

Class 5 Data Visualization with ggplot2

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Using GGPLOT

The ggplot2 package needs to be installed as it does not come with R “out of the box”.

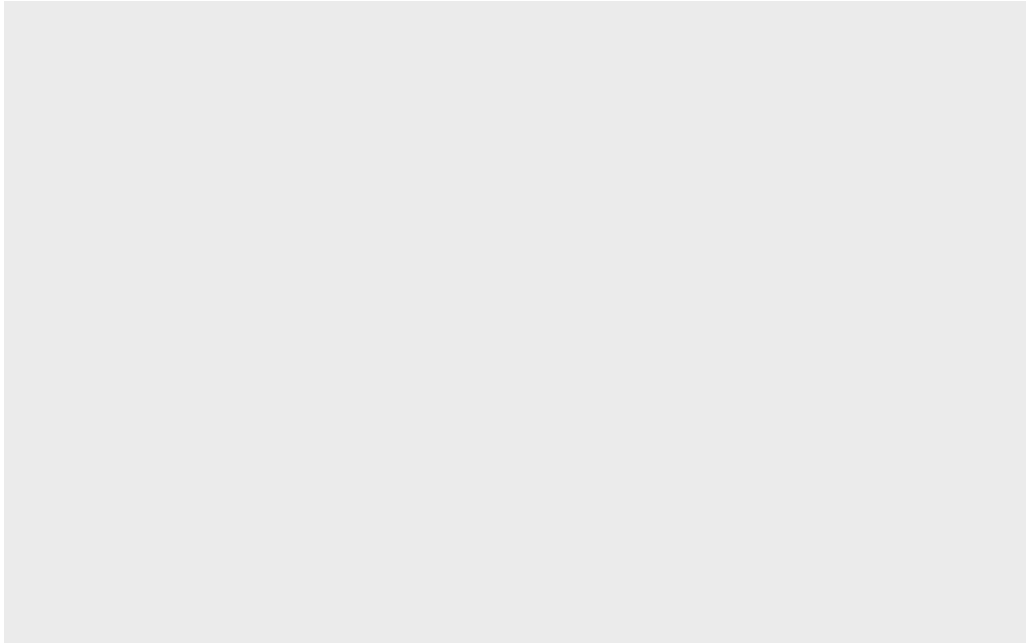
We use the `install.packages()` function to do this.

```
head(cars)
```

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

To use ggplot I need to load it up before I can call any of the functions in the package. I do this with the `library()` function.

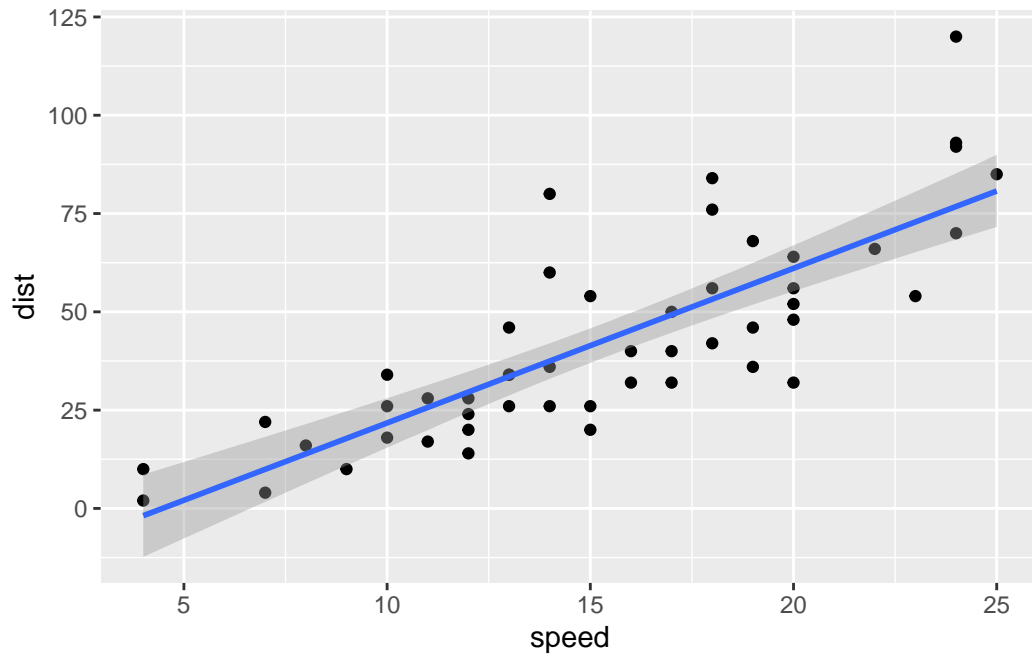
```
library(ggplot2)  
ggplot()
```



All ggplot figures have at least 3 things: - data (the stuff we want to plot) - aesthetic mapping (aes vales) - geoms

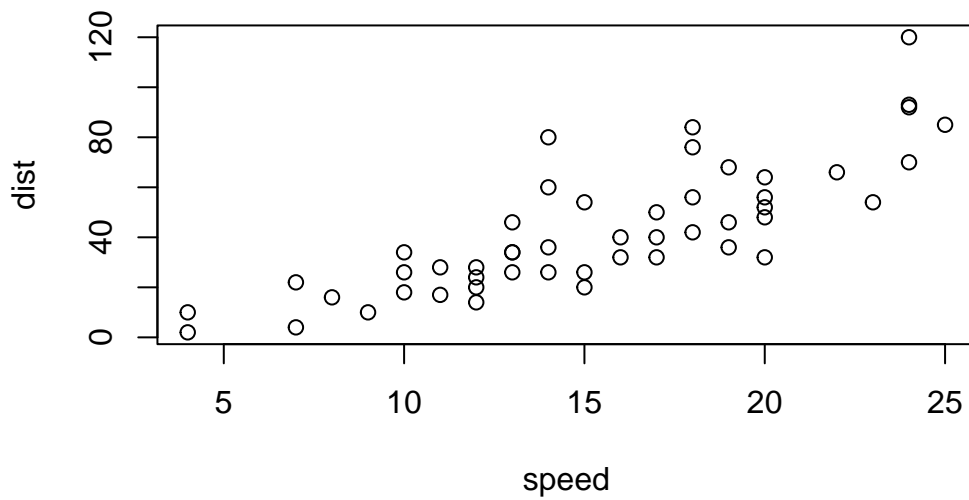
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(method="lm")
```

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



ggplot is not the only graphing system in R there are lots of others. There is even “base R” graphics.

```
plot(cars)
```

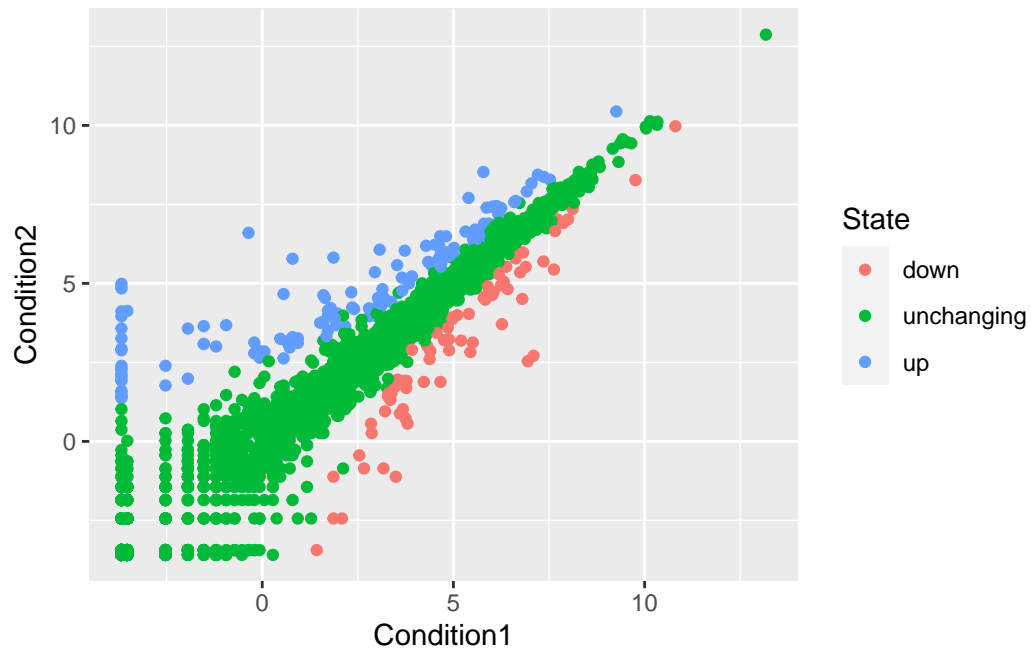


Expression dataset

```
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, color=State) +
  geom_point()
```



```
sum(genes$State == "up")
```

```
[1] 127
```

```
head(genes$State)
```

```
[1] "unchanging" "unchanging" "unchanging" "unchanging" "unchanging"
[6] "unchanging"
```

```
head(genes$State == "up")
```

```
[1] FALSE FALSE FALSE FALSE FALSE FALSE
```

```
#install.packages("dplyr")
```

```
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
head(genes)
```

	Gene	Condition1	Condition2	State
1	A4GNT	-3.6808610	-3.4401355	unchanging
2	AAAS	4.5479580	4.3864126	unchanging
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```
sum(genes$State == "up")
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```
[1] 127
```