

# Class 05: 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 plots in R. These include:

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

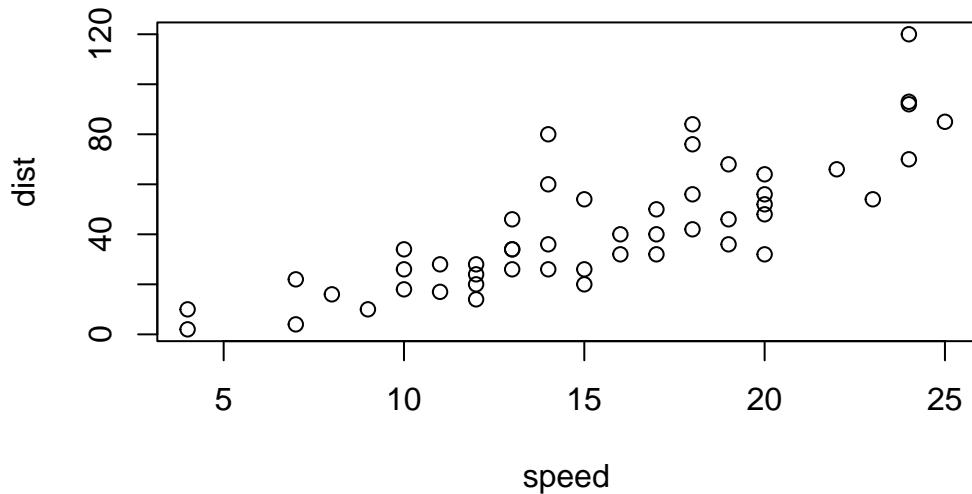
Here is a simple “base” R plot.

```
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()** functions.

```
plot(cars)
```



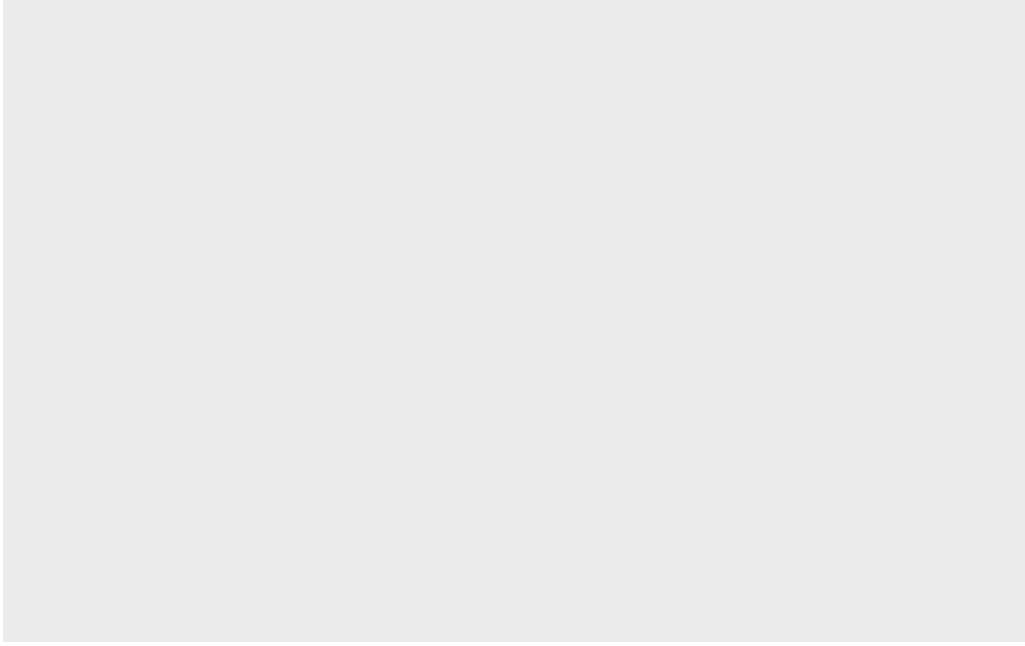
Key-point: Base R is quick but simple looking.

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

First, we need to install this add-on package. For this we can use the `install.packages()` function - WE DO THIS IN THE CONSOLE, NOT our report.

Second, we need to load the package with the `library()` function everytime we want to use it.

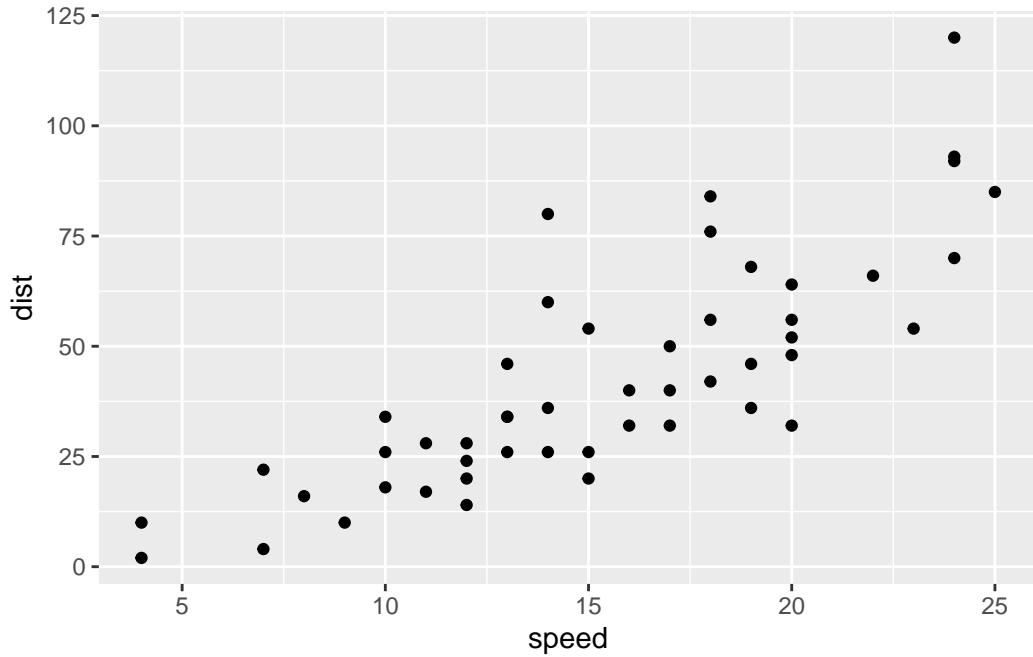
```
library(ggplot2)
ggplot(cars)
```



Every ggplot is composed of at least 3 layers:

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

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



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

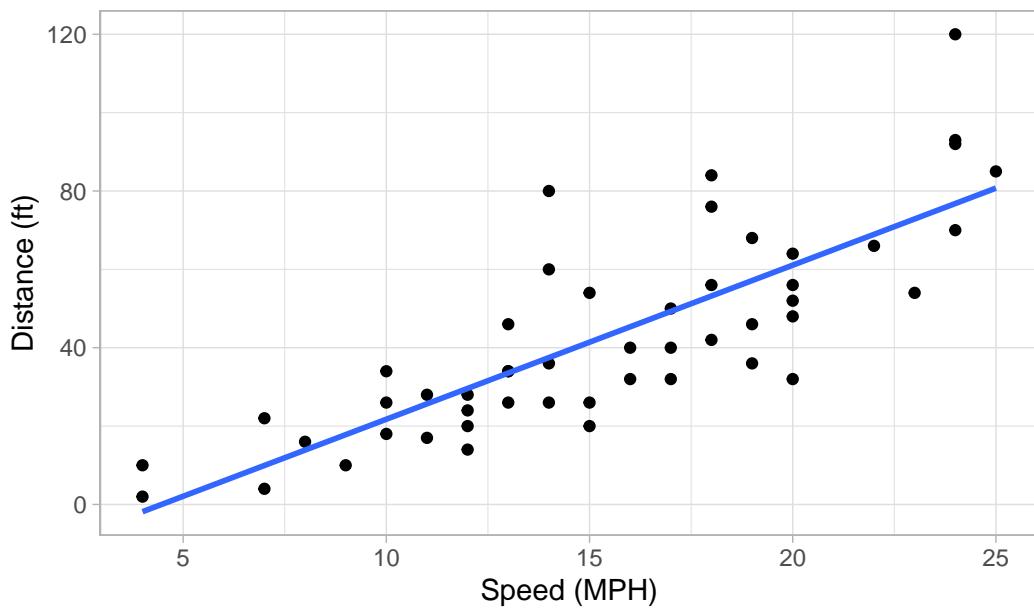
Lets add more layers to our ggplot

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 = "Speed vs Distance Plot",
    x = "Speed (MPH)",
    y = "Distance (ft)"
  ) +
  theme_light()

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

## Speed vs Distance Plot



## Going further - Gene Expression Dataset

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 dataset

```
nrow(genes)
```

[1] 5196

```
ncol(genes)
```

```
[1] 4
```

```
colnames(genes)
```

```
[1] "Gene"      "Condition1" "Condition2" "State"
```

Q2. How many upregulated genes are there

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

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

	down	unchanging	up
	72	4997	127

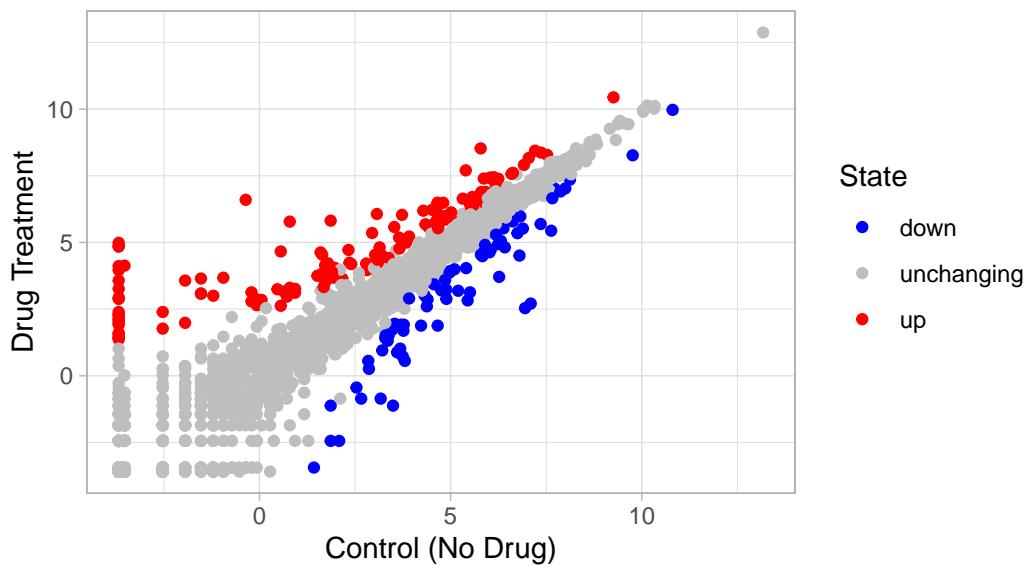
Make a v1 figure

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

p +
  scale_color_manual(values = c("blue", "grey", "red")) +
  labs(
    title = "Gene Expression Changes Upon Drug Treatment",
    subtitle = "another scatterplot made with ggplot",
    x = "Control (No Drug)",
    y = "Drug Treatment"
  ) +
  theme_light()
```

## Gene Expression Changes Upon Drug Treatment

another scatterplot made with ggplot



## More Plotting Examples - gapminder Dataset

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

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

```
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 countries are in this dataset

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

```
[1] 142
```

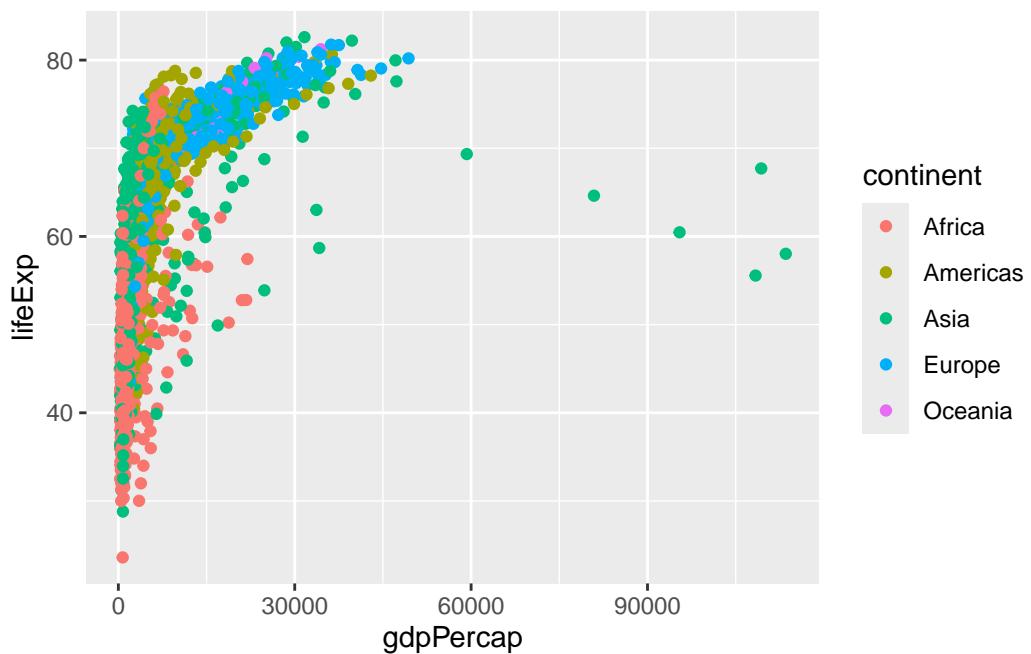
Q5. Number of continents

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

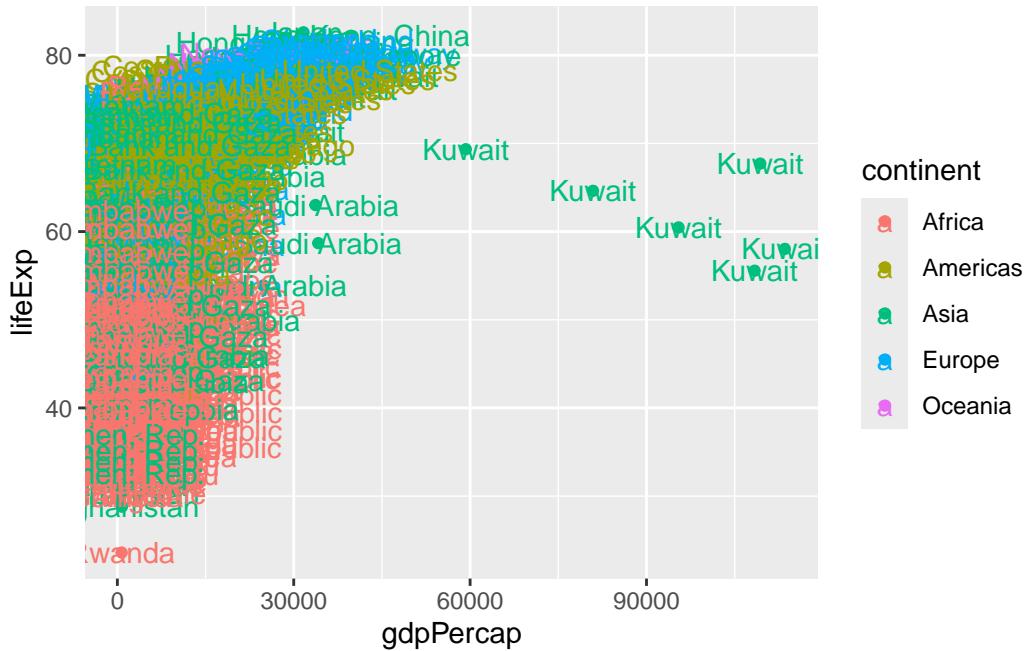
```
[1] "Asia"      "Europe"     "Africa"     "Americas"   "Oceania"
```

Version 1 plot

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



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

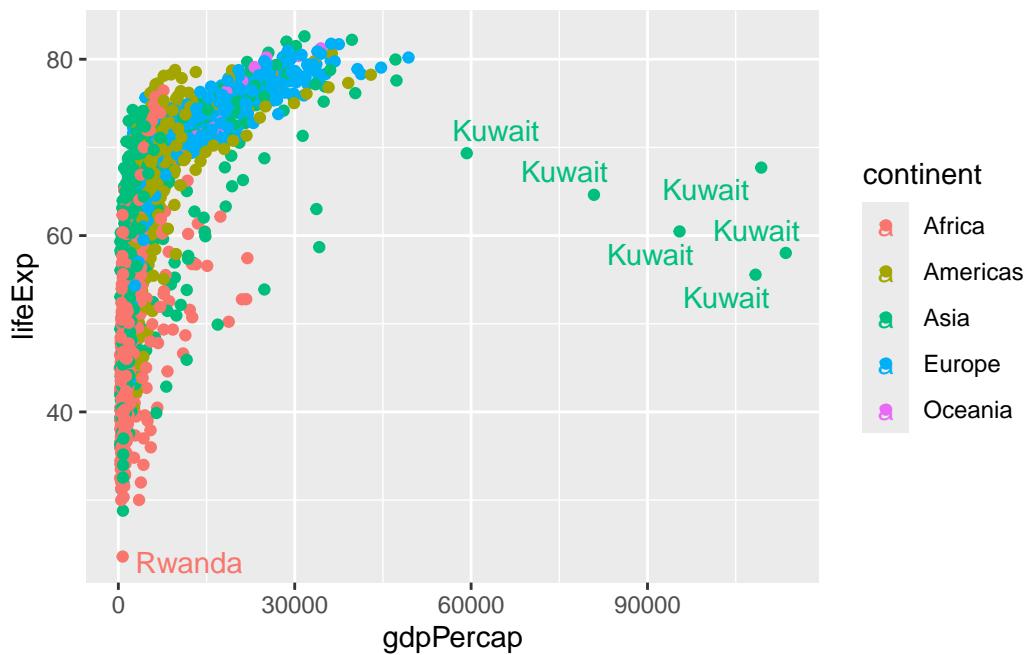


I can use the `ggrepel` package to make more sensible labels here

```
library(ggrepel)

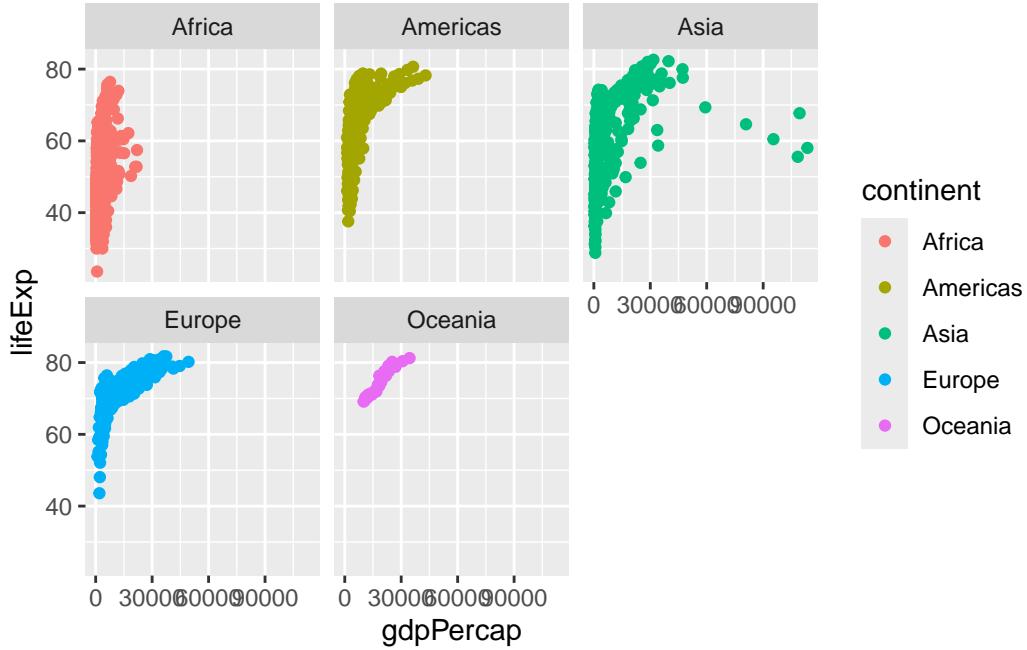
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, colour = continent, label = country) +
  geom_point() +
  geom_text_repel()
```

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



I want a separate pannel per continent

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



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

1. **Layered Grammar of Graphics:** ggplot uses a consistent, layered approach. You build plots by adding layers (data, aesthetics, geoms, themes) with the `+` operator. This makes complex plots easier to construct and modify, compared to base R where each plot type often requires a different function and many arguments [1], [3], [2], [4], [5].
2. **Publication-Quality Defaults:** ggplot produces attractive, publication-ready figures by default. Base R plots are quick but often require a lot of manual tweaking to look polished [1], [3], [2], [4], [5].
3. **Declarative Syntax:** In ggplot, you declare what you want to show (e.g., which variables map to which aesthetics), rather than specifying every detail step-by-step as in base R [1], [3], [2], [4], [5].
4. **Consistency and Reproducibility:** ggplot's approach is consistent across plot types, making it easier to learn and reproduce complex visualizations. Base R can be more idiosyncratic, with different functions and arguments for each plot type [1], [3], [2], [4], [5].
5. **Customization and Extensibility:** ggplot makes it easy to add layers (like trend lines, color scales, themes) and customize every aspect of the plot. Base R allows pixel-level control but is more cumbersome for complex customizations [1], [3], [2], [4], [5].