class05_data_visualization

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using GGPLOT

The ggplot2 package needs to be installed here as it does not come with R "out of the box". Used the `install.packages()` function to do it.

To use ggplot, you need to load it before using any of the functions it comes with. Do this with the `library()` function.

```r
head(cars)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

```r
library(ggplot2)
ggplot(cars) +
  aes(x=speed,y=dist) +
  geom_point() +
  labs(title="Distance to Stop at Differenrt Speeds of Cars",
       x="Speed (MPH)",
       y="Distance (Ft)",
       subtitle="This is a plot with a line of best fit",
       caption="Dataset: Cars")+
  geom_smooth(method = "lm",se=FALSE)
```

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

Distance to Stop at Differenrt Speeds of Cars
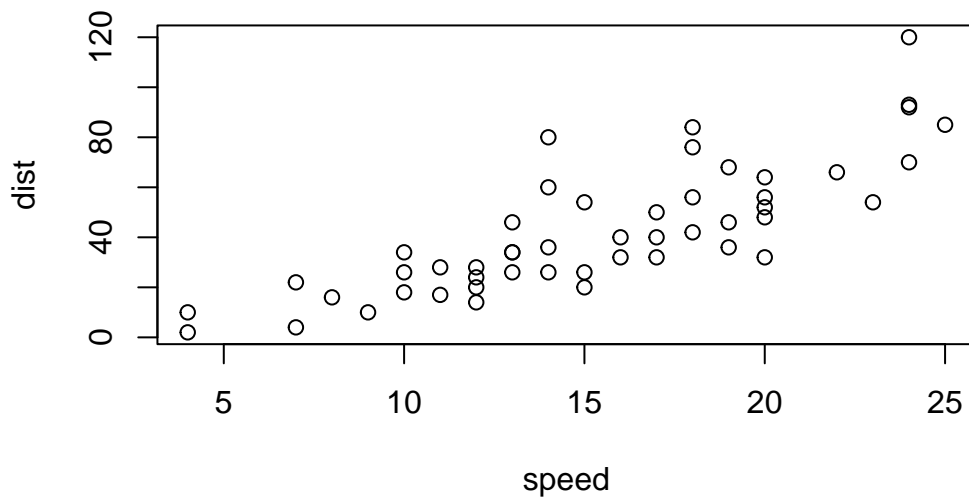This is a plot with a line of best fit
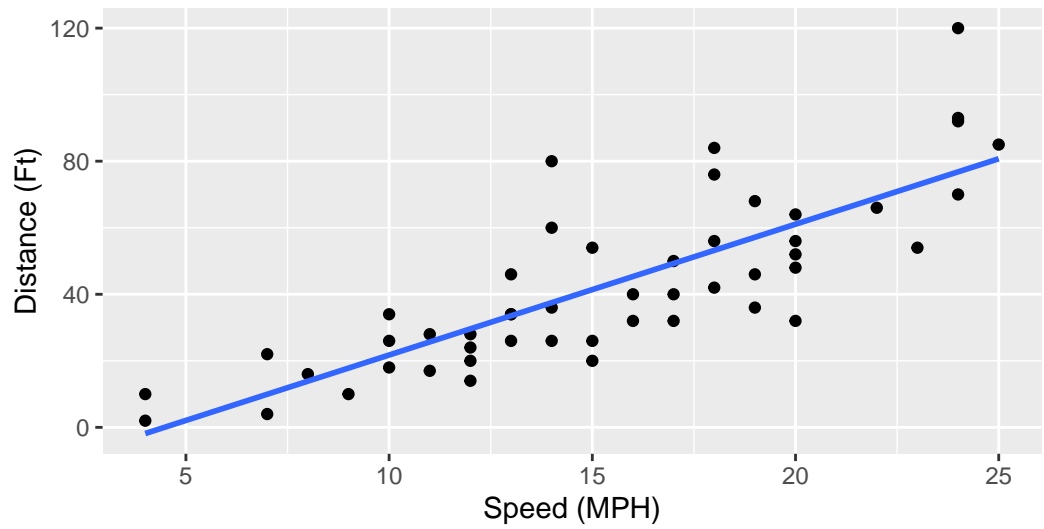
Dataset: Cars

All ggplot figures have at least 3 things. 1- data 2- aesthetic mapping 3- geoms

There are lots of graphing systems in R, including one that comes with it.

```
plot(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$State)
```

```
      down unchanging         up
        72       4997        127
```

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

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

```
library(ggplot2)
p <- ggplot(genes)+
  aes(x=Condition1,y=Condition2, col=State) +
  geom_point()+
  scale_colour_manual( values=c("orange","green","white") )+
   labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug)",
       y="Drug Treatment")
p
```

Gene Expression Changes Upon Drug Treatment