

# Class 5: Data Viz 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.

```
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 this to the `plot()` function.

```
plot(cars)
```



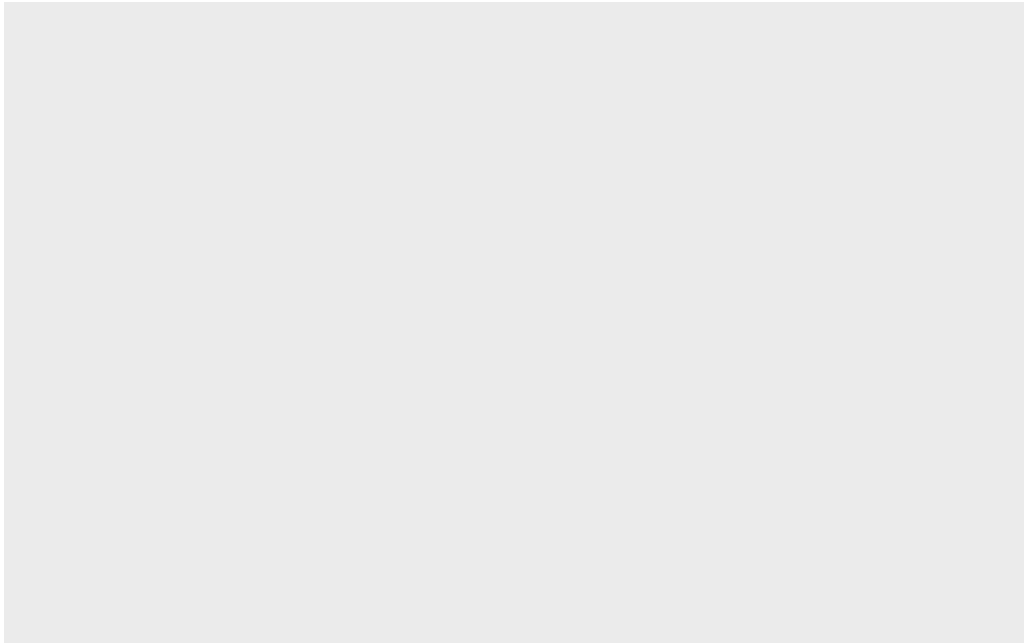
Key-point: Base R is quick but not so nice looking in some folks eyes.

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 `library()` function every time we want to use it.

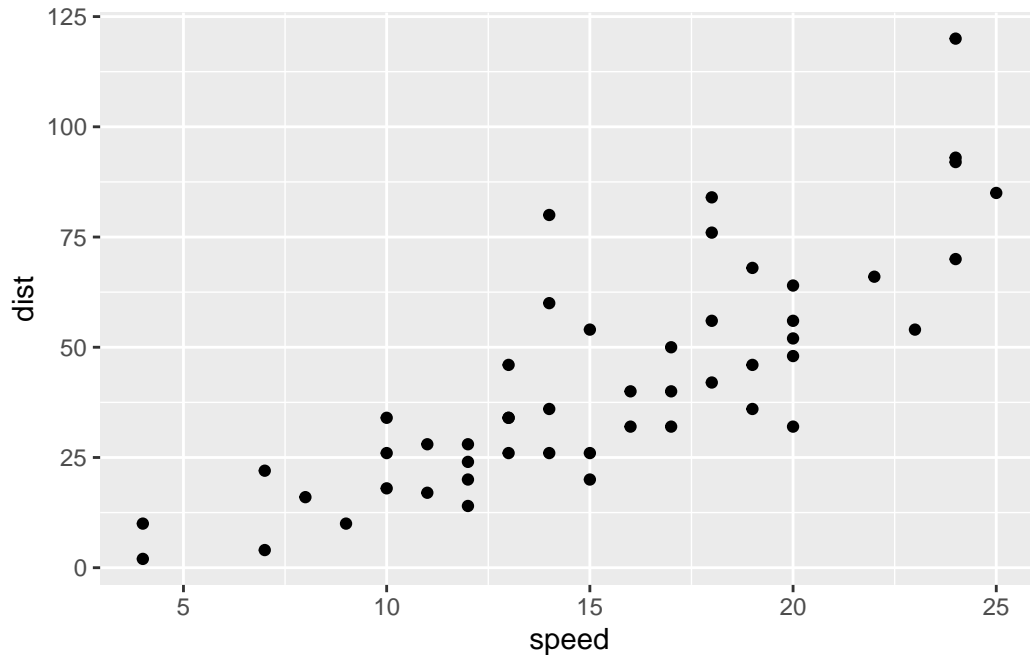
```
library(ggplot2)
ggplot(cars)
```



Every ggplot is composed of at least 3 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 sort how the plot appears

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



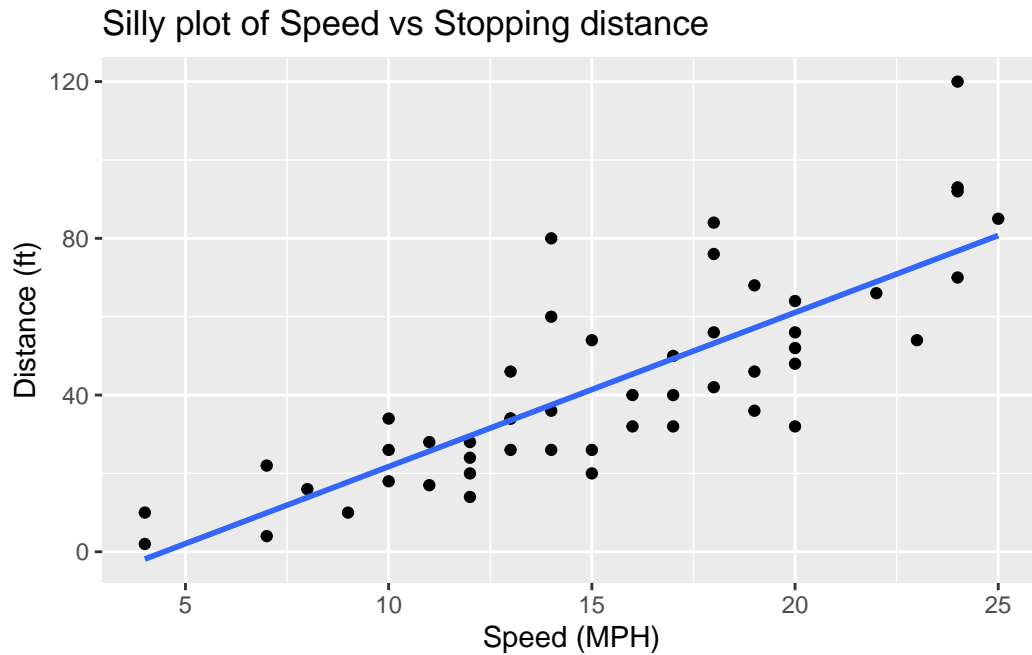
Key point: For simple “canned” graphs base R is quicker but as things get more custom and elaborate then ggplot wins out...

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)” Chnage the theme...

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

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



```
theme_bw()
```

```
<theme> List of 144
```

```
$ line                                     : <ggplot2::element_line>
  ..@ colour      : chr "black"
  ..@ linewidth   : num 0.5
  ..@ linetype    : num 1
  ..@ lineend     : chr "butt"
  ..@ linejoin    : chr "round"
  ..@ arrow       : logi FALSE
  ..@ arrow.fill  : chr "black"
  ..@ inherit.blank: logi TRUE
$ rect                                     : <ggplot2::element_rect>
  ..@ fill        : chr "white"
  ..@ colour      : chr "black"
  ..@ linewidth   : num 0.5
  ..@ linetype    : num 1
  ..@ linejoin    : chr "round"
  ..@ inherit.blank: logi TRUE
$ text                                    : <ggplot2::element_text>
  ..@ family      : chr ""
  ..@ face        : chr "plain"
```

```

..@ italic      : chr NA
..@ fontweight  : num NA
..@ fontwidth   : num NA
..@ colour      : chr "black"
..@ size        : num 11
..@ hjust       : num 0.5
..@ vjust       : num 0.5
..@ angle       : num 0
..@ lineheight  : num 0.9
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..@ inherit.blank: logi TRUE
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..@ fontweight  : num NA
..@ fontwidth   : num NA
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..@ hjust       : NULL
..@ vjust       : NULL
..@ angle       : NULL
..@ lineheight  : NULL
..@ margin      : NULL
..@ debug       : NULL
..@ inherit.blank: logi TRUE
$ point          : <ggplot2::element_point>
..@ colour      : chr "black"
..@ shape       : num 19
..@ size        : num 1.5
..@ fill        : chr "white"
..@ stroke      : num 0.5
..@ inherit.blank: logi TRUE
$ polygon        : <ggplot2::element_polygon>
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..@ colour      : chr "black"
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..@ linetype    : num 1
..@ linejoin    : chr "round"
..@ inherit.blank: logi TRUE
$ geom           : <ggplot2::element_geom>
..@ ink         : chr "black"

```

```

..@ paper      : chr "white"
..@ accent     : chr "#3366FF"
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..@ borderwidth: num 0.5
..@ linetype   : int 1
..@ bordertype : int 1
..@ family     : chr ""
..@ fontsize  : num 3.87
..@ pointsize  : num 1.5
..@ pointshape : num 19
..@ colour     : NULL
..@ fill       : NULL
$ spacing      : 'simpleUnit' num 5.5points
  ..- attr(*, "unit")= int 8
$ margins      : <ggplot2::margin> num [1:4] 5.5 5.5 5.5 5.5
$ aspect.ratio : NULL
$ axis.title   : NULL
$ axis.title.x : <ggplot2::element_text>
  ..@ family    : NULL
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  ..@ italic    : chr NA
  ..@ fontweight: num NA
  ..@ fontwidth : num NA
  ..@ colour    : NULL
  ..@ size      : NULL
  ..@ hjust     : NULL
  ..@ vjust     : num 1
  ..@ angle     : NULL
  ..@ lineheight: NULL
  ..@ margin    : <ggplot2::margin> num [1:4] 2.75 0 0 0
  ..@ debug     : NULL
  ..@ inherit.blank: logi TRUE
$ axis.title.x.top : <ggplot2::element_text>
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  ..@ face      : NULL
  ..@ italic    : chr NA
  ..@ fontweight: num NA
  ..@ fontwidth : num NA
  ..@ colour    : NULL
  ..@ size      : NULL
  ..@ hjust     : NULL
  ..@ vjust     : num 0
  ..@ angle     : NULL

```

```

..@ lineheight      : NULL
..@ margin          : <ggplot2::margin> num [1:4] 0 0 2.75 0
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$ axis.title.y            : <ggplot2::element_text>
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..@ size             : NULL
..@ hjust            : NULL
..@ vjust            : num 1
..@ angle            : num -90
..@ lineheight       : NULL
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..@ family           : NULL
..@ face             : NULL
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..@ fontweight       : num NA
..@ fontwidth        : num NA
..@ colour           : chr "#4D4D4DFF"

```



```

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..@ face          : NULL
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..@ fontweight    : num NA
..@ fontwidth     : num NA
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..@ angle         : NULL
..@ lineheight    : NULL
..@ margin        : <ggplot2::margin> num [1:4] 2.2 0 0 0
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..@ size          : NULL
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..@ vjust         : num 0
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..@ lineheight    : NULL
..@ margin        : <ggplot2::margin> num [1:4] 0 0 2.2 0
..@ debug         : NULL
..@ inherit.blank: logi TRUE
$ axis.text.x.bottom   : NULL
$ axis.text.y          : <ggplot2::element_text>
..@ family        : NULL
..@ face          : NULL
..@ italic        : chr NA

```

```

..@ fontweight      : num NA
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..@ hjust           : num 1
..@ vjust           : NULL
..@ angle           : NULL
..@ lineheight      : NULL
..@ margin           : <ggplot2::margin> num [1:4] 0 2.2 0 0
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$ axis.text.y.left   : NULL
$ axis.text.y.right  : <ggplot2::element_text>
..@ family          : NULL
..@ face            : NULL
..@ italic          : chr NA
..@ fontweight      : num NA
..@ fontwidth       : num NA
..@ colour          : NULL
..@ size            : NULL
..@ hjust           : num 0
..@ vjust           : NULL
..@ angle           : NULL
..@ lineheight      : NULL
..@ margin           : <ggplot2::margin> num [1:4] 0 0 0 2.2
..@ debug           : NULL
..@ inherit.blank   : logi TRUE
$ axis.text.theta    : NULL
$ axis.text.r        : <ggplot2::element_text>
..@ family          : NULL
..@ face            : NULL
..@ italic          : chr NA
..@ fontweight      : num NA
..@ fontwidth       : num NA
..@ colour          : NULL
..@ size            : NULL
..@ hjust           : num 0.5
..@ vjust           : NULL
..@ angle           : NULL
..@ lineheight      : NULL
..@ margin           : <ggplot2::margin> num [1:4] 0 2.2 0 2.2
..@ debug           : NULL
..@ inherit.blank   : logi TRUE

```

```

$ axis.ticks : <ggplot2::element_line>
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  ..@ inherit.blank: logi TRUE
$ axis.ticks.x : NULL
$ axis.ticks.x.top : NULL
$ axis.ticks.x.bottom : NULL
$ axis.ticks.y : NULL
$ axis.ticks.y.left : NULL
$ axis.ticks.y.right : NULL
$ axis.ticks.theta : NULL
$ axis.ticks.r : NULL
$ axis.minor.ticks.x.top : NULL
$ axis.minor.ticks.x.bottom : NULL
$ axis.minor.ticks.y.left : NULL
$ axis.minor.ticks.y.right : NULL
$ axis.minor.ticks.theta : NULL
$ axis.minor.ticks.r : NULL
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$ axis.ticks.length.x : NULL
$ axis.ticks.length.x.top : NULL
$ axis.ticks.length.x.bottom : NULL
$ axis.ticks.length.y : NULL
$ axis.ticks.length.y.left : NULL
$ axis.ticks.length.y.right : NULL
$ axis.ticks.length.theta : NULL
$ axis.ticks.length.r : NULL
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$ axis.minor.ticks.length.x.bottom : NULL
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$ axis.minor.ticks.length.y.left : NULL
$ axis.minor.ticks.length.y.right : NULL
$ axis.minor.ticks.length.theta : NULL
$ axis.minor.ticks.length.r : NULL
$ axis.line : <ggplot2::element_blank>
$ axis.line.x : NULL

```

```

$ axis.line.x.top           : NULL
$ axis.line.x.bottom        : NULL
$ axis.line.y               : NULL
$ axis.line.y.left          : NULL
$ axis.line.y.right         : NULL
$ axis.line.theta           : NULL
$ axis.line.r               : NULL
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  ..@ linejoin               : NULL
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$ legend.spacing.y          : NULL
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$ legend.key.spacing        : NULL
$ legend.key.spacing.x      : NULL
$ legend.key.spacing.y      : NULL
$ legend.key.justification   : NULL
$ legend.frame              : NULL
$ legend.ticks              : NULL
$ legend.ticks.length       : 'rel' num 0.2
$ legend.axis.line          : NULL
$ legend.text               : <ggplot2::element_text>
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  ..@ vjust                  : NULL
  ..@ angle                  : NULL
  ..@ lineheight             : NULL

```

```

..@ margin      : NULL
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..@ inherit.blank: logi TRUE
$ legend.text.position      : NULL
$ legend.title              : <ggplot2::element_text>
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..@ face                 : NULL
..@ italic               : chr NA
..@ fontweight           : num NA
..@ fontwidth            : num NA
..@ colour               : NULL
..@ size                 : NULL
..@ hjust                : num 0
..@ vjust                : NULL
..@ angle                : NULL
..@ lineheight           : NULL
..@ margin               : NULL
..@ debug               : NULL
..@ inherit.blank: logi TRUE
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$ legend.position.inside   : NULL
$ legend.direction         : NULL
$ legend.byrow             : NULL
$ legend.justification     : chr "center"
$ legend.justification.top : NULL
$ legend.justification.bottom : NULL
$ legend.justification.left : NULL
$ legend.justification.right : NULL
$ legend.justification.inside : NULL
[list output truncated]
@ complete: logi TRUE
@ validate: logi TRUE

```

## Going further

Read some 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 wee dataset?

```
nrow(genes)
```

```
[1] 5196
```

Q2. How many “up” regulated genes are there?

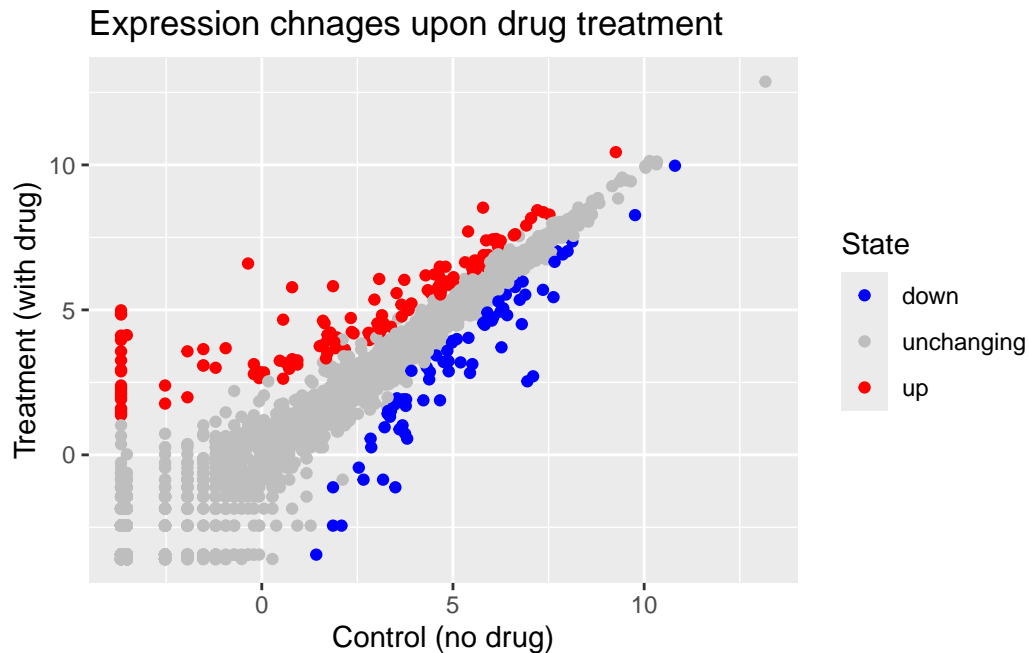
```
table(genes$State)
```

|      |            |     |
|------|------------|-----|
| down | unchanging | up  |
| 72   | 4997       | 127 |

A useful function for counting up occurrences of things in a vector is the `table()` function.

Make a v1 figure

```
p<-ggplot(genes) +
  aes(x= Condition1,
      y= Condition2,
      col=State) +
  geom_point() +
  labs(title= "Expression chnages upon drug treatment",
       x="Control (no drug)",
       y="Treatment (with drug)")
p + scale_colour_manual(values = c("blue", "gray","red"))
```



```
##More PLOtting library(gapminder)
```

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

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

Lets have a wee peak

```
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  |

Q4. How many different country values are in this dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

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

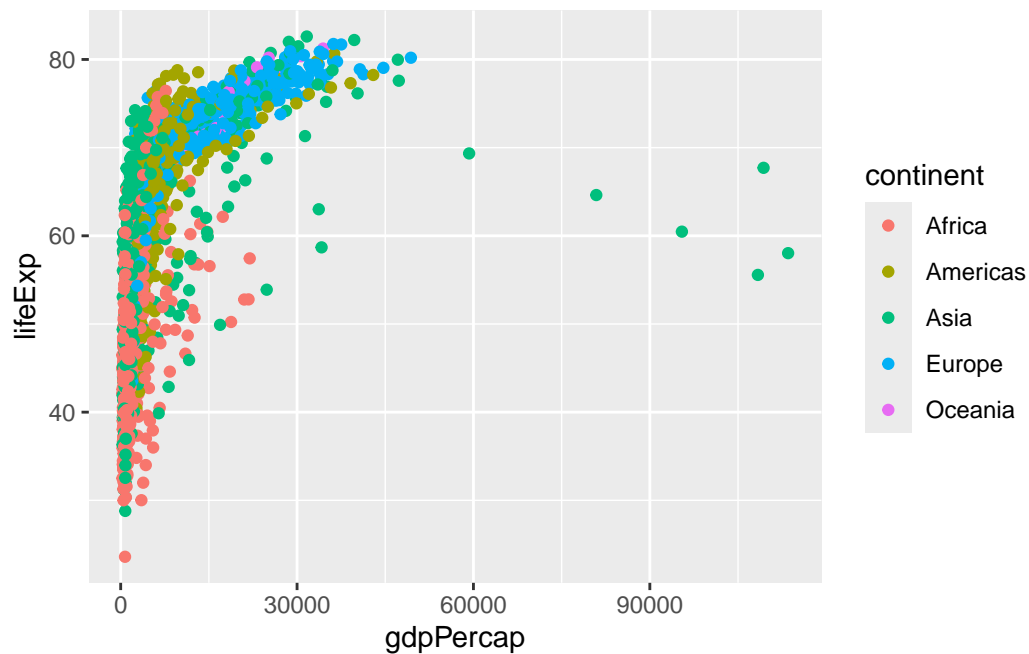
```
[1] 142
```

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

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

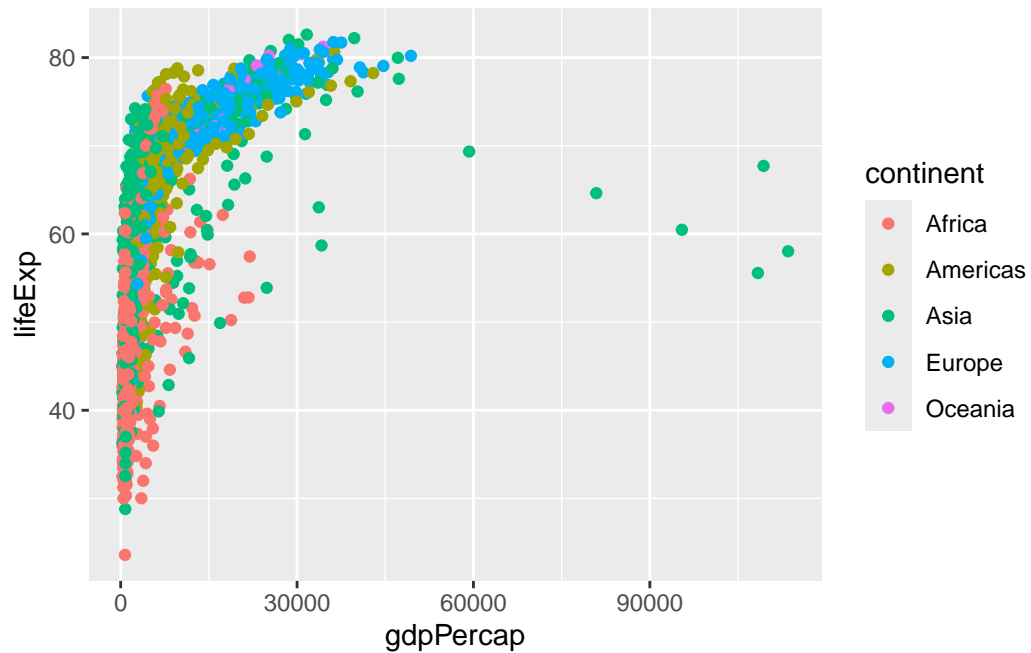
```
[1] "Asia"      "Europe"    "Africa"    "Americas" "Oceania"
```

```
ggplot(gapminder) +  
  aes(gdpPercap, lifeExp, color=continent) +  
  geom_point()
```



```
ggplot(gapminder) +  
  aes(gdpPercap, lifeExp, color=continent, label=country) +  
  geom_point()
```



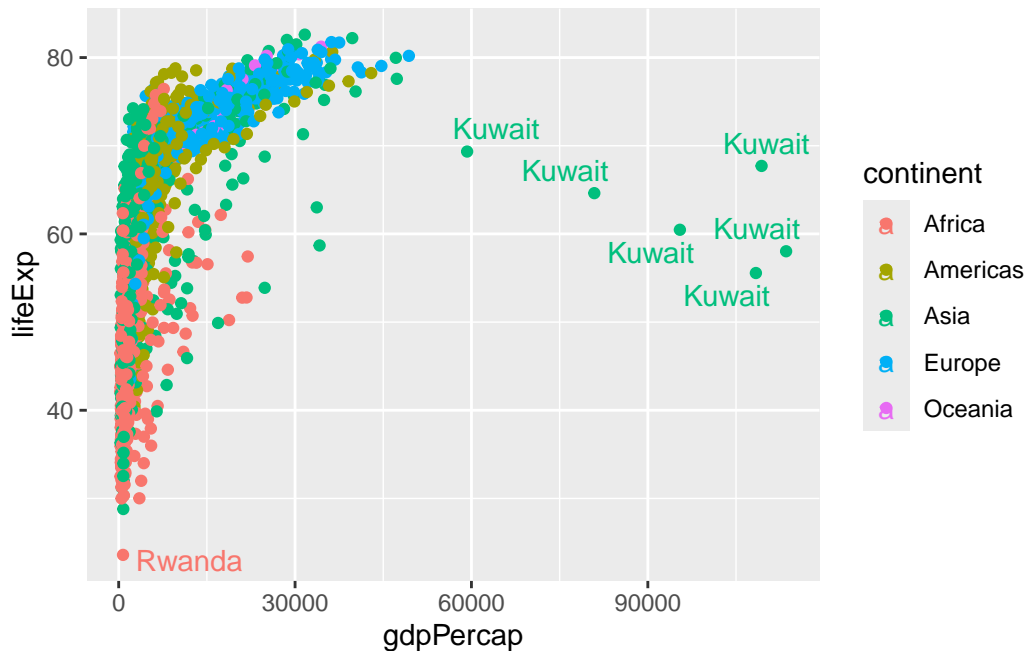


I can use the **ggrepel** package to make more sensible labels here.

```
library(ggrepel)

ggplot(gapminder) +
  aes(gdpPerCap, lifeExp, color=continent, label=country) +
  geom_point() +
  geom_text_repel()
```

Warning: ggrepel: 1697 unlabeled data points (too many overlaps). Consider increasing max.overlaps



I want a separate panel per continent

```
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, color=continent, label=country) +
  geom_point() +
  geom_text_repel() +
  facet_wrap(~continent)
```

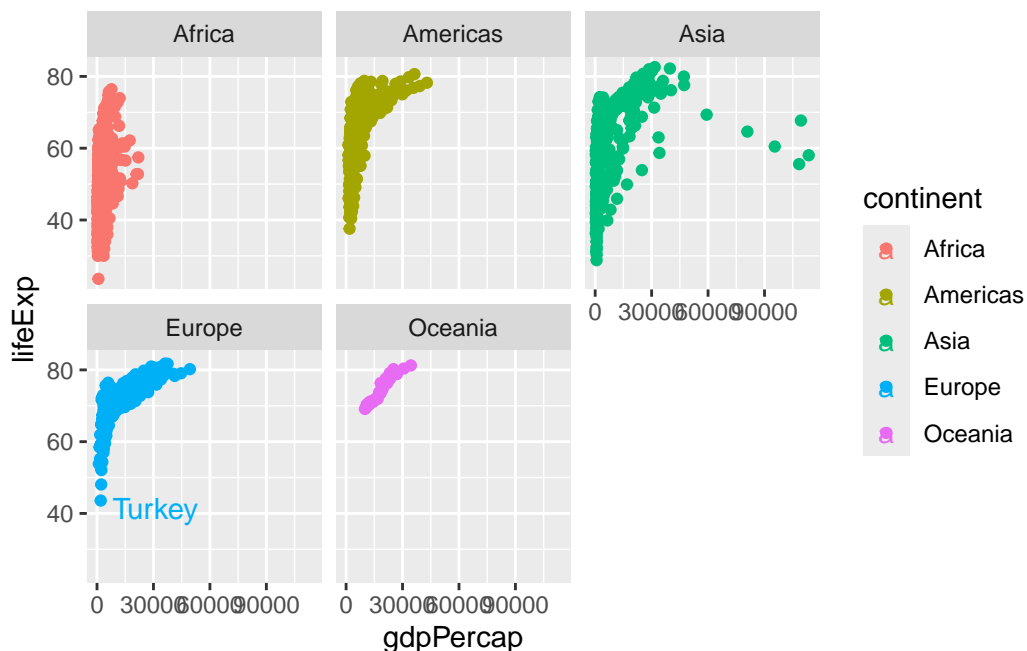
Warning: ggrepel: 624 unlabeled data points (too many overlaps). Consider increasing max.overlaps

Warning: ggrepel: 359 unlabeled data points (too many overlaps). Consider increasing max.overlaps

Warning: ggrepel: 300 unlabeled data points (too many overlaps). Consider increasing max.overlaps

Warning: ggrepel: 24 unlabeled data points (too many overlaps). Consider increasing max.overlaps

Warning: ggrepel: 396 unlabeled data points (too many overlaps). Consider increasing max.overlaps



ggplot2 offers several advantages over base R plots:

1. **Layered Grammar:** ggplot2 uses a consistent, layered approach for building plots, making it easier to add or modify elements (data, aesthetics, geoms) step by step [1], [2], [3], [5], [4].
2. **Publication Quality:** ggplot2 produces visually appealing, publication-quality figures with sensible defaults, which are harder to achieve with base R without extensive tweaking [1], [2], [3], [4].
3. **Customization:** Customizing complex plots is more straightforward in ggplot2. Adding legends, themes, or combining multiple plots is easier and less error-prone than in base R [1], [2], [3].
4. **Consistency:** The syntax and logic are consistent across different plot types, reducing the need to learn many separate functions as in base R [1], [2], [3], [5].
5. **Extensibility:** ggplot2 is part of a larger ecosystem, allowing integration with other packages for advanced graphics and analysis [1].

What do you think is the most important advantage for your own work?