

class05

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Quarto

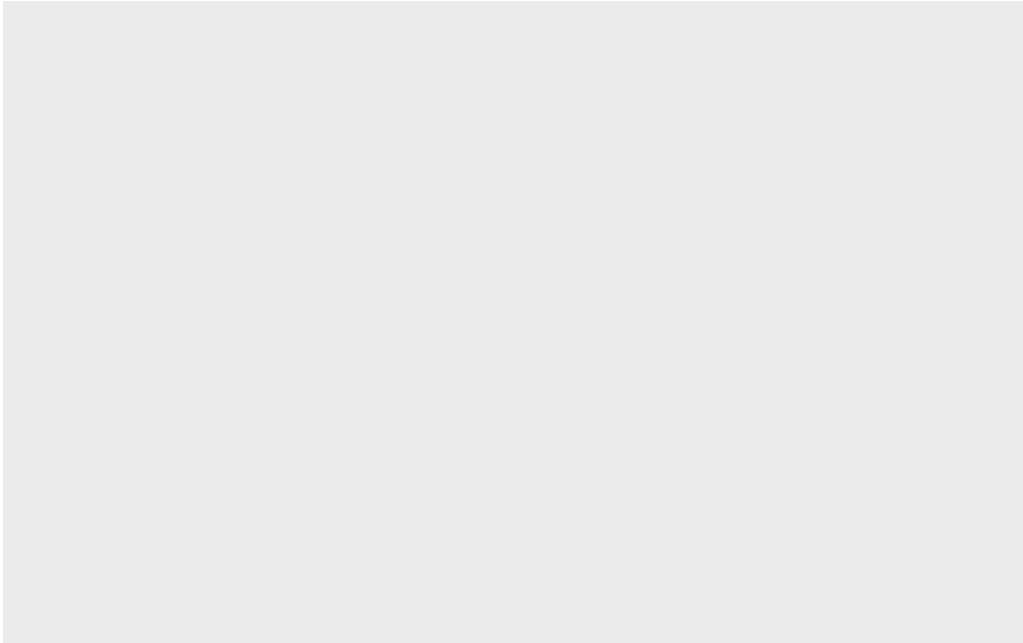
Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see <https://quarto.org>.

Running Code

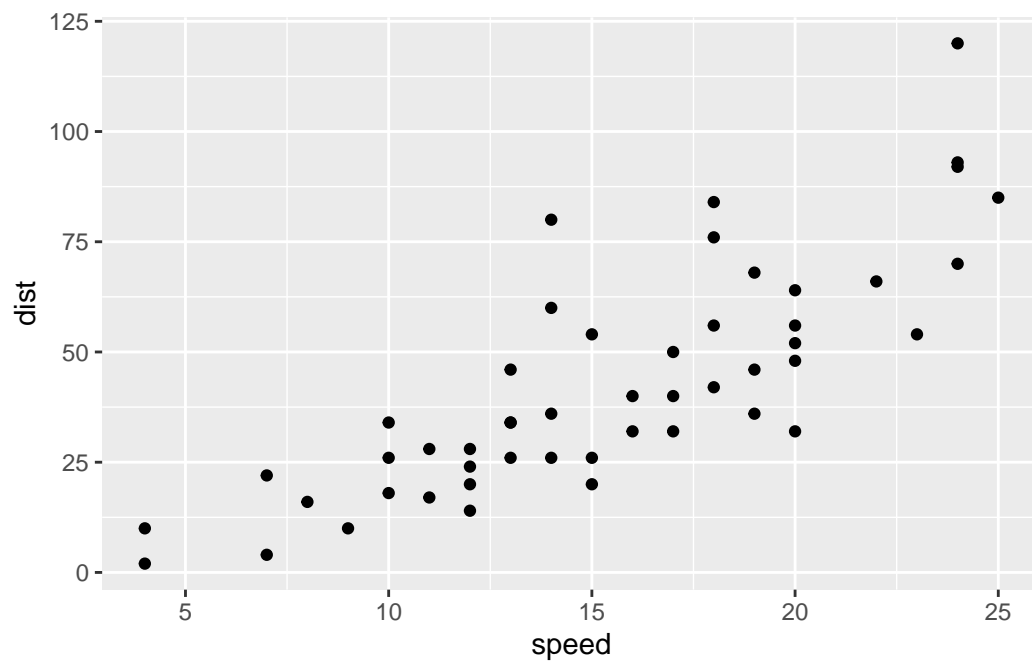
When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
#install.packages("ggplot2")
```

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



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

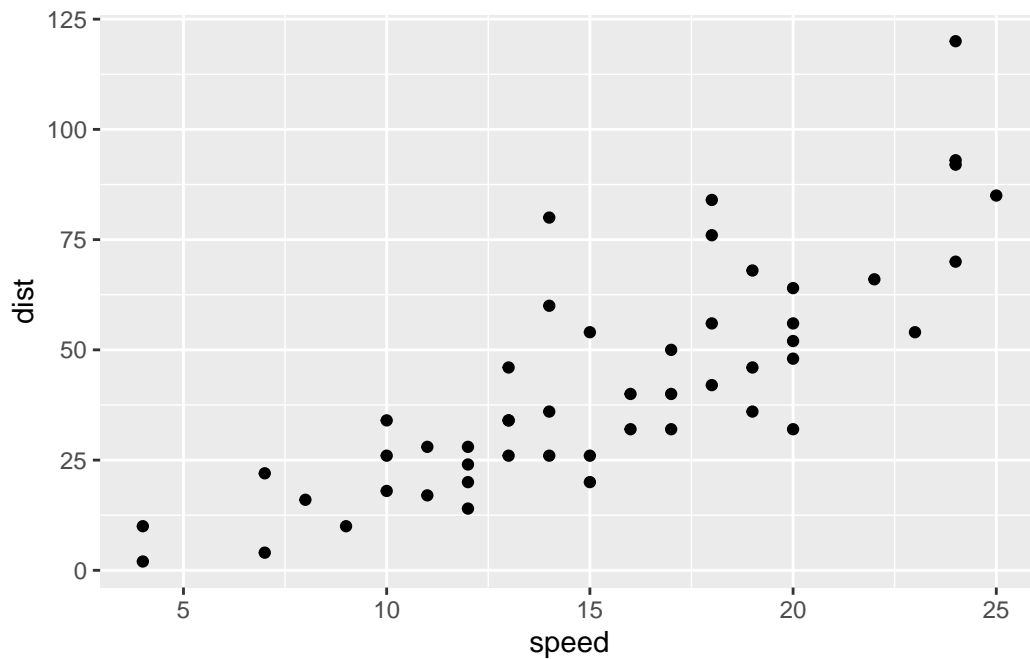


Q. add a line to show the relationship of speed to stopping distance (i.e. add another “layer”)

```
p <- ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(se=FALSE, method="lm")
```

Q. Add a title and subtitle for the plot

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

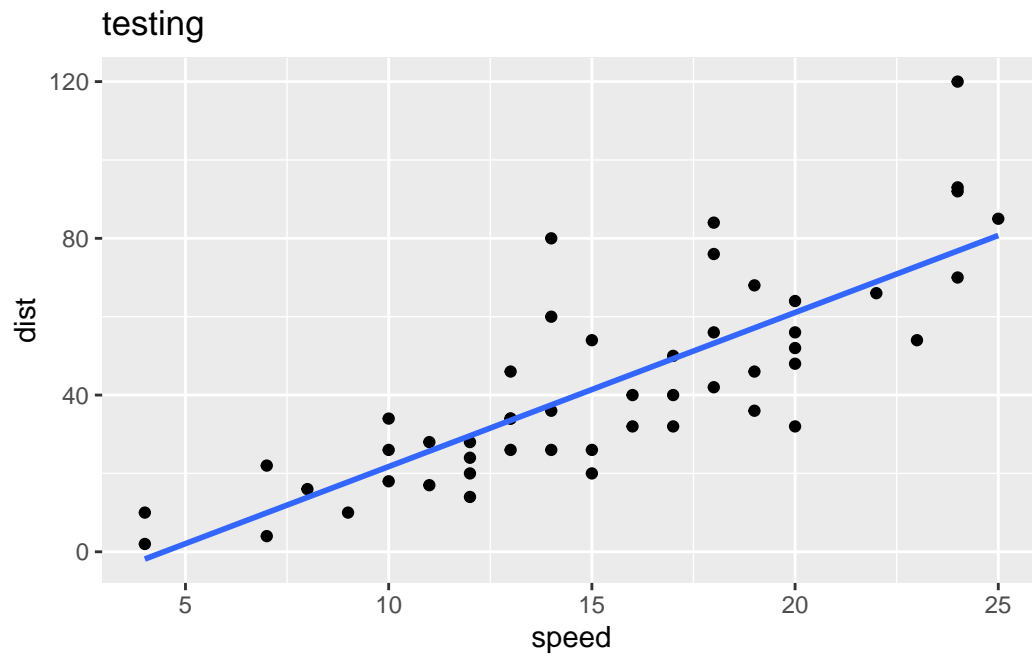


Q. add a line to show the relationship of speed to stopping distance (i.e. add another “layer”)

I can always save anyggplot object (i.e. plot) and then use it later for adding more layers.

```
p + ggtitle("testing")
```

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

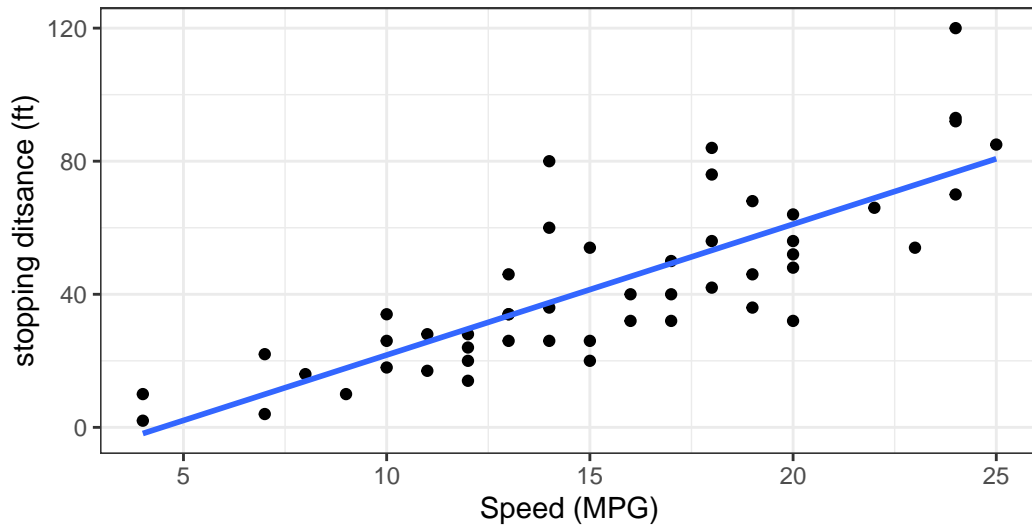


```
p + labs(title = "My first gg plot", subtitle = "stopping ditance of old cars", caption = "B")  
  theme_bw()
```

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

My first gg plot

stopping dittance of old cars



BIMM143

```
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

Q. How many columns are there?

```
ncol(genes)
```

```
[1] 4
```

Q. what re the column names?

```
colnames(genes)
```

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

Q. How many “up” and “down” regulated genes are there?

```
#genes$State
```

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

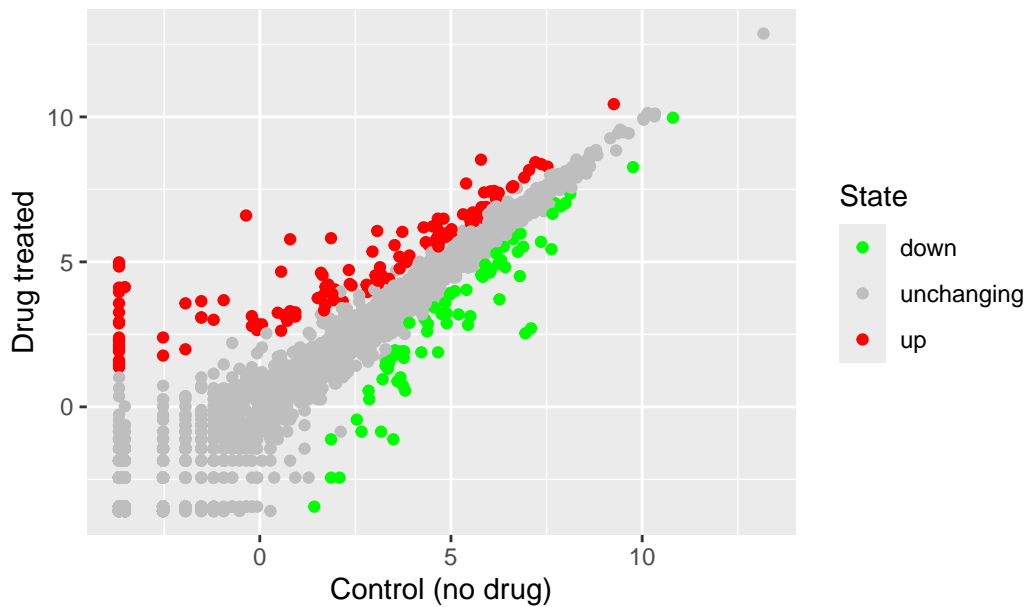
down	unchanging	up
72	4997	127

Custom color plot

Q. Make a first plot of this data

```
ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  scale_color_manual( values = c("green", "gray","red")) +  
  geom_point() +  
  labs(title="Gene expression changes upon drug treatment", x = "Control (no drug)", y = "Drug")
```

Gene expression changes upon drug treatment



```
#theme_bw()
```

Using different geoms

Let's plot some aspects of the in-built 'mtcars' dataset.

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

Q. Scatter plot of 'mpg' vs 'disp'

```
p1 <- ggplot(mtcars) +
  aes(x=mpg, y=disp)+
  geom_point()
```

Q. boxplot of 'gear' vs 'disp'

```
p2 <- ggplot(mtcars) +  
  aes(x=gear, y=disp, group=gear)+  
  geom_boxplot()
```

Q. barplot of 'carb'

```
p3 <- ggplot(mtcars) +  
  aes(x=carb)+  
  geom_bar()
```

Smooth of 'disp' vs 'qsec'

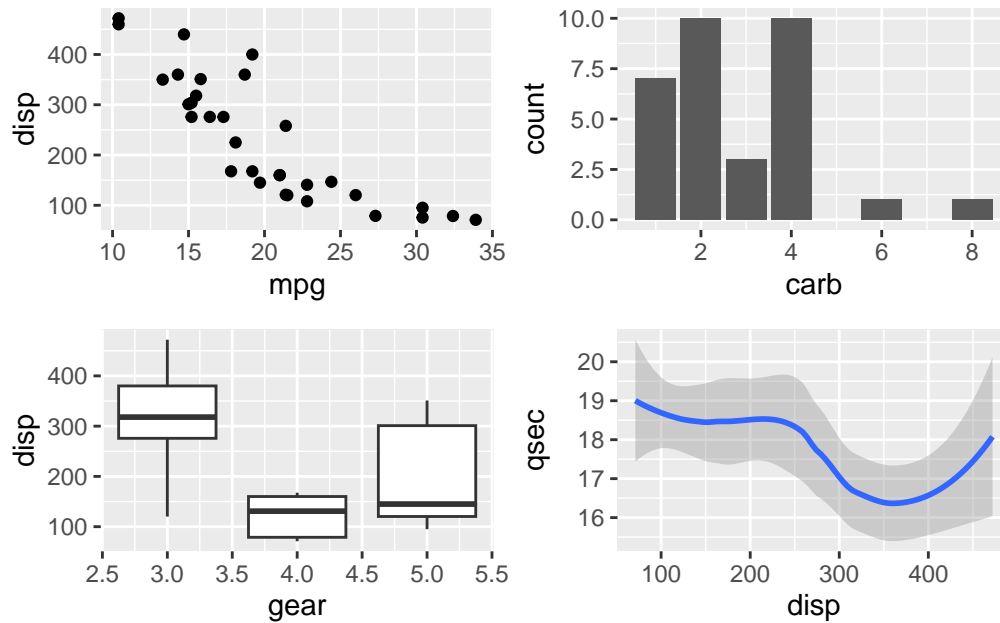
```
p4 <- ggplot(mtcars) +  
  aes(x=disp, y=qsec)+  
  geom_smooth()
```

I want to combine all these plots into one figure with multiple pannels

We can use **patchwork** package to do this.

```
library(patchwork)  
  
(p1 / p2 | p3 / p4)
```

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'



```
ggsave(filename = "myplot.png", width=10, height = 10)
```

``geom_smooth()`` using method = 'loess' and formula = 'y ~ x'

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

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

Q. How many countries are in this dataset?

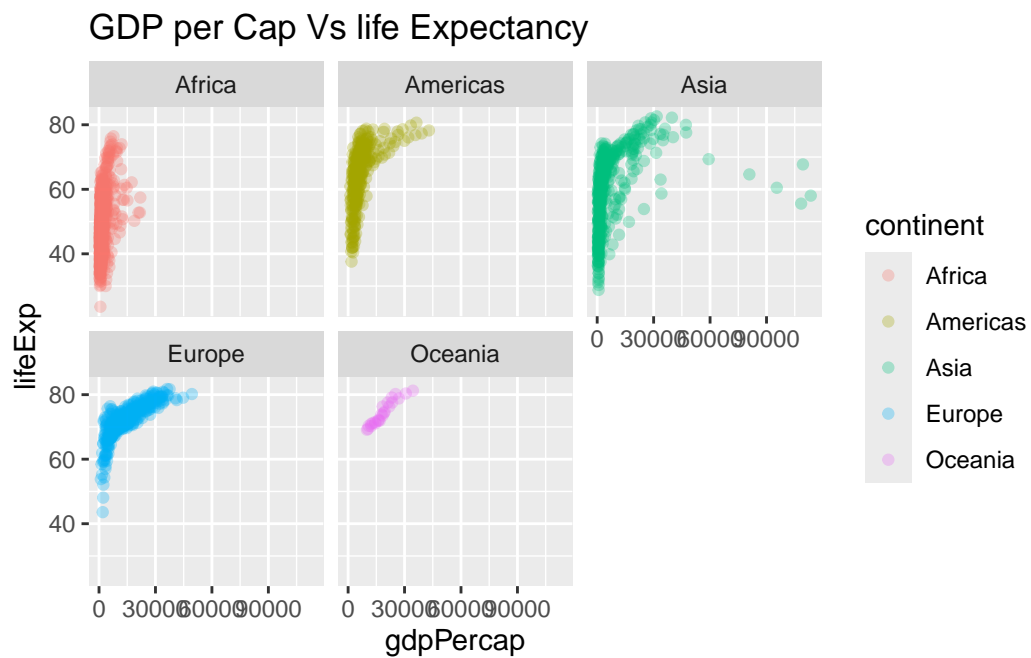
```
#gapminder$country
#table(gapminder$country)
```

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

```
[1] 142
```

Q plot `gdpPercap` vs `lifeExp` color by continent

```
ggplot(gapminder) +
  aes(x=gdpPerCap, y=lifeExp, col=continent) +
  geom_point(alpha = 0.3) +
  facet_wrap(~continent) +
  labs(title="GDP per Cap Vs life Expectancy", x = "gdpPerCap", y = "lifeExp")
```



```
#theme_bw()
```