

Class 5: Data visualization

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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” R I can simply call the `plot()` function:

```
plot(cars)
```



To use the `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 always need at least 3 things:

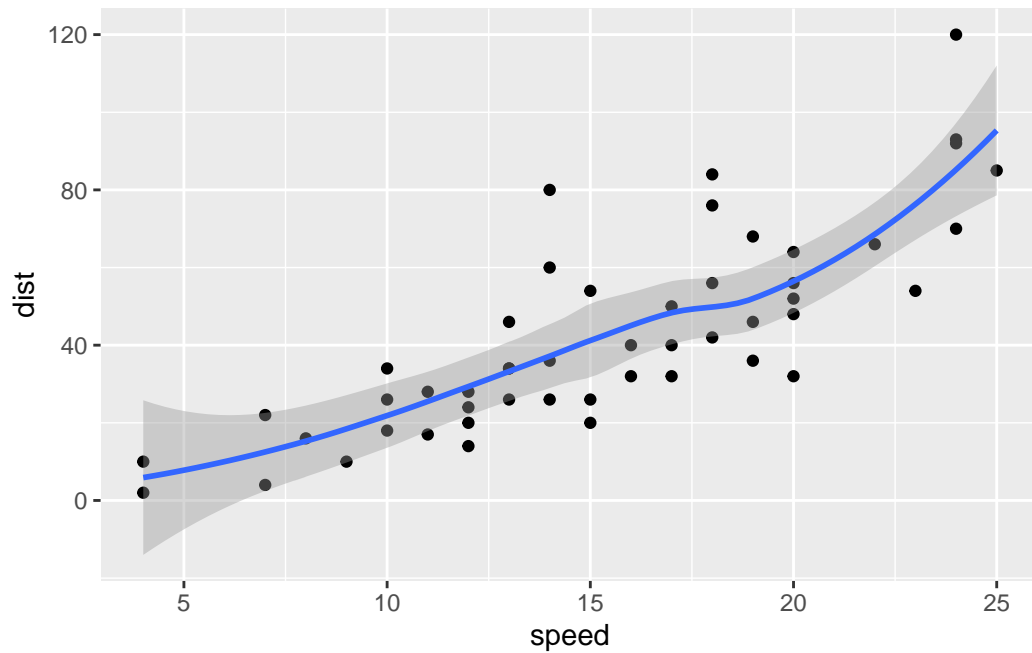
- **data** (i.e. what I want to plot)
- **aes** (i.e. the aesthetic mapping of the data to the plot I want)
- the **geoms** (i.e. how I want to plot the data)

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



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

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

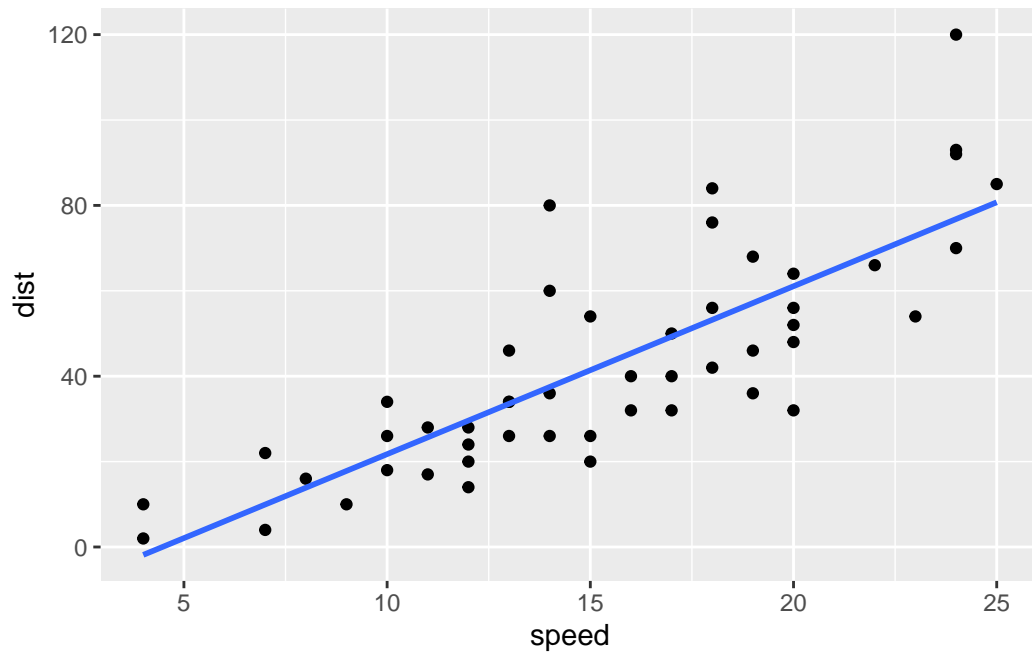


GGplot is much more verbose than base R plots but it has a consistent layer system that I can use to make just about any plot.

Let's make a plot with a straight line fit - i.e. a linear model with no standard error shown.

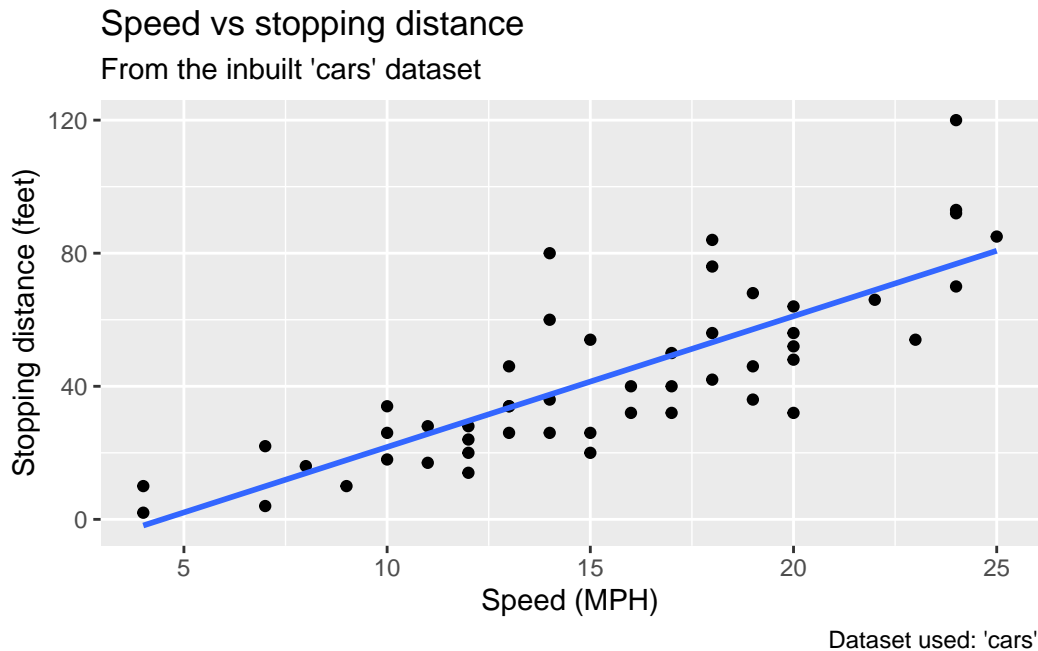
```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(se=FALSE, method="lm")
```

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



```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(se=FALSE, method="lm") +  
  labs(title="Speed vs stopping distance",  
        x="Speed (MPH)",  
        y="Stopping distance (feet)",  
        subtitle="From the inbuilt 'cars' dataset",  
        caption="Dataset used: 'cars'")
```

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



A more complicated plot

Let's plot some gene 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

Q1. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

Q2. How can we summarize the last column - the “State” column?

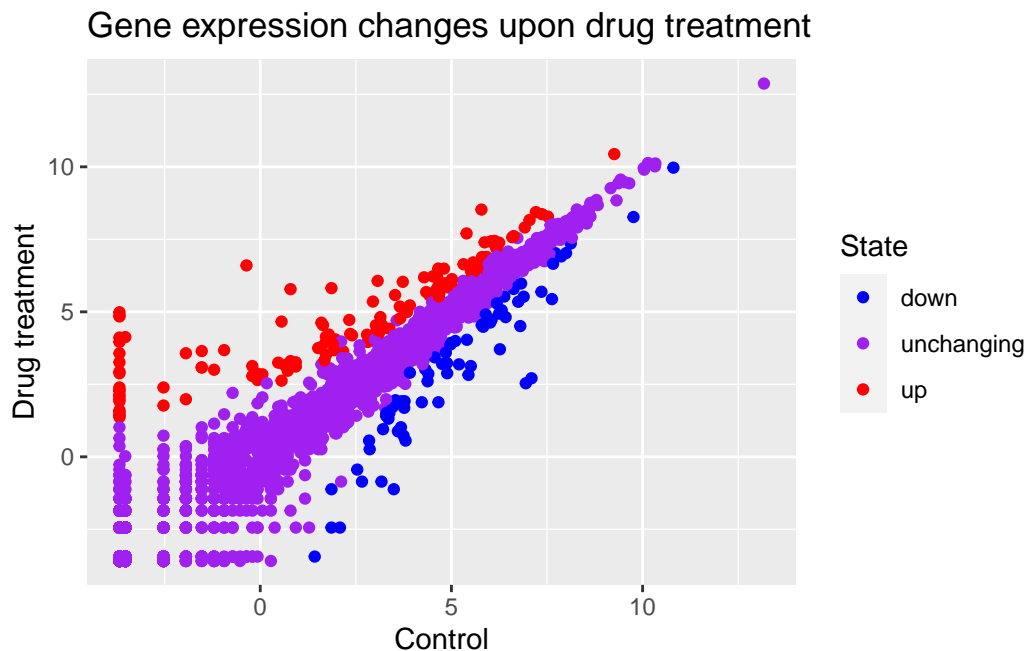
```
table(genes$State)
```

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

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

I can call `p` when I want to plot or add to it.

```
p + labs(title="Gene expression changes upon drug treatment",  
         x="Control", y="Drug treatment") +  
  scale_colour_manual( values=c("blue","purple","red") )
```



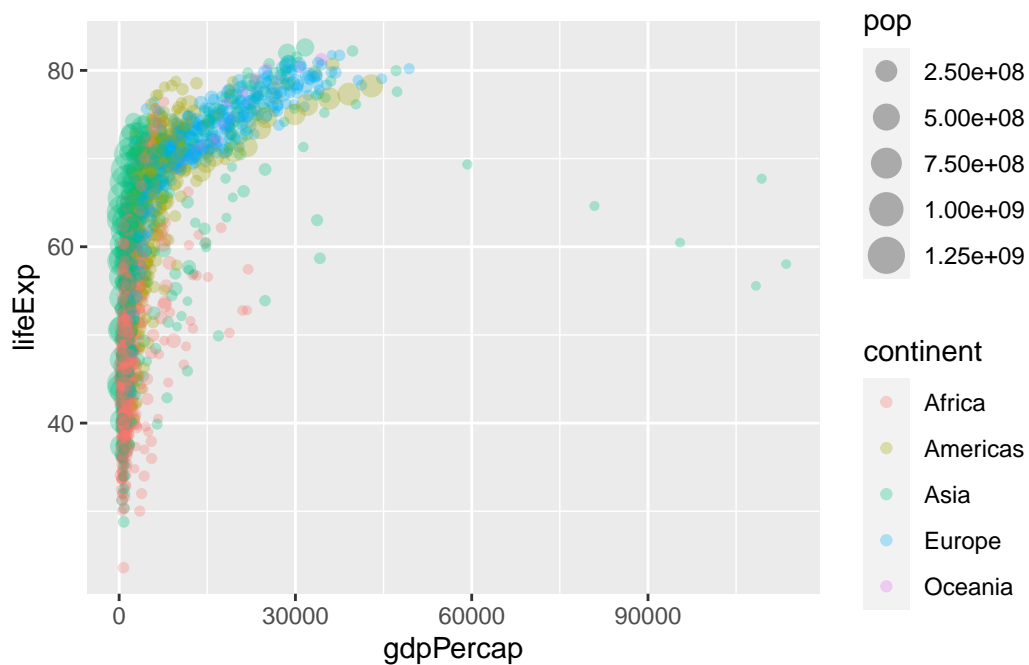
Going further

Here I'll 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

```
ggplot(gapminder) +
  aes(x= gdpPercap, y=lifeExp, col=continent, size=pop) +
  geom_point(alpha=0.3)
```



A very useful layer to add sometimes is for facetting.

```
ggplot(gapminder) +
  aes(x= gdpPercap, y=lifeExp, col=continent, size=pop) +
  geom_point(alpha=0.3) +
  facet_wrap(~continent)
```

