

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

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

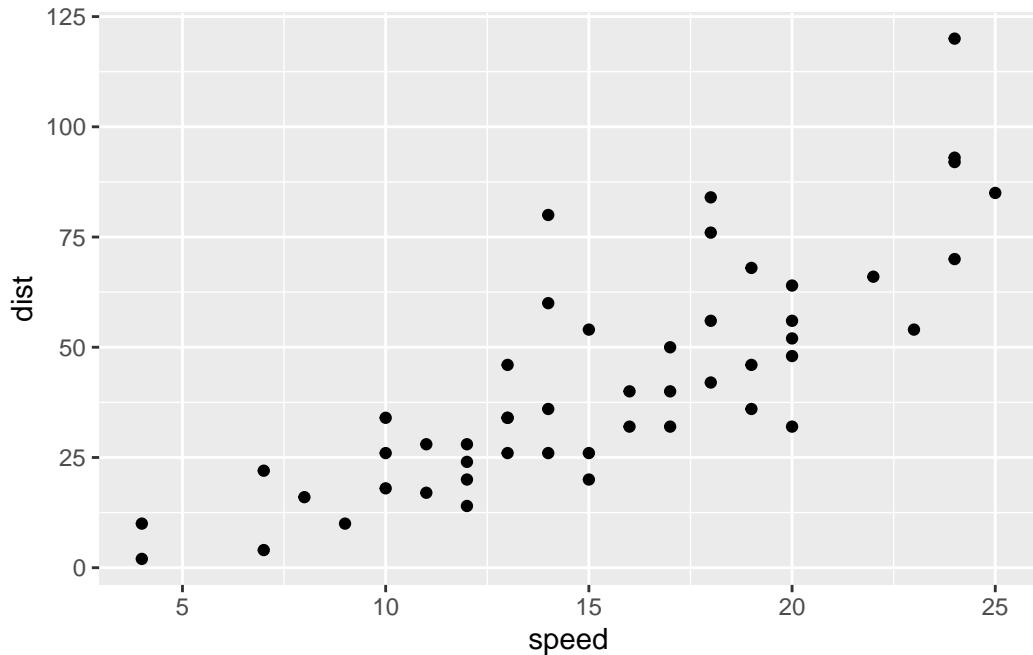
```
library(ggplot2)
ggplot(cars)
```



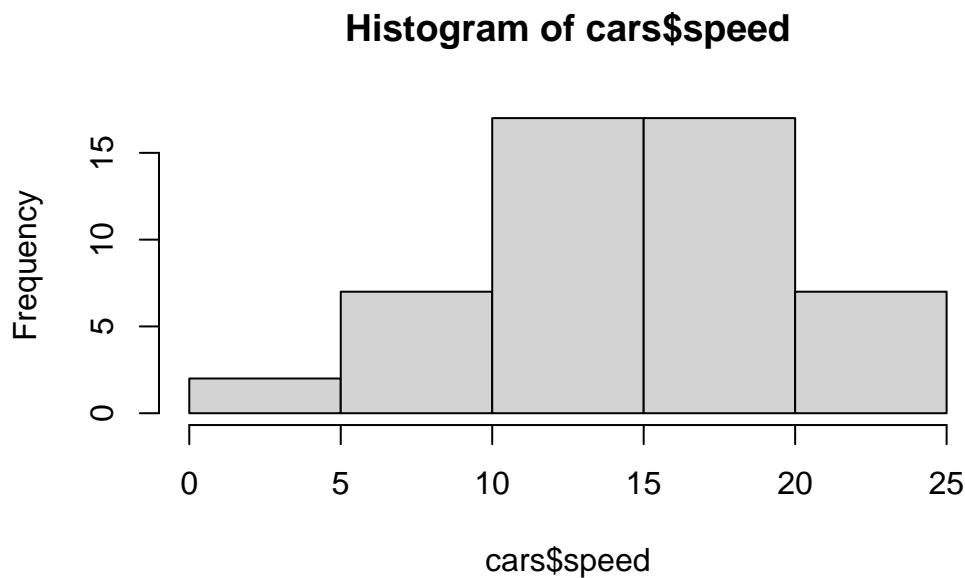
Every ggplot is composed of at least 3 layers:

- **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()
```



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

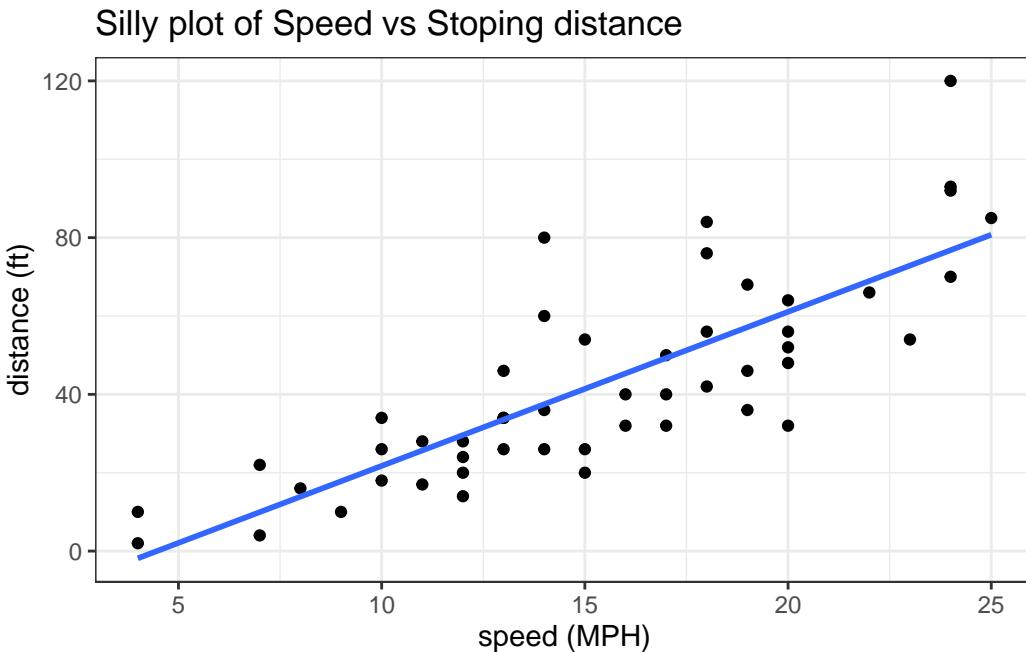


Key point: For simple “canned” graphs base R is quicker and more concise but as things get more custom the elaborate then ggplot wins out...

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...

```
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 genes are in this wee dataset

```
nrow(genes)
```

[1] 5196

```
ncol(genes)
```

[1] 4

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

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

[1] 127

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

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

down	unchanging	up
72	4997	127

fraction

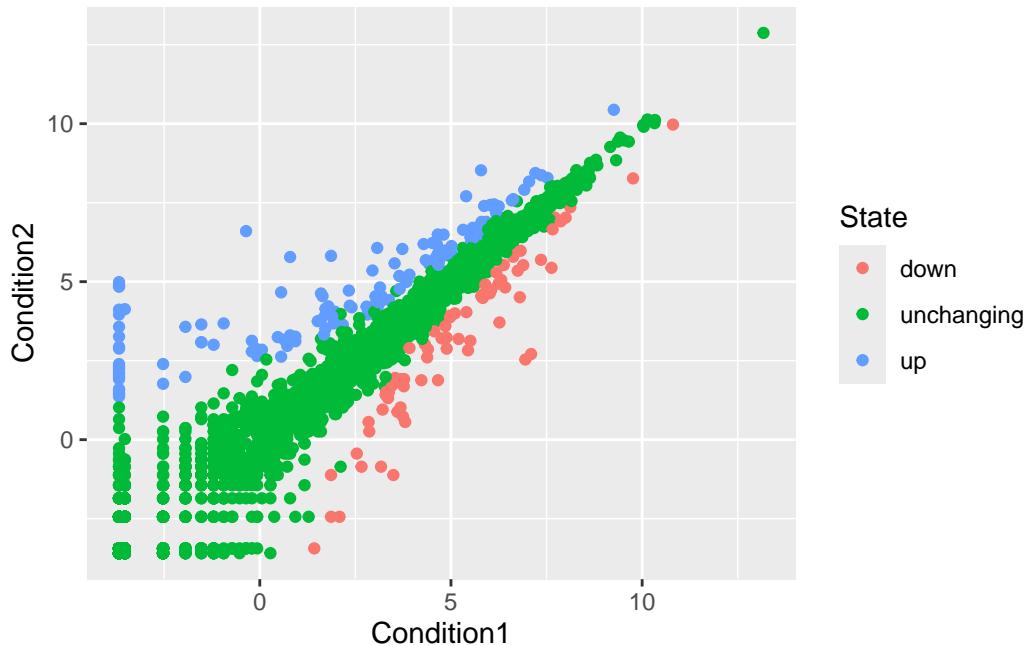
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

down	unchanging	up
1.39	96.17	2.44

Make a v1 figure

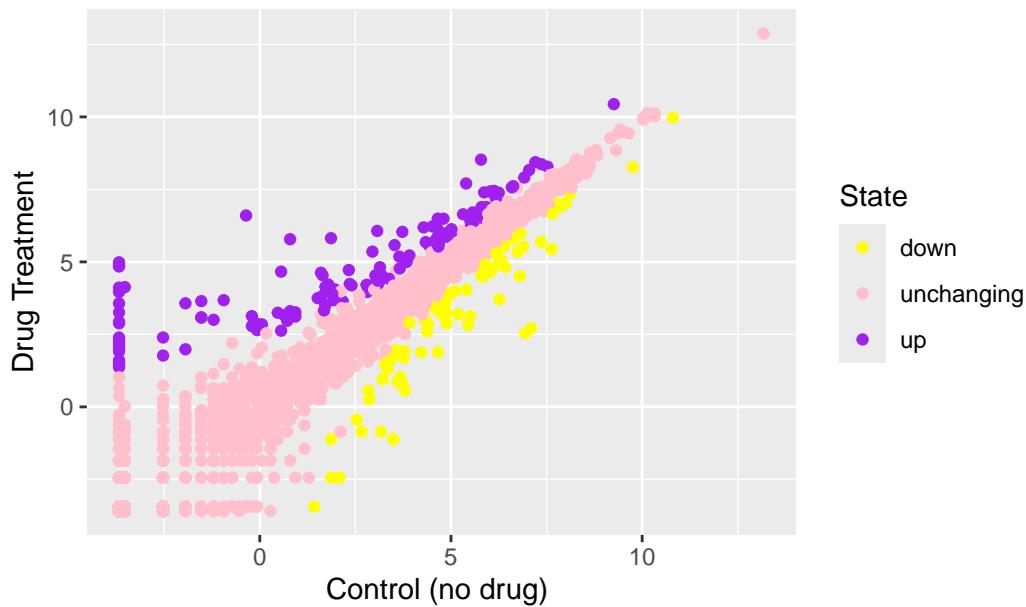
```
p <- ggplot(genes) +  
  aes(x=Condition1,  
       y=Condition2,  
       col=State) +  
  geom_point()
```

```
p
```



```
p + scale_colour_manual(values=c("yellow","pink","purple")) +  
  labs(title="Gene Expression Changes Upon Drug Treatment",  
       x="Control (no drug) ",  
       y="Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment



More Plotting

Read gapmider

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

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
```

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

Afghanistan	Albania	Algeria
12	12	12
Angola	Argentina	Australia
12	12	12
Austria	Bahrain	Bangladesh
12	12	12
Belgium	Benin	Bolivia
12	12	12
Bosnia and Herzegovina	Botswana	Brazil
12	12	12
Bulgaria	Burkina Faso	Burundi
12	12	12
Cambodia	Cameroon	Canada
12	12	12
Central African Republic	Chad	Chile
12	12	12
China	Colombia	Comoros
12	12	12
Congo, Dem. Rep.	Congo, Rep.	Costa Rica
12	12	12
Cote d'Ivoire	Croatia	Cuba
12	12	12
Czech Republic	Denmark	Djibouti
12	12	12
Dominican Republic	Ecuador	Egypt
12	12	12
El Salvador	Equatorial Guinea	Eritrea
12	12	12
Ethiopia	Finland	France
12	12	12
Gabon	Gambia	Germany
12	12	12
Ghana	Greece	Guatemala
12	12	12

Guinea		Guinea-Bissau		Haiti
12		12		12
Honduras		Hong Kong, China		Hungary
12		12		12
Iceland		India		Indonesia
12		12		12
Iran		Iraq		Ireland
12		12		12
Israel		Italy		Jamaica
12		12		12
Japan		Jordan		Kenya
12		12		12
Korea, Dem. Rep.		Korea, Rep.		Kuwait
12		12		12
Lebanon		Lesotho		Liberia
12		12		12
Libya		Madagascar		Malawi
12		12		12
Malaysia		Mali		Mauritania
12		12		12
Mauritius		Mexico		Mongolia
12		12		12
Montenegro		Morocco		Mozambique
12		12		12
Myanmar		Namibia		Nepal
12		12		12
Netherlands		New Zealand		Nicaragua
12		12		12
Niger		Nigeria		Norway
12		12		12
Oman		Pakistan		Panama
12		12		12
Paraguay		Peru		Philippines
12		12		12
Poland		Portugal		Puerto Rico
12		12		12
Reunion		Romania		Rwanda
12		12		12
Sao Tome and Principe		Saudi Arabia		Senegal
12		12		12
Serbia		Sierra Leone		Singapore
12		12		12
Slovak Republic		Slovenia		Somalia

	12	12	12
South Africa		Spain	Sri Lanka
	12		12
Sudan		Swaziland	Sweden
	12		12
Switzerland		Syria	Taiwan
	12		12
Tanzania		Thailand	Togo
	12		12
Trinidad and Tobago		Tunisia	Turkey
	12		12
Uganda		United Kingdom	United States
	12		12
Uruguay		Venezuela	Vietnam
	12		12
West Bank and Gaza		Yemen, Rep.	Zambia
	12		12
Zimbabwe			
	12		

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

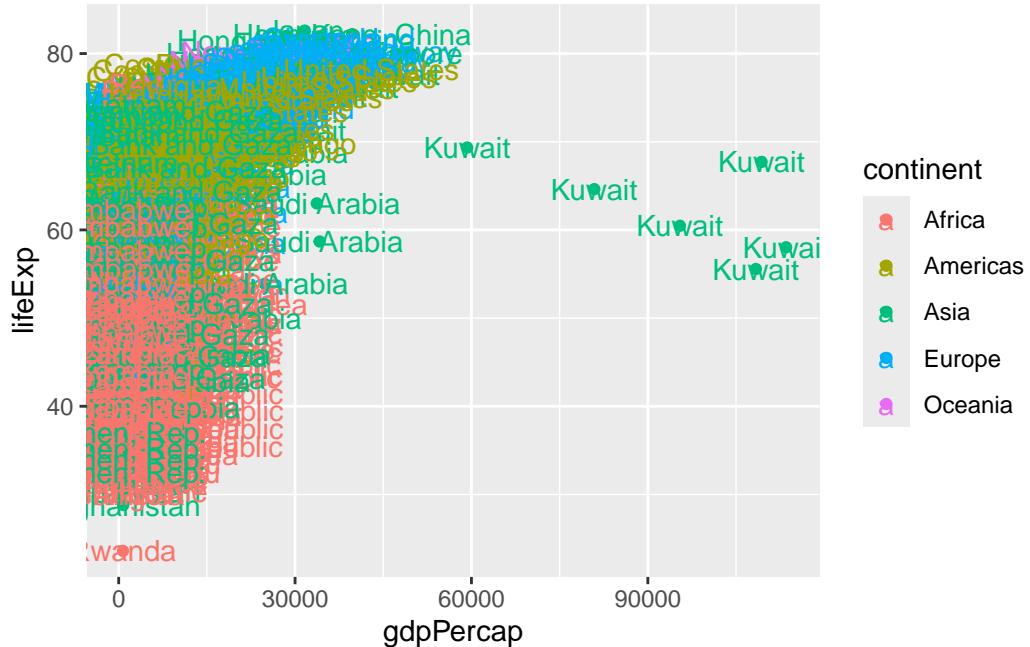
```
[1] 142
```

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

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

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

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

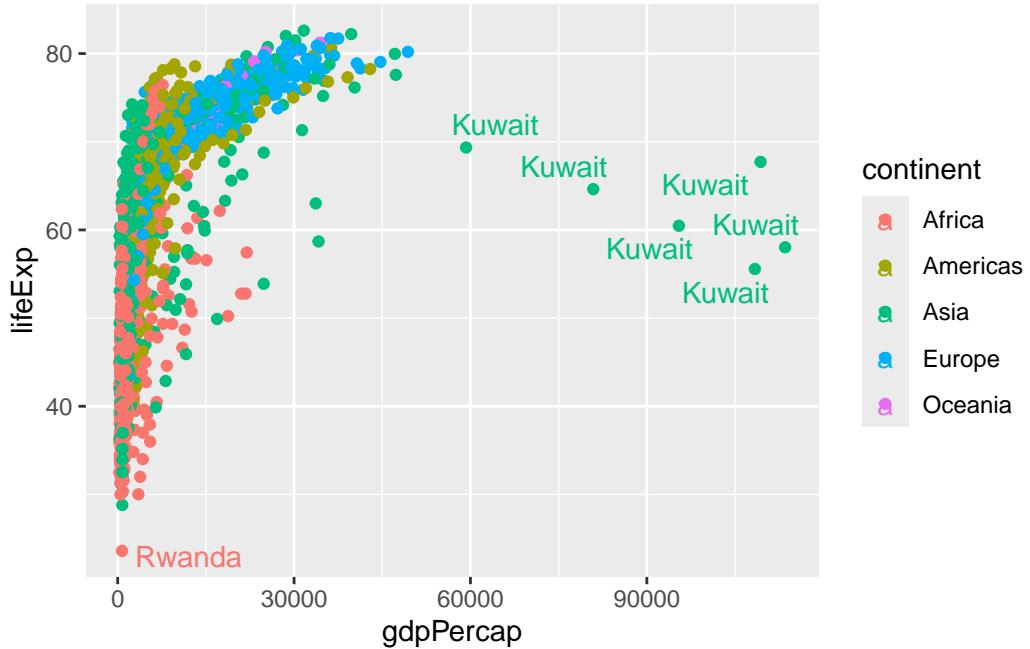


I can use `ggrepel` package to make more sensible labels here.

```
library(ggrepel)

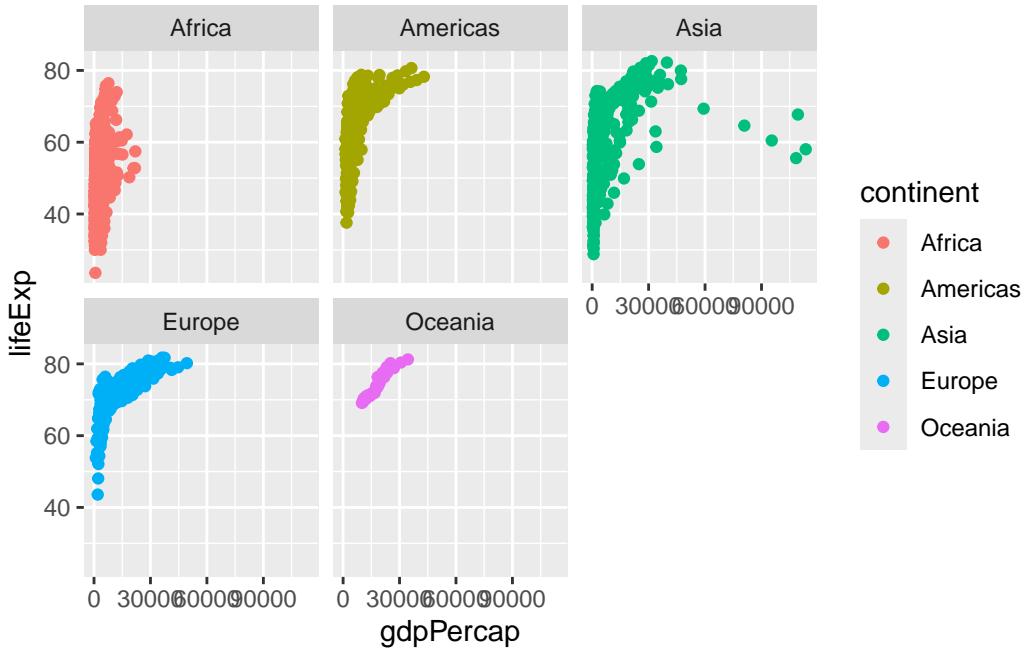
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col=continent, label=country) +
  geom_point() +
  geom_text_repel()
```

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



I want a separate panel per continent

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



#[#]Summary

The main advantages of ggplot over base R plotting are:

Let's focus on the main advantages of ggplot2 over base R plotting:

1. ggplot2 uses a layered approach (data, aesthetics, geometry), making it easier to build complex, publication-quality plots by adding layers step by step. Base R requires different functions and many arguments for each plot type, which can be fiddly and time-consuming to refine for publication-quality figures.
2. ggplot2 provides sensible defaults for aesthetics and themes, so plots look visually appealing with less manual tweaking. Base R gives full control but often needs more effort to polish.
3. ggplot2 code is more concise for complex plots, while base R is quicker for simple, exploratory plots but gets verbose and complicated for advanced visualizations.
4. ggplot2 makes it easier to automate and reproduce plots, especially for reports, since the same code structure applies to different datasets and plot types.