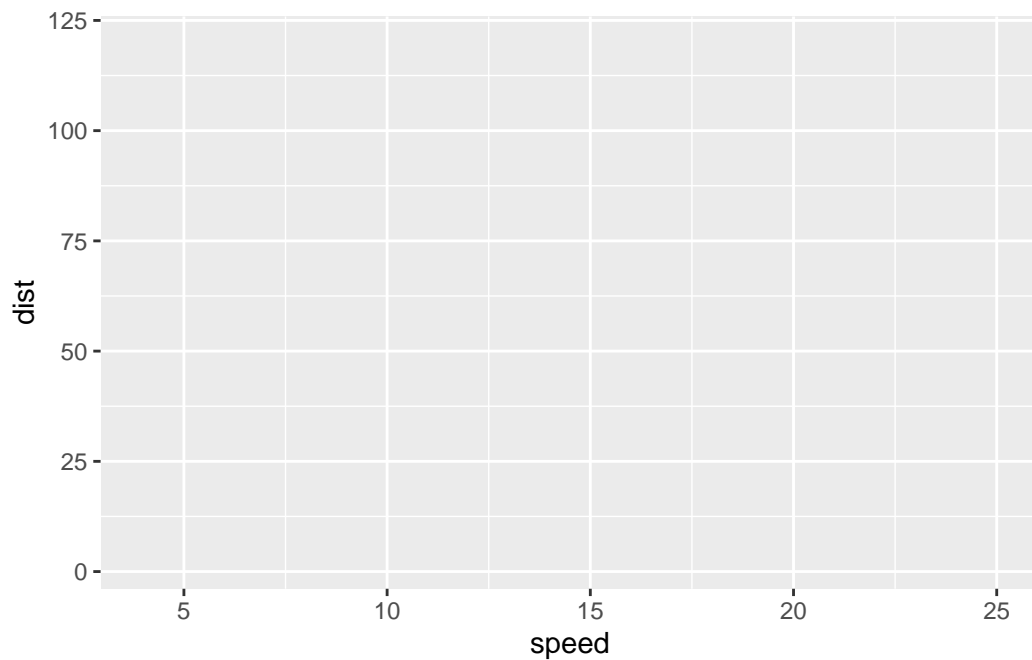


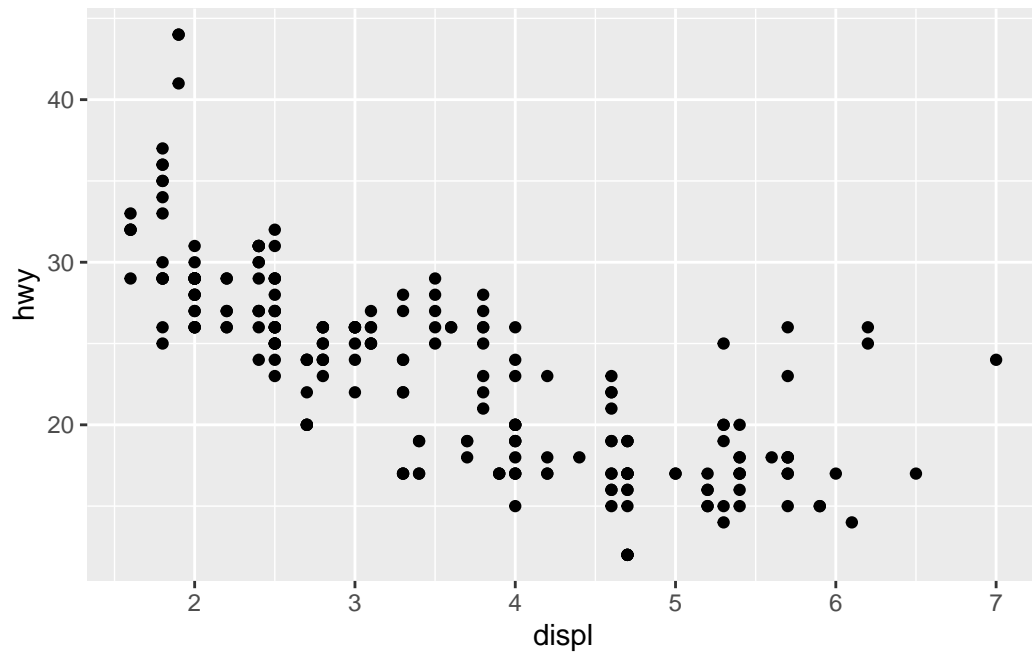
Class 05: Data Visualization with GGLOT

Tahmid Ahmed

```
#install.packages("ggplot2")  
library(ggplot2)  
ggplot(cars) + aes(x=speed, y=dist)
```

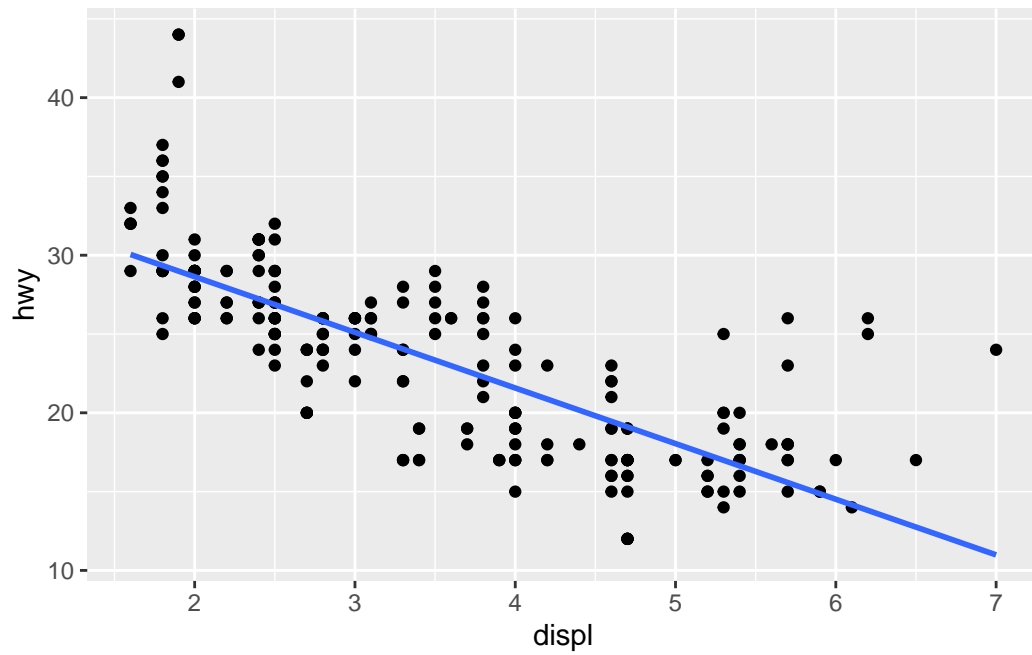


```
ggplot(mpg) + aes(x=displ, y=hwy) +geom_point()
```



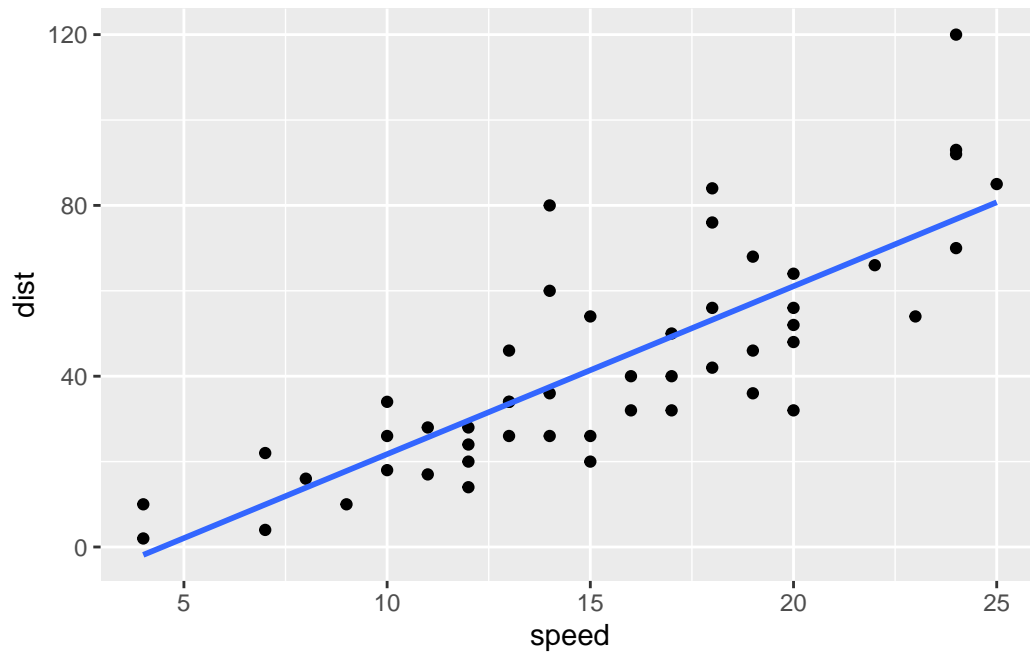
```
ggplot(mpg) + aes(x=displ, y=hwy) + geom_point() + geom_smooth(method= lm, se= FALSE)
```

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



```
ggplot(cars) + aes(x=displ, y=hwy) + geom_point() + geom_smooth(method=lm, se= FALSE)
```

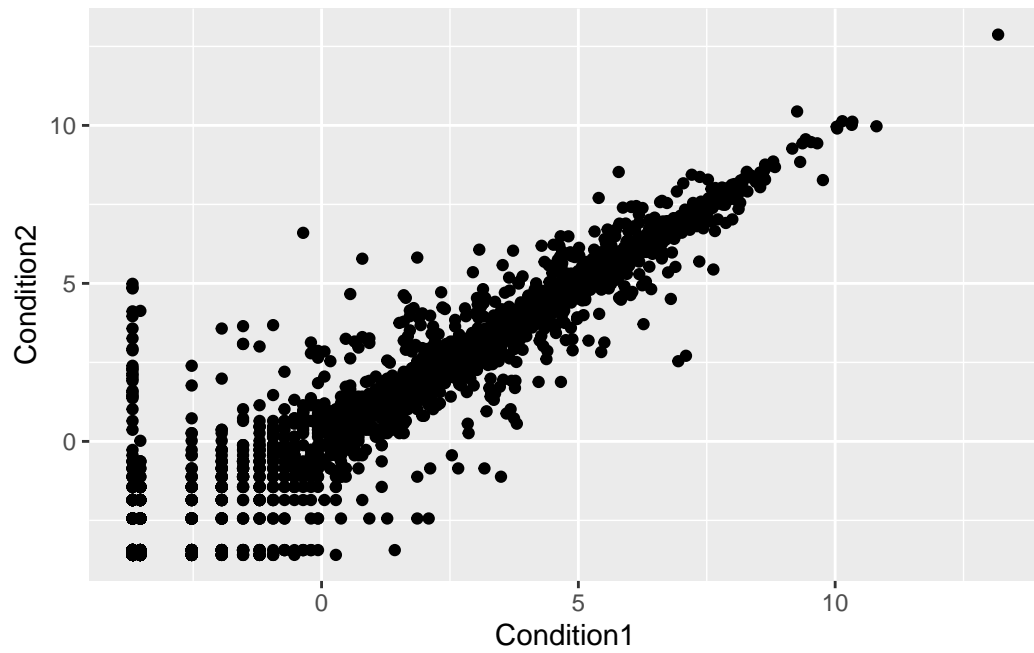
`geom_smooth()` using formula 'y ~ x'



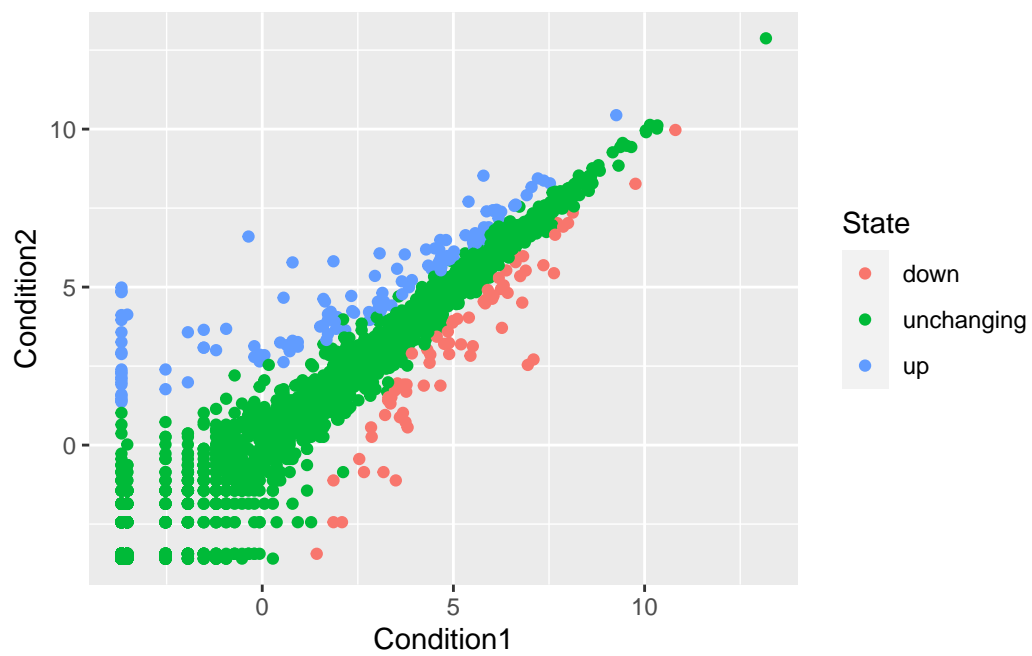
```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

	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

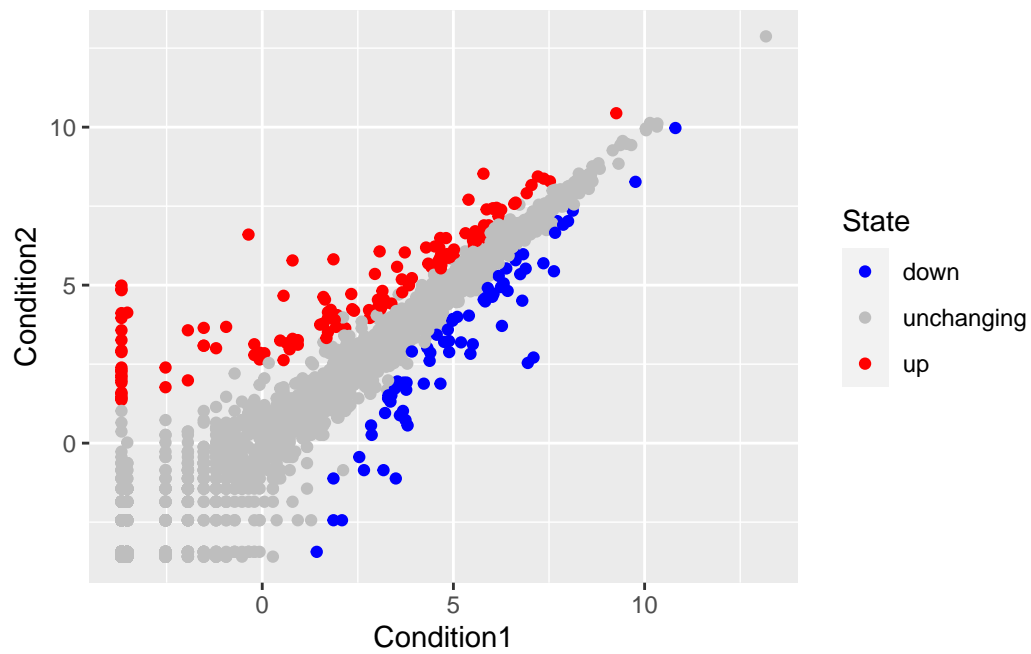
```
ggplot(genes) + aes(x=Condition1, y=Condition2) + geom_point()
```



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



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



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

Gene Expression Changes Upon Drug Treatment

