Class 5: Data Visualization with GGPlot

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Today we are exploring the **ggplot** package and how to make nice figures in R.

There are lots of ways to make figures and plot in R. These include:

-so called "base" R -and add on packages like **ggplot2**

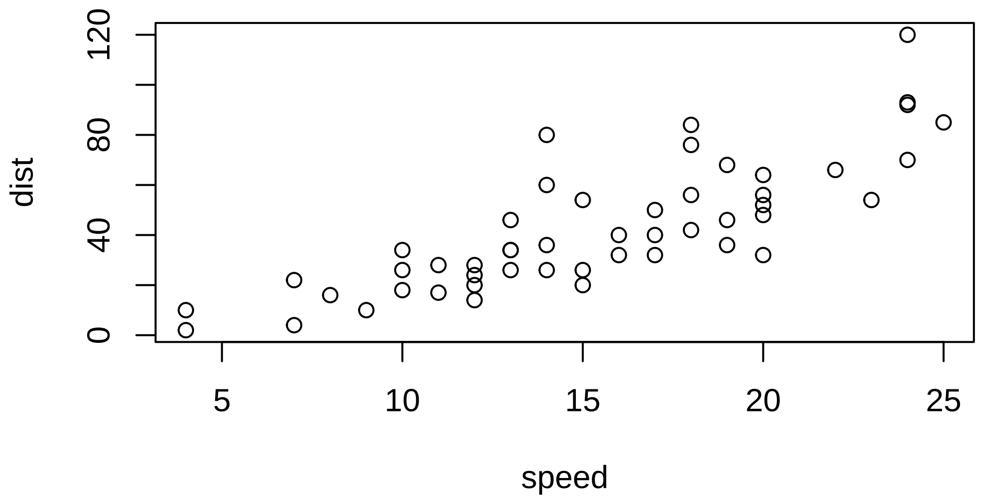
Here is a simple "base" R plot.

```r
head(cars)
```

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

We can simply pass to the 'plot()' function.

```r
plot(cars)
```



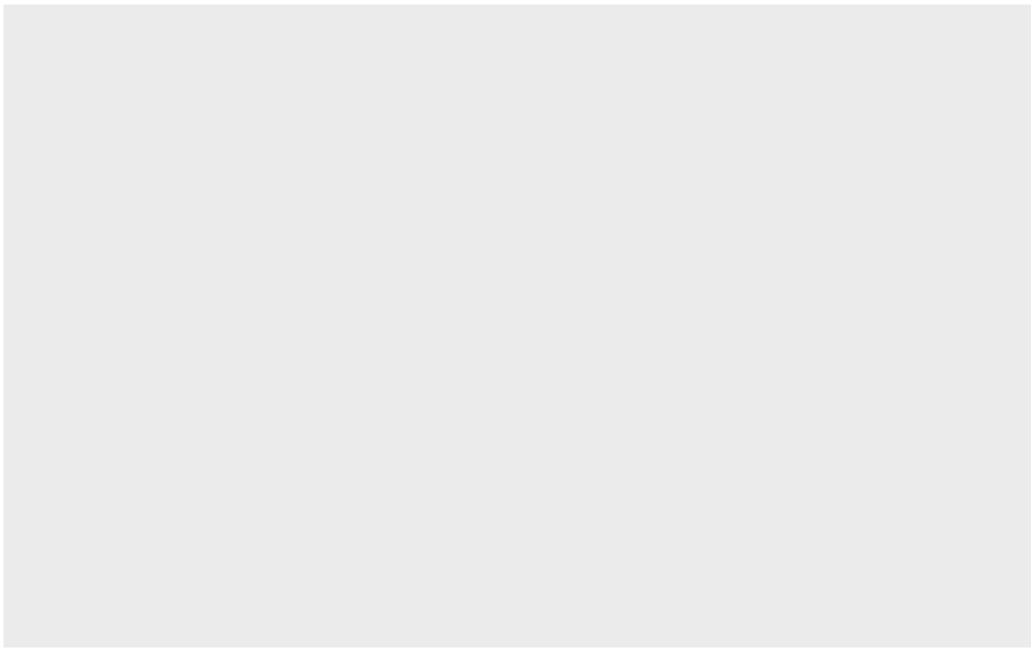
Key-point: Base R is quick but not so nice and simple looking in some folks eyes.

Let's see how we can plot this with **ggplot2**…

1st I need to install this add-on package. For this we use the 'install.packages()' function - **WE DO THIS IN THE CONSOLE, NOT our report**. This is a one time only deal.

2nd we need to load the package with the 'library()' function every time we want to use it.

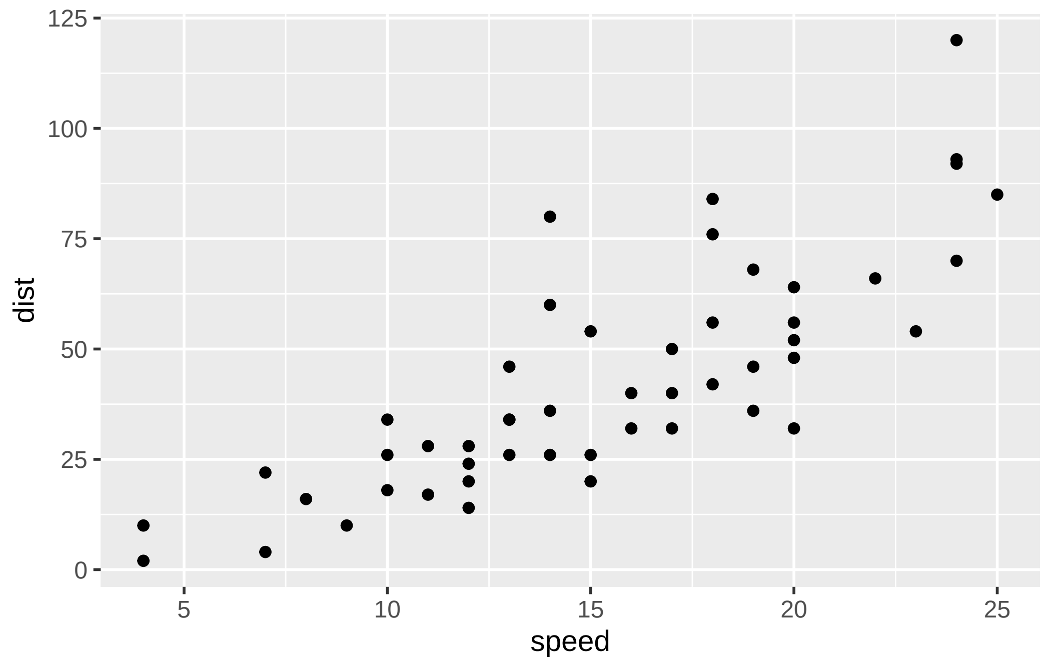
```r
library(ggplot2)
ggplot(cars)
```



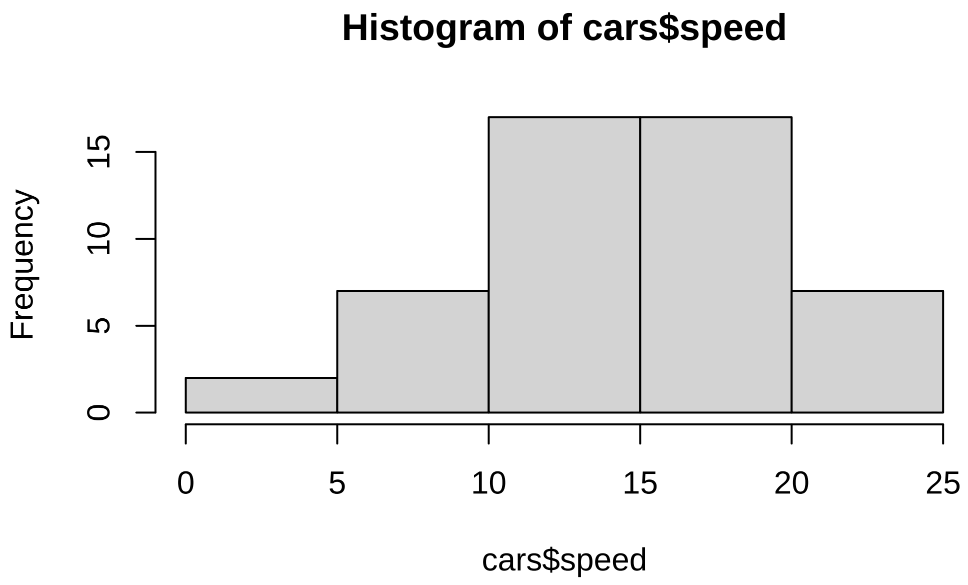
Every ggplot is composed of at least three layers:

-**data**(i.e. a data.frame with the things you want to plot), -aesthetics **aes()** that map the columns of data to your plot features (i.e. aesthetics) -geoms like **geom_point()** that srt how the plot appears

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



```r
hist(cars$speed)
```



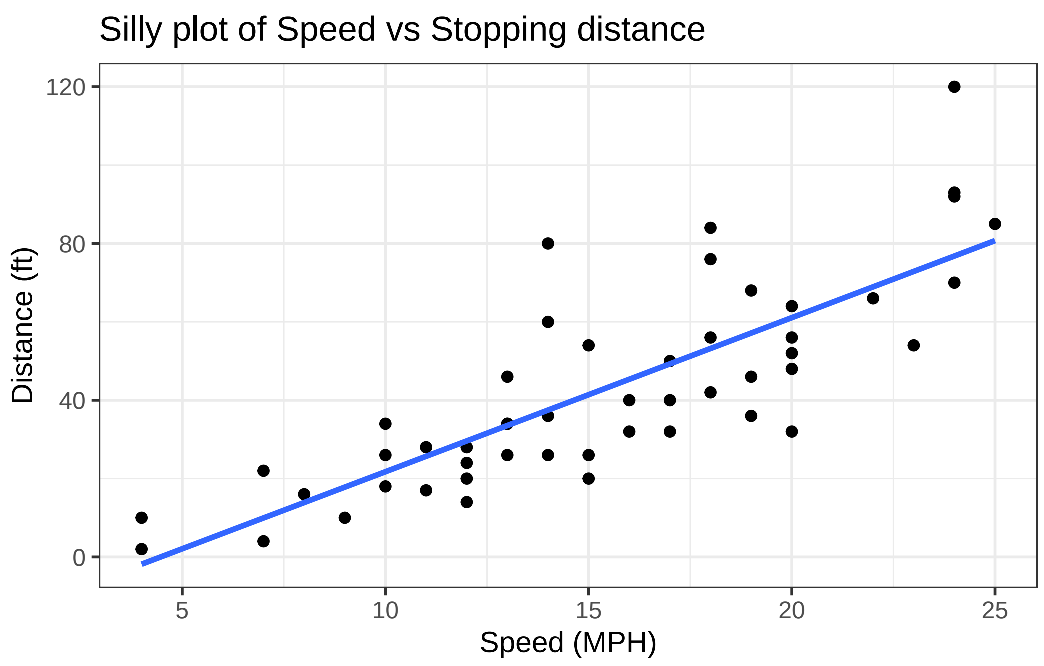
Key point: For simple "canned" graphs base R is quicker but as things get more custom and elaborate then ggplot wins out…

Let's add more layers to our ggplot

Add a line showing the relationship between x and y Add a title Add custom axis labels "Speed (MPH)" and "Distance (ft)" Change the theme….

```r
ggplot(cars)+
  aes(x=speed,y=dist)+
  geom_point()+
  geom_smooth(method="lm",se=FALSE)+
  labs(title="Silly plot of Speed vs Stopping distance",
       x="Speed (MPH)",
       y="Distance (ft)") +
  theme_bw()
```

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



Going further

Read some gene expression data

```r
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?

```r
nrow(genes)
```

```
[1] 5196
```

> Q2. How many "up" regulated genes are there?

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

```
[1] 127
```

A useful funtion for counting up occurances of things in a vector is the 'table()' function.

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

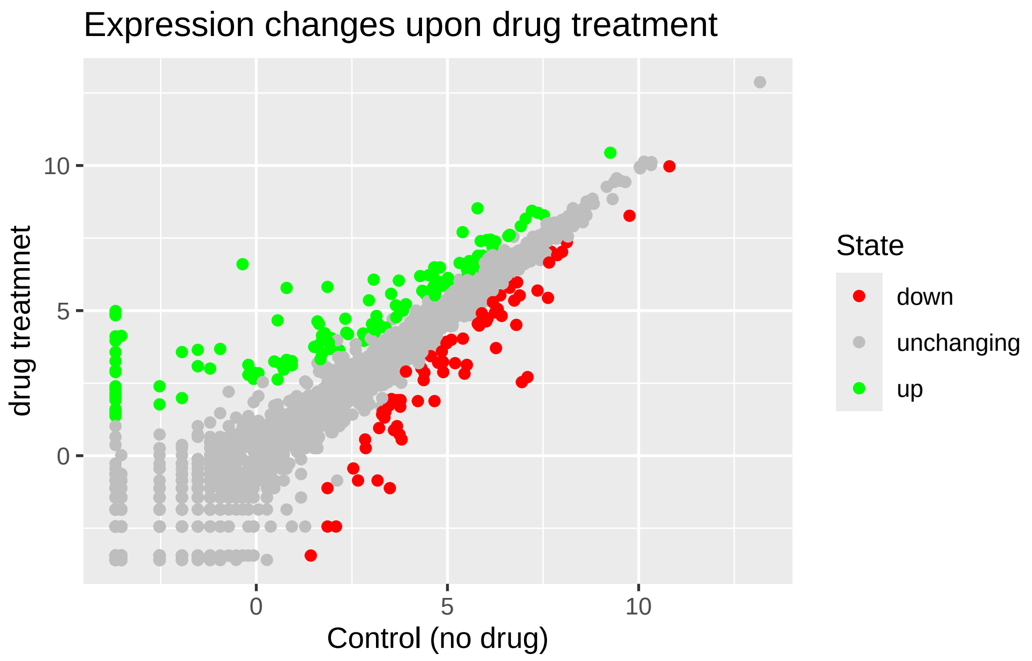
```

      down unchanging         up 
        72       4997        127 
```

Make a v1 figured

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

```
p+
  scale_color_manual(values=c("red","gray","green"))+
  labs(title="Expression changes upon drug treatment",
       x="Control (no drug)",
       y="drug treatmnet")
```



More Plotting example

Read in the gapminder mindset

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

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

Lets have a peek

```
head(gapminder,3)
```

```
      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
```

```
tail(gapminder,3)
```

```
      country continent year lifeExp      pop gdpPercap
1702 Zimbabwe    Africa 1997  46.809 11404948  792.4500
1703 Zimbabwe    Africa 2002  39.989 11926563  672.0386
1704 Zimbabwe    Africa 2007  43.487 12311143  469.7093
```

Q.4 How many diffeent country values are in this dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

```
length(table(gapminder$country))
```

```
[1] 142
```

Q5. How many different continent values are in this dataset?

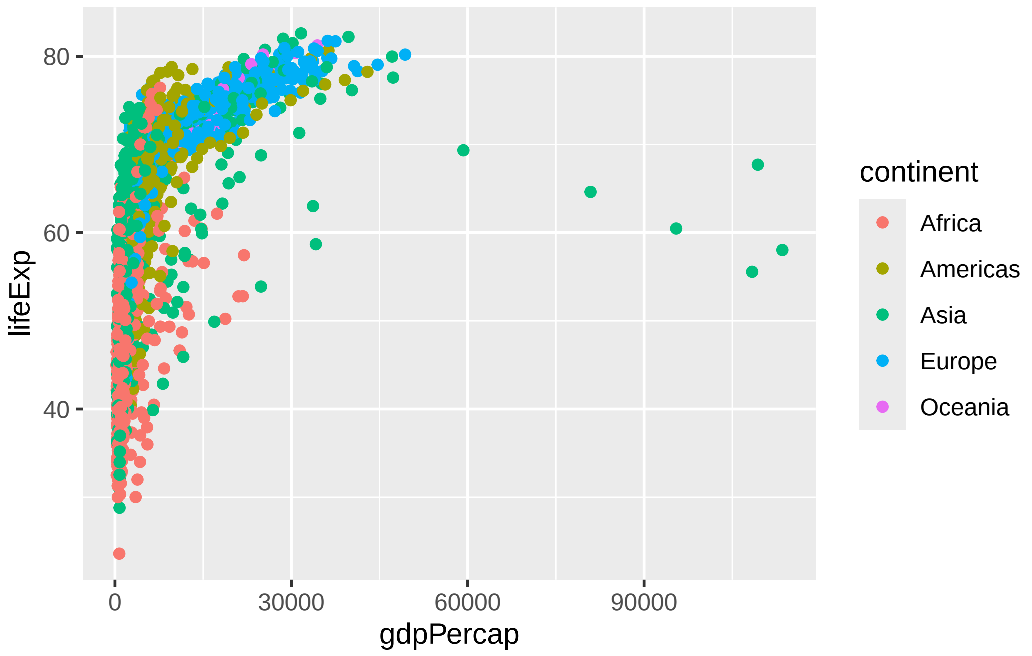
```
length(table(gapminder$continent))
```

```
[1] 5
```

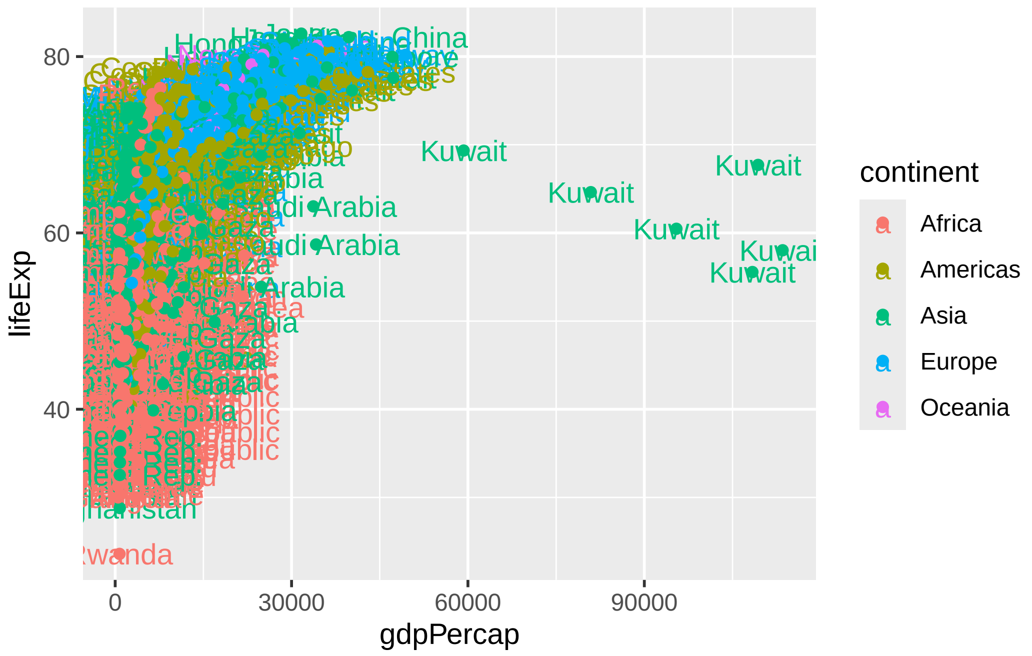
```
unique(gapminder$continent)
```

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

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

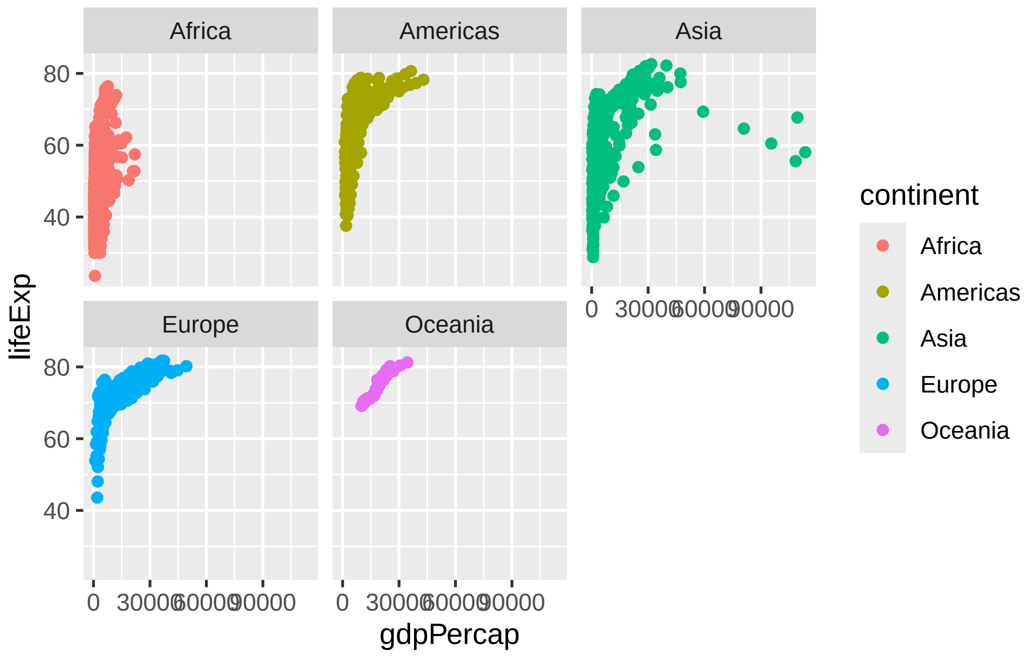


```
ggplot(gapminder)+
  aes(x=gdpPercap,y=lifeExp,col=continent,label=country)+
  geom_text()+
  geom_point()
```



```r
library(ggrepel)
```

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



I can use the **ggrepel** package to make more sensible labels here.

I want a seperate pannel per continent.

ggplot2 offers several advantages over base R plots:

1. **Layered grammar**: ggplot2 builds plots by adding layers (data, aesthetics, geoms), making complex visualizations easier to construct and modify step-by-step [1], [2], [3], [4].
2. **Consistency**: The same syntax and logic apply across different plot types, reducing the need to learn new functions for each visualization [1], [2], [3], [4].
3. **Publication quality**: ggplot2 produces attractive, professional figures with sensible defaults, which are often more visually appealing than base R plots [1], [2], [3], [4].
4. **Customization**: It is easier to customize legends, colors, themes, and other elements, especially for complex plots [1], [2], [3].
5. **Scalability**: ggplot2 handles large datasets and complex plots more efficiently, and code can be reused and automated for reproducibility [1], [2], [3].
6. **Community and resources**: Extensive documentation, cheat sheets, and examples are available, making it easier to learn and troubleshoot [2], [3], [4].

Base R plots are quick for simple, exploratory graphics, but ggplot2 excels for refined, layered, and publication-ready figures [1], [2], [3], [4]. What aspect do you want to explore further?