

Lab-5.R

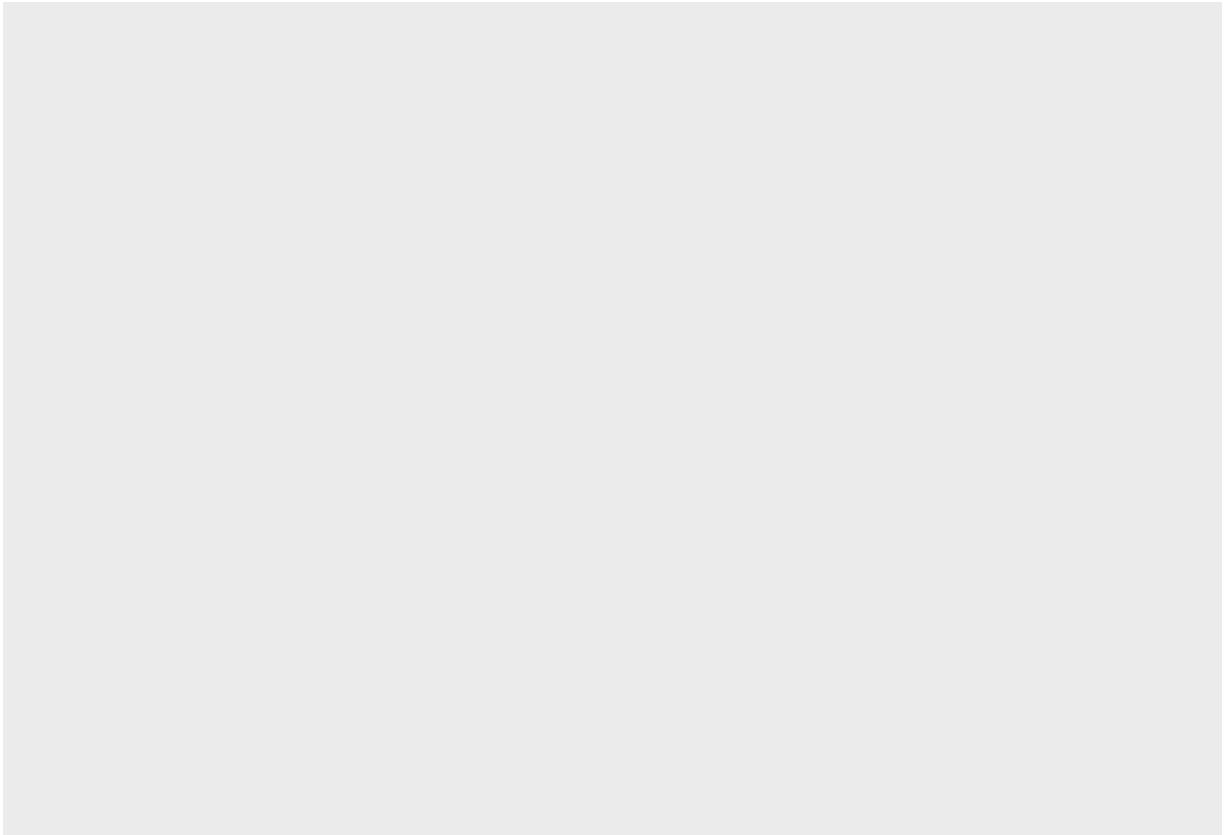
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2022-02-06

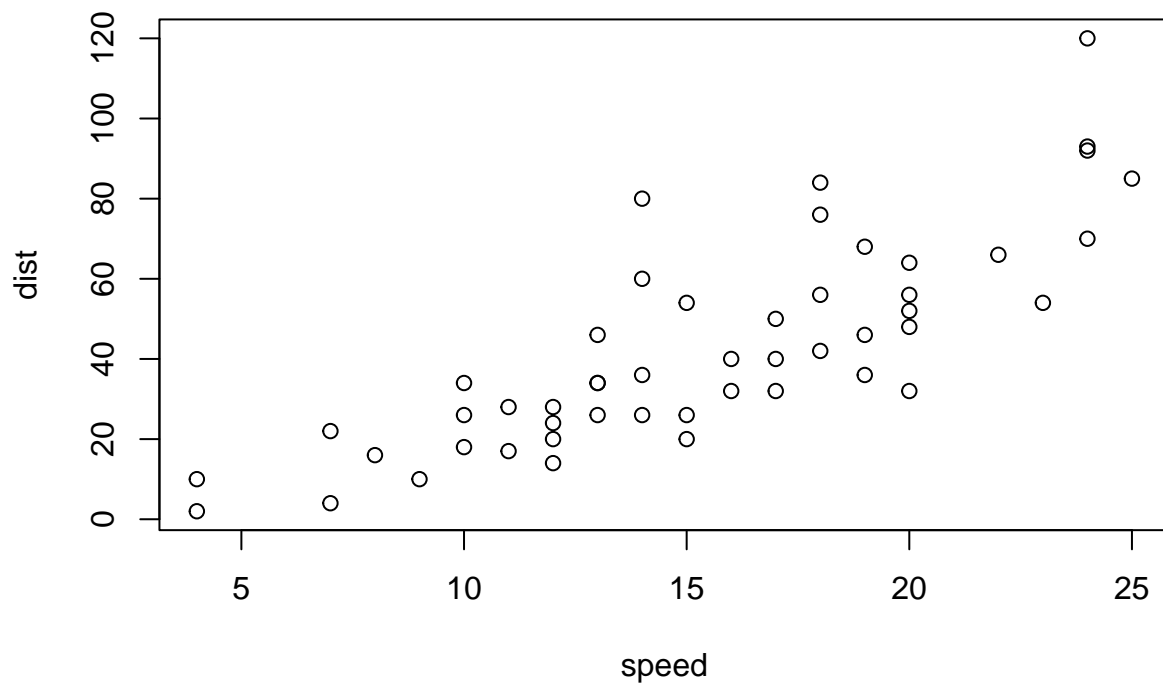
```
# Week 5 Data Visualization Lab
```

```
library(ggplot2)  
ggplot(cars)
```

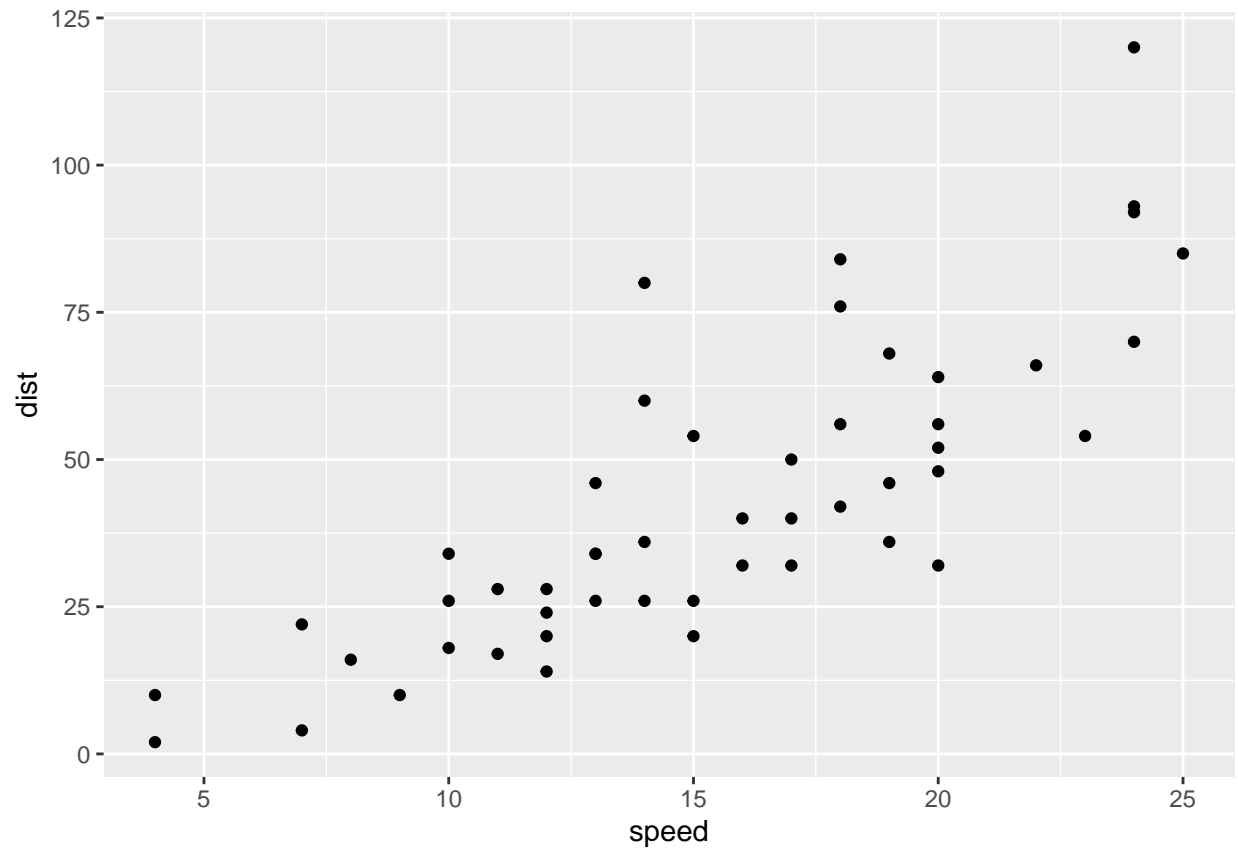
```
View(cars)  
ggplot(cars)
```



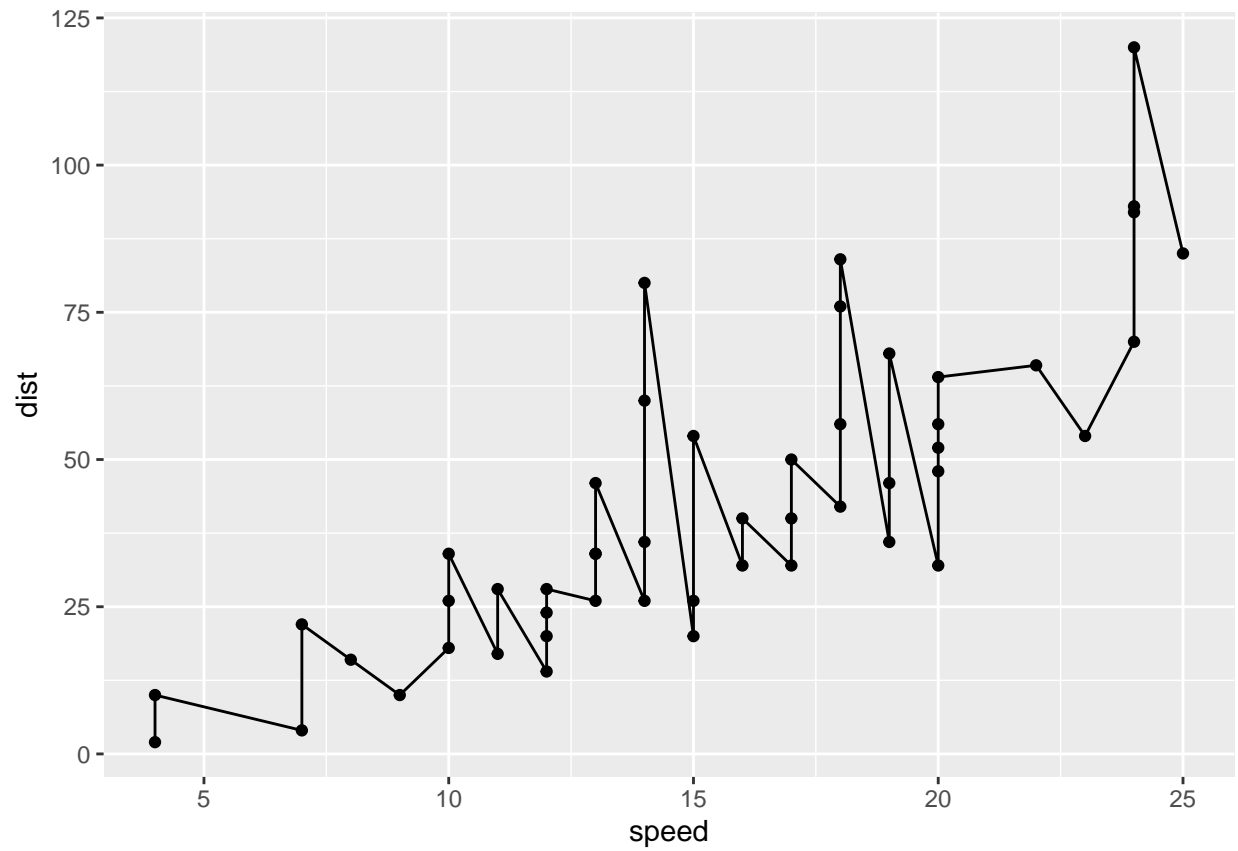
```
# A quick base R plot  
plot(cars)
```



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

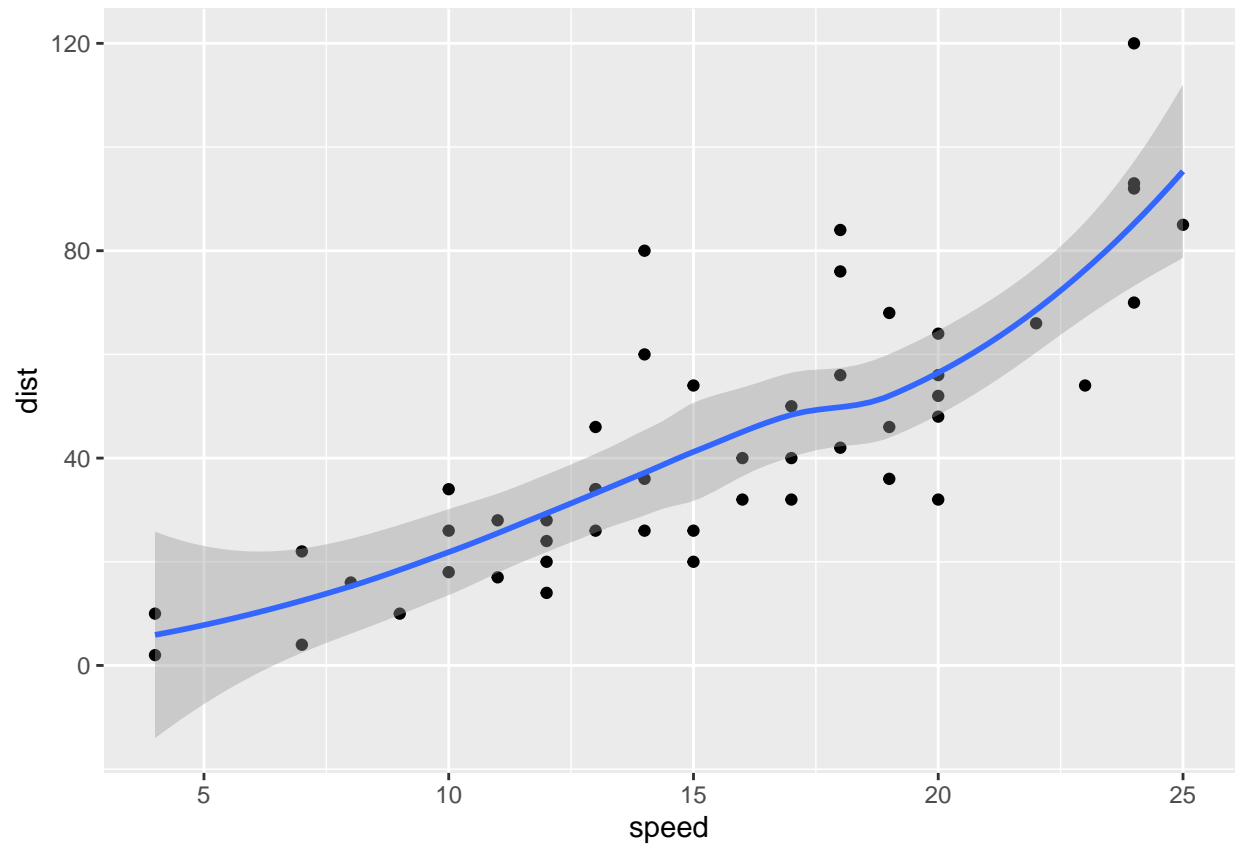


```
p <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()  
# Add a line geom with geom_line()  
p + geom_line()
```



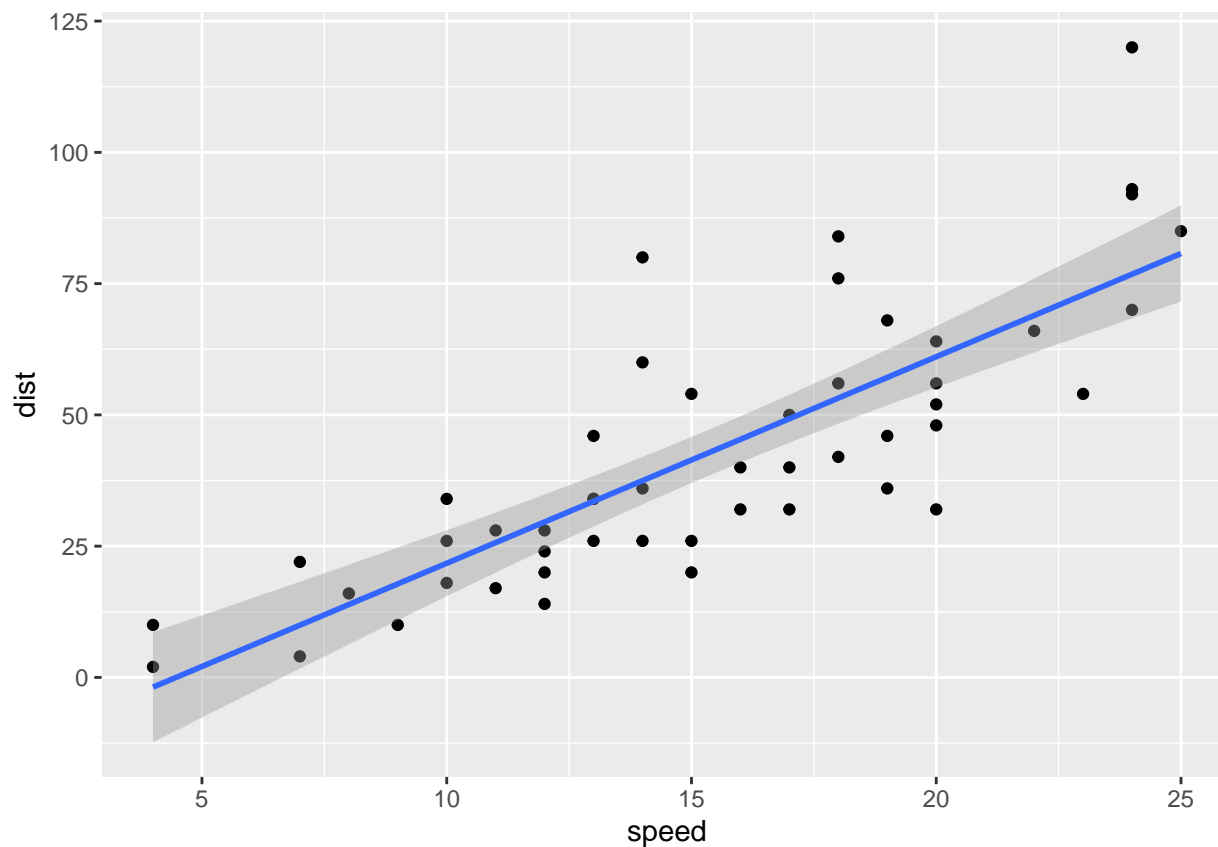
```
# Add a trend line close to the data  
p + geom_smooth()
```

```
## '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)
```

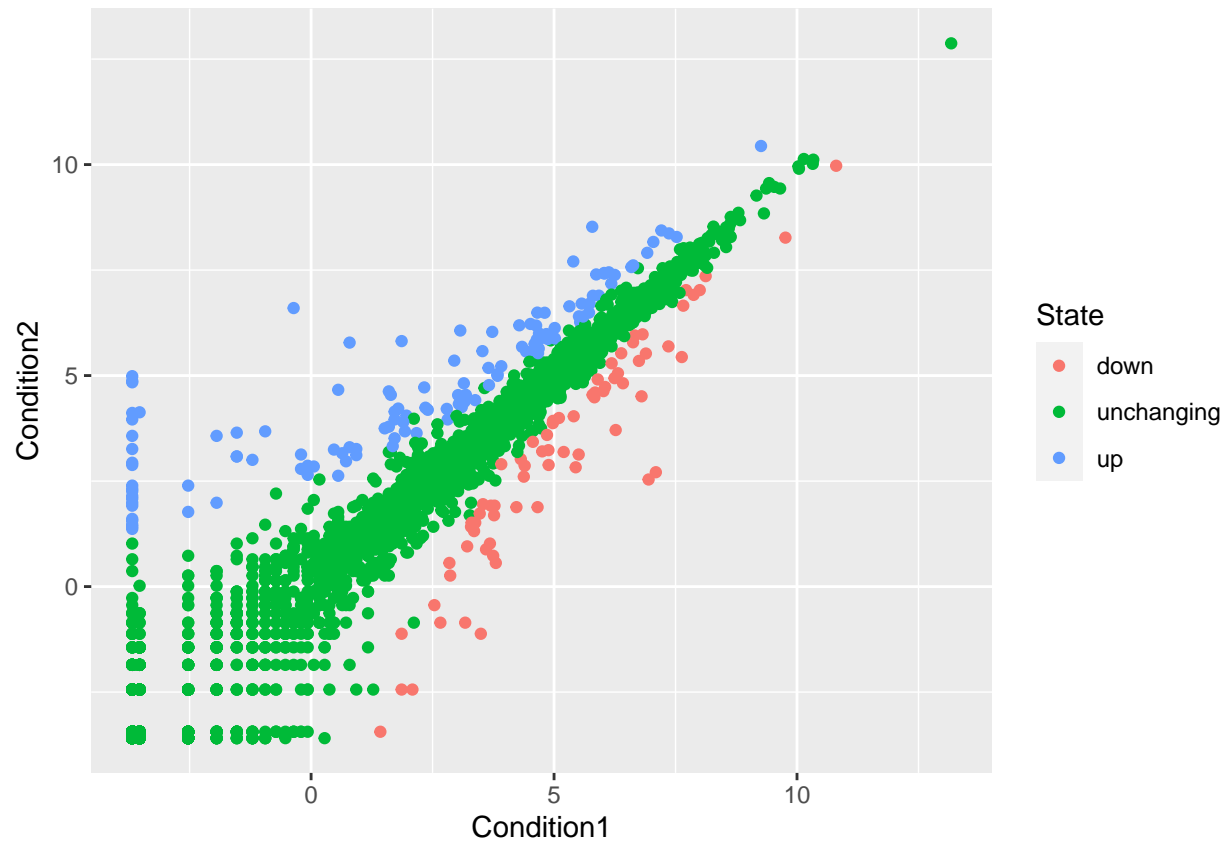
```
##      Gene Condition1 Condition2      State
## 1   A4GNT -3.6808610 -3.4401355  unchanging
## 2   AAAS  4.5479580  4.3864126  unchanging
## 3  AASDH  3.7190695  3.4787276  unchanging
## 4   AATF  5.0784720  5.0151916  unchanging
## 5   AATK  0.4711421  0.5598642  unchanging
## 6 AB015752.4 -3.6808610 -3.5921390  unchanging
```

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

```
##
##      down unchanging      up
##      1.39      96.17      2.44
```

```
#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

