

Class5: Data Visualization

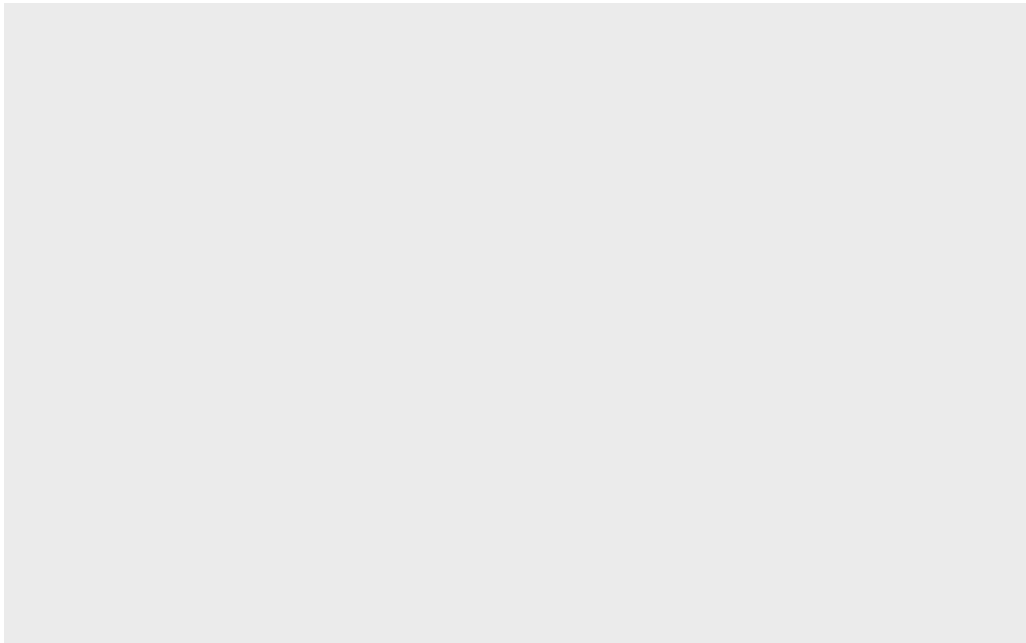
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Using GGPLOT

To use ggplot2 we first need to install it on our computers. To do this we will use the function `install.packages()`.

Before I use any package functions, I have to load them up with a `library()` call, like so:

```
# install.packages("ggplot2")  
library(ggplot2)  
ggplot(cars)
```

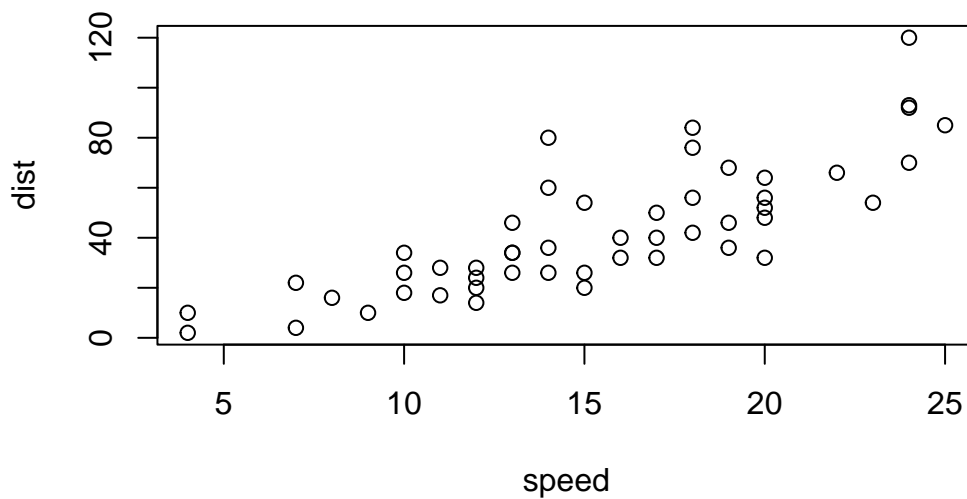


```
head(cars)
```

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

There's always the "base R" graphics system, i.e. `plot()`

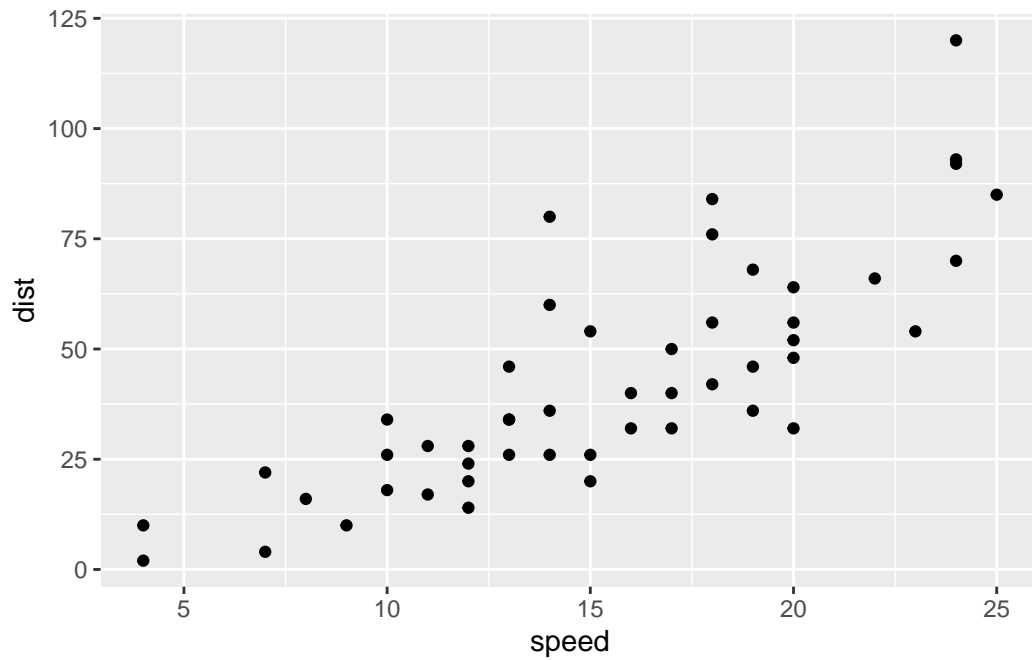
```
plot(cars)
```



To use ggplot, I need to spell out at least 3 things: - data (the stuff I want to plot as a data.frame) - aesthetics (`aes()` values - how the data map to the plot) - geoms (how I want things drawn)

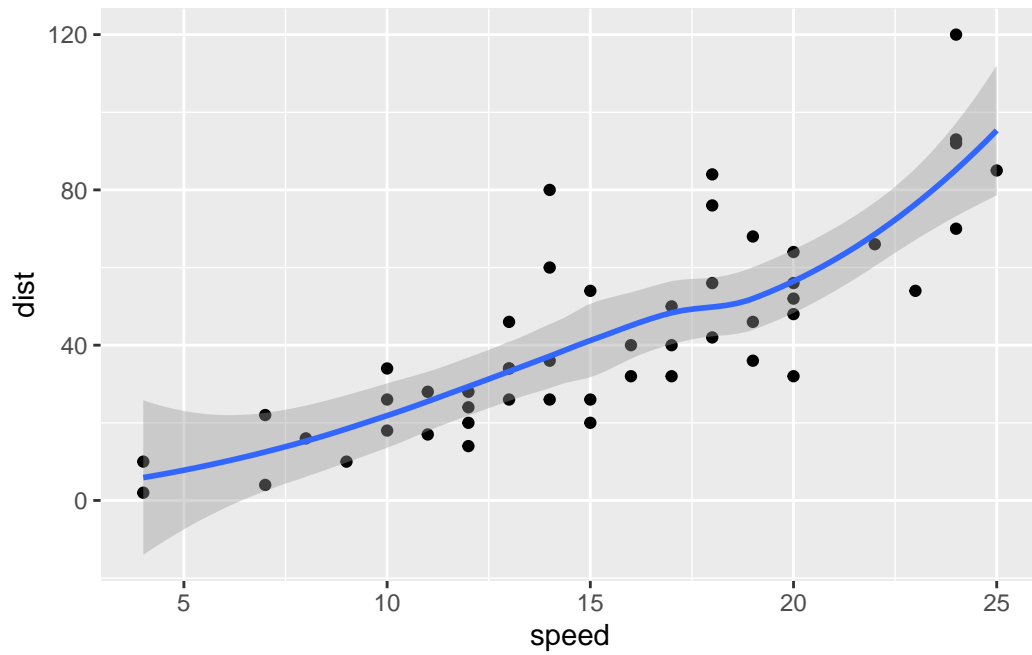
```
ggplot(cars) +  
  aes(x=speed, y=dist) +
```

```
geom_point()
```



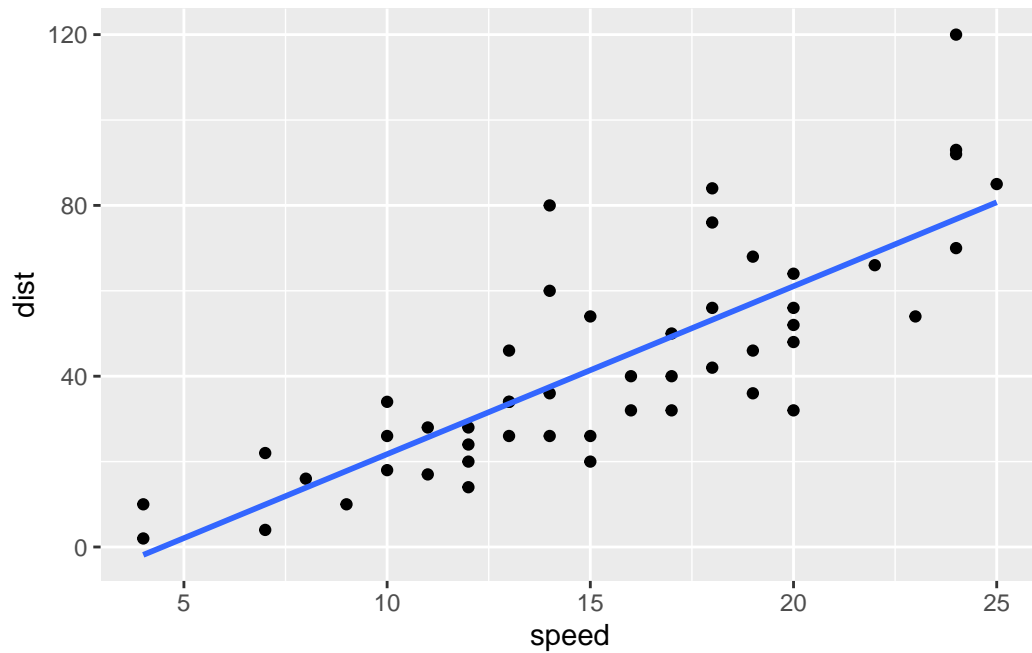
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth()
```

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



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

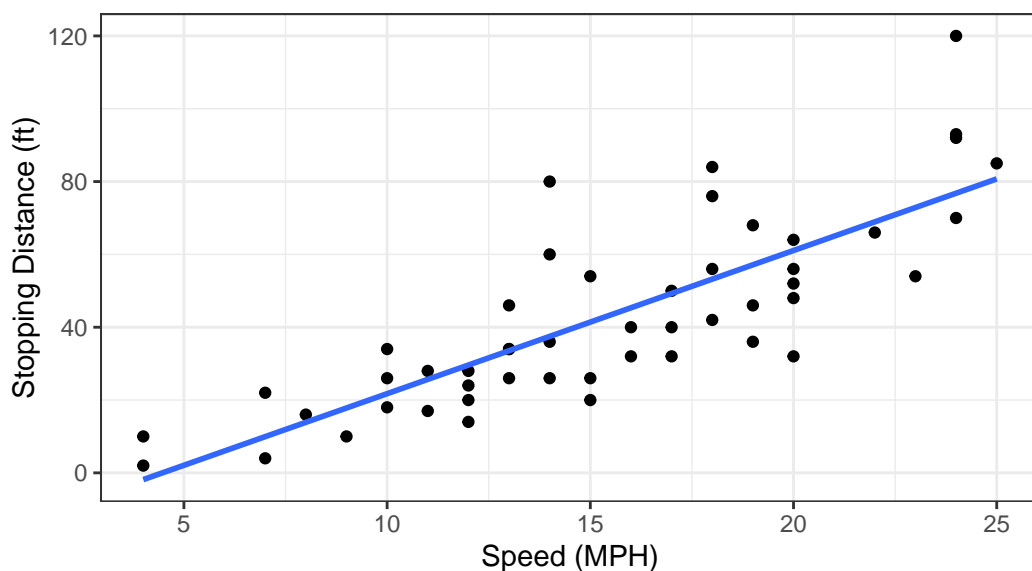
`geom_smooth()` using formula = 'y ~ x'



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

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

Speed and Stopping Distances of Cars



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

to get how many genes there are (how many rows)

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

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

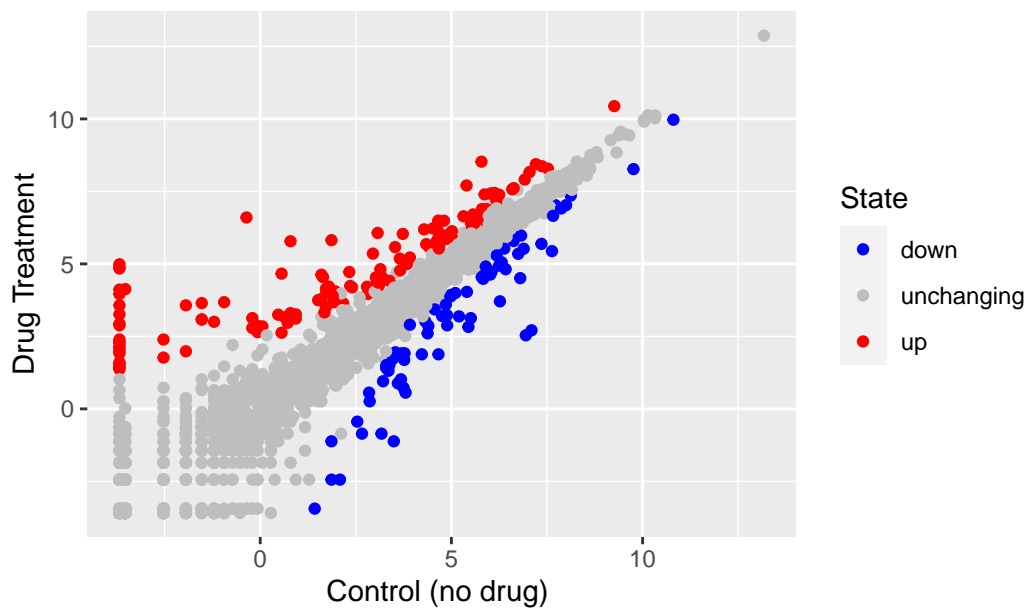
down	unchanging	up
72	4997	127

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

down	unchanging	up
1.39	96.17	2.44

```
p <- ggplot(genes)+  
  aes(x=Condition1, y=Condition2, col=State)+  
  geom_point()  
p + scale_colour_manual(values=c("blue","grey","red"))+  
  labs(title="Gene Expression Changes Upon Drug Treatment",  
        x="Control (no drug) ",  
        y="Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment



```
# 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

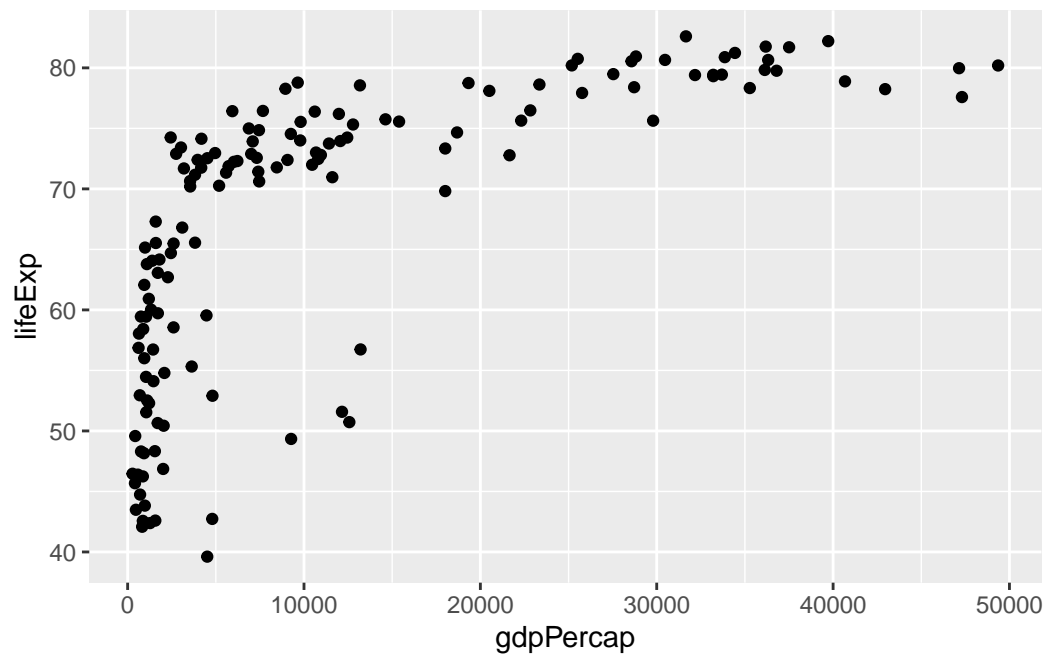
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

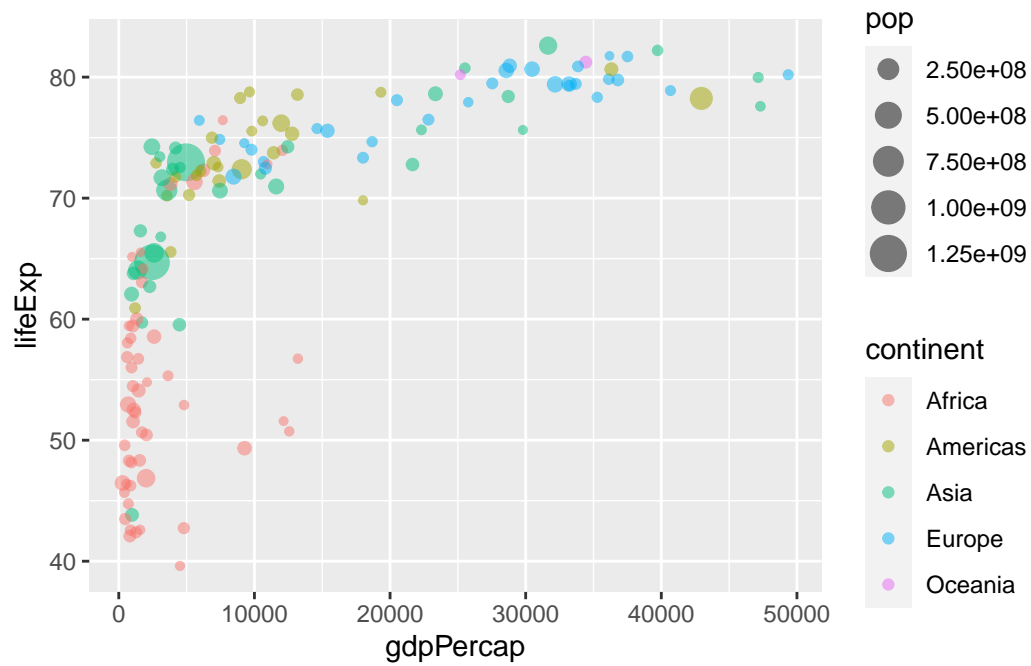
```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
```



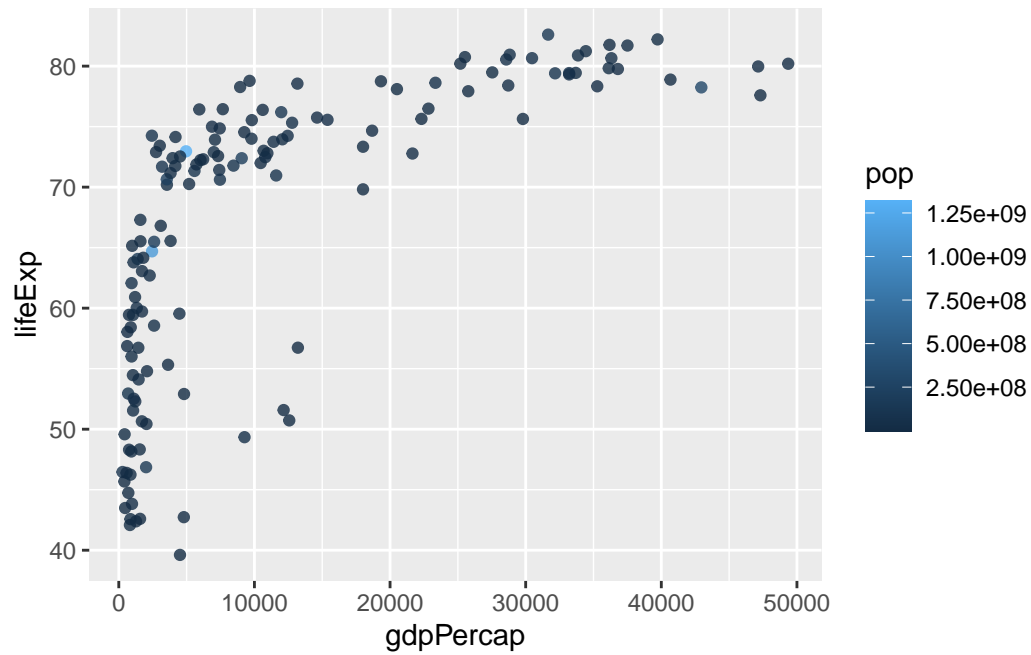
```
geom_point()
```



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

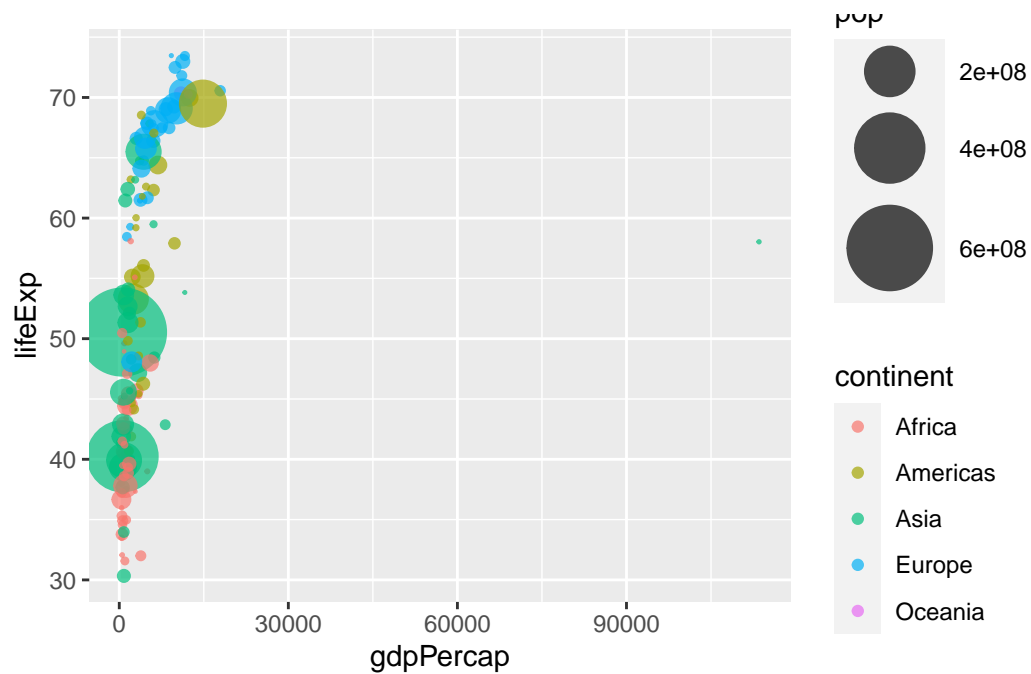


```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007)+
  aes(x=gdpPercap, y=lifeExp, color=pop) +
  geom_point(alpha=0.8)
```



```
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 = 15)
```



```
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 = 15) +
  facet_wrap(~year)
```

