

Class 5 Data Visualization with ggplot2

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Using GGLOT

Use `install.packages()` function to install ggplot2 function.

```
head(cars)
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10

Must load ggplot before you can use its functions in a session. Do this using `library()` function.

```
library(ggplot2)
```

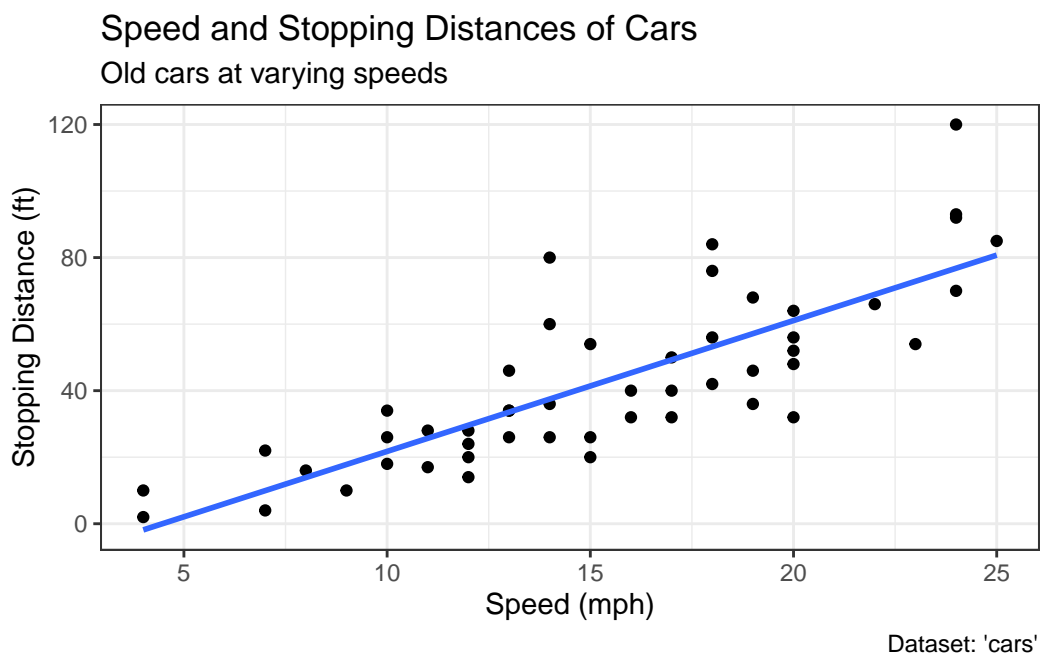
Three components of ggplot figures:

1. data (what we want to plot)
2. aesthetic mapping (aes)
3. geometries (geom)

Adding fit lines:

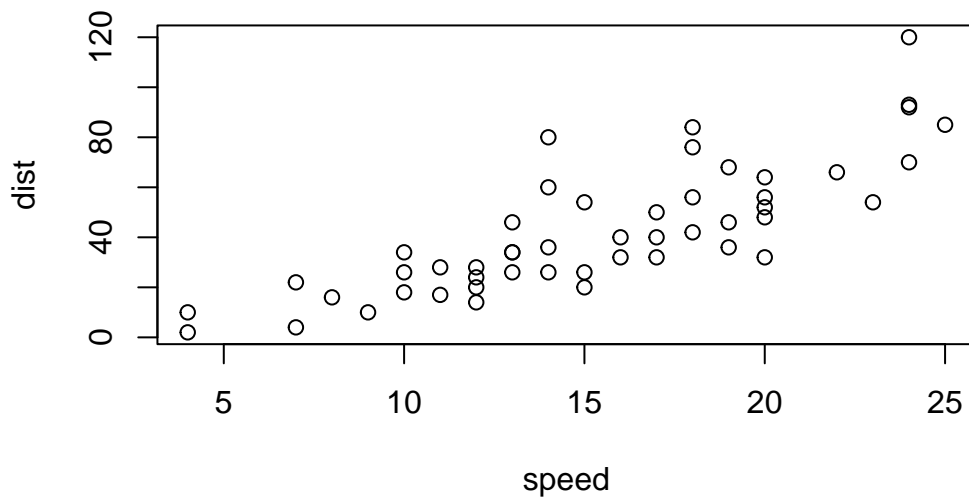
```
ggplot(cars) + aes(speed,dist) + geom_point() + geom_smooth(method="lm", se=FALSE) + theme_minimal() +  
  labs(title="Speed and Stopping Distances of Cars",  
        x="Speed (mph)",  
        y="Stopping Distance (ft)",  
        subtitle = "Old cars at varying speeds",  
        caption="Dataset: 'cars'")
```

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



There are other options for plotting in R, such as “base R” graphics.

```
plot(cars)
```



Anti-Viral Drug

```
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

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

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

```
[1] 127
```

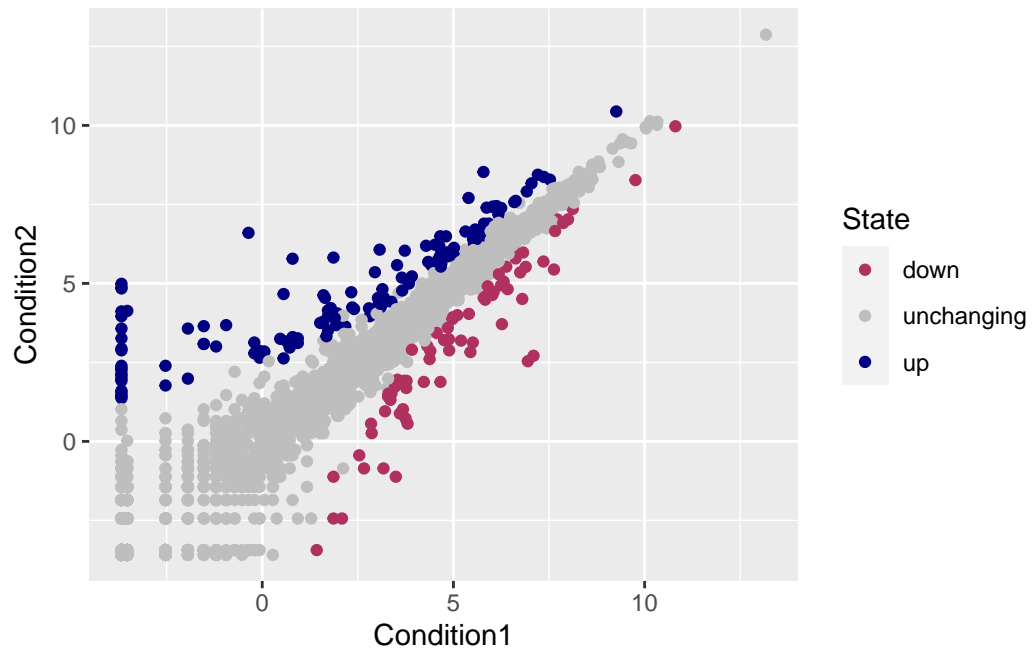
```
table(genes$State)/nrow(genes)
```

	down	unchanging	up
	0.01385681	0.96170131	0.02444188

Fraction of up-regulated genes = 0.024

Changing colors:

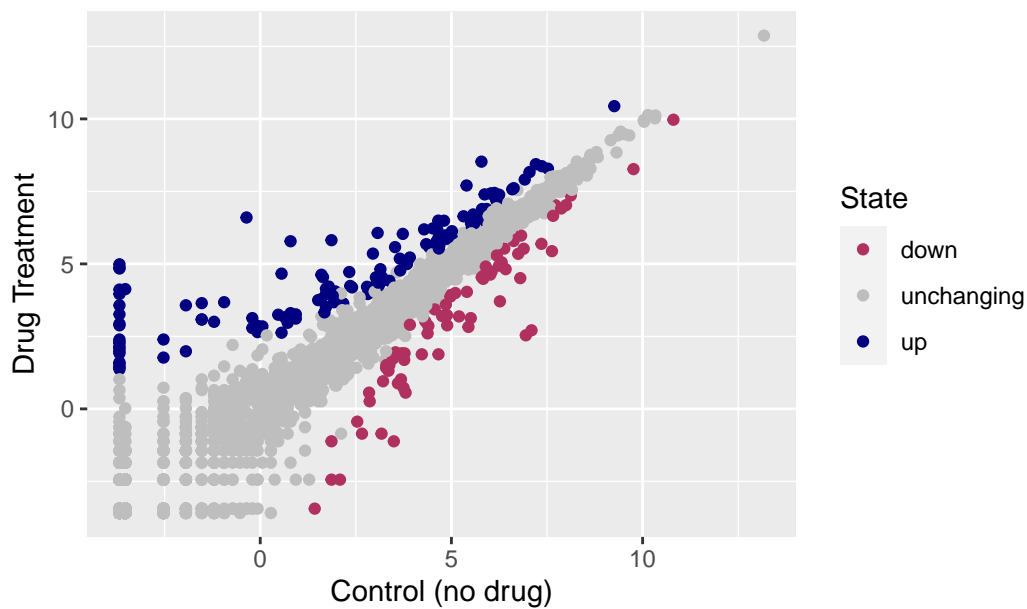
```
p <- ggplot(genes) + aes(Condition1, Condition2, col=State) + geom_point()
p <- p + scale_color_manual(values=c("maroon", "gray", "navy"))
p
```



Adding titles:

```
p + labs(title="Gene Expression Changes Upon Drug Treatment",  
         x="Control (no drug)",  
         y="Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment



Gapminder (population data)

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

gapminder <- read.delim(url)

# install.packages("dplyr") ## un-comment to install if needed
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

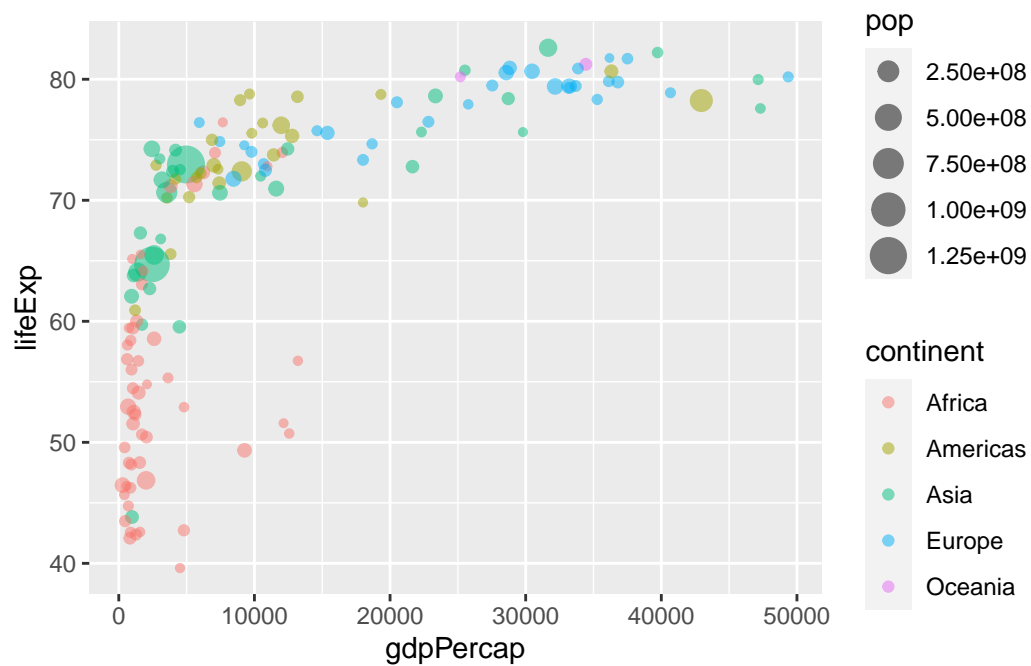
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

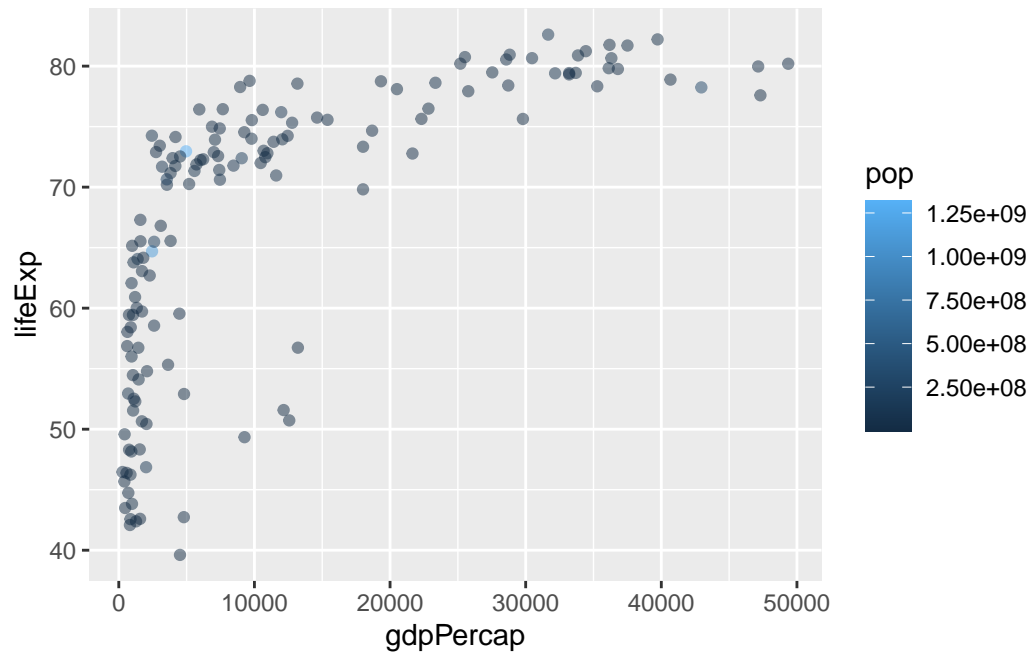
Mapping size and categorical color:

```
ggplot(gapminder_2007) +  
  aes(gdpPercap, lifeExp, color=continent, size=pop) +  
  geom_point(alpha=0.5)
```



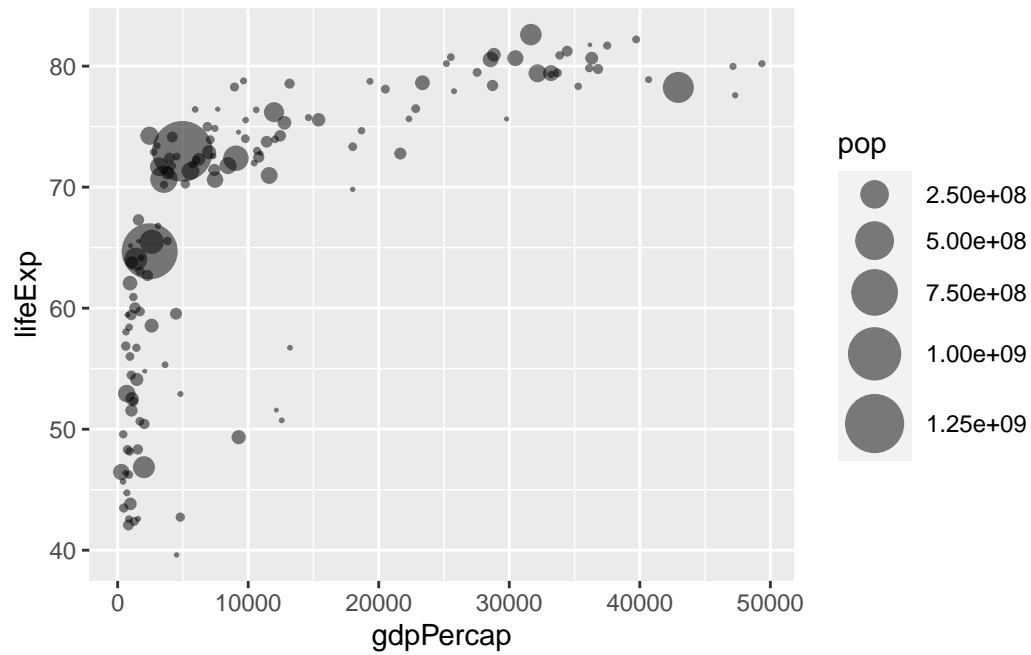
Mapping continuous color

```
ggplot(gapminder_2007) +  
  aes(gdpPercap, lifeExp, color=pop) +  
  geom_point(alpha=0.5)
```



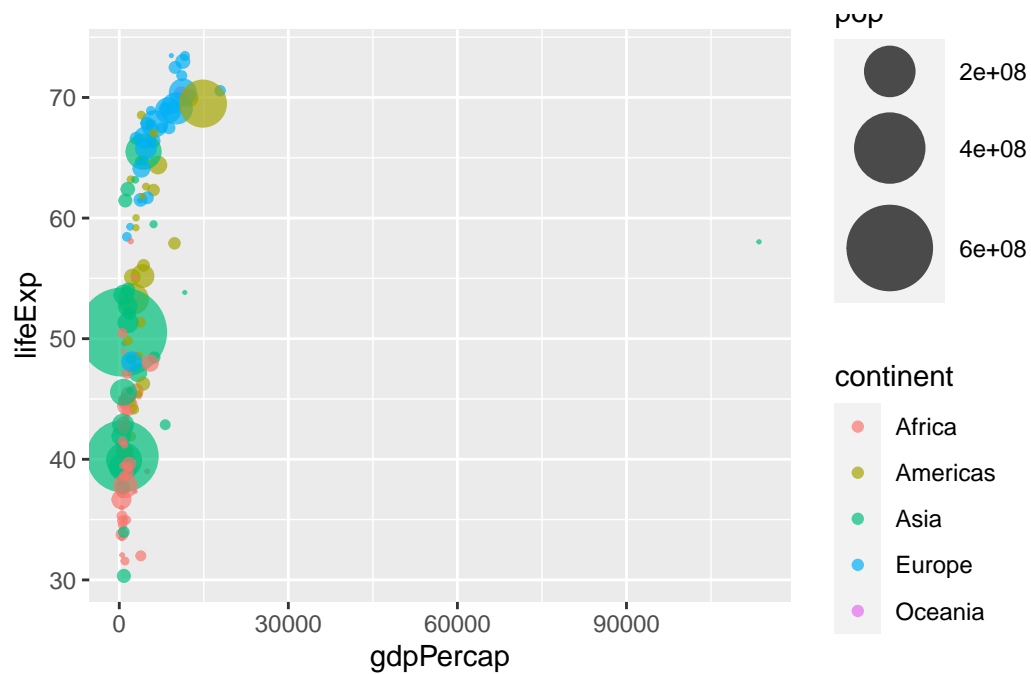
Mapping point size

```
ggplot(gapminder_2007) +  
  aes(gdpPercap, lifeExp, size=pop) +  
  geom_point(alpha=0.5) +  
  scale_size_area(max_size=10)
```

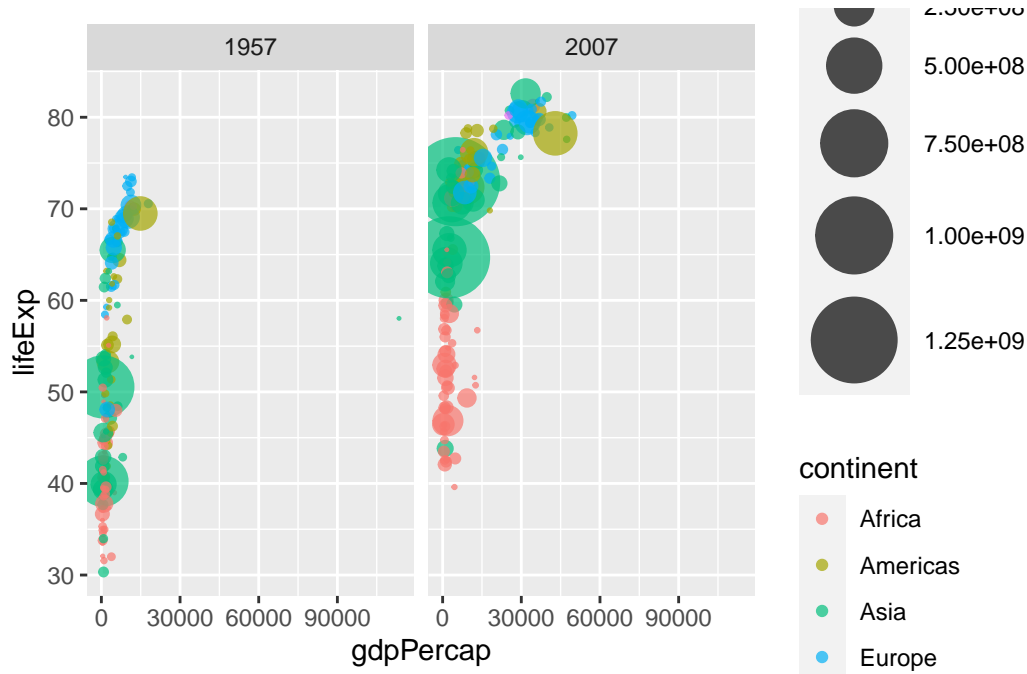
Repeat for 1957

```
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957) +
  aes(gdpPercap, lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 15)
```



Both 2007 and 1957

```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)
ggplot(gapminder_1957) +
  aes(gdpPercap, lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 15) +
  facet_wrap(~year)
```



Quarto

Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see <https://quarto.org>.

Running Code

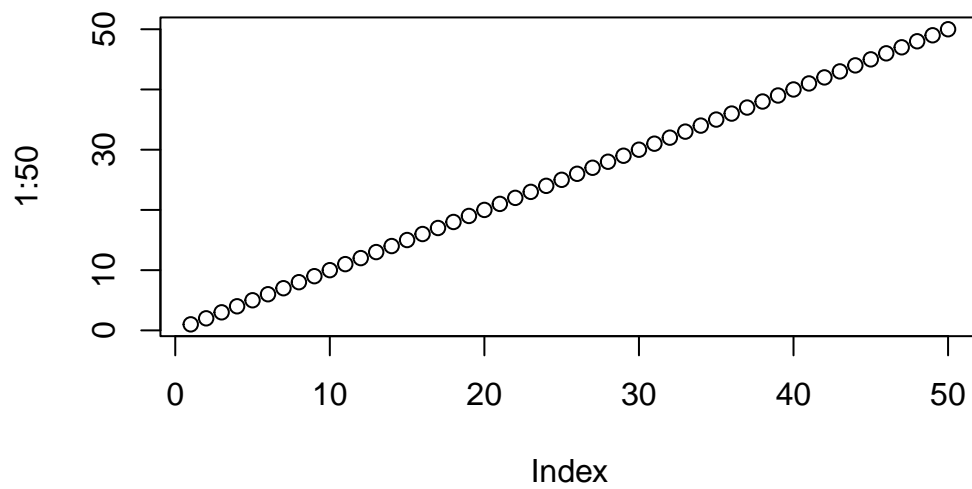
This is some of my text.

```
log(100)
```

```
[1] 4.60517
```

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
plot(1:50)
```



You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).