

Class 5: Data Viz with ggplot

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Background

There are lot's of ways to make figures in R. These include so-called “base R” graphics (e.g. `plot()`) and tones of add-on packages like **ggplot2**.

For example here we make the same plot with both:

```
head(cars)
```

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

```
plot(cars)
```



First I need to install the package with the command `install.packages()`

N.B. We never run an install cmd in a quarto code chunk or we will end up re-installing packages many many times - which is not what we want!

Every time we want to use one of these “add-on” packages we need to load it up in R with the `library()` function:

```
library(ggplot2)
```

```
ggplot(cars)
```



Every ggplot needs at least 3 things:

- The **data**, the stuff you want plotted
- The **aesthetics**, how the data map to the plot
- The **geometry**, the type of plot

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



Add a line to better show relationship between speed and dist

```
p <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  labs(title="Stopping distance of old cars", subtitle = "Data from the `cars` object", x="Speed", y="Distance")
```

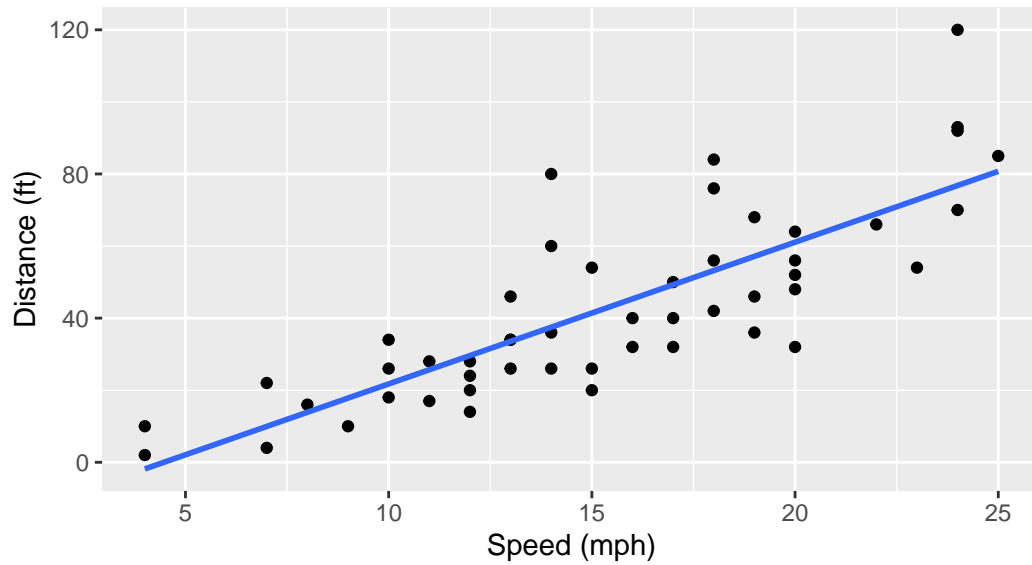
render it out

```
p
```

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

Stopping distance of old cars

Data from the `cars` object

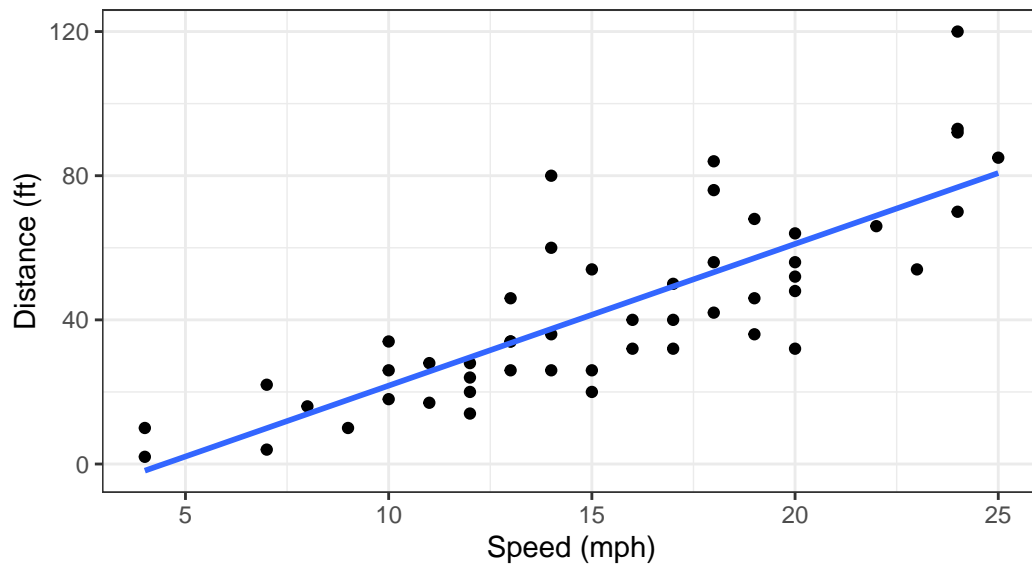


```
p + theme_bw()
```

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

Stopping distance of old cars

Data from the `cars` object



Gene expression plot

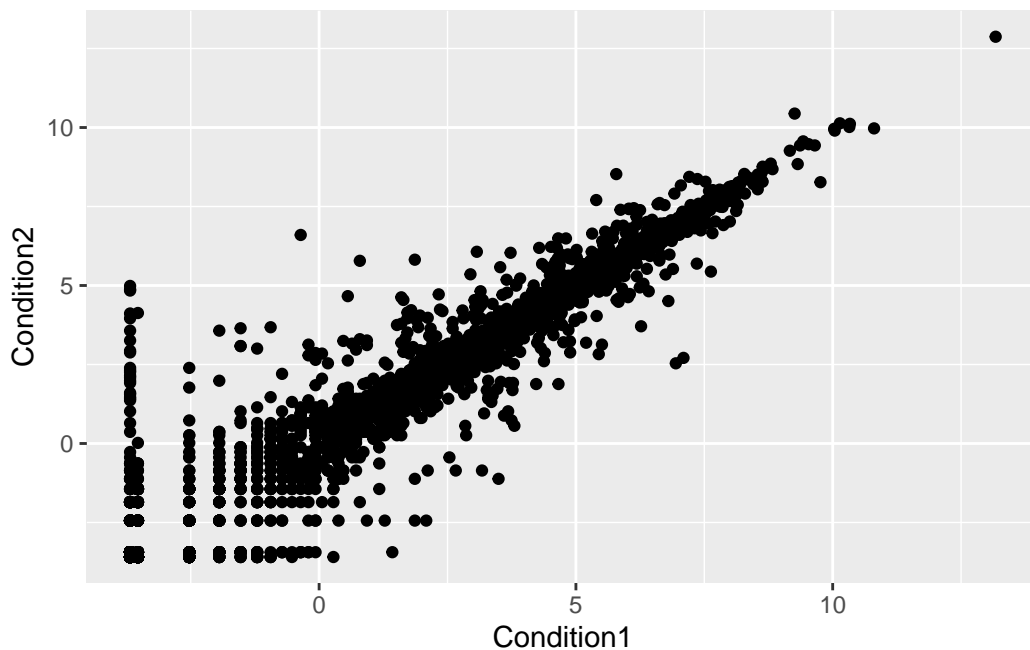
We can read the input data from the class website

```
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

A first version plot

```
ggplot(genes) +
  aes(Condition1, Condition2) +
  geom_point()
```



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

```

down  unchanging      up
  72    4997         127

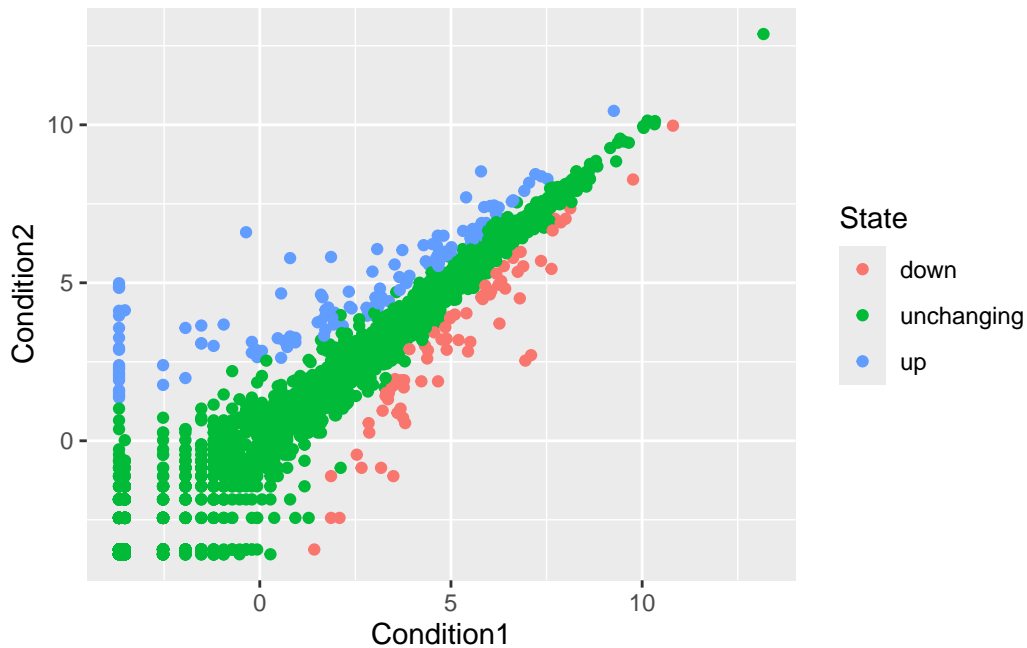
```

Version 2 let's color by **State** so we can see the “up” and “down” significant genes compared to all the “unchanging” genes

```

ggplot(genes) +
  aes(Condition1, Condition2, col=State) +
  geom_point()

```

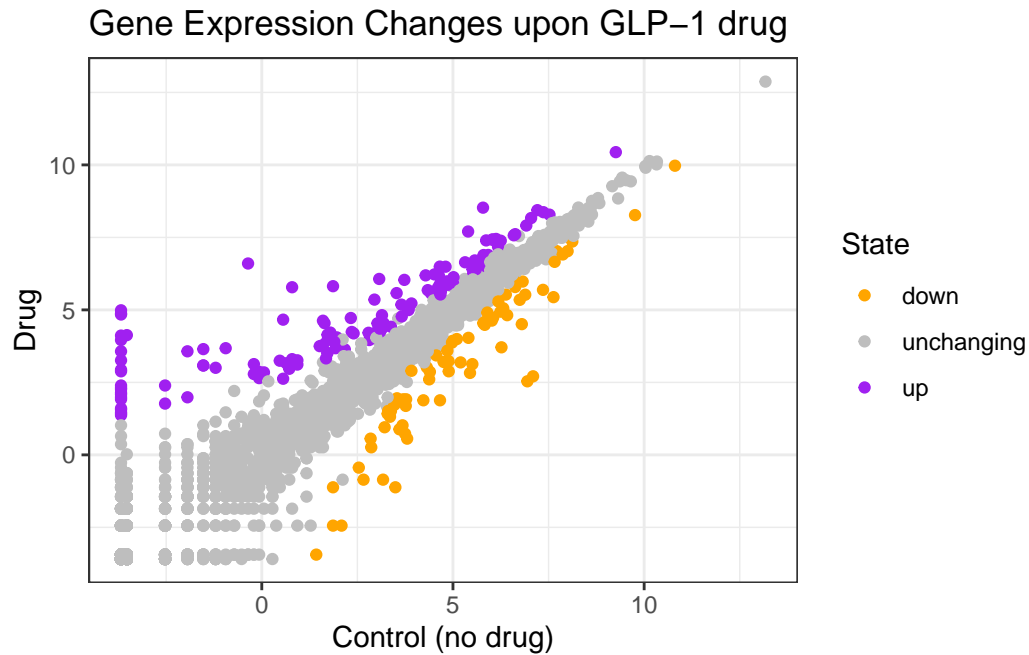


Version 3 plot, let's modify the default colors to something we like

```

ggplot(genes) +
  aes(Condition1, Condition2, col=State) +
  geom_point() +
  scale_colour_manual( values=c("orange", "gray", "purple")) +
  labs(x="Control (no drug)", y="Drug", title="Gene Expression Changes upon GLP-1 drug") +
  theme_bw()

```



Going Further

Let's have a look at the famous **gapminder**

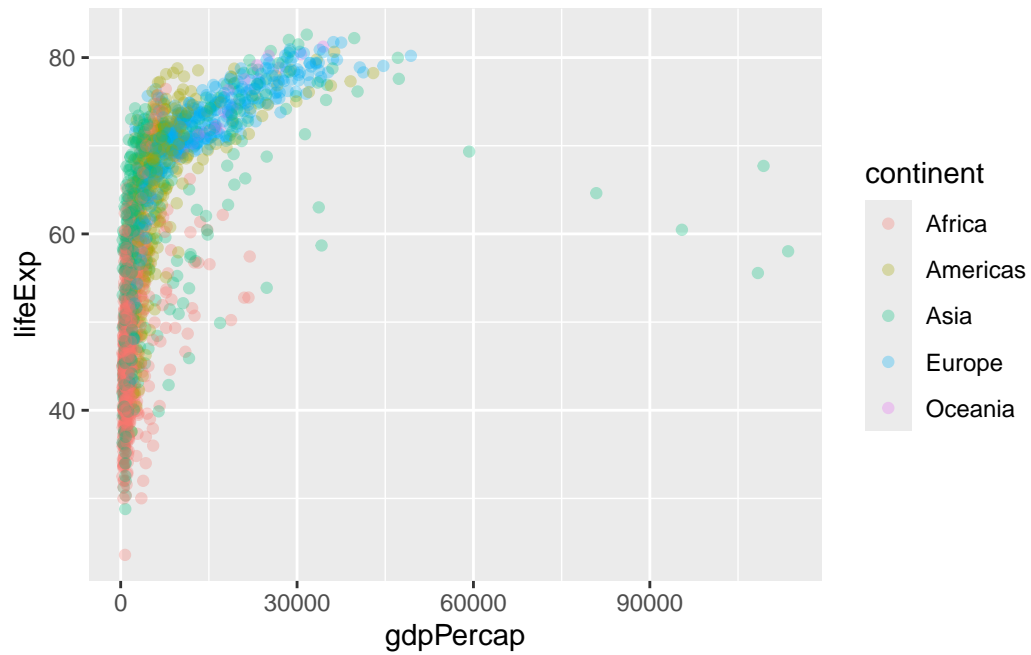
```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"

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

```
head(gapminder, 3)
```

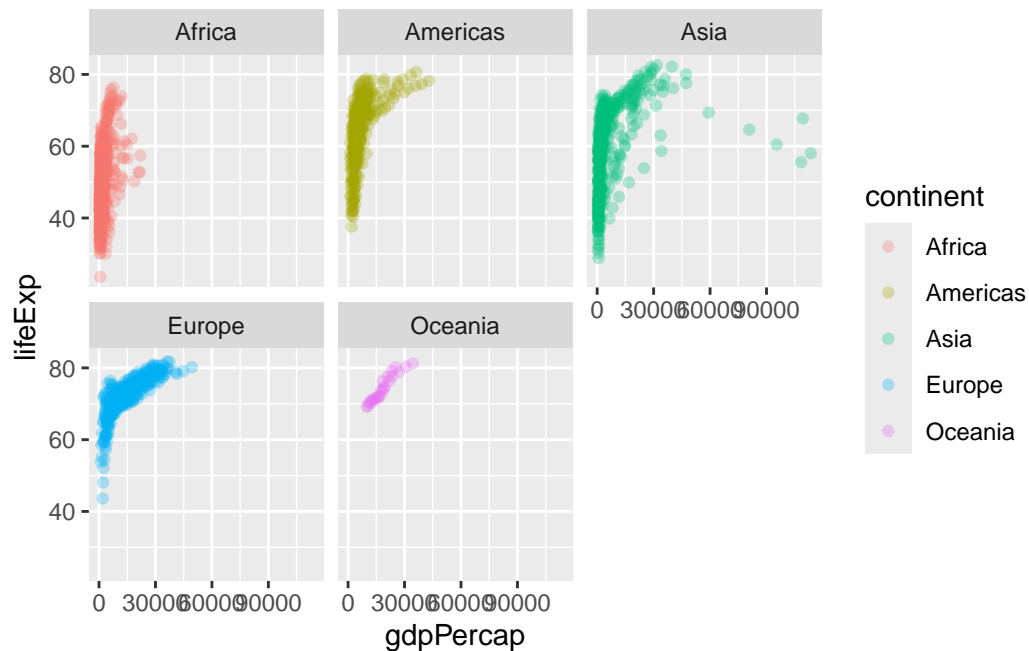
	country	continent	year	lifeExp	pop	gdpPercap
1	Afghanistan	Asia	1952	28.801	8425333	779.4453
2	Afghanistan	Asia	1957	30.332	9240934	820.8530
3	Afghanistan	Asia	1962	31.997	10267083	853.1007

```
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col=continent) +
  geom_point(alpha=0.3)
```

Let's “facet” (i.e. make a separate plot) by continent rather than the big hot mess above.

```
ggplot(gapminder) +  
  aes(gdpPercap, lifeExp, col=continent) +  
  geom_point(alpha=0.3) +  
  facet_wrap(~continent)
```



Custom plots

How big is this gapminder dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

I want to “filter” down to a subset of this data. I will use the **dplyr** package to help me.

First I need to install it and then load it up... `install.packages("dplyr")` and then `library(dplyr)`

```
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 <- filter(gapminder, year==2007)
head(gapminder_2007)
```

	country	continent	year	lifeExp	pop	gdpPercap
1	Afghanistan	Asia	2007	43.828	31889923	974.5803
2	Albania	Europe	2007	76.423	3600523	5937.0295
3	Algeria	Africa	2007	72.301	33333216	6223.3675
4	Angola	Africa	2007	42.731	12420476	4797.2313
5	Argentina	Americas	2007	75.320	40301927	12779.3796
6	Australia	Oceania	2007	81.235	20434176	34435.3674

```
filter(gapminder_2007, country=="Ireland")
```

	country	continent	year	lifeExp	pop	gdpPercap
1	Ireland	Europe	2007	78.885	4109086	40676

```
filter(gapminder, year==2007, country=="Ireland")
```

	country	continent	year	lifeExp	pop	gdpPercap
1	Ireland	Europe	2007	78.885	4109086	40676

```
filter(gapminder, year==2007, country=="United States")
```

	country	continent	year	lifeExp	pop	gdpPercap
1	United States	Americas	2007	78.242	301139947	42951.65

Q. Make a plot comparing 1977 and 2007 for all countries

```
input <- filter(gapminder, year %in% c(1977, 2007))
head(input)
```

	country	continent	year	lifeExp	pop	gdpPercap
1	Afghanistan	Asia	1977	38.438	14880372	786.1134
2	Afghanistan	Asia	2007	43.828	31889923	974.5803
3	Albania	Europe	1977	68.930	2509048	3533.0039
4	Albania	Europe	2007	76.423	3600523	5937.0295
5	Algeria	Africa	1977	58.014	17152804	4910.4168
6	Algeria	Africa	2007	72.301	33333216	6223.3675

```
ggplot(input) +
  aes(gdpPercap, lifeExp, col=continent) +
  geom_point(alpha=0.5) +
  facet_wrap(~year)
```

