

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 packages on the planet.

There are many 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 datasets.

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

```
# ggplot(cars)
```

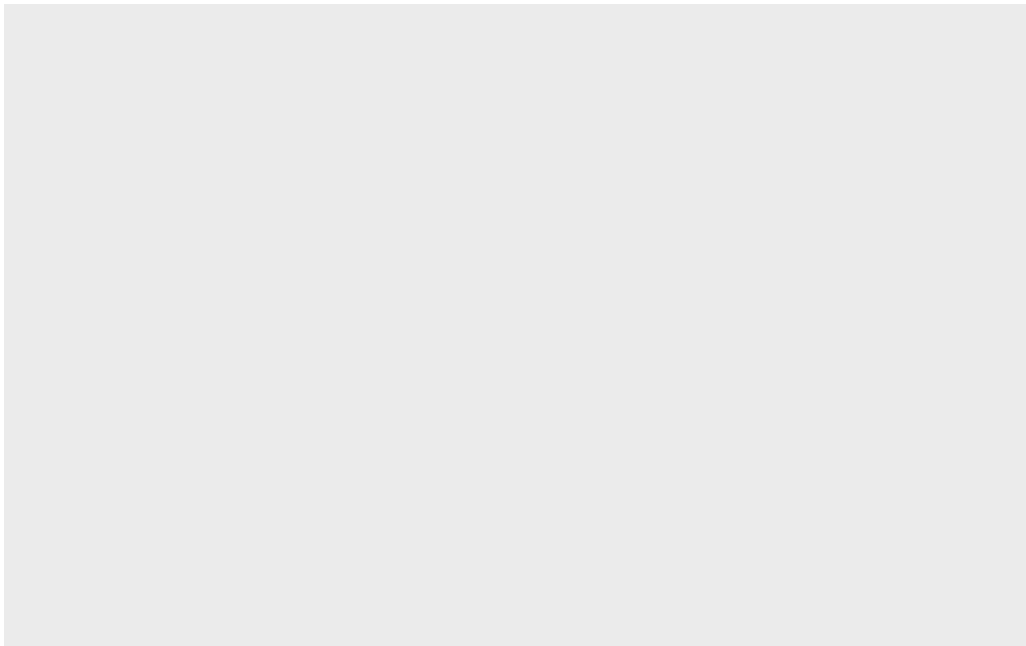
I need to install the package first to my computer. To do this, I can use the function `install.packages("ggplot2")`

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

```
library(ggplot2)
```

Now I can finally use ggplot.

```
ggplot(cars)
```



Every ggplot has at least 3 things:

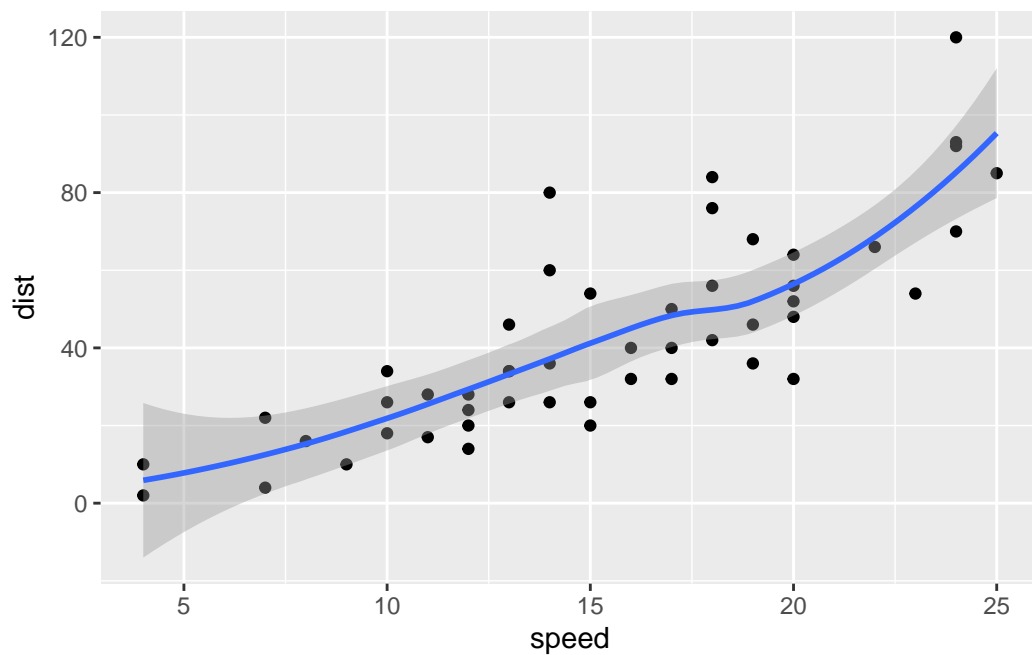
- **Data:** the data.frame with the data you want to plot
- **Aes:** the aesthetic mapping of the data to the plot
- **Geom:** how you want the plot to look, ie. points, lines, columns, etc.

```
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() +  
  geom_smooth()
```

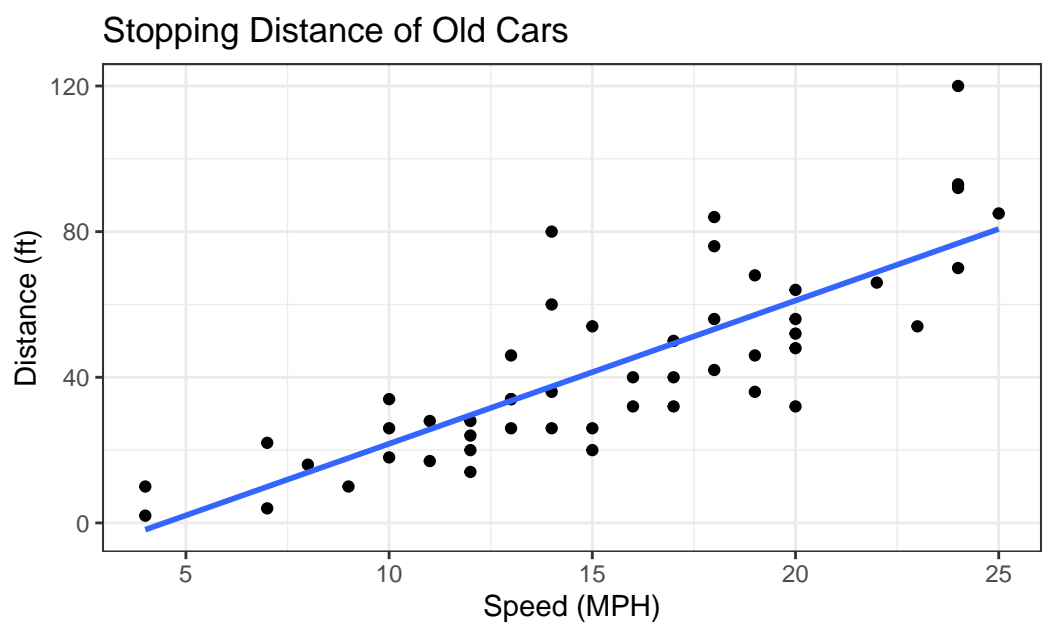
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'



I want a linear model and no standard error bounds shown on my plot. I also want nicer axis labels, a title, etc.

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

```
round(sum(genes$State == "up") / nrow(genes) * 100 , 2)
```

```
[1] 2.44
```

```
n.gene <- nrow(genes)
n.up <- sum(genes$State == "up")

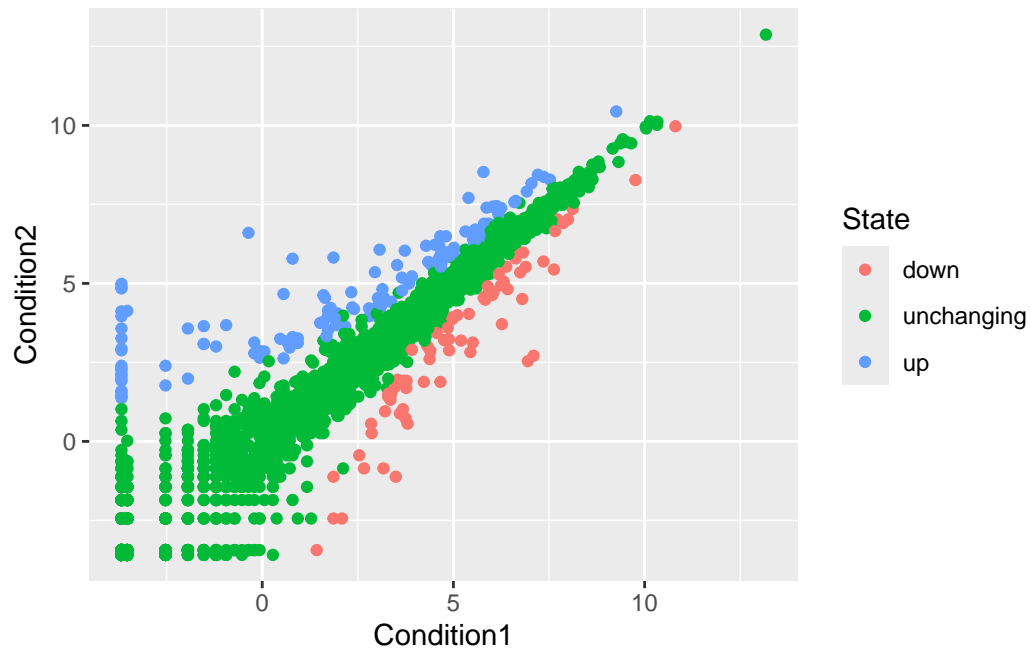
up.percent <- n.up/n.gene * 100
round(up.percent, 2)
```

```
[1] 2.44
```

```
head(genes, 2)
```

	Gene	Condition1	Condition2	State
1	A4GNT	-3.680861	-3.440135	unchanging
2	AAAS	4.547958	4.386413	unchanging

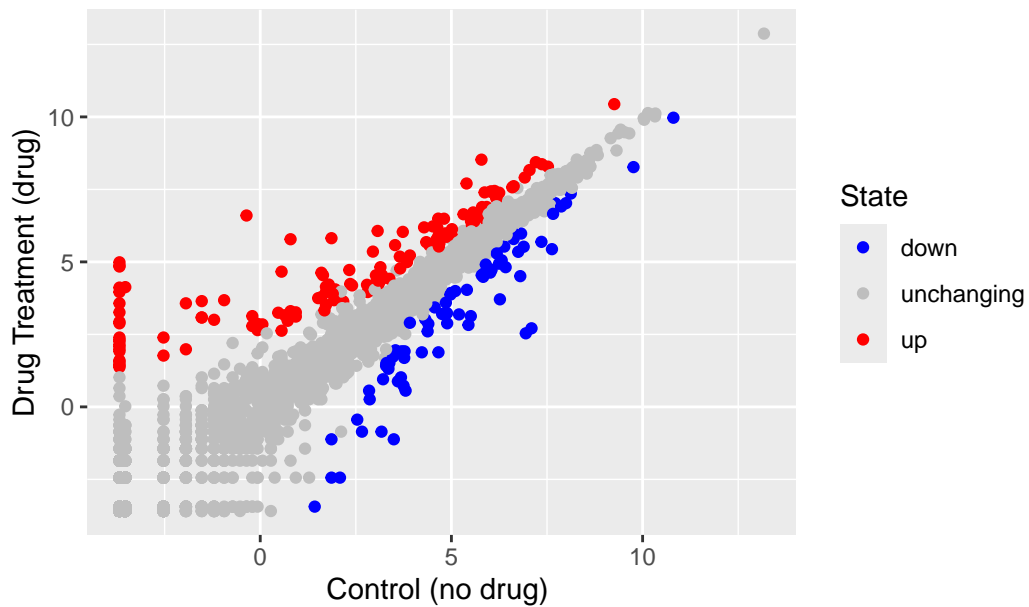
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
```



Change the colors and labelling.

```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  scale_color_manual( values=c("blue","gray","red") ) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment (drug)")
```

Gene Expression Changes Upon Drug Treatment



Exploring the Gapminder Dataset

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

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

Q. How many entries rows are in this dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

Q. How many columns?

```
ncol(gapminder)
```

```
[1] 6
```

```
dim(gapminder)
```

```
[1] 1704    6
```

```
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

```
table(gapminder$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 are there in this dataset?

```
table(gapminder$continent)
```

Africa	Americas	Asia	Europe	Oceania
624	300	396	360	24

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

```
unique(gapminder$continent)
```

```
[1] "Asia"      "Europe"    "Africa"    "Americas"  "Oceania"
```

```
length(unique(gapminder$continent))
```

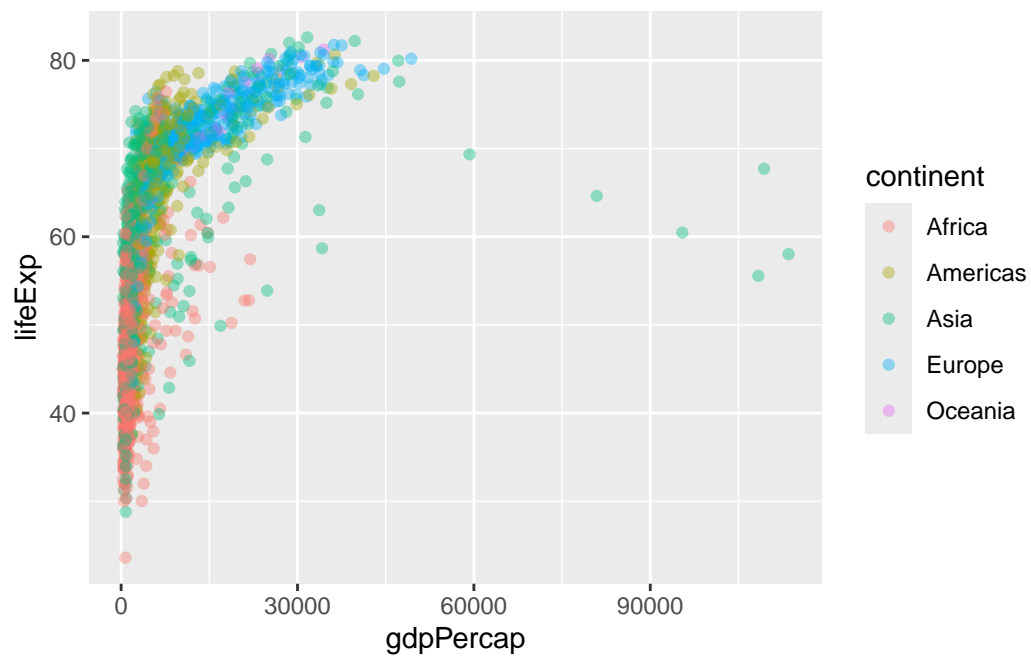
```
[1] 5
```

Q. How many countries are there in this dataset?


```
length(unique(gapminder$country))
```

```
[1] 142
```

```
ggplot(gapminder) +  
  aes(x=gdpPercap, y=lifeExp, col=continent) +  
  geom_point(alpha=0.4)
```



2007 dataset.

```
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
```

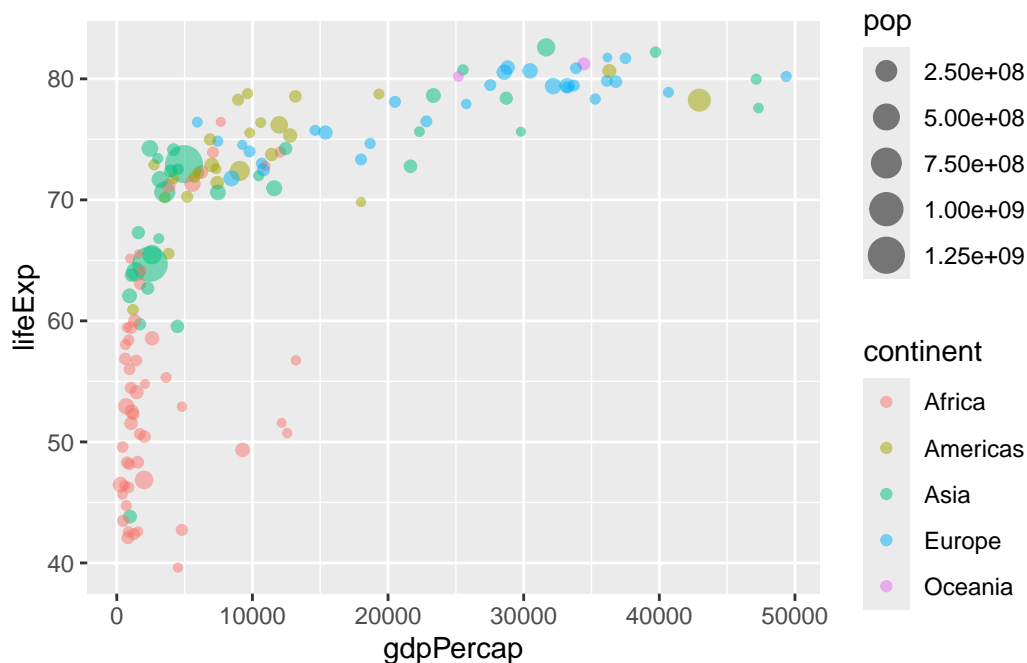
```
gapminder_2007 <- filter (gapminder, year==2007)
```

```
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=0.5)
```



```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point() +
  facet_wrap(~continent)
```

