

Class 5: Data Visualization with ggplot

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Today we will have our first play with the **ggplot2** package - one of the most popular graphics package son the planet.

There are amny plotting systems in R. These include so called “*base*” plotting/graphics.

```
plot(cars)
```



Base plot is generally rather short code and somewhat dull plots ~ but it is always there for you and is fast for big data sets.

If I want to use **ggplot2** it takes some more work.

```
# ggplot(cars)
```

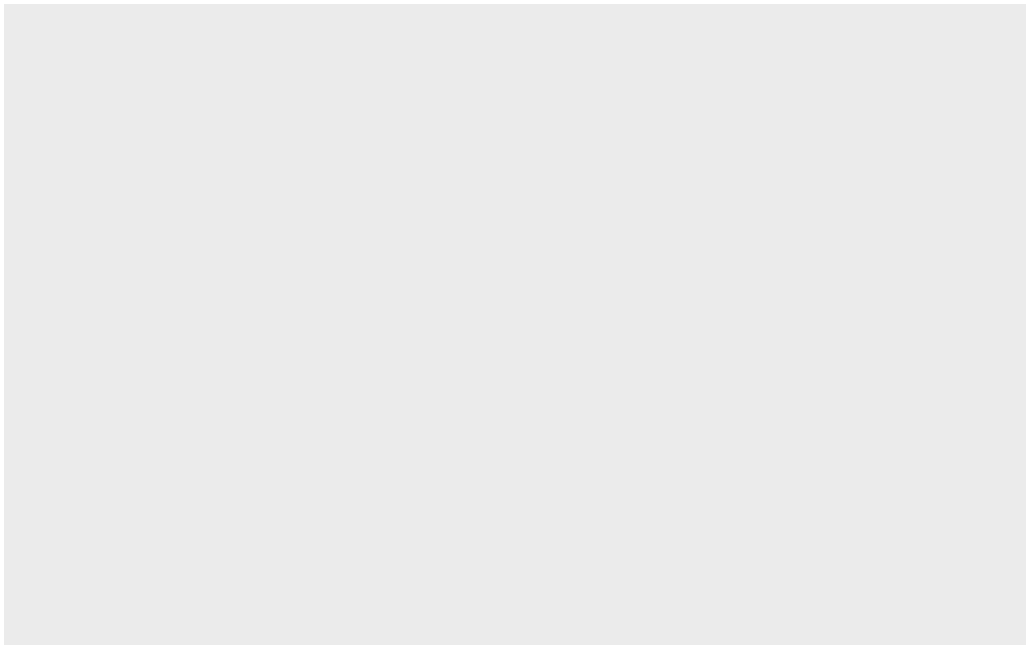
I need to install the package first to my computer. To do this I can use the function `install.packages(ggplot2)`

Every time I want to use a package I need to load it up with a `library()` call.

```
# install.packages(ggplot2)
library(ggplot2)
```

Now finally I can use ggplot

```
ggplot(cars)
```



Every ggplot has at least 3 things:

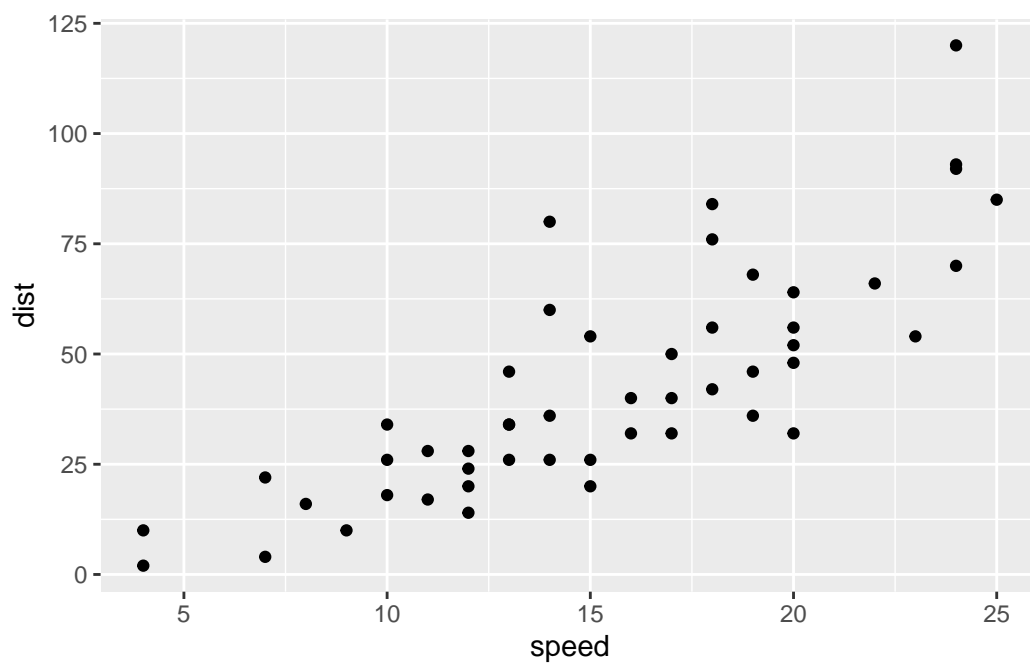
- **data** (the data.frame with the data you want to plot)
- **aes** (the aesthetic mapping of the data to the plot)

- **geom** (how do you want the plot to look, points, lines, etc.)

```
head(cars)
```

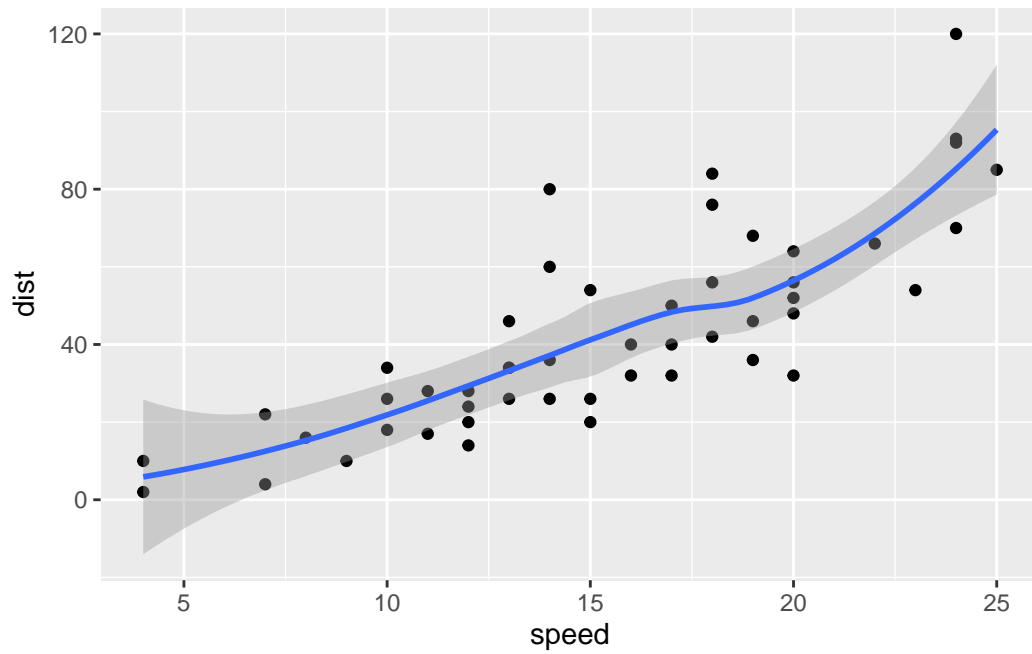
	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10

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



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

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

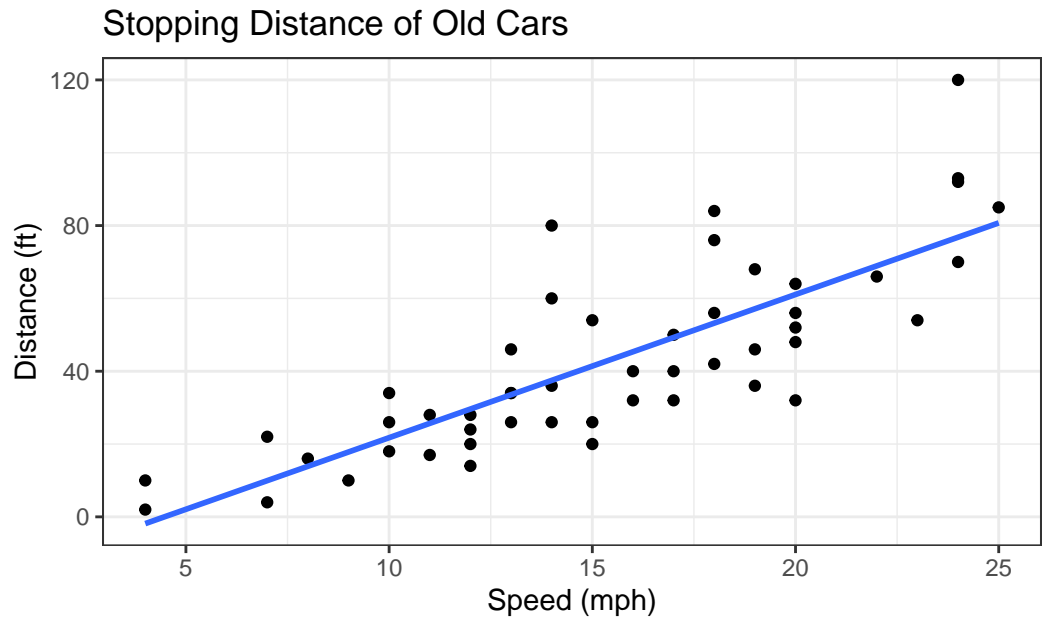


I want a liner model and no standard error bounds shown.

```
bp<- ggplot(cars) + aes(x = speed, y = dist) + geom_point()

bp + geom_smooth(se = FALSE, method = "lm") +
  labs(title = "Stopping Distance of Old Cars",
        x = "Speed (mph)", y = "Distance (ft)",
        caption = "From the 'cars' dataset") + theme_bw()
```

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



From the 'cars' dataset

A more complicated scatter plot

Here we make a plot of 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

```
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)[3]/ nrow(genes) * 100, 2)
```

```
up  
2.44
```

```
n.gene <- nrow(genes)  
n.up <- sum(genes$State == "up")  
  
up.percent <- n.up/n.gene * 100  
round(up.percent, 2)
```

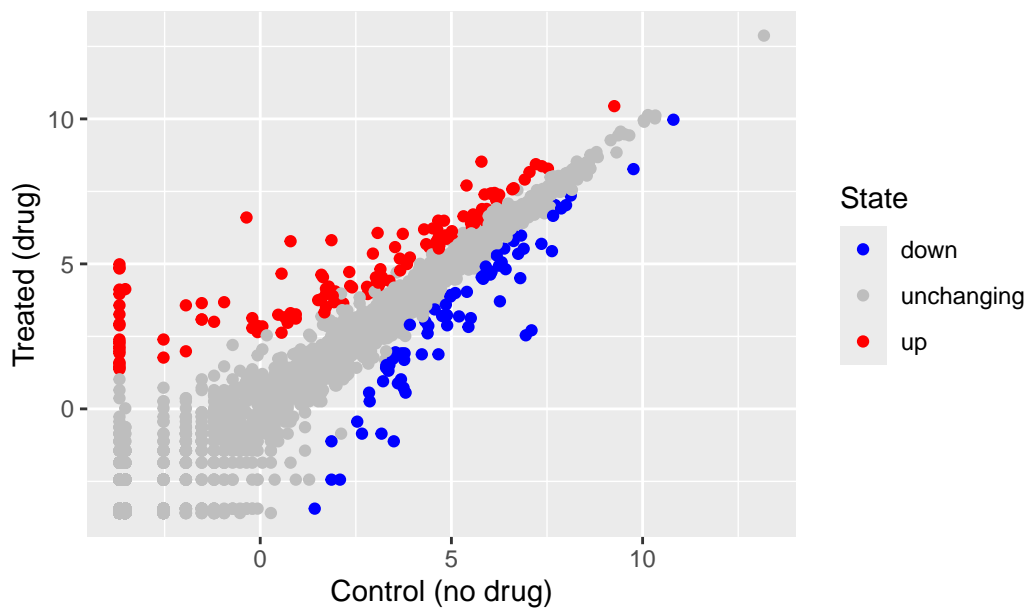
```
[1] 2.44
```

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

Change the colors and the labels that were provided for the plot.

```
t + scale_colour_manual(values = c("blue", "grey", "red")) +  
  labs(title = "Gene Expression Changes with Drug Treatment",  
       x= "Control (no drug)", y= "Treated (drug)")
```

Gene Expression Changes with Drug Treatment



Exploring the gapmider dataset

Here we will load up the gapmider dataset to get practice with different aes mappings.

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.  
gapmider <- read.delim(url)
```

Q. How many entries rows are in this dataset?

```
nrow(gapmider)
```

```
[1] 1704
```

Q. How many columns are in this dataset?

```
ncol(gapmider)
```

```
[1] 6
```

```
dim(gapmider)
```

```
[1] 1704    6
```

```
head(gapmider)
```

	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

```
table(gapmider$year)
```

1952	1957	1962	1967	1972	1977	1982	1987	1992	1997	2002	2007
142	142	142	142	142	142	142	142	142	142	142	142

Q. How many continents?

```
table(gapmider$continent)
```

Africa	Americas	Asia	Europe	Oceania
624	300	396	360	24

I could use the `unique()` function...

```
length(unique(gapmider$continent))
```

```
[1] 5
```

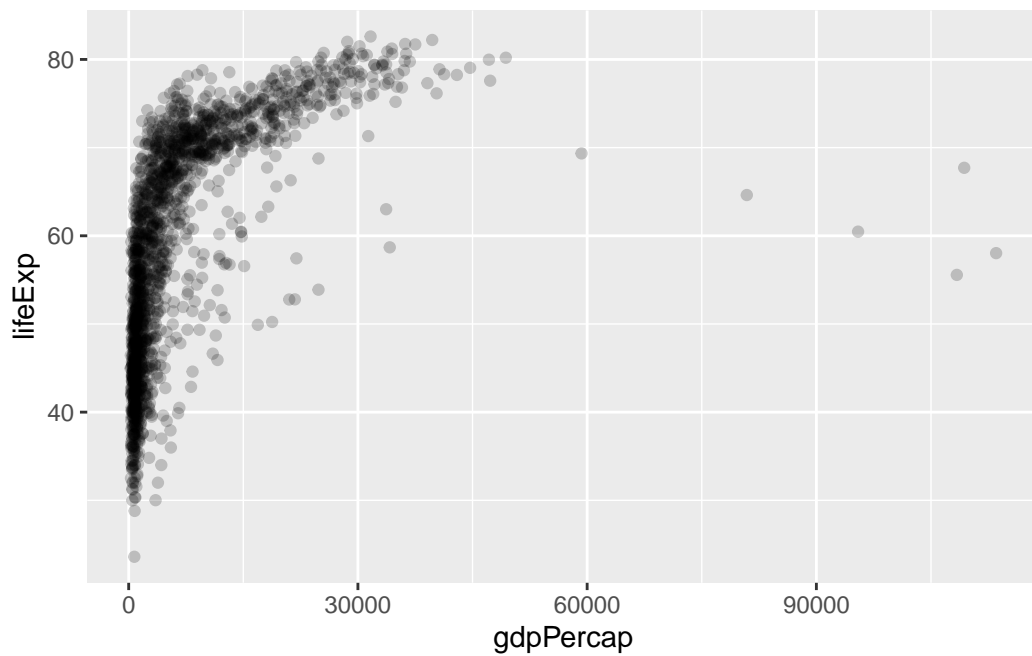
Q. How many countries are there in this dataset?

```
# unique(gapmider$country)
length(unique(gapmider$country))
```

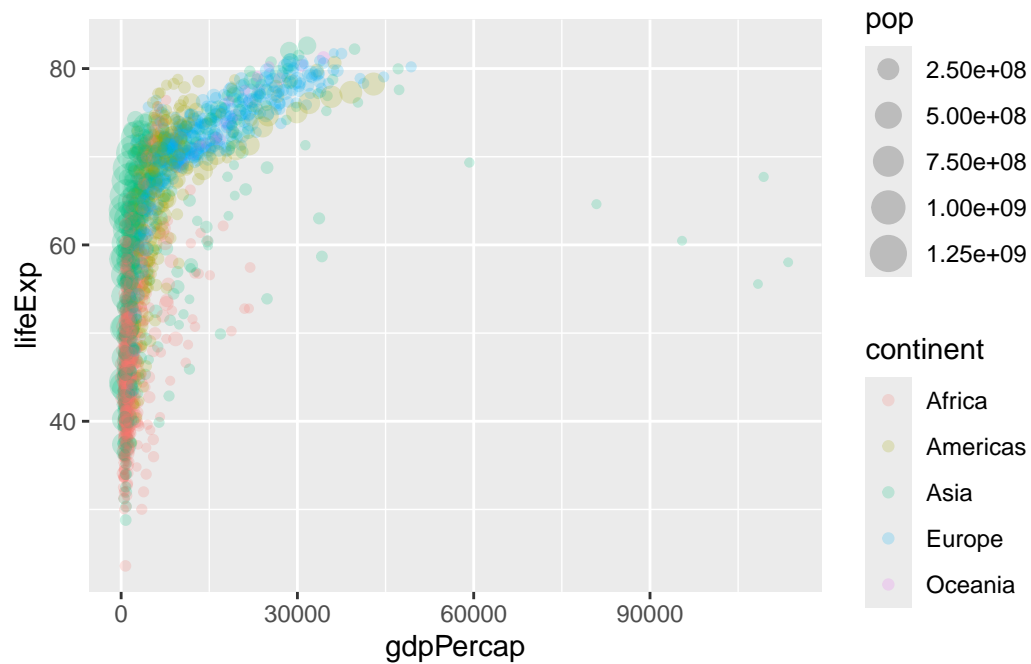
```
[1] 142
```



```
ggplot(gapmider) + aes(x = gdpPercap, y = lifeExp) +  
  geom_point(alpha = 0.2)
```



```
ggplot(gapmider) + aes(x = gdpPercap, y = lifeExp,  
                        col = continent, size = pop) +  
  geom_point(alpha = 0.2)
```



```
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

```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

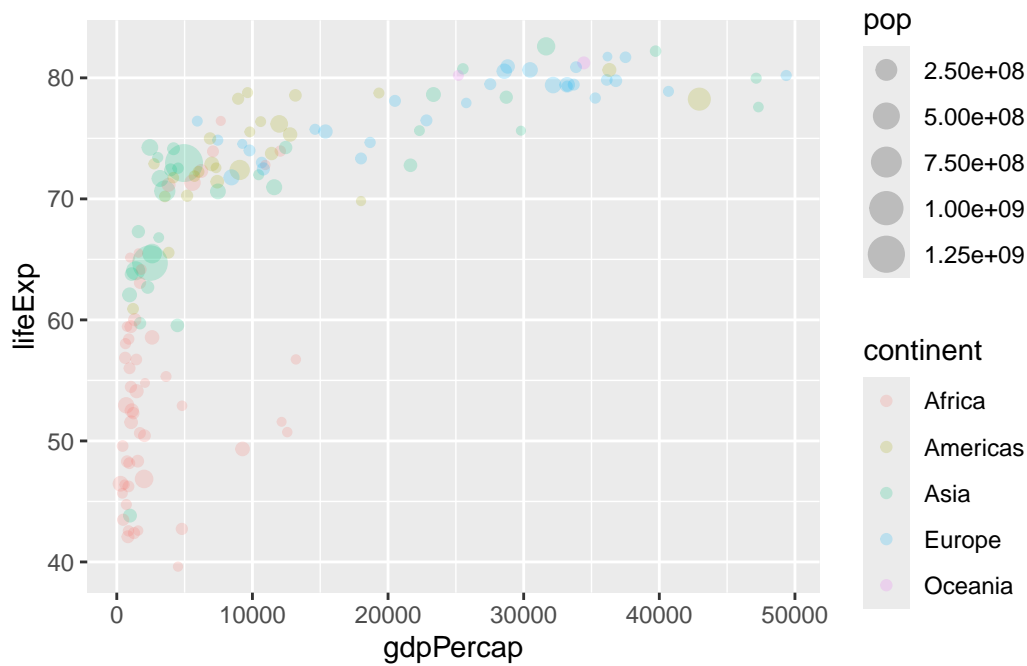
```
head(gapminder_2007)
```

	country	continent	year	lifeExp	pop	gdpPercap
1	Afghanistan	Asia	2007	43.828	31889923	974.5803
2	Albania	Europe	2007	76.423	3600523	5937.0295

3	Algeria	Africa	2007	72.301	33333216	6223.3675
4	Angola	Africa	2007	42.731	12420476	4797.2313
5	Argentina	Americas	2007	75.320	40301927	12779.3796
6	Australia	Oceania	2007	81.235	20434176	34435.3674

Plot of 2007 with population and continent data

```
ggplot(gapminder_2007) + aes(x = gdpPercap,
                             y = lifeExp, col = continent,
                             size = pop) +
  geom_point(alpha = 0.2)
```



```
ggplot(gapminder) + aes(x = gdpPercap, y = lifeExp,
                        col = continent, size = pop) +
  geom_point(alpha = 0.2) + facet_wrap(~continent)
```

