Class 5 Data Visualization with ggplot2

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Using GGPLOT

The ggplot2 package does not come installed with R. Use the `install.package()` function to do so.

```
head(cars)
```

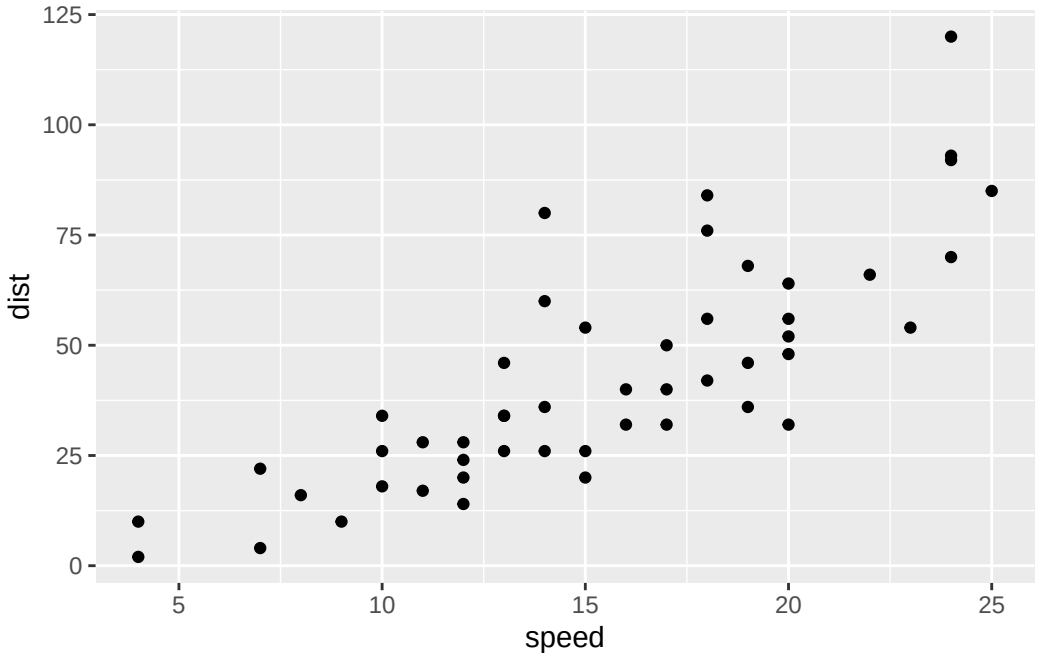
```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

To use ggplot I need to load up before I can call any of the functions in the package. Use the `library()` function to do this.

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

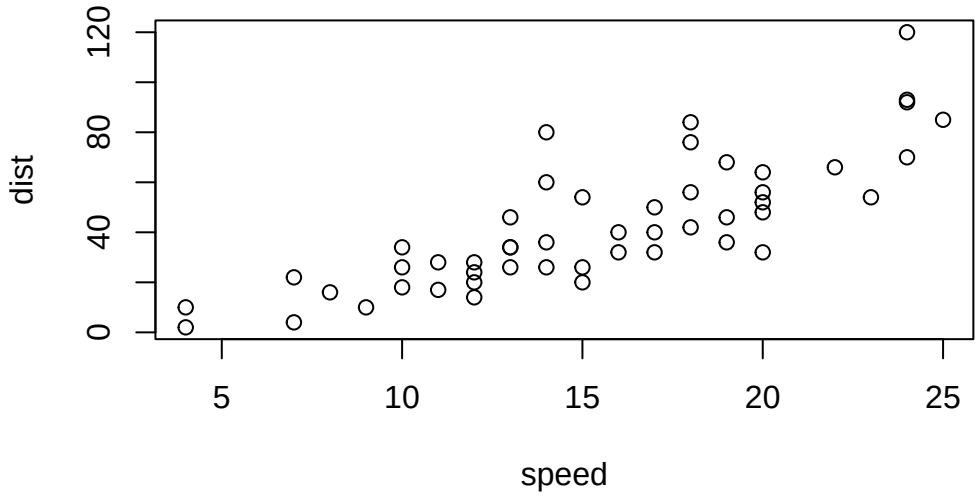
All ggplot figures have at least 3 things: - data(the stuff we want to plot) - aesthetic mapping(assigned visual aspects to your data) - geoms (how our dataset will be visualized)

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



ggplot is not the only graphing system in R - there are lots of others. There are even "base R" graphics (remember the plot function?).

```
plot(cars)
```



Lab 5

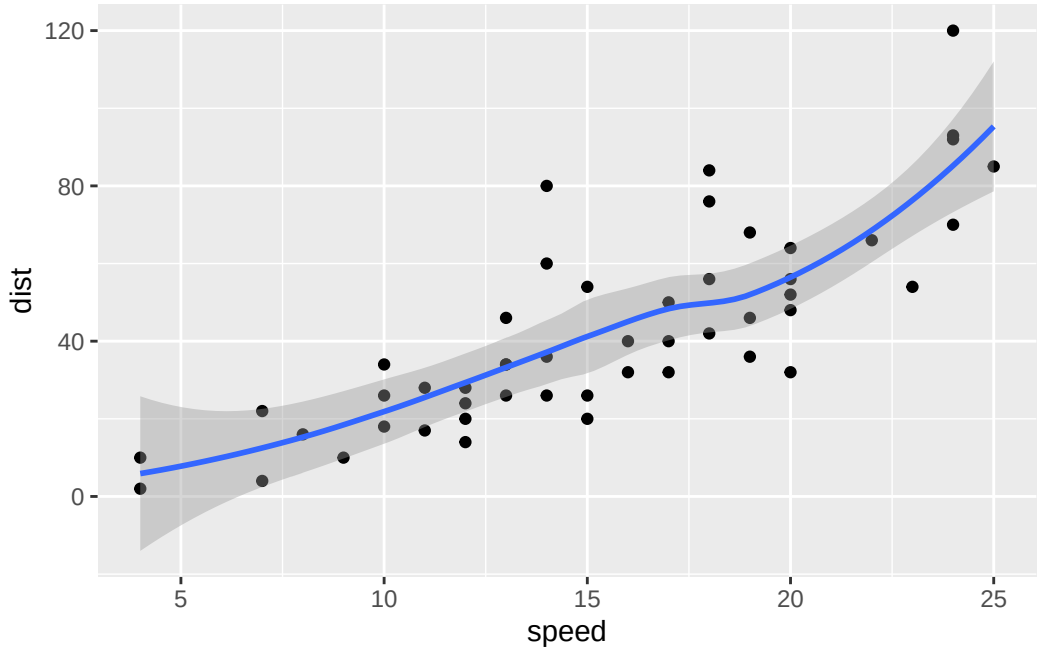
6. Creating Scatterplots

Cars Plot

Adding a trendline:

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

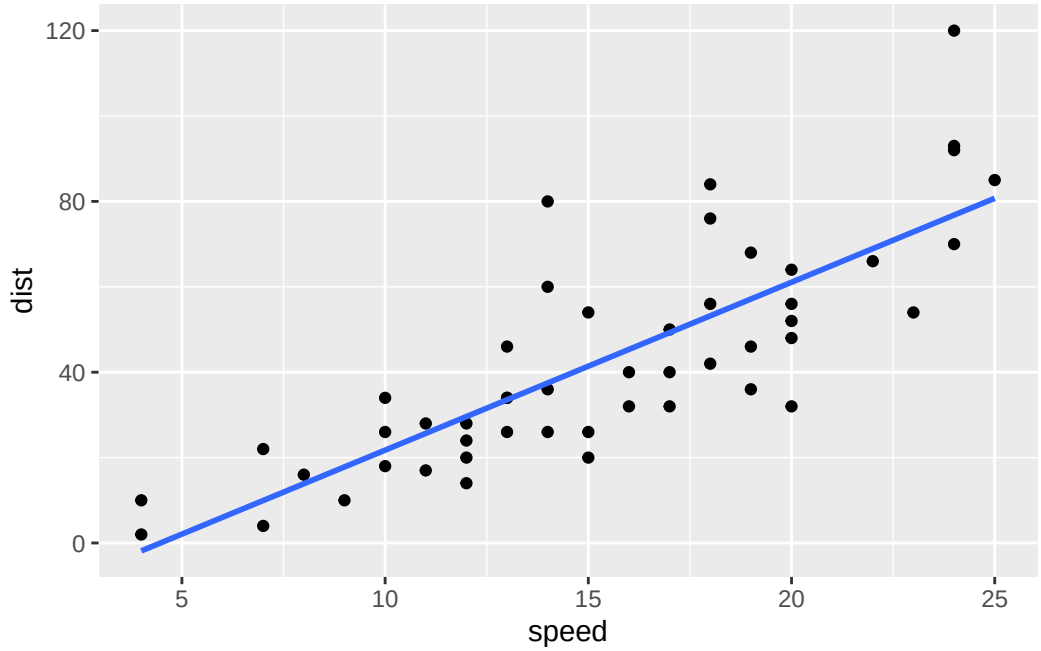
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



straightening the line and removing the shaded region:

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

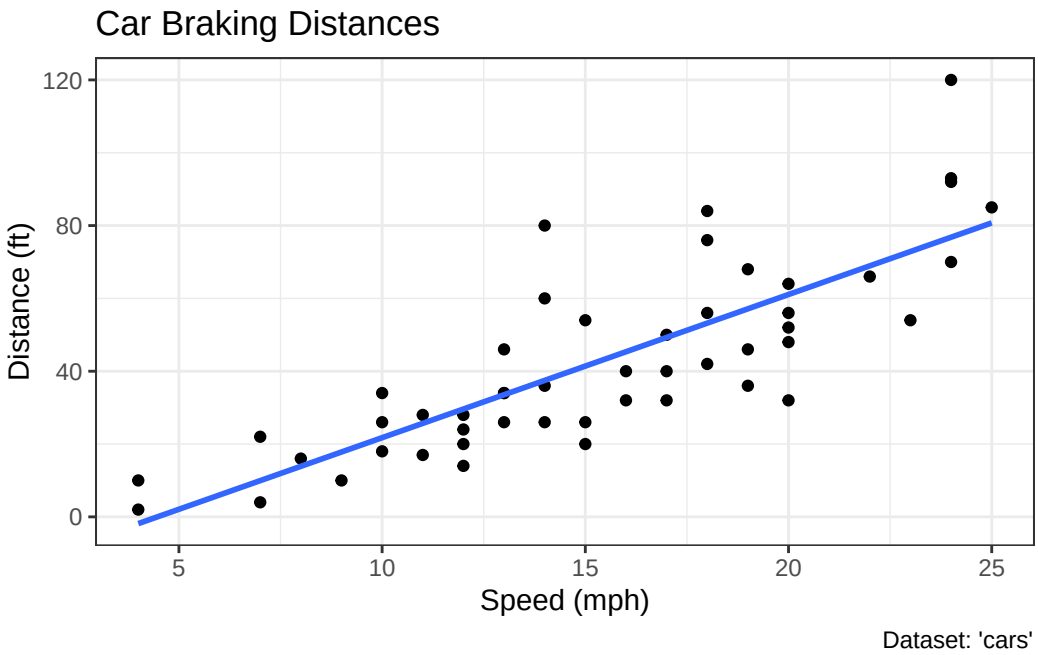
```
`geom_smooth()` using formula = 'y ~ x'
```



Adding labels and removing color:

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  labs(title="Car Braking Distances", x="Speed (mph)", y="Distance (ft)", caption="Dataset
  theme_bw()
```

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



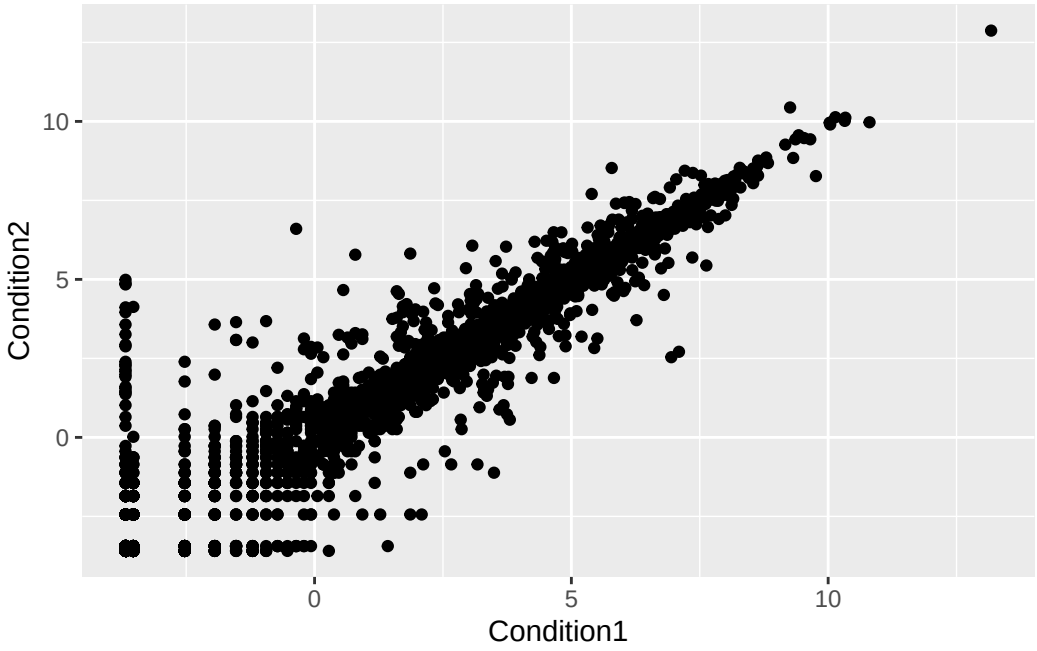
Genes Plot

```
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
```

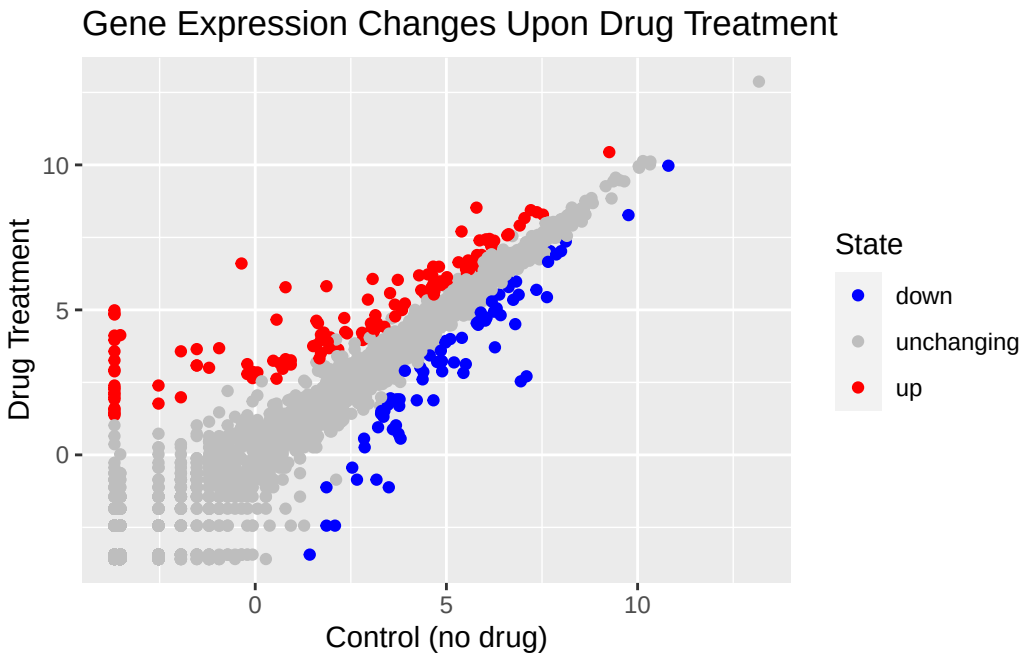
Basic Scatterplot:

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



Adding/changing the colors and adding labels:

```
p + aes(color=State) +
  scale_color_manual(values = c("blue", "gray", "red")) +
  labs(title = "Gene Expression Changes Upon Drug Treatment", x = "Control (no drug)", y =
```



7. Going Further

```
library(gapminder)
library(dplyr)
```

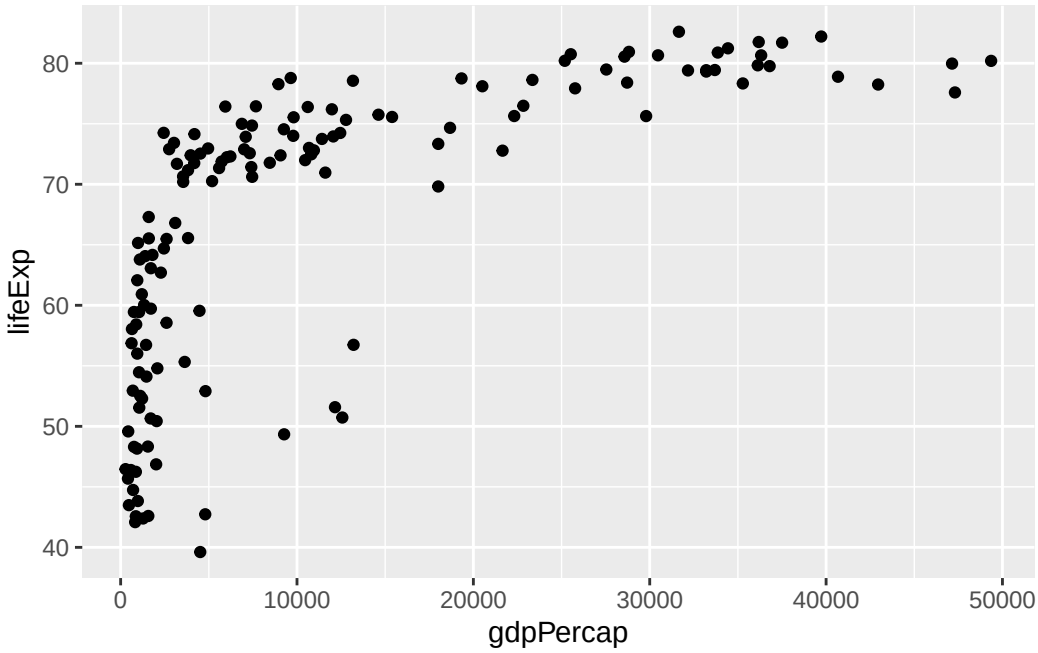
```
Attaching package: 'dplyr'
```

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

    filter, lag
```

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

    intersect, setdiff, setequal, union
```

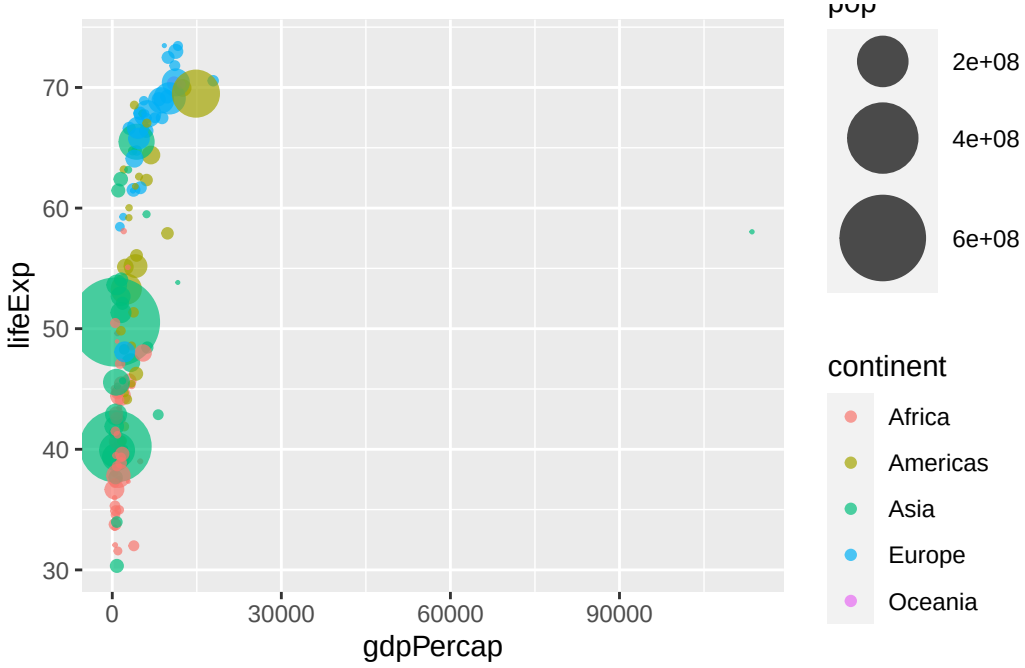
Basic Scatterplot:

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



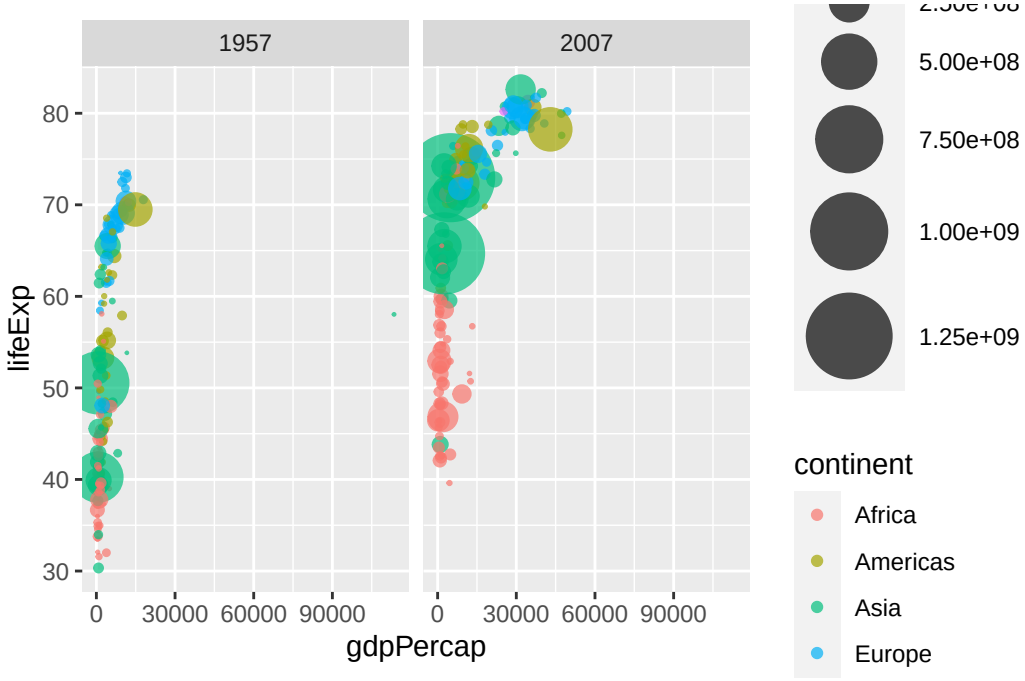
1957 Data Plot:

```
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)
```



Comparing 1957 to 2007:

```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)
ggplot(gapminder_1957) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 15) +
  facet_wrap(~year)
```


1957
2007
lifeExp
80
70
60
50
40
30
0
30000
60000
90000
gdpPercap
5.00e+08
7.50e+08
1.00e+09
1.25e+09
continent
Africa
Americas
Asia
Europe