Class 5: Data Viz with ggplot

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Today we are exploring the **gggplot**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 in **ggplot2**

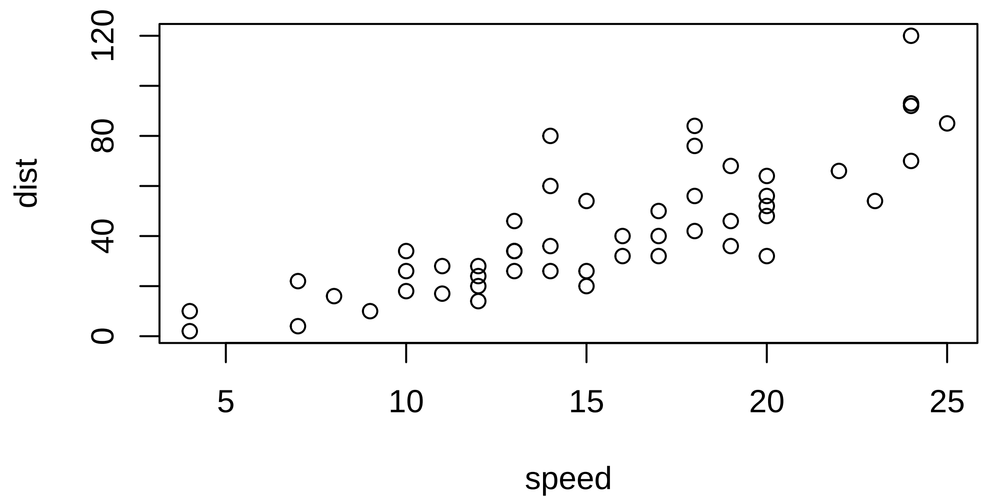
Here is a simple "base" R plot.

```
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 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 **ggplot**…

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.

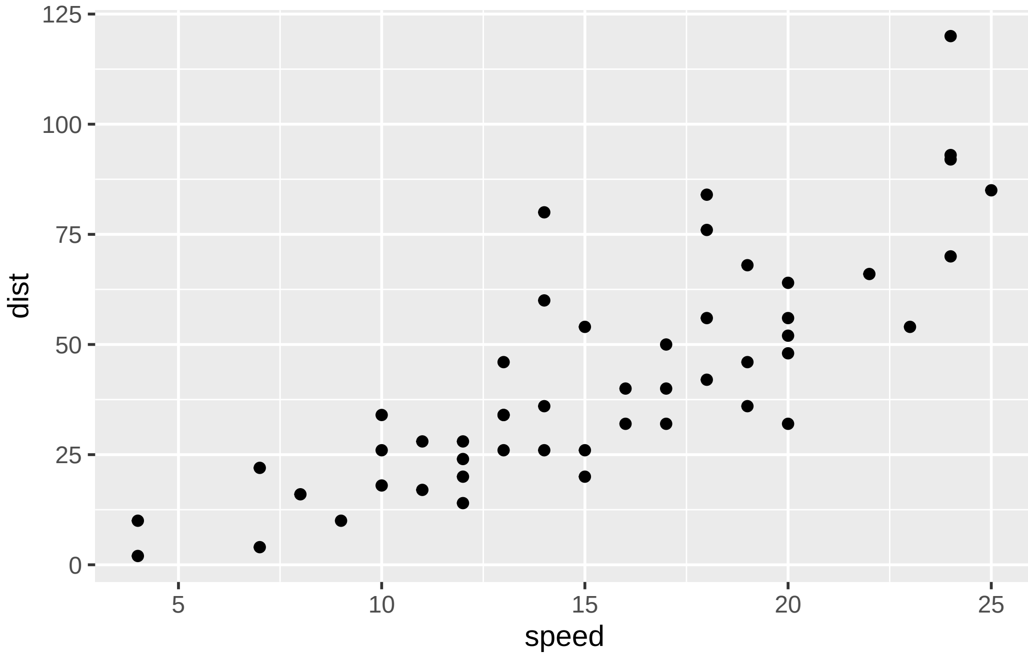
2nd We need to load the package with `library()` function every time we want to use it.

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

Every ggplot is composed of at leasr 3 layers:

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

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



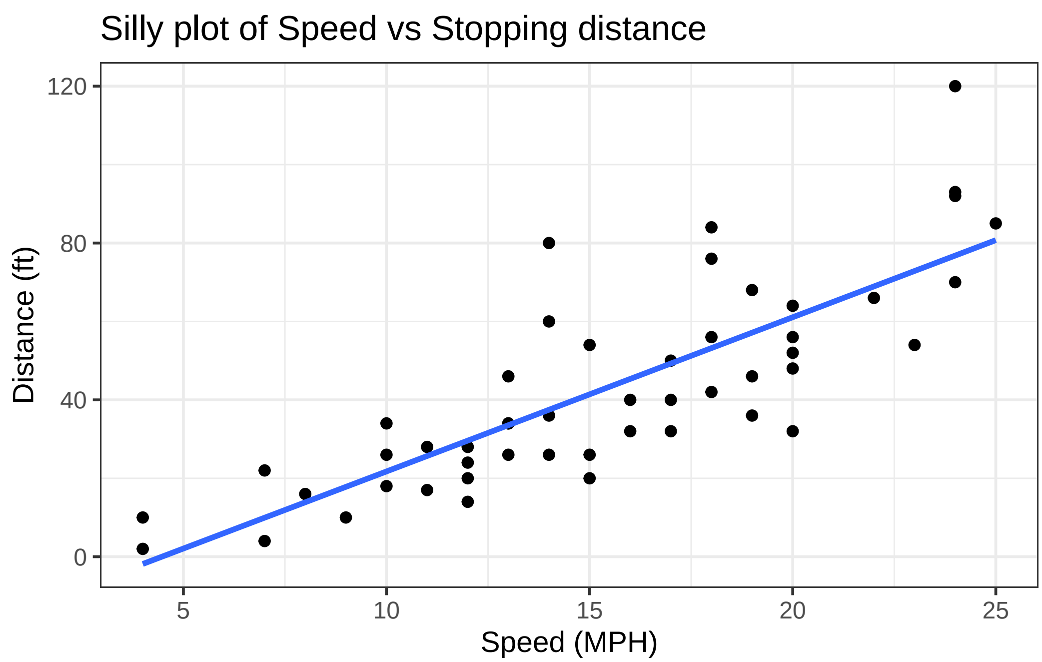
> Key point: For simple "canned" graphs base R is quicker but as things get more custom and elobrate then ggplot wins out…

Let's add more layers to out 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…

```
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

```
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 gene are in this wee dataset?

```
nrow(genes)
```

```
[1] 5196
```

```r
ncol(genes)
```

```
[1] 4
```

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

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

```
[1] 127
```

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

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

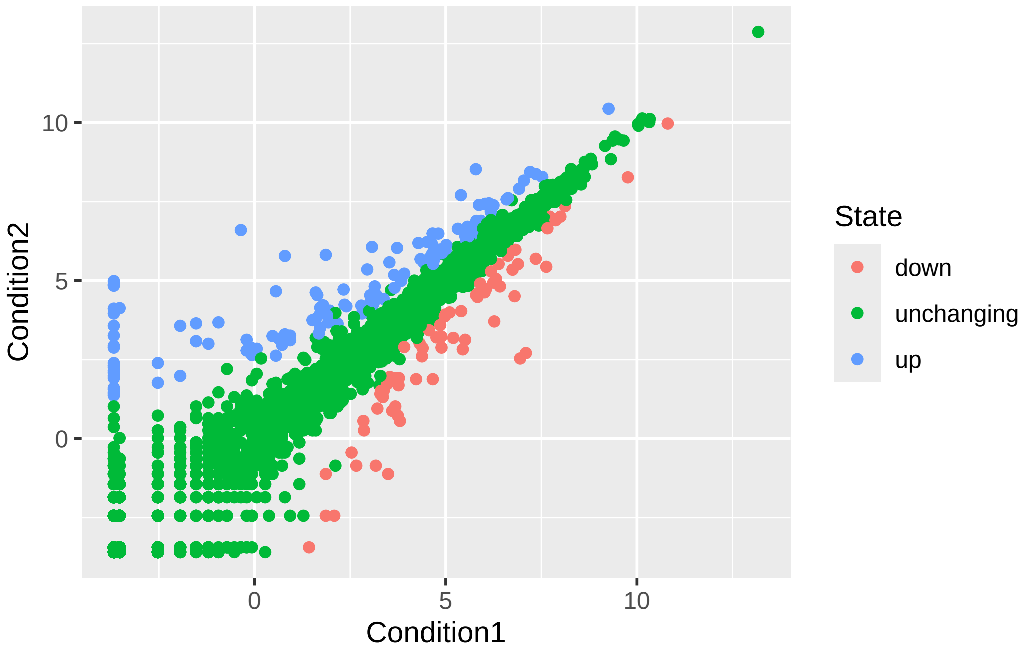
```

      down unchanging         up 
        72       4997        127 
```

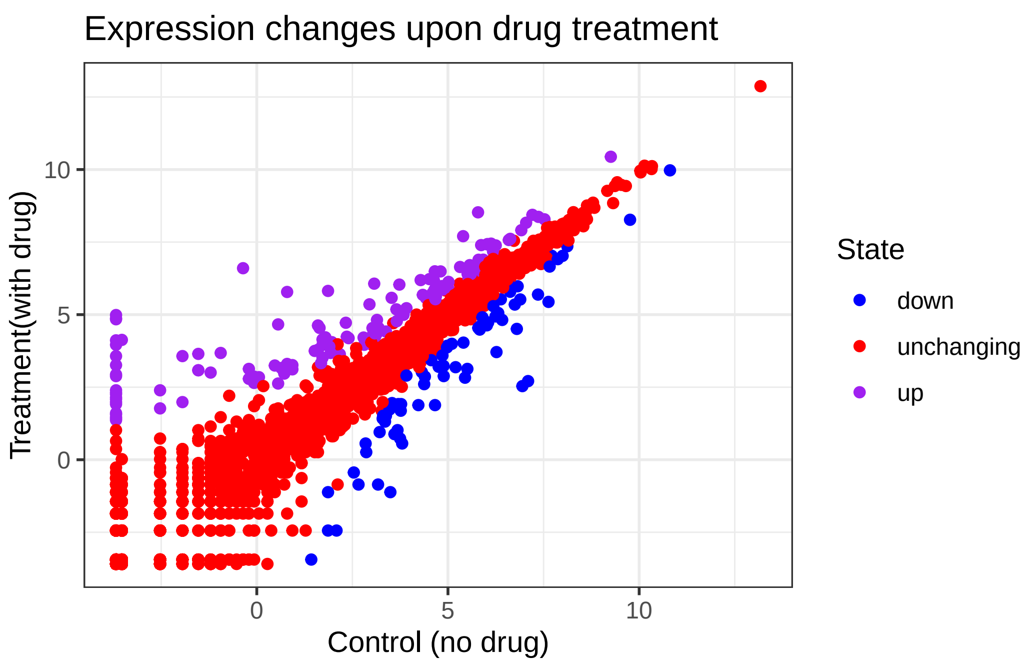
Make a v1 figure

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

p
```




```
p +
  scale_colour_manual(values=c("blue", "red", "purple")) + labs(title="Expression changes upo
     x="Control (no drug)",
     y= "Treatment(with drug)") +
  theme_bw()
```



More plotting

Read in the gapminder database

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

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

Let's 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
```

```
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
```

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

```r
nrow(gapminder)
```

```
[1] 1704
```

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

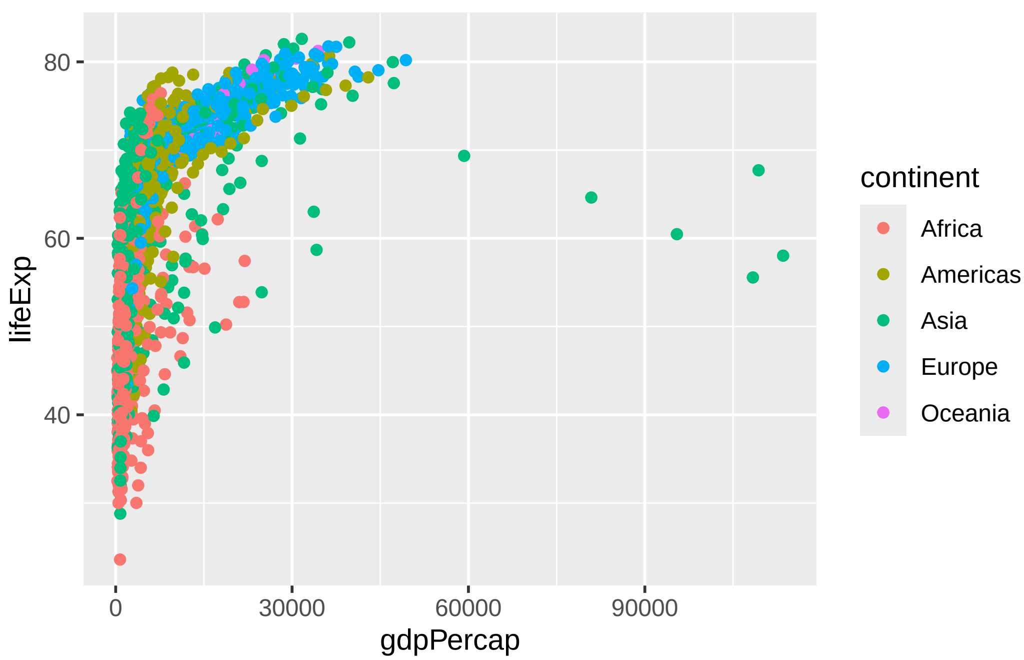
```
[1] 142
```

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

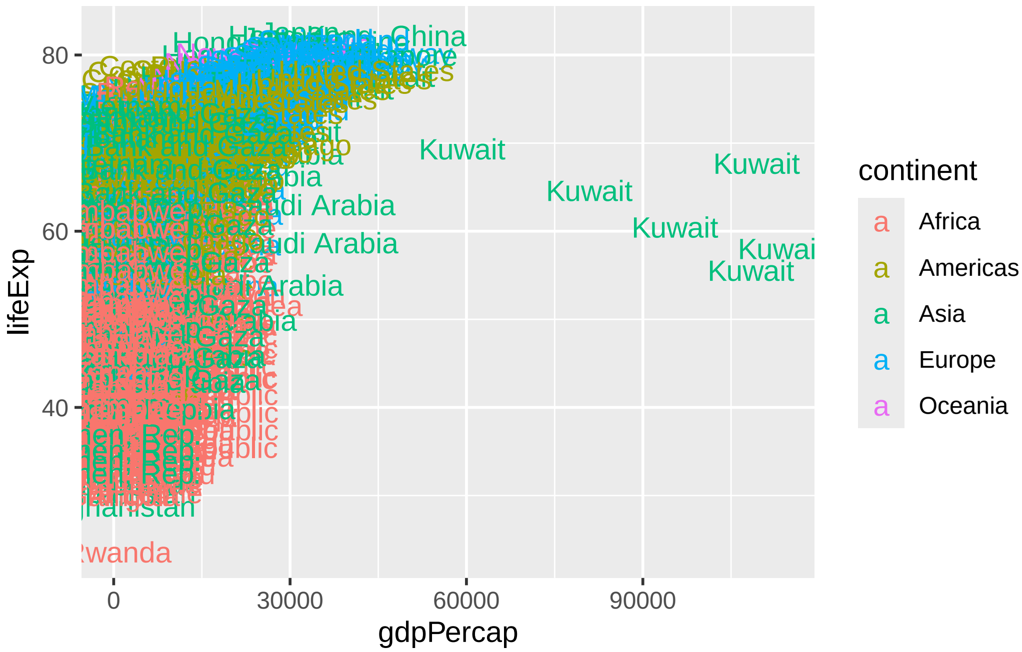
```r
unique(gapminder$continent)
```

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

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



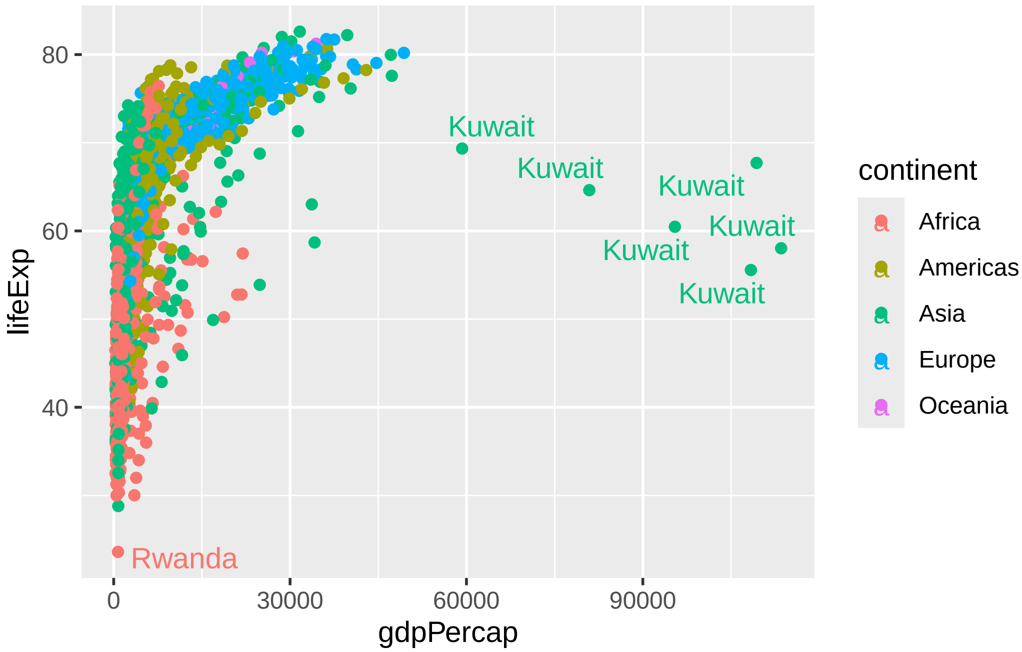
```r
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col=continent, label=country) +
  geom_text()
```



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

```r
library(ggrepel)
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col=continent, label=country) +
  geom_point() +
  geom_text_repel()
```

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



I want a seperate pannel per continent

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

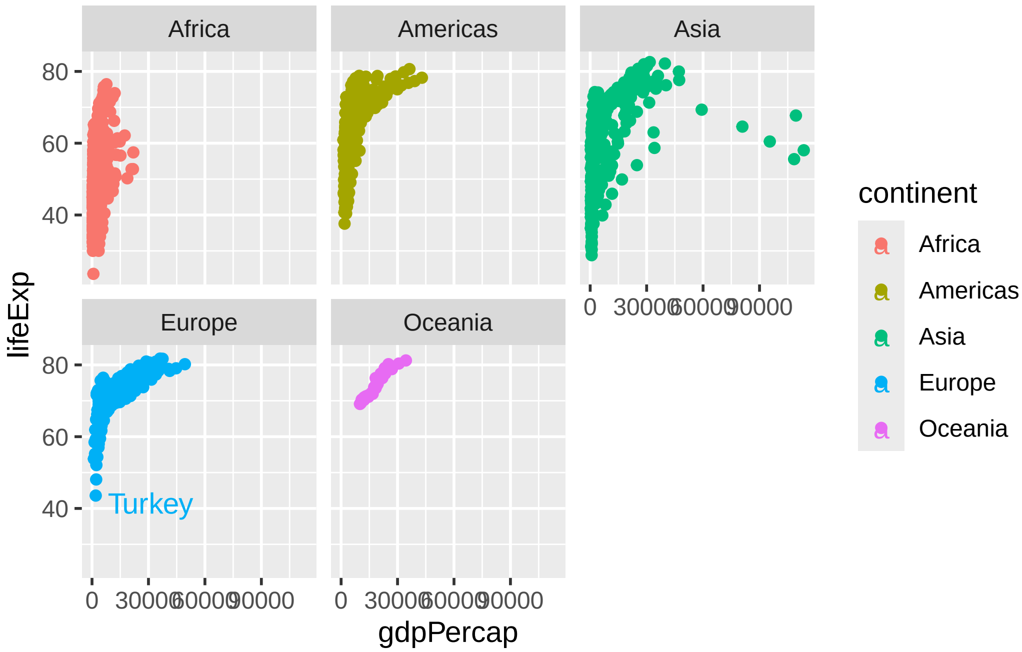
```
Warning: ggrepel: 624 unlabeled data points (too many overlaps). Consider
increasing max.overlaps
```

```
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
```



Summary

The main advantges of ggplot over base R plot are :

1. **Grammar of Graphics** – ggplot2 is built on a clear, consistent "grammar" that separates data, aesthetics, and geometries. This makes it easier to construct complex plots step-by-step and to modify individual layers without rewriting the whole graph.
2. **Layered Design** – You can add multiple geometric objects (points, lines, ribbons, etc.) on top of each other with +. This encourages incremental building and easy tweaking of components such as annotations, smoothers, or facets.
3. **Automatic Aesthetic Mapping** – Mapping variables to colour, shape, size, or transparency is handled inside aes(). ggplot2 automatically generates appropriate legends and scales, reducing boilerplate code.
4. **Faceting for Small-Multiples** – facet_wrap() and facet_grid() split data into a matrix of sub-plots with minimal effort, a feature that requires considerable manual work in base graphics.
5. **Theme System** – Consistent styling is achieved through reusable themes (theme_minimal(), theme_bw(), custom theme() objects). Changing fonts, backgrounds, or gridlines across many plots is straightforward.
6. **Built-in Statistical Transformations** – Geoms like geom_smooth(), geom_histogram(), and geom_boxplot() automatically compute summaries (e.g., density, counts, quantiles) without extra code.

7. **Extensibility** – A large ecosystem of extensions (e.g., ggrepel, gganimate, sf for spatial data) builds on the same grammar, allowing you to add labels, animations, or map layers with minimal learning curve.
8. **Publication-Ready Output** – Fine-grained control over every visual element, combined with seamless integration with ggsave() for PDF, PNG, or vector formats, makes it easier to produce figures that meet journal standards.
9. **Consistency Across Plot Types** – Whether you are creating a scatterplot, heatmap, or choropleth, the same syntax (ggplot(data) + geom_*() + …) applies, reducing the mental load of remembering different function signatures.