

Class 5: Data visualization lab

Lilia Jimenez (PID:A16262599)

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Week 3 Data visualization lab

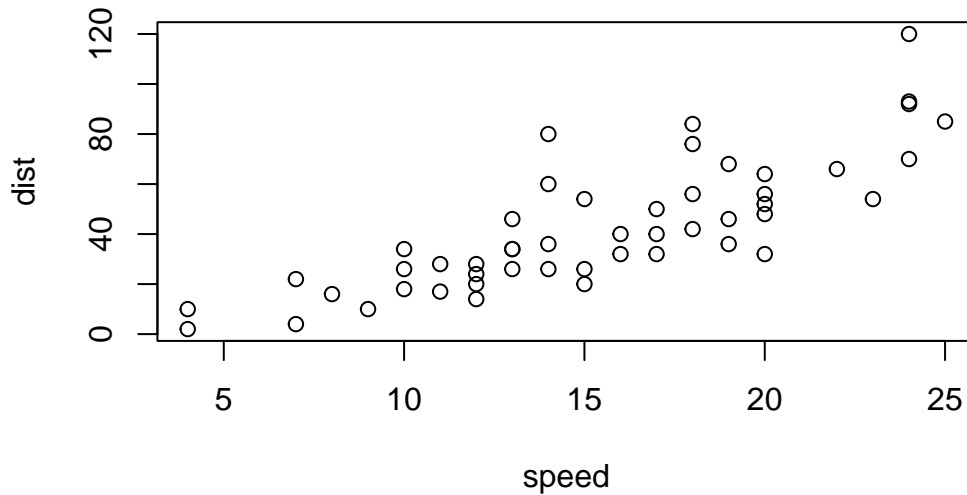
install the package ggplot2 `install.packages("ggplot2")`

Any time I want to use this package I need to load it

```
library(ggplot2)
```

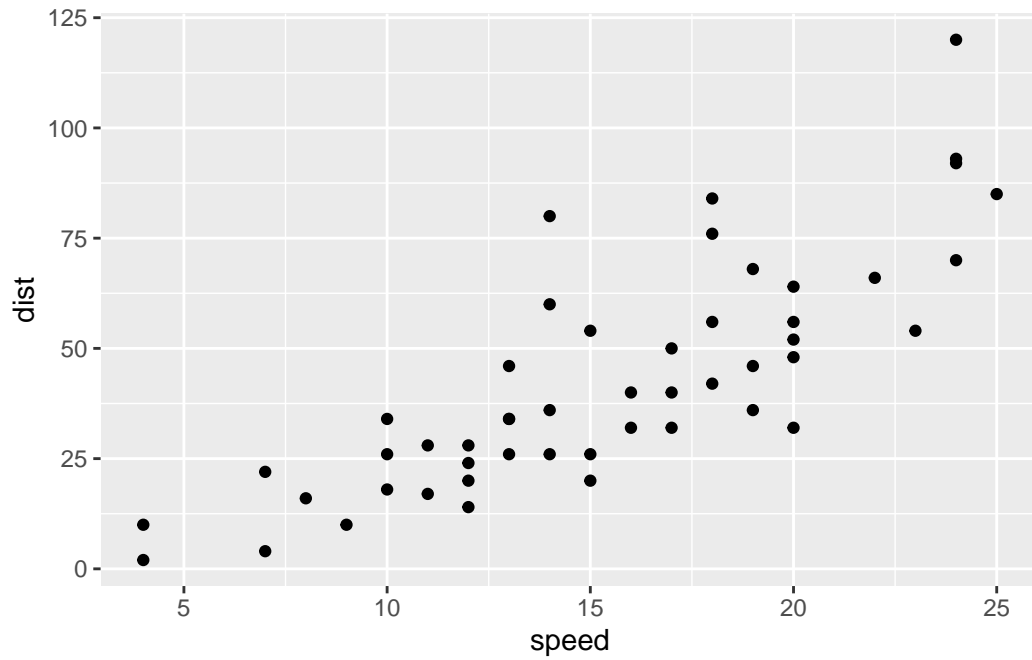
`#View(cars)` #A quick baseR plot -not ggplot2

```
plot(cars)
```



our first ggplot #we need data + aes + geoms

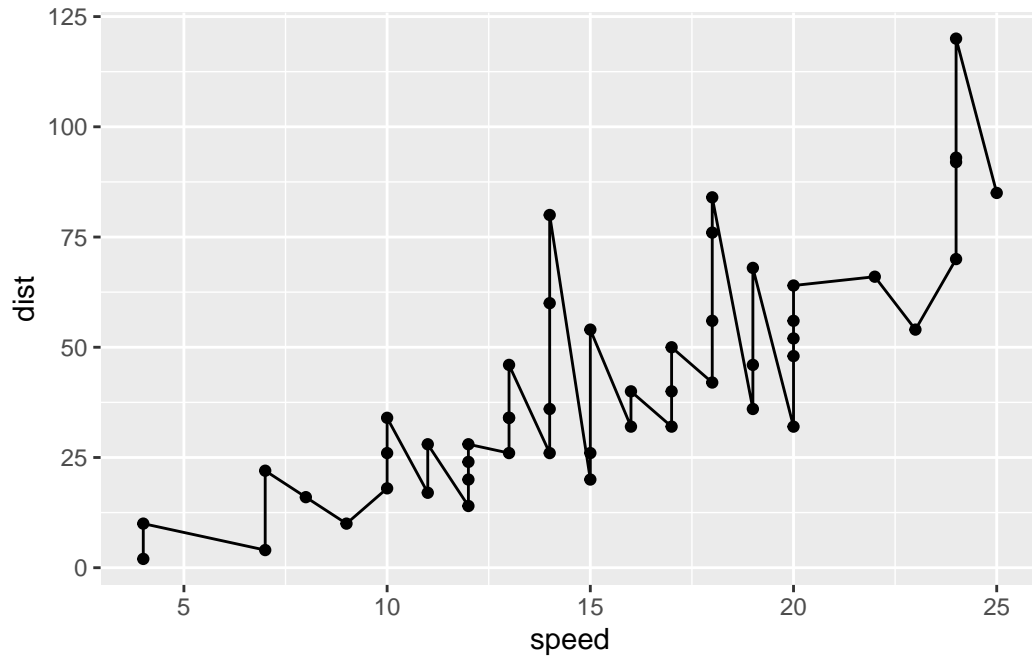
```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```



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

#add a line geom with geom_line

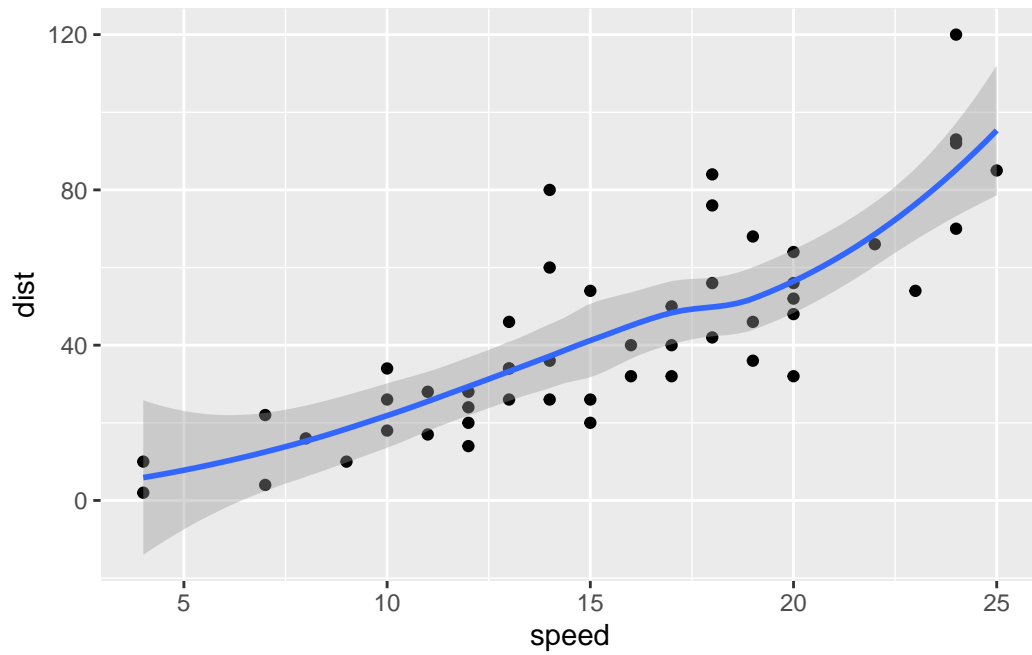
```
p + geom_line()
```



#add a trend line close to the data

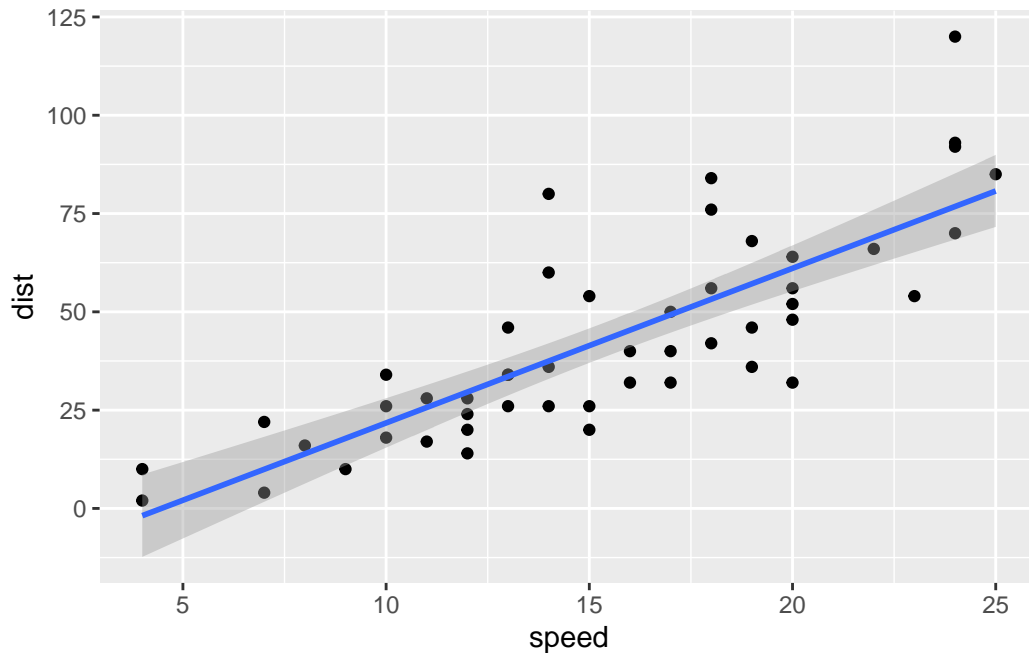
```
p + geom_smooth()
```

`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 |

first plot attempt

```
g<-ggplot(data=genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
#add some color
g + scale_colour_manual(values = c("blue","gray","red")) +
labs(title=("Gene expression changes"), x="Control(No drug)", y="Drug treatment") +
theme_bw()
```

Gene expression changes

