

# Class 5 Data Visualization with ggplot

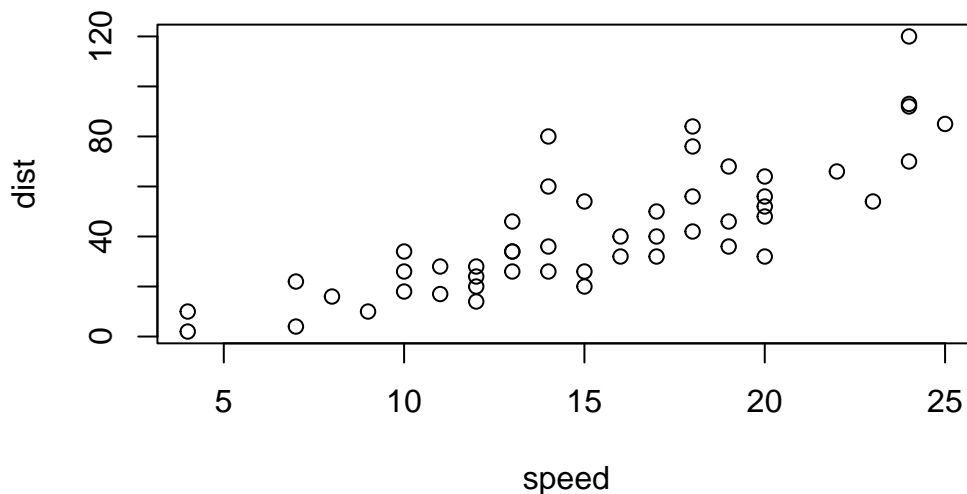
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#Graphics systems in R

There are many graphic systems in R for making plots and figures. We have already played a little with “**base R**” graphics and the `plot()` function.

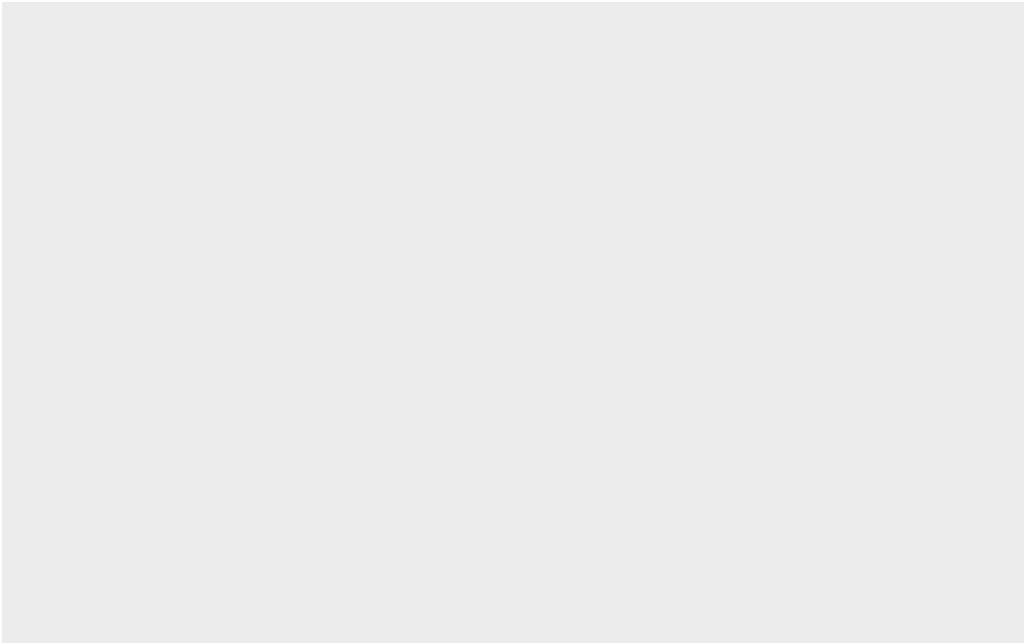
Today we will start learning about a popular graphics package called `ggplot2()`. This is an add on package- we need to install it. We will use the `install.packages()` function to do so.

```
plot(cars)
```



Before I can use the functions from a package I have to load up the package from my “library”. We use the `library(ggplot)` command to load it up.

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



Every ggplot needs at least 3 parts to work: - Data (the numbers that will do into your plot)  
- aes (aesthetics- how the columns of data map to the plot aesthetics) - geoms ( how the plot actually looks points, bars, lines,...)

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



For simple plots ggplot is more verbose- it takes more code, than a base R plot.

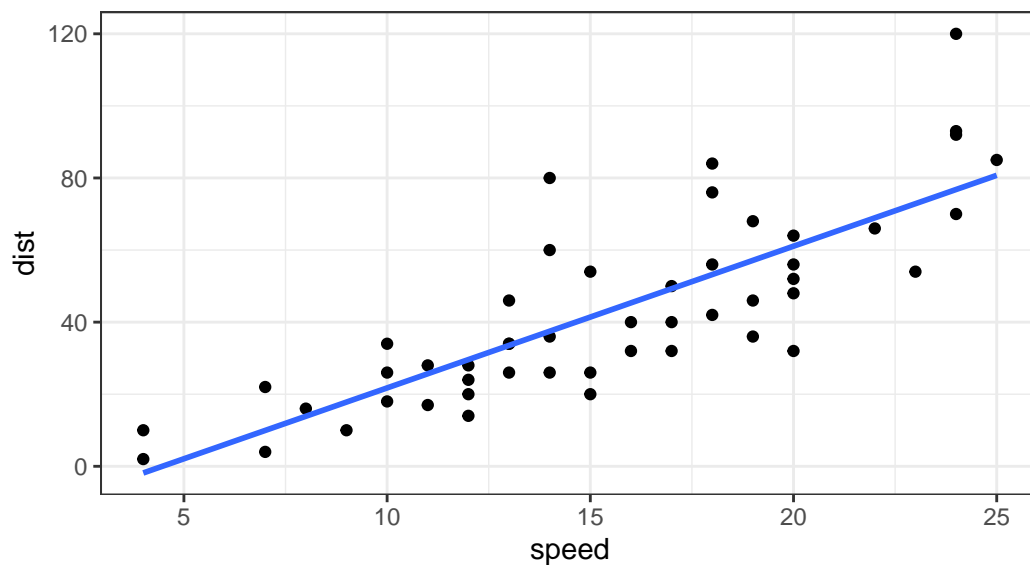
Add some more layers to our ggplot

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

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

## Stopping Distance of Old Cars

A sample plot



```
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
```

```
ncol(genes)
```

```
[1] 4
```

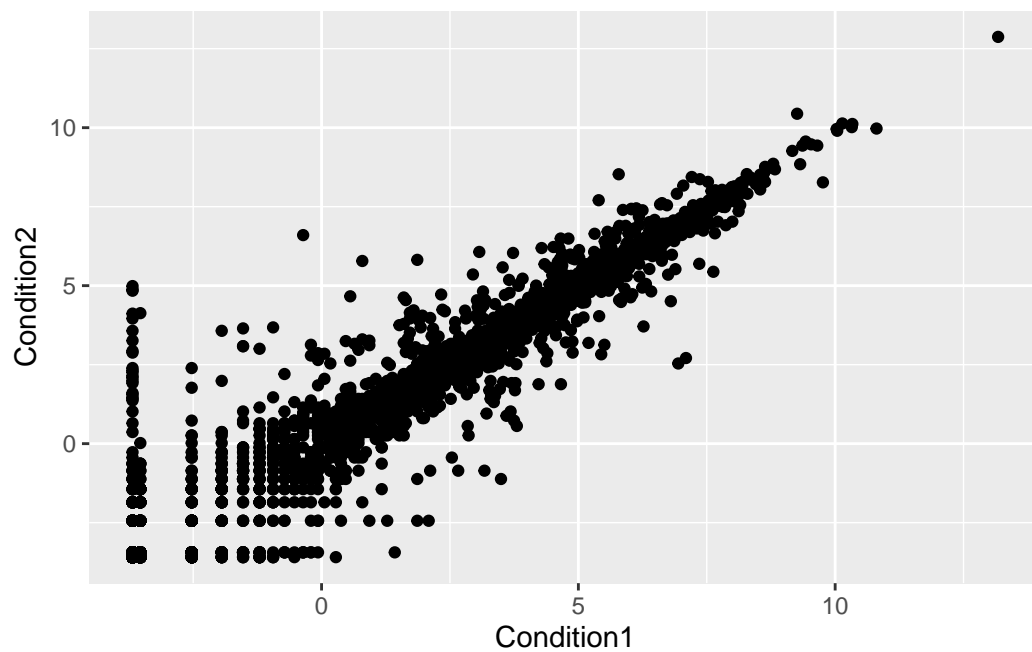
```
table(genes$State)
```

down	unchanging	up
72	4997	127

```
127/5196
```

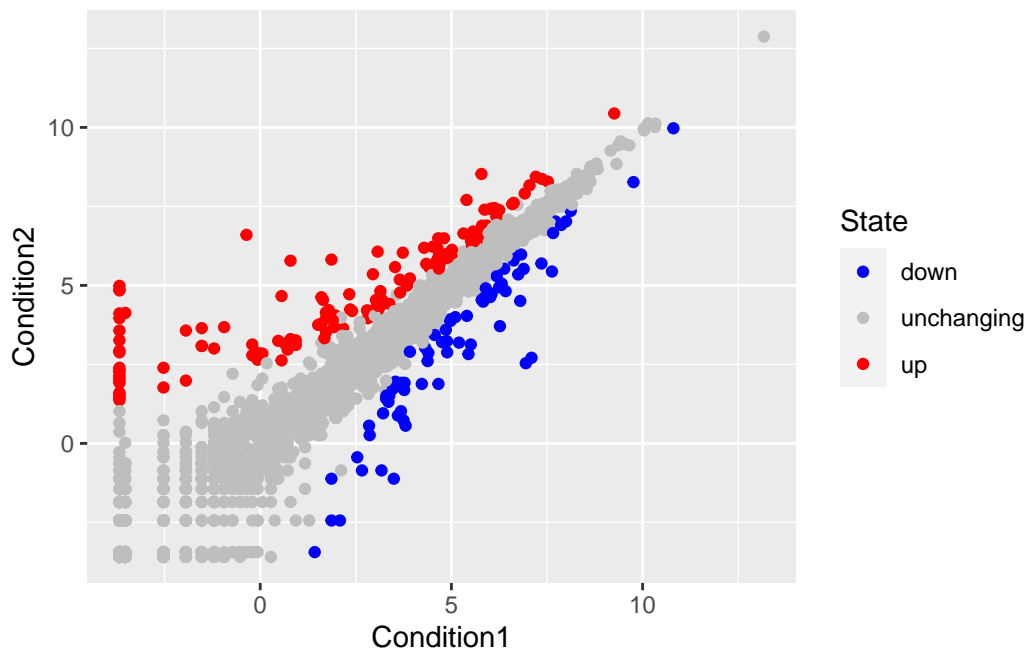
```
[1] 0.02444188
```

```
ggplot(genes)+aes(x=Condition1, y=Condition2)+ geom_point()
```



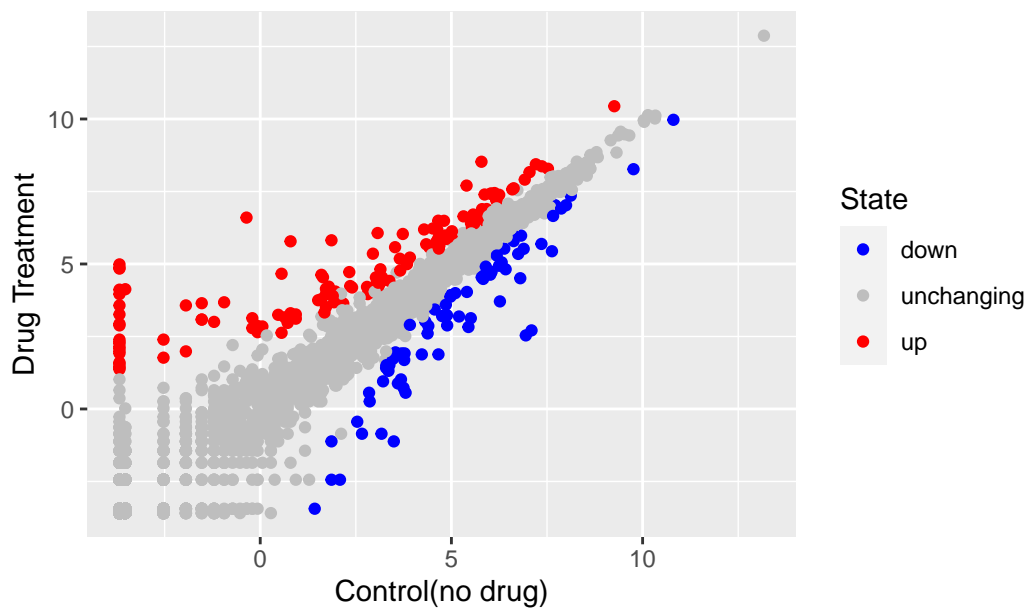
```
p= ggplot(genes)+aes(x=Condition1, y=Condition2, col=State)+ geom_point()
```

```
p+scale_color_manual(values=c("blue","grey","red"))
```



```
p+scale_color_manual(values=c("blue","grey","red"))+ labs(title="Gene Expression Changes U
```

Gene Expression Changes Upon Drug Treatment



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

Attaching package: 'gapminder'

The following object is masked \_by\_ '.GlobalEnv':

gapminder

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

Attaching package: 'dplyr'

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

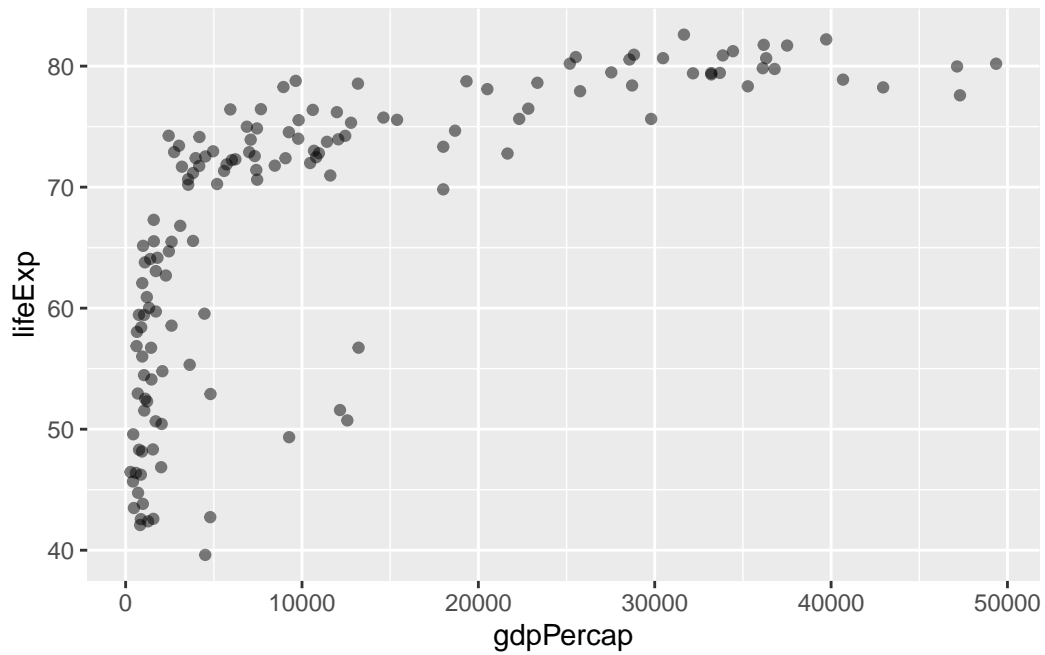
filter, lag

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

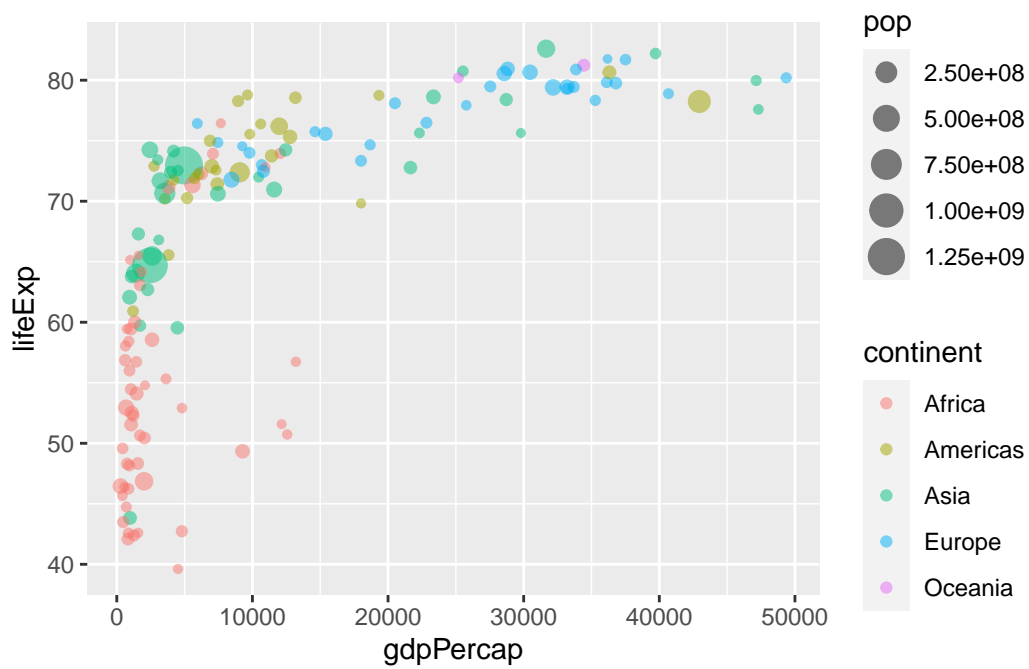
intersect, setdiff, setequal, union

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

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

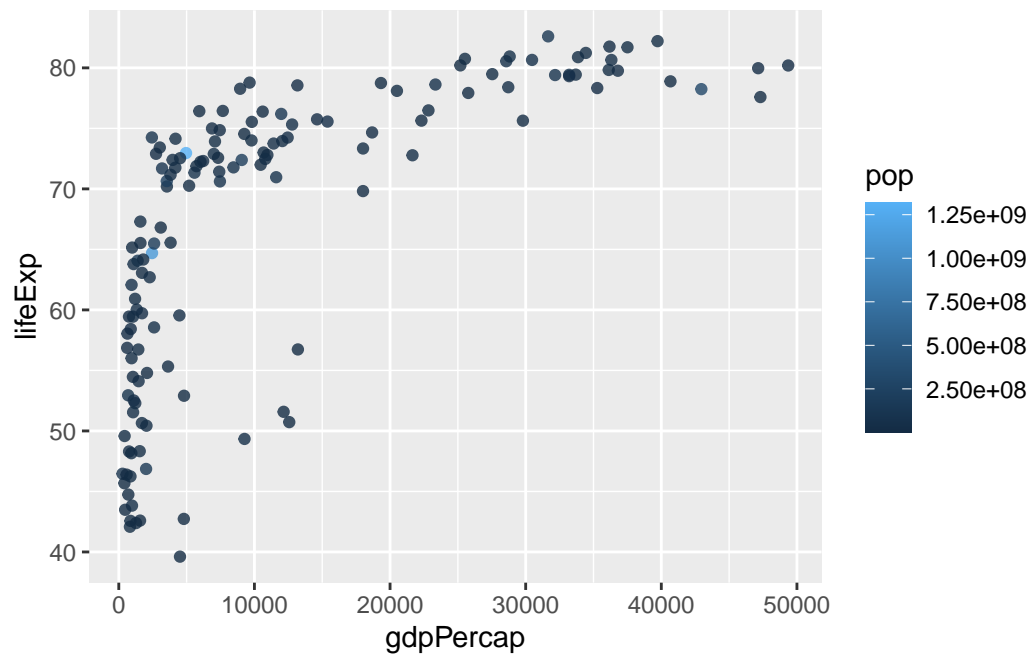


```
ggplot(gapminder_2007)+aes(x=gdpPercap, y=lifeExp, col=continent, size=pop)+ geom_point(al
```

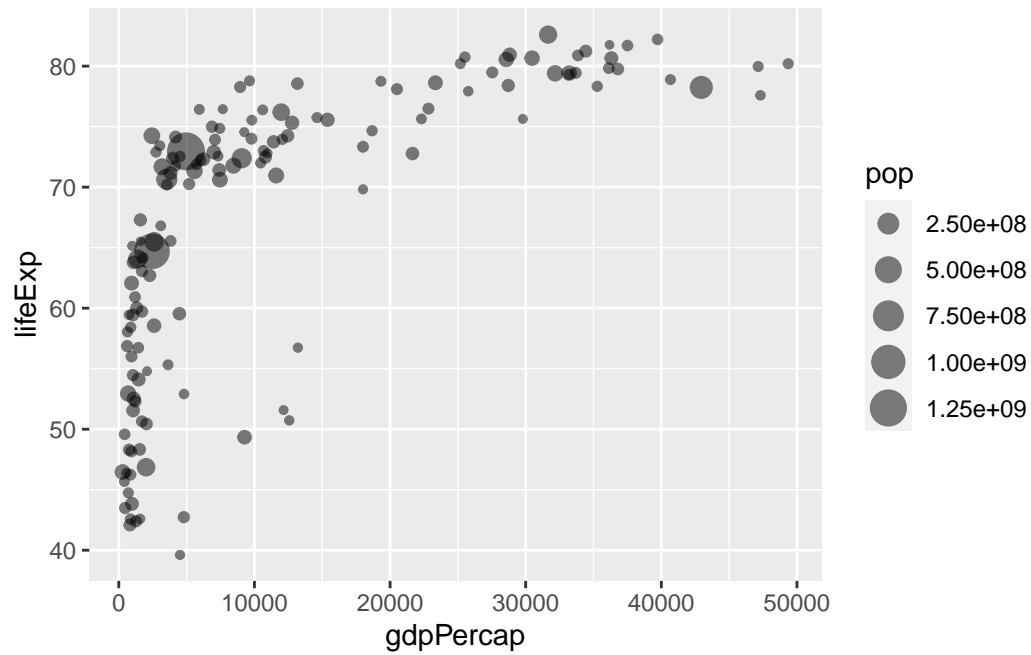




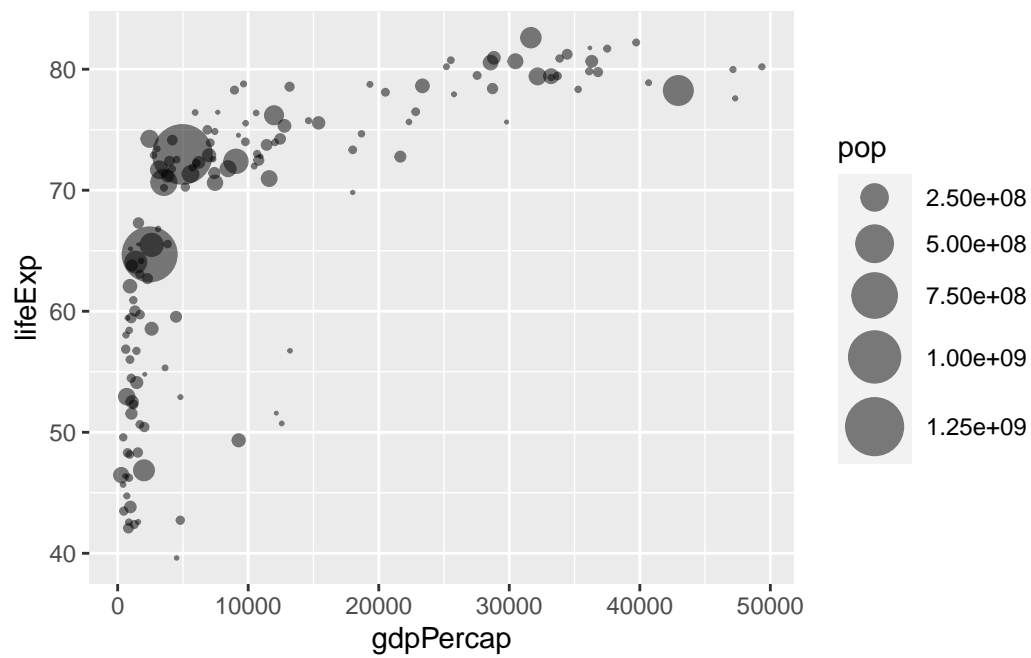
```
ggplot(gapminder_2007)+aes(x=gdpPercap, y=lifeExp, col=pop)+ geom_point(alpha=0.8)
```



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



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



```
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957)+aes(x=gdpPercap, y=lifeExp, col=continent, size=pop)+ geom_point(al
```

