

# Class 5: Data Visualization

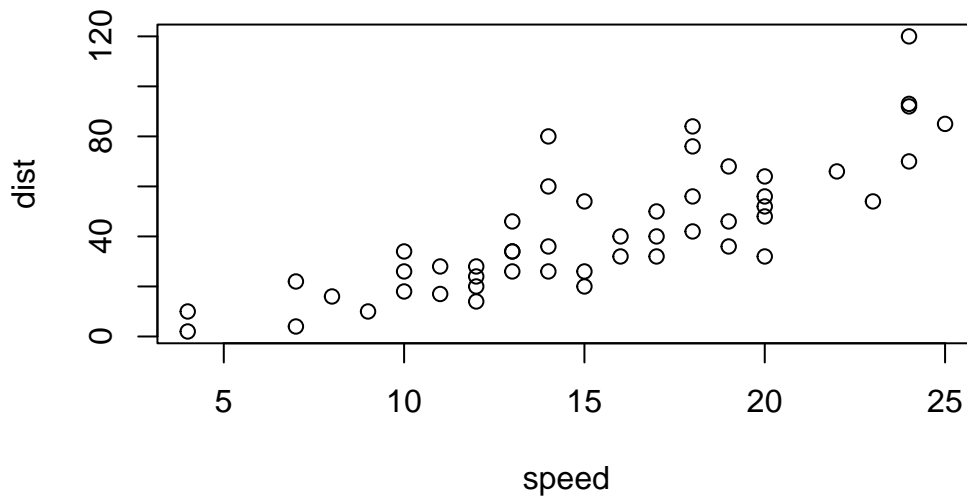
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## Plotting in R

R has multiple plotting and graphics systems. The most popular of which is **ggplot2**.

We have already played with “base” R graphics. This comes along with R “out of the box”. (WoW)

```
plot(cars)
```



Compared to base R plots ggplot is much more verbose - I need to write more code to get simple plots like the above.

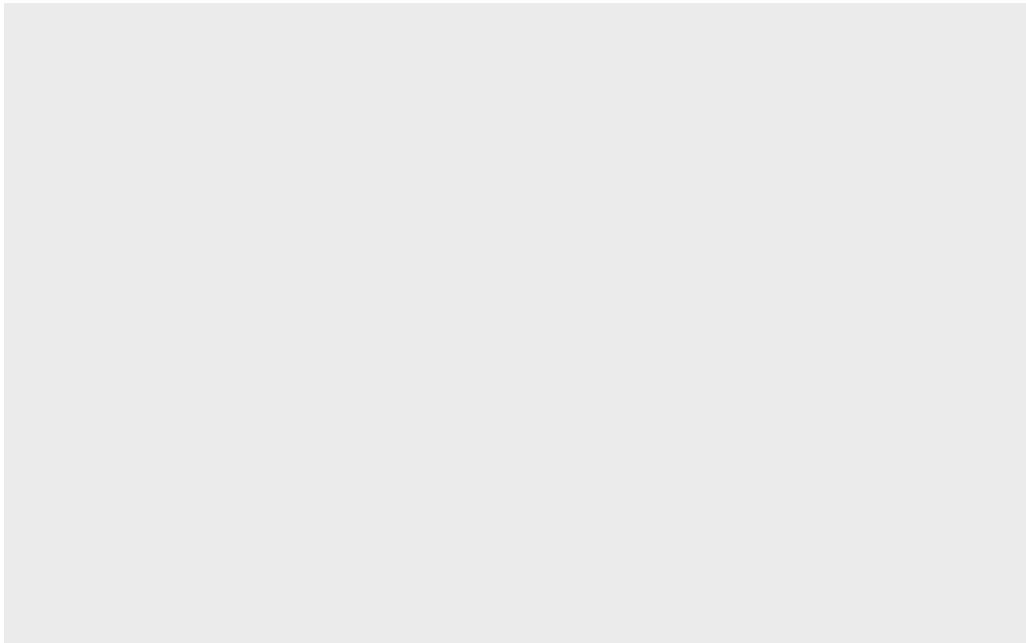
To use ggplot I need to first install the ggplot2 package. To install any package in R, I use the `install.packages()` command along with the package name.

The install is a one time only requirement. The package is now on our computer. I don't need to re-install it.

However, I can't just use it without loading it up with a `library()` call.

```
library(ggplot2)
```

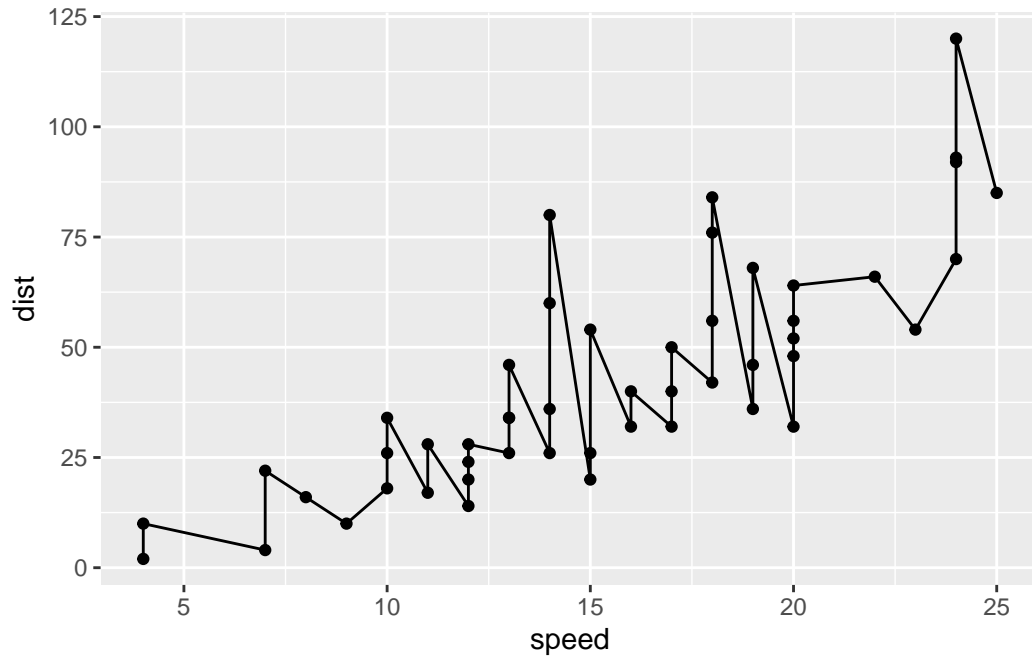
```
ggplot(cars)
```



All ggplot figures need at least 3 things:

- data (this is the `data.frame` with our numbers)
- aesthetics (`aes()`, how our data maps to the plot)
- geoms (do u want lines, points, columns, etc...)

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



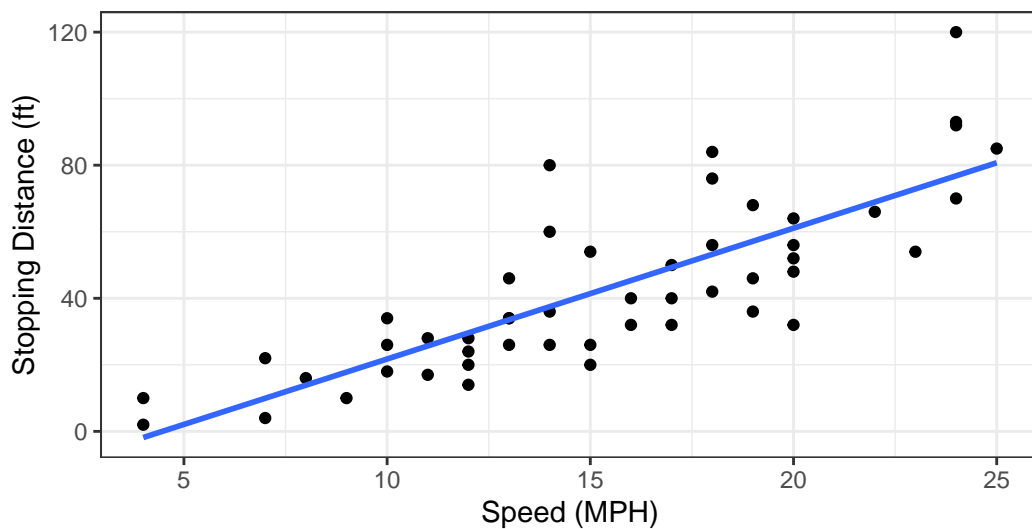
That is not we want, unfortunately.

```
ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  labs(title="Speed and Stopping Distances of Cars",
        x="Speed (MPH)",
        y="Stopping Distance (ft)",
        subtitle = "Back in the Old Old Time",
        caption="Dataset: 'cars'") +
  geom_smooth(method = "lm", se=FALSE) +
  theme_bw()
```

`geom\_smooth()` using formula = 'y ~ x'

## Speed and Stopping Distances of Cars

Back in the Old Old Time



Dataset: 'cars'

```
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

The `head()` will only print the first 6 rows by default.

```
nrow(genes)
```

```
[1] 5196
```

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

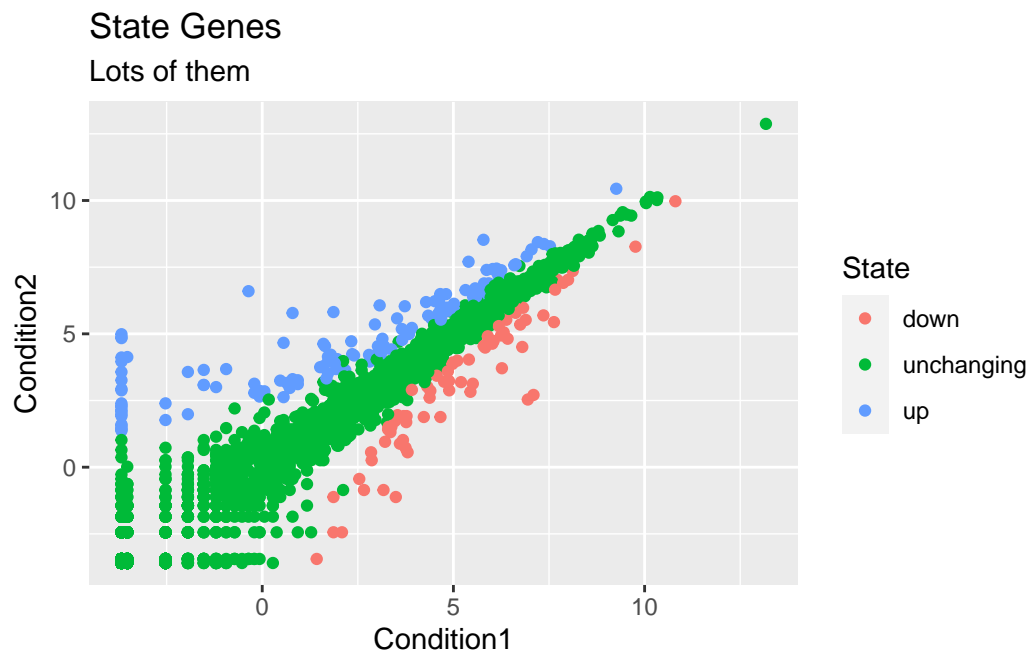
down	unchanging	up
72	4997	127

```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

down	unchanging	up
1.39	96.17	2.44

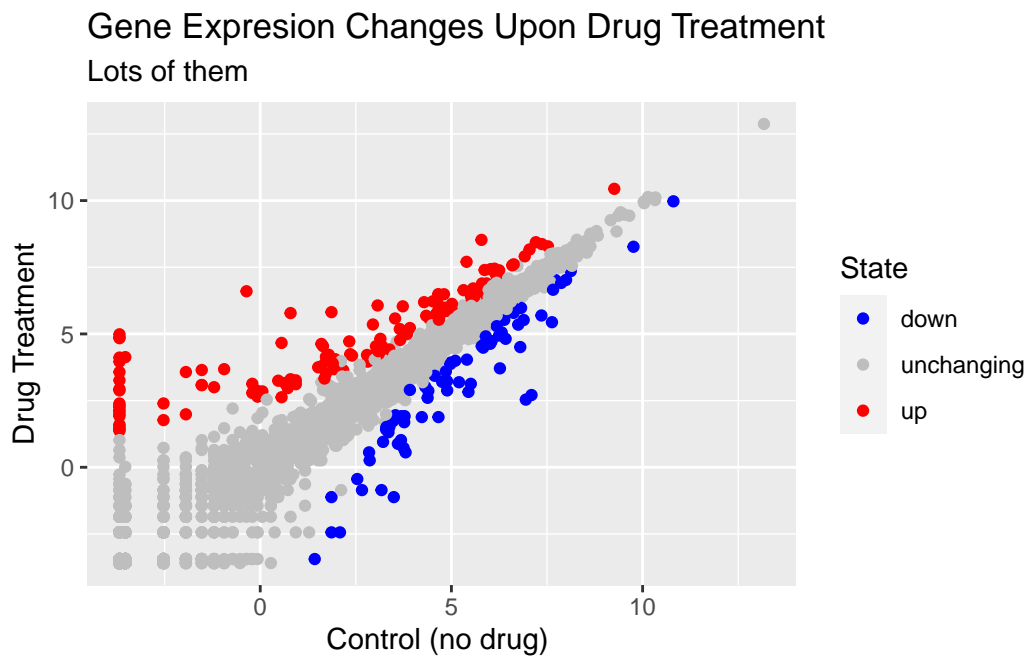
```
q <- ggplot(genes) +
  aes(Condition1, Condition2, color=State) +
  geom_point() +
  labs(title = "State Genes",
       subtitle = "Lots of them")
```

q



Can do **bold** and *italics*

```
q + scale_colour_manual( values=c("blue","gray","red") ) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment")
```



```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder."
gapminder <- read.delim(url)

library(dplyr)
```

Attaching package: 'dplyr'

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

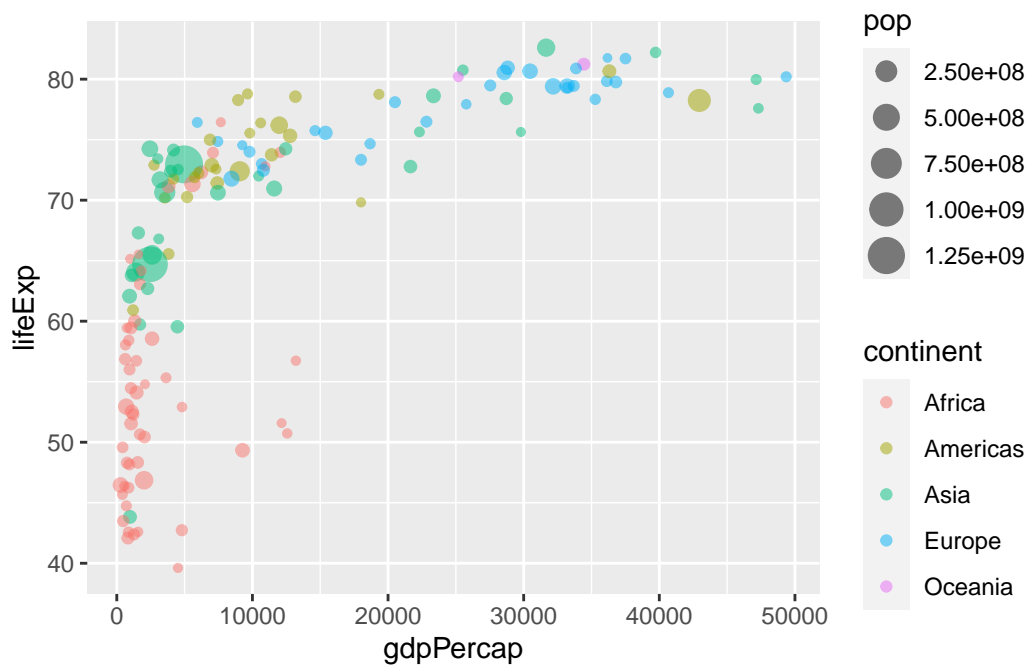
filter, lag

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

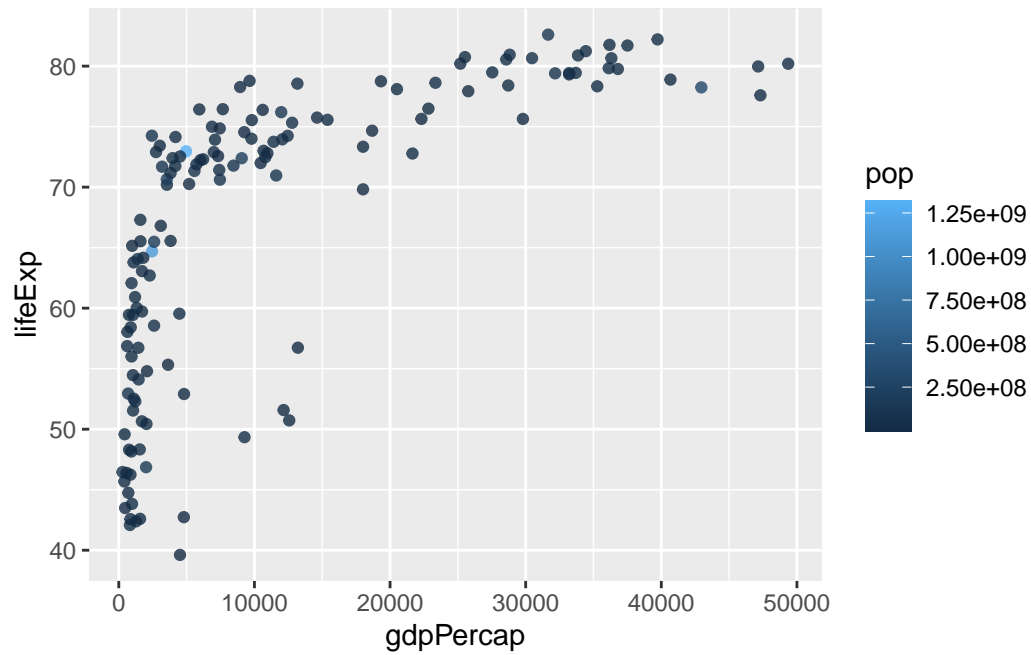
```
intersect, setdiff, setequal, union
```

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

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

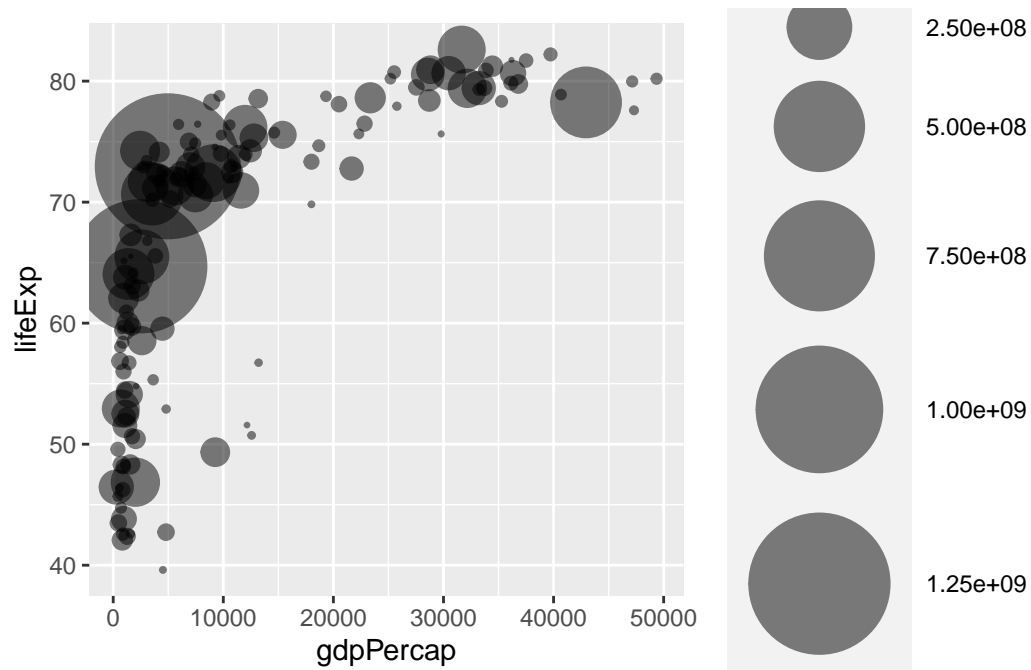


```
ggplot(gapminder_2007) +  
  aes(x = gdpPercap, y = lifeExp, color = pop) +  
  geom_point(alpha=0.8)
```



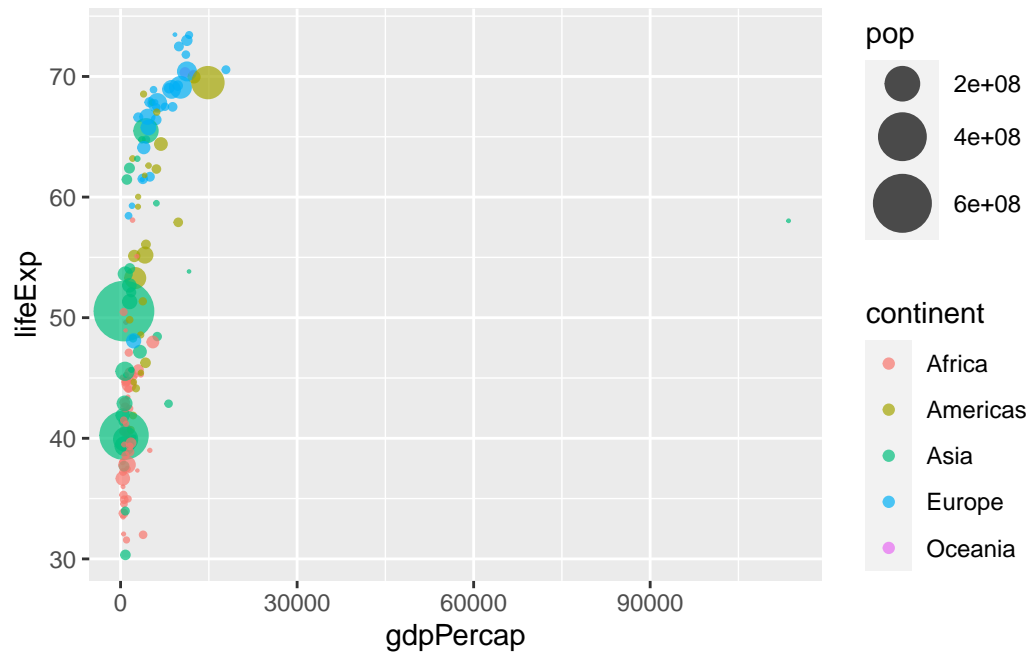
```
ggplot(gapminder_2007) +  
  geom_point(aes(x = gdpPercap, y = lifeExp,  
                 size = pop), alpha=0.5) +  
  scale_size_area(max_size = 25)
```





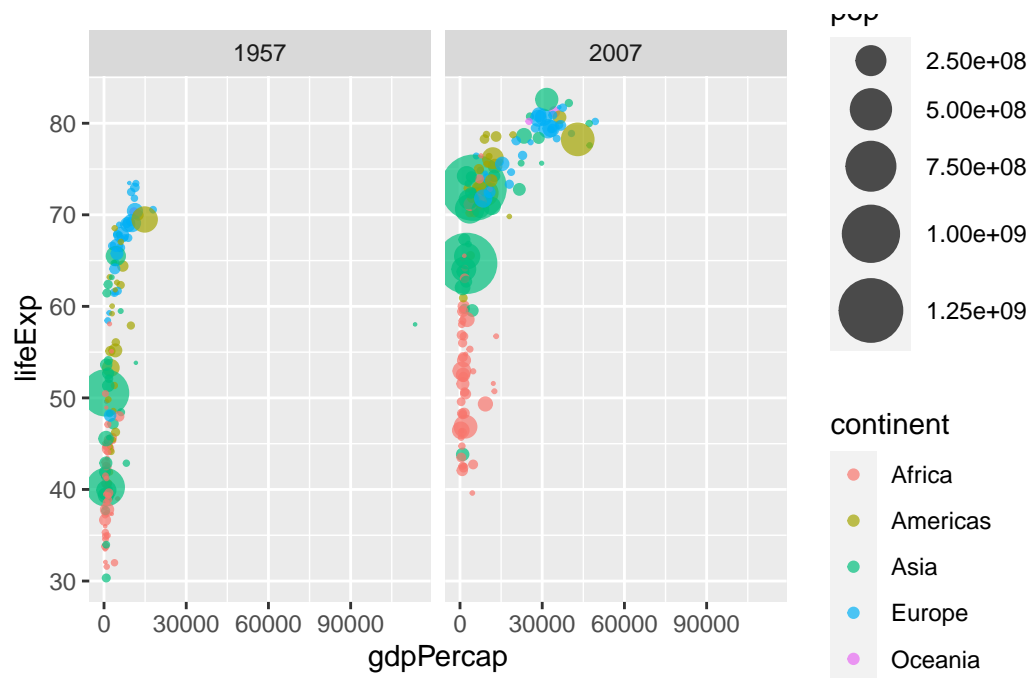
```
gapminder_1957 <- gapminder %>% filter(year==1957)

ggplot(gapminder_1957) +
  aes(x = gdpPerCap, y = lifeExp, color=continent,
      size = pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 10)
```



```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
                 size = pop), alpha=0.7) +
  scale_size_area(max_size = 11) +
  facet_wrap(~year)
```



[data-to-viz.com](http://data-to-viz.com)