Class 5: Data Visualization

Jae (A16138412)

Base R graphics vs ggplot2

There are many graphics systems available in R, including so-called "base" R graphics and the very popular **ggplot2** package.

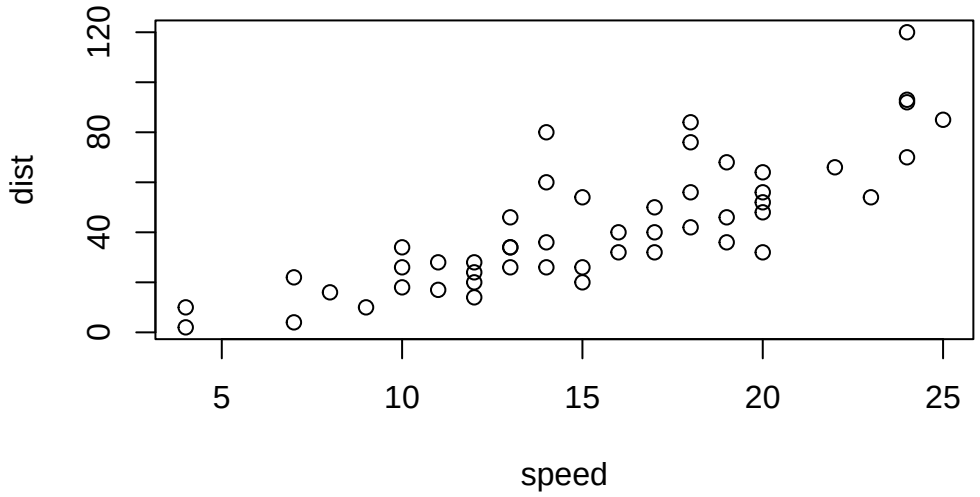
To compare these let's play with the inbuilt `cars` dataset.

```
head(cars)
```

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

To use "base" I can simply call the `plot()` function:

```
plot(cars)
```



To use `ggplot2` package I first need to install it with the function `install.packages("ggplot2")`.

I will run this in my R console (i.e. the R brain) as I do not want to re-install it every time I render my report...

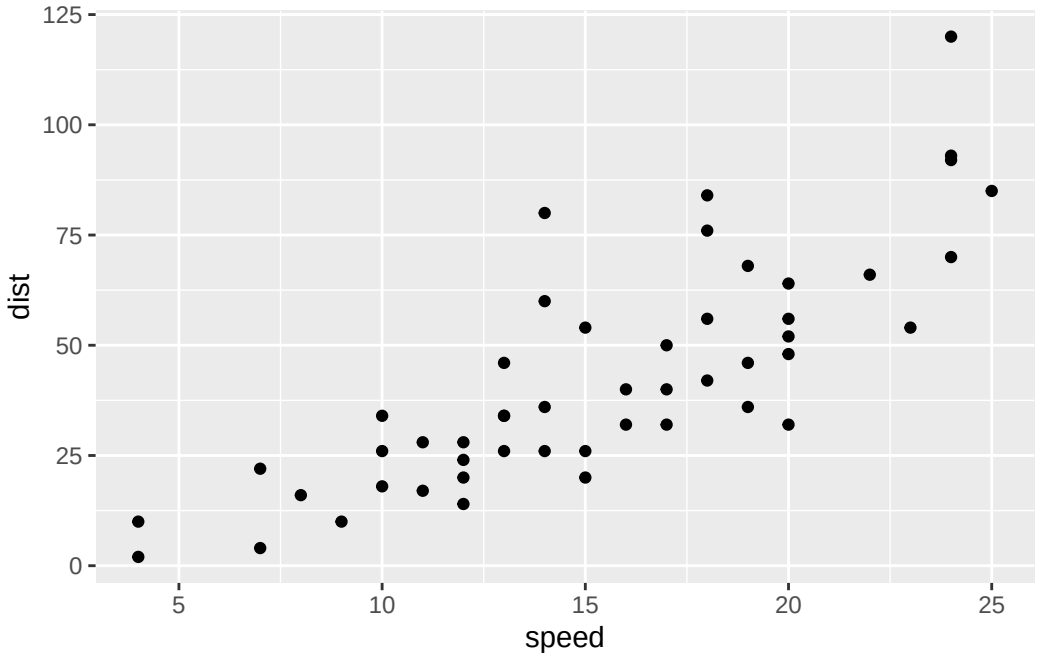
The main function in this package is called `ggplot()`. Can i just call it?

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

To make a figure with ggplot I need always at least 3 things:

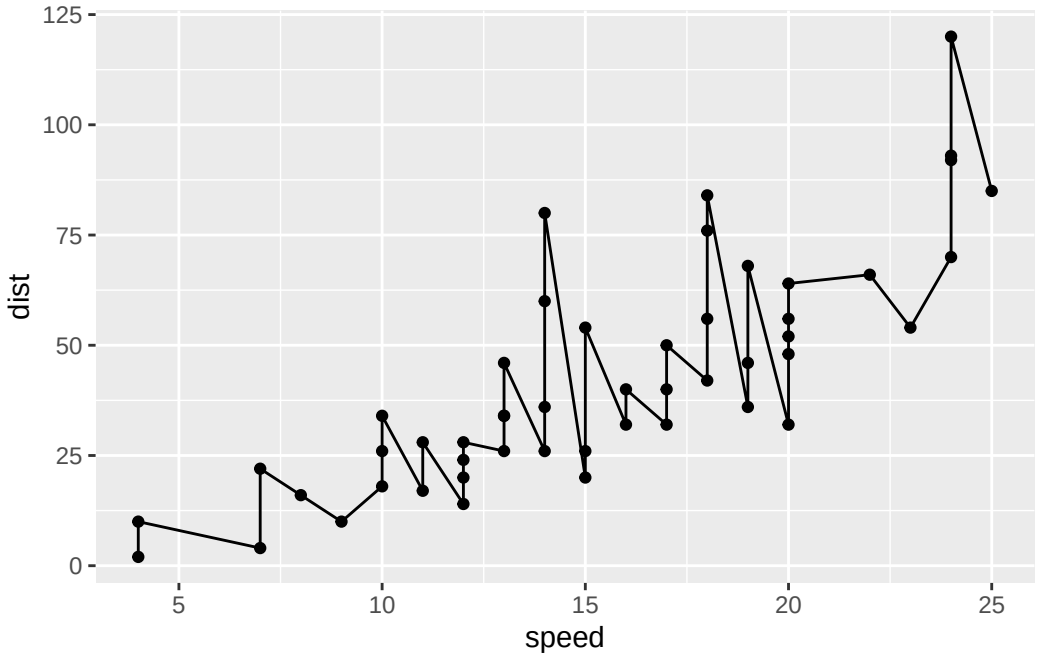
- data
- aes
- geom

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



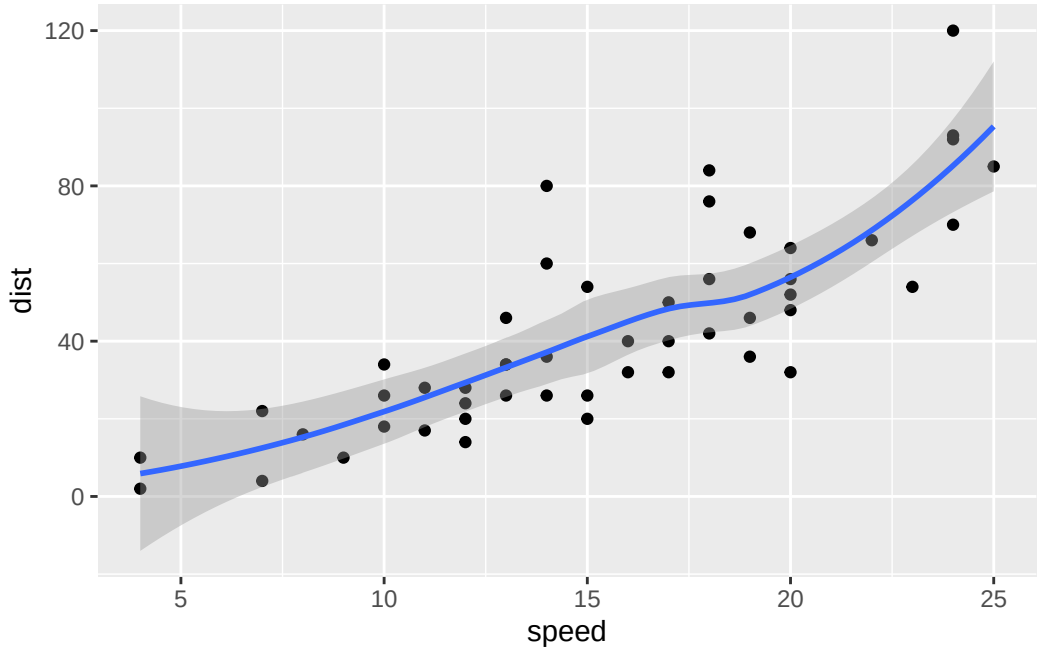
If I want to add more things I can just keep adding layers

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




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

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



ggplot is much more verbose than base R plots for standard plots but it has a consistent layer system that I can use to make just about any plot

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

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

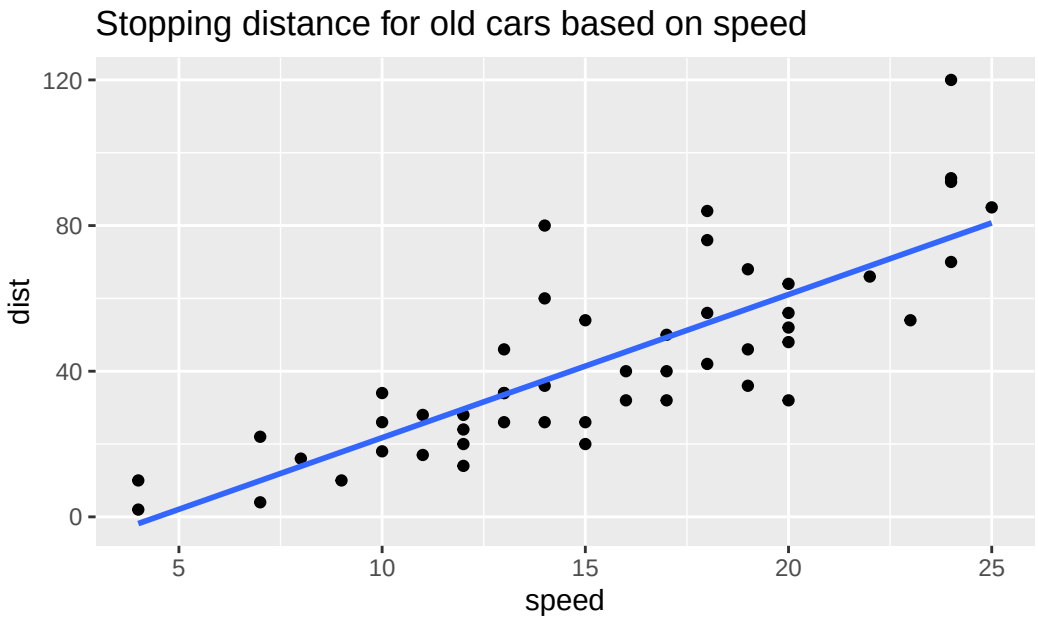


Figure 1. The distance required to come to a stop increases as the speed increases.

A more complicated plot

Let's lot some gene expression data The code below reads the results of a differential expression analysis where a new anti-viral drug is being tested.

```
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
```

Q. How many genes are in this dataset?

```
nrow(genes)
```

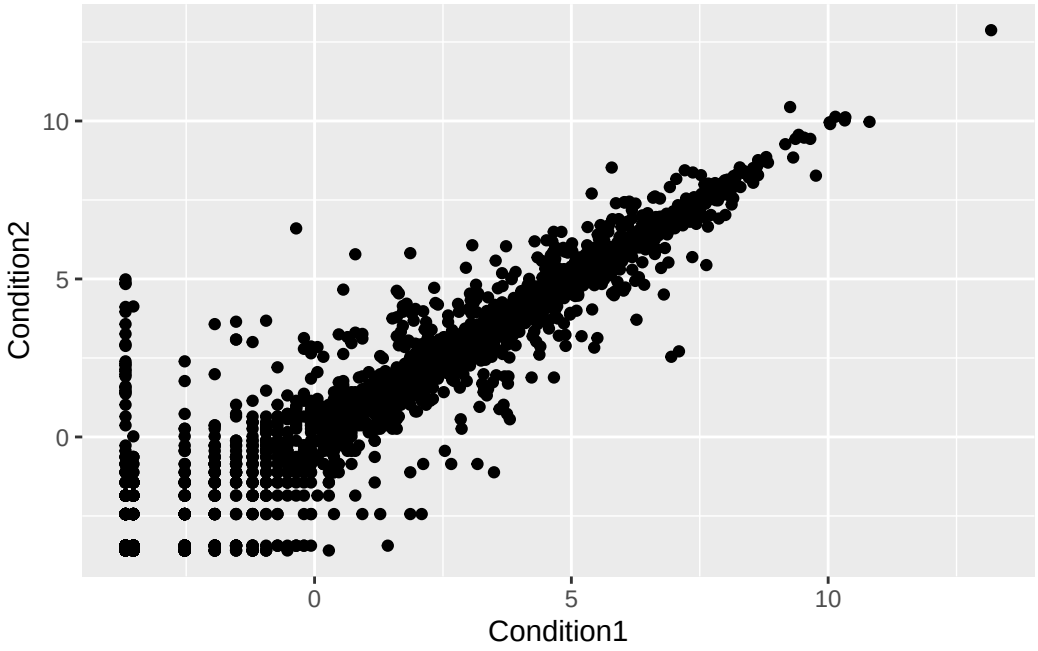
```
[1] 5196
```

Q. How can we summerize the last column ("State")?

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

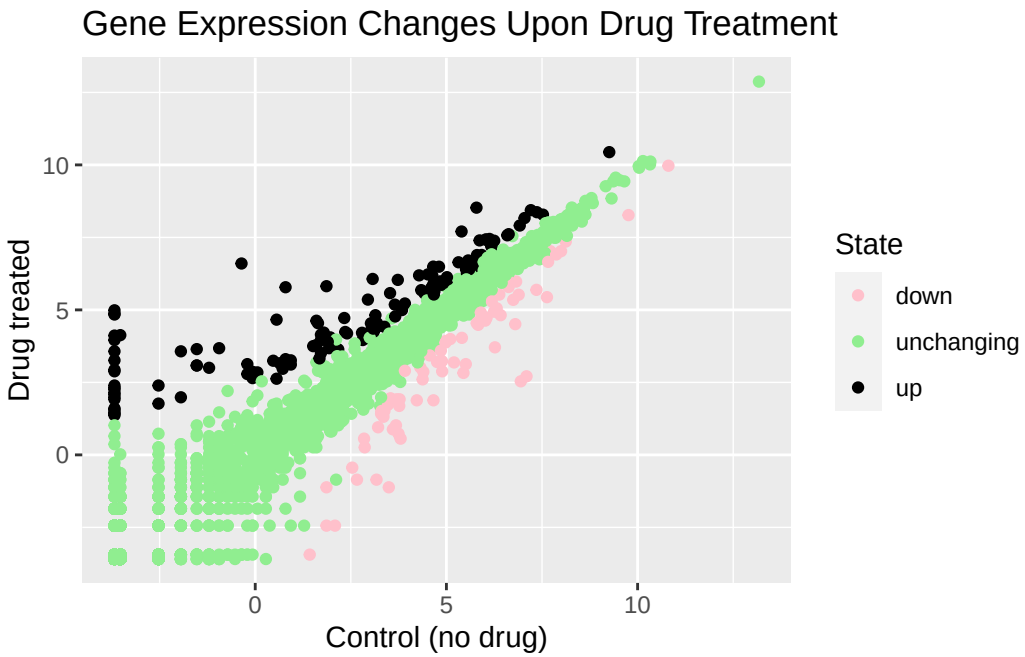
```
    down unchanging          up
      72        4997         127
```

```
ggplot(genes)+aes(x=Condition1, y=Condition2)+geom_point()
```




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

```
p+labs(title="Gene Expression Changes Upon Drug Treatment",x="Control (no drug)",y="Drug t
```



Going Further

Here I read a slightly larger dataset:

```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.

gapminder <- read.delim(url)
head(gapminder)
```

```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
4 Afghanistan      Asia 1967  34.020 11537966  836.1971
5 Afghanistan      Asia 1972  36.088 13079460  739.9811
6 Afghanistan      Asia 1977  38.438 14880372  786.1134
```

```
n<-ggplot(gapminder)+aes(x=gdpPercap, y=lifeExp)+geom_point()
```

```
m<-n+aes(color=continent,size=pop)+geom_point(alpha=0.3)
```

A very useful layer to add sometimes is for "faceting"

```
m+facet_wrap(~continent)
```