

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 plots 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.

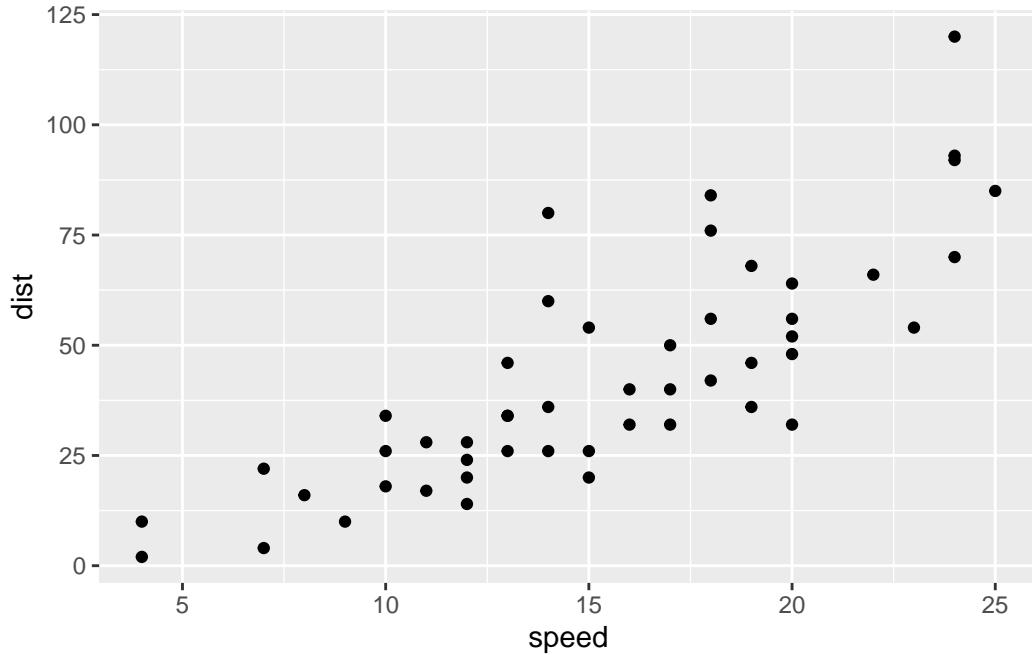
```
library(ggplot2)
ggplot(cars)
```



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...

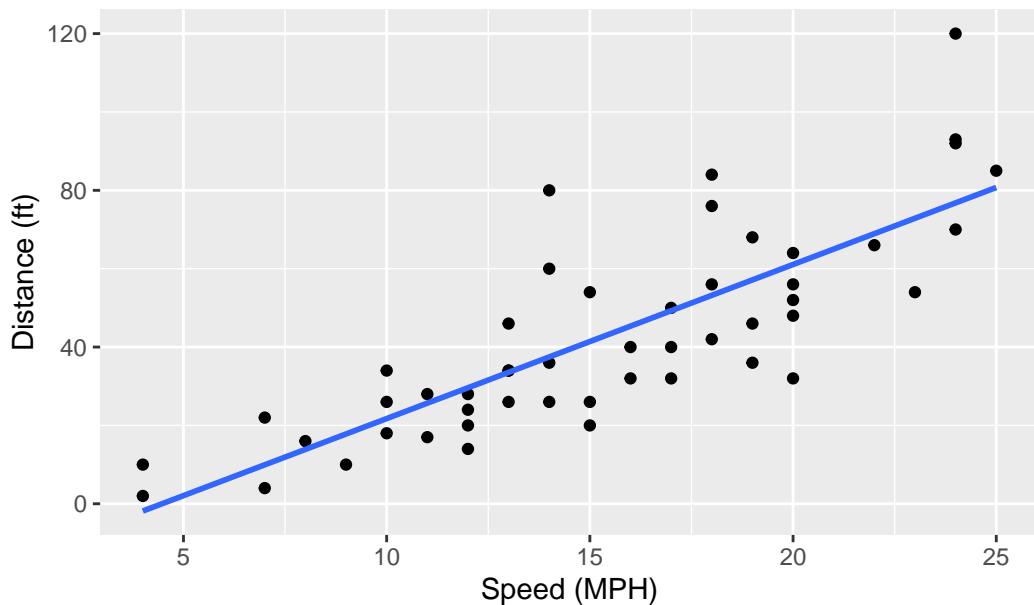
Let's add more layers to our ggplot

Add a line showing the relationship between x and y Add a title Add custom axis labels “Speed (MPH)” and “Distance (ft)” Change 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'
```

Silly plot of Speed vs Stopping distance



```
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"
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..@ margin       : NULL
..@ debug        : NULL
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$ point          : <ggplot2::element_point>
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..@ shape        : num 19
..@ size         : num 1.5
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..@ inherit.blank: logi TRUE
$ geom           : <ggplot2::element_geom>
..@ ink           : chr "black"

```

```

..@ paper      : chr "white"
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..@ bordertype : int 1
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..@ pointsize  : num 1.5
..@ pointshape : num 19
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..@ fill        : NULL
$ spacing          : 'simpleUnit' num 5.5points
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```

```

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```

```

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```

```

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..@ vjust           : NULL
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$ axis.text.theta          : NULL
$ axis.text.r             : <ggplot2::element_text>
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..@ hjust           : num 0.5
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..@ angle           : NULL
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```

```

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$ axis.ticks.y          : NULL
$ axis.ticks.y.left     : NULL
$ axis.ticks.y.right    : NULL
$ axis.ticks.theta      : NULL
$ axis.ticks.r          : NULL
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$ axis.ticks.length.theta: 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
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$ axis.line.x          : NULL

```

```

$ axis.line.x.top          : NULL
$ axis.line.x.bottom       : NULL
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$ axis.line.y.left         : NULL
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..@ angle                  : NULL
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```

```

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$ 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)
```

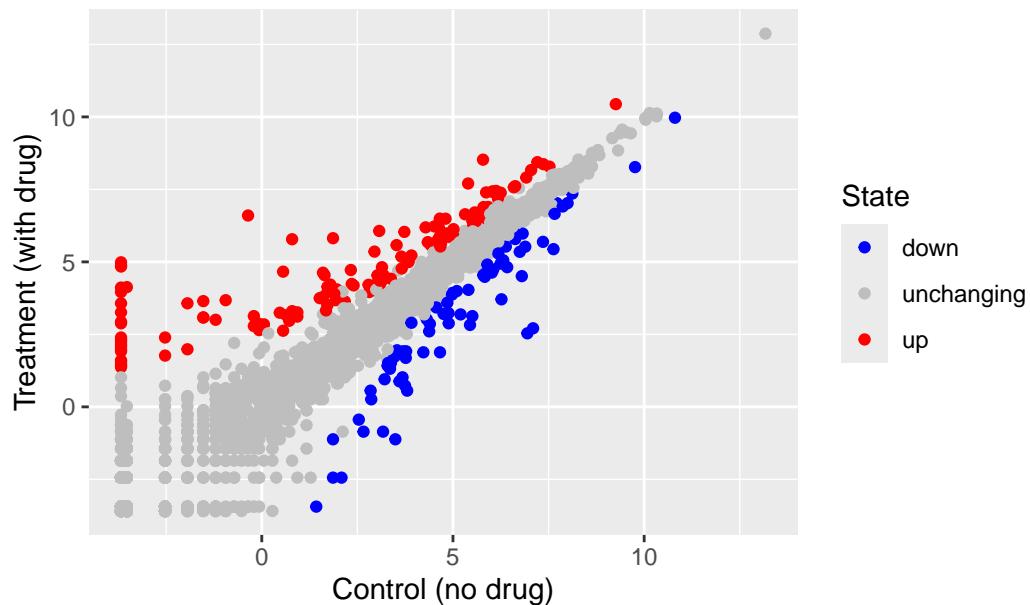
	down	unchanging	up
	72	4997	127

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 changes upon drug treatment",
       x="Control (no drug)",
       y="Treatment (with drug)")
p + scale_colour_manual(values = c("blue", "gray", "red"))
```

Expression changes upon drug treatment



```
##More Plotting library(gapminder)
```

```
# 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

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

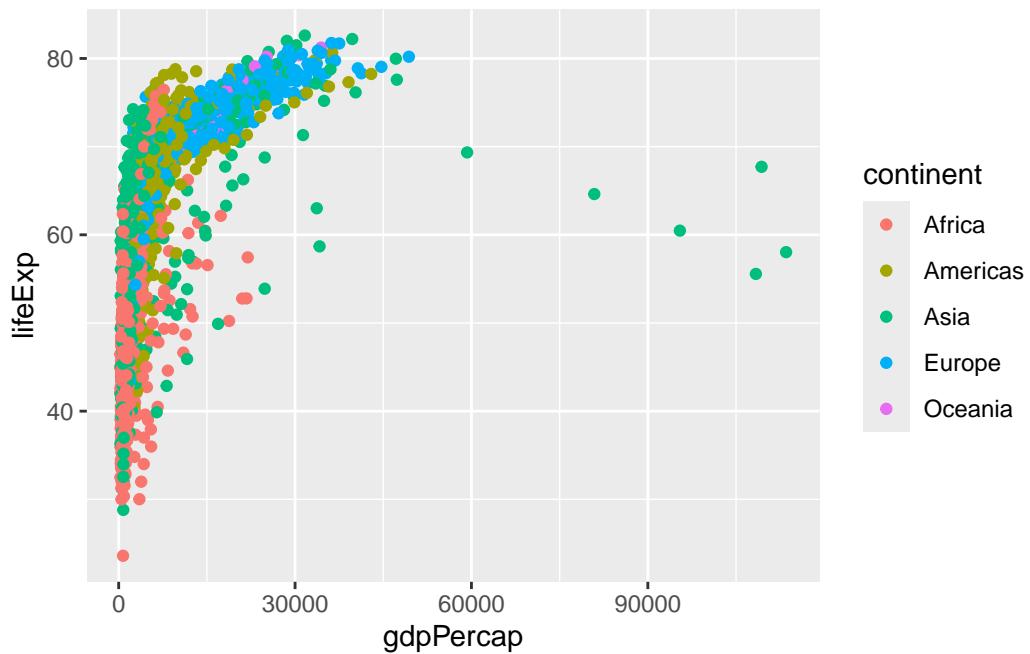
```
[1] 142
```

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

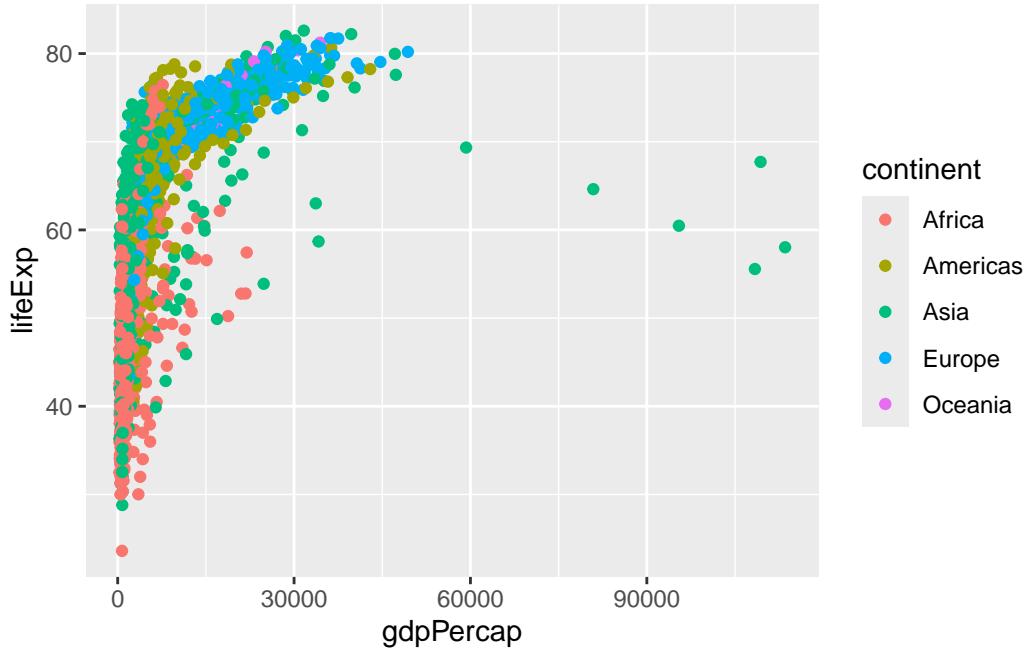
```
unique(gapminder$continent)
```

```
[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()
```

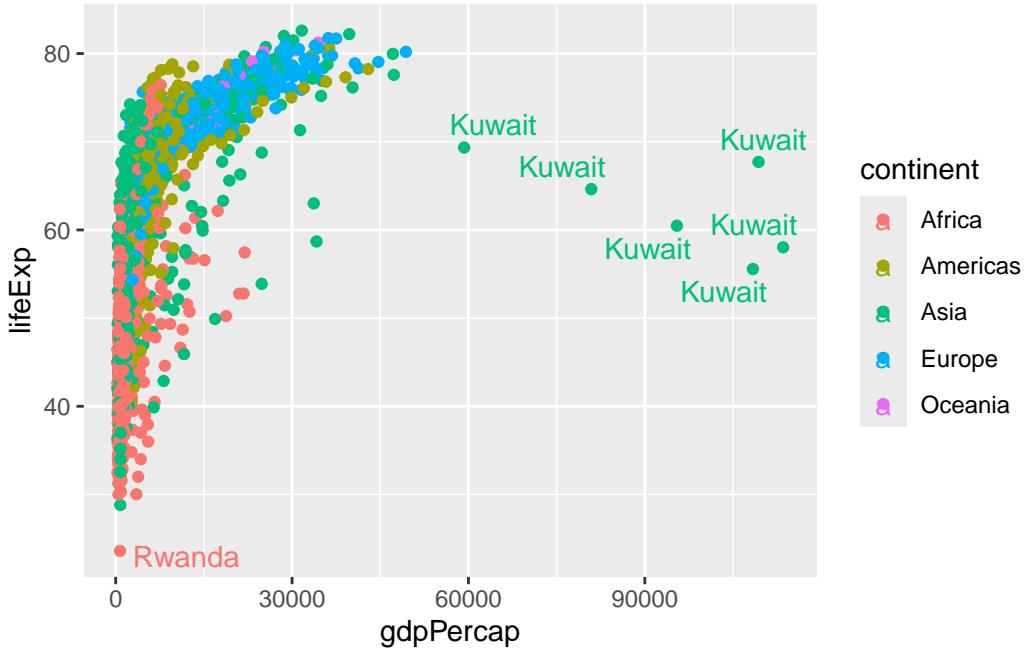


I can use the `ggrepel` package to make more sensible labels here.

```
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)
```

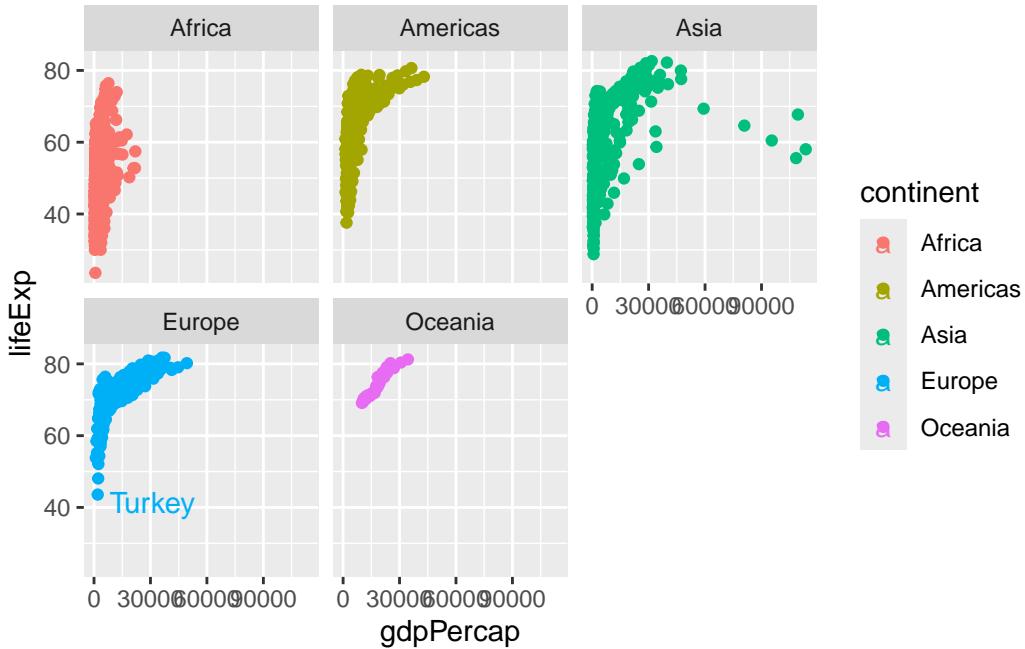
Warning: ggrepel: 624 unlabeled data points (too many overlaps). Consider increasing max.overlaps

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?