

Class 5: Data Visualization with GGLOT

Alma

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Our first plot 1

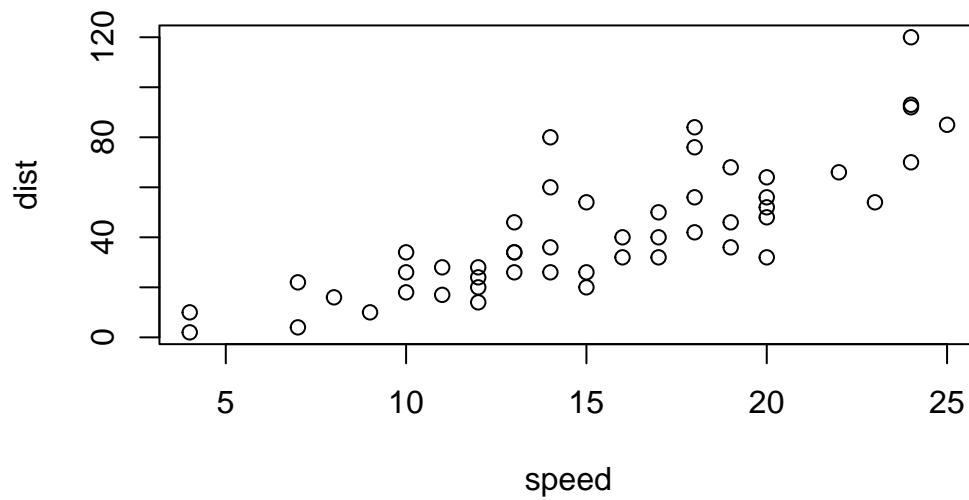
Our first plot

R has base graphics

```
head (cars)
```

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

```
plot (cars)
```



How would I plot this with `ggplot2`? No, need to install using `install.packages()` function. Don't install in the code chunk since you will render the function every time. You can add a `#`

Before I can use this package I need to load with a `library()` call.

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

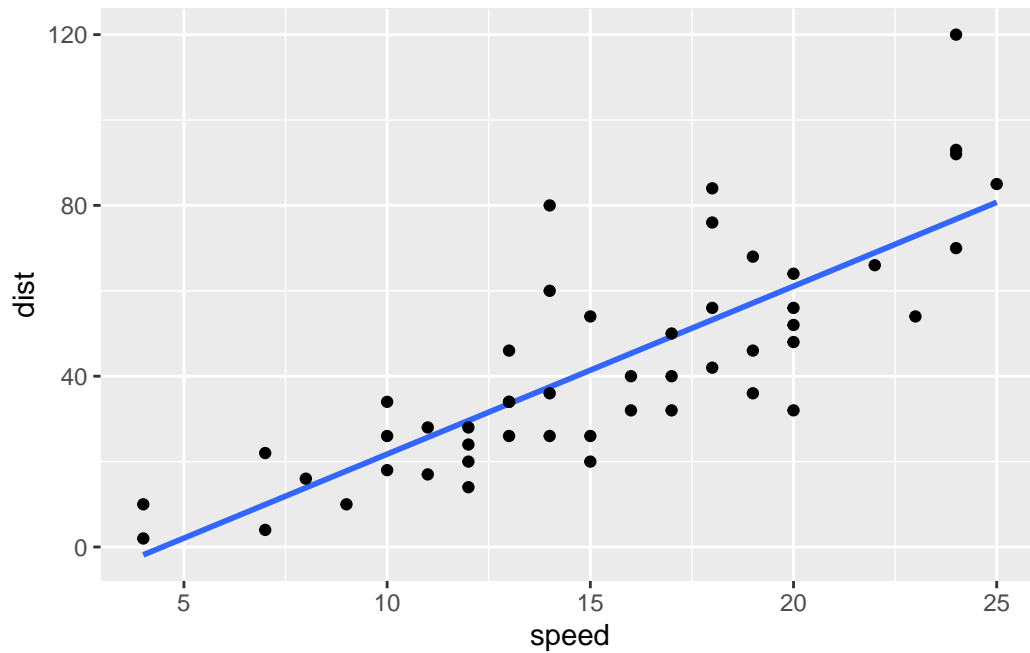


Every ggplot needs at least 3 layers:

- Data** (i.e. the data frame we have)
- Aesthetic** (the aesthetic mapping of our data to what we want to plot)
- Geoms**(how we want to plot this stuff)

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

`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

Q1. how many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

There are 5196 genes in this data set.

```
colnames(genes)
```

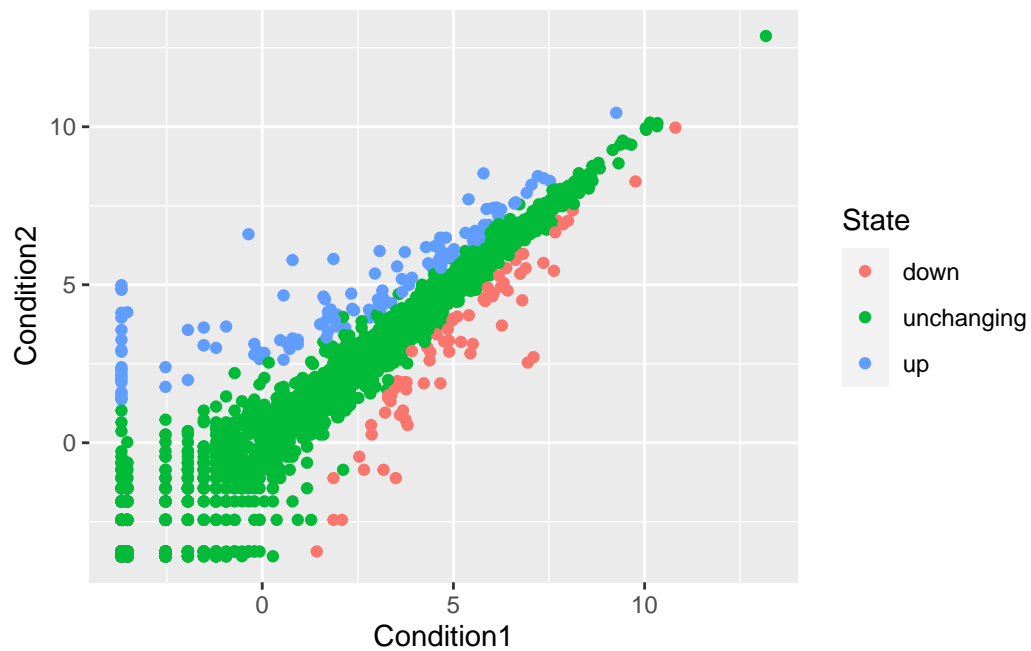
```
[1] "Gene"          "Condition1" "Condition2" "State"
```

```
table(genes$State)
```

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

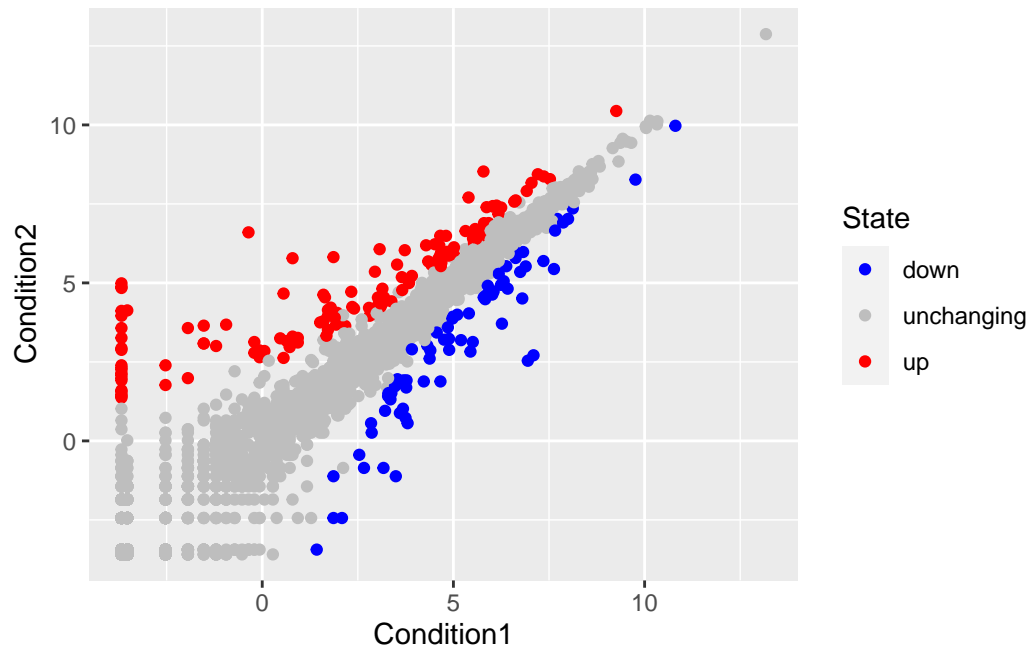
```
p <- ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()
```

p



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

```
c
```



Alpha has to be in the `geom_point` to make the points transparent

To change the axis labels from Condition1 to Control, you have to use `lab(x = "Control")`

```
c + labs(x = "Control (No Drug)", y = "Drug Treatment")
```

