Class 5: Data Visualization

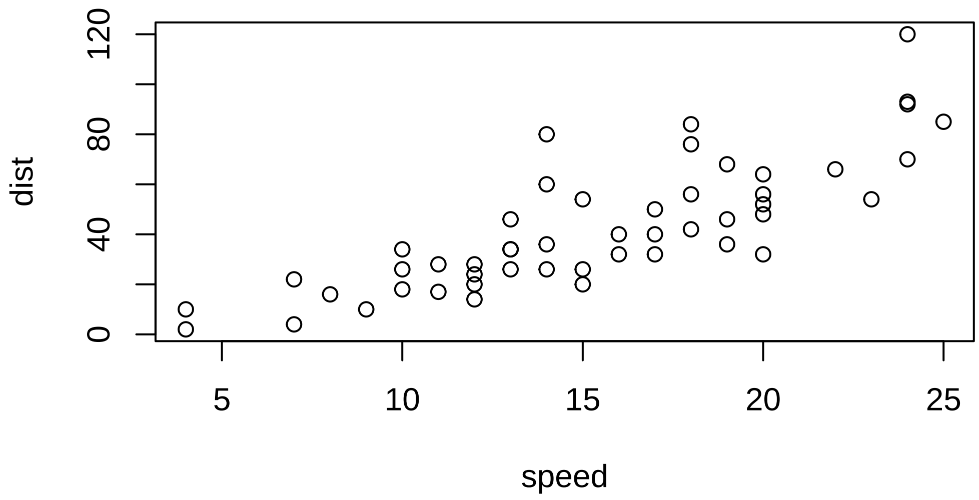
Andres Sandoval

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”.

```
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.

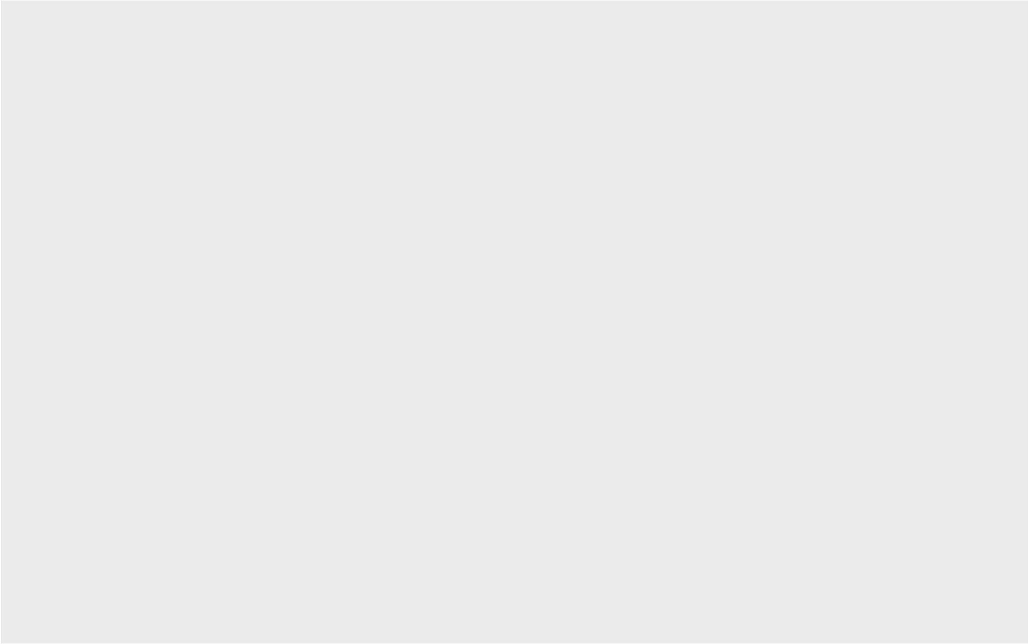
To use ggplot I need to first install the ggplot2 package. To install any package in R, use the `install.packages()` command along with the package name.

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.

```r
#install.packages("ggplot2")
library(ggplot2)
```

```r
ggplot(cars)
```

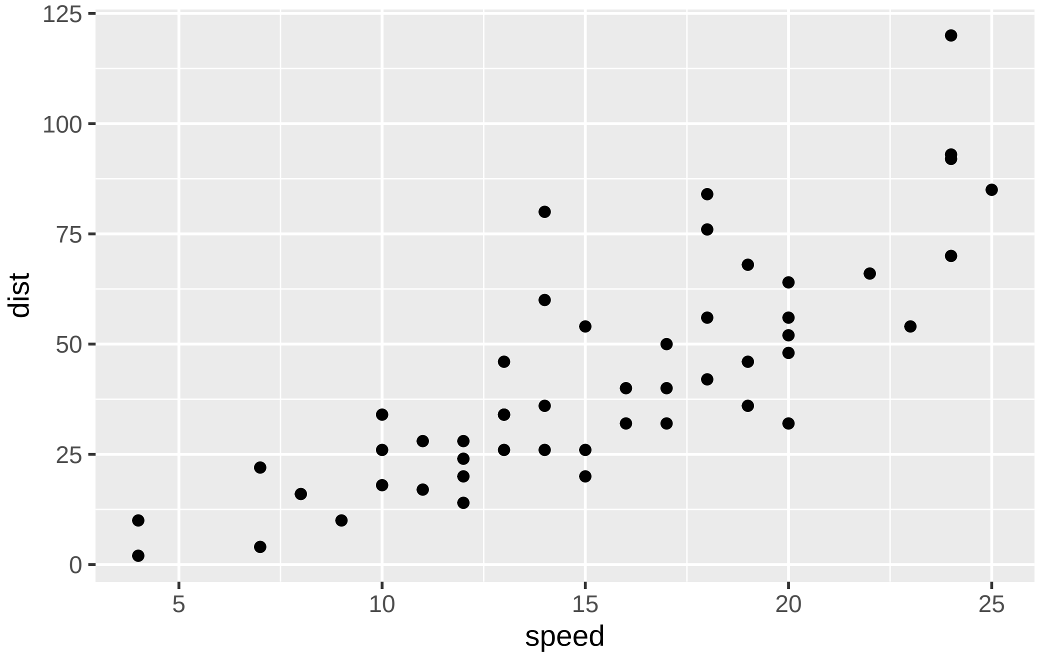


All ggplot figures need at least three things:

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

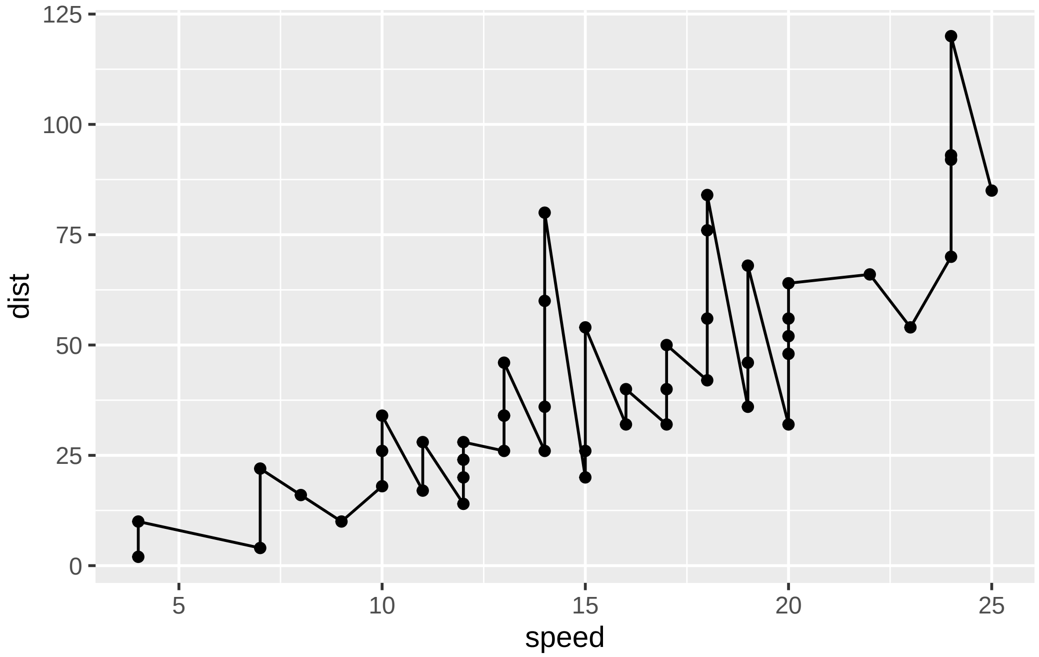
```r
bb <- ggplot(data=cars) +
  aes(x = speed, y = dist) +
  geom_point()
```

```
bb
```



I want a trend line to show the relationship between speed and stopping distance

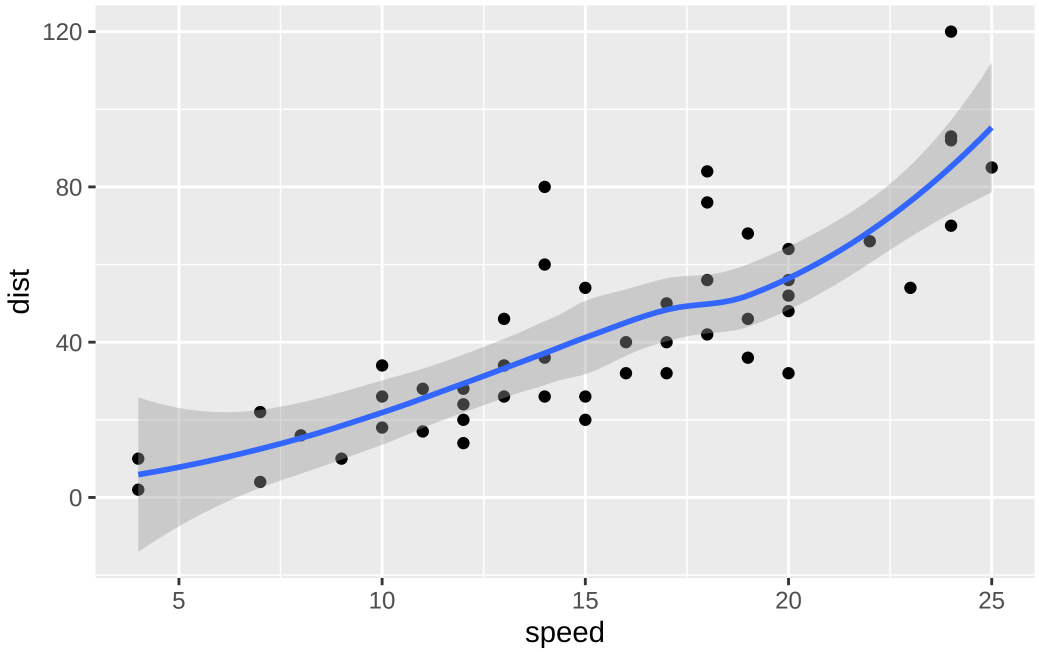
```
ggplot(data=cars) +
  aes(x = speed, y = dist) +
  geom_point() +
  geom_line()
```



That is not what we want

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

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



Gene

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
```

head(dataset) function will print out teh first 6 rows of the data set

```
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
```

Total genes

```
nrow(genes)
```

```
[1] 5196
```

Column Names and Number of columns

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

Number of Upregulated Genes

```
table(genes[,"State"])
```

```

      down unchanging         up 
        72       4997        127 
```

Fraction of total genes

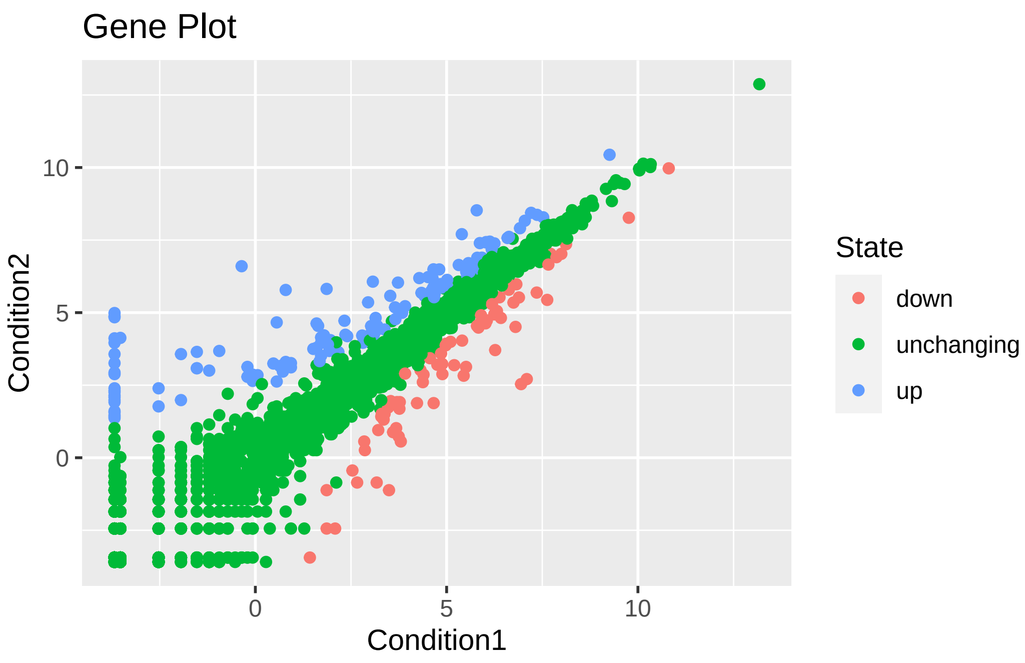
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

```

      down unchanging         up 
      1.39      96.17       2.44 
```

Saved the plot as p

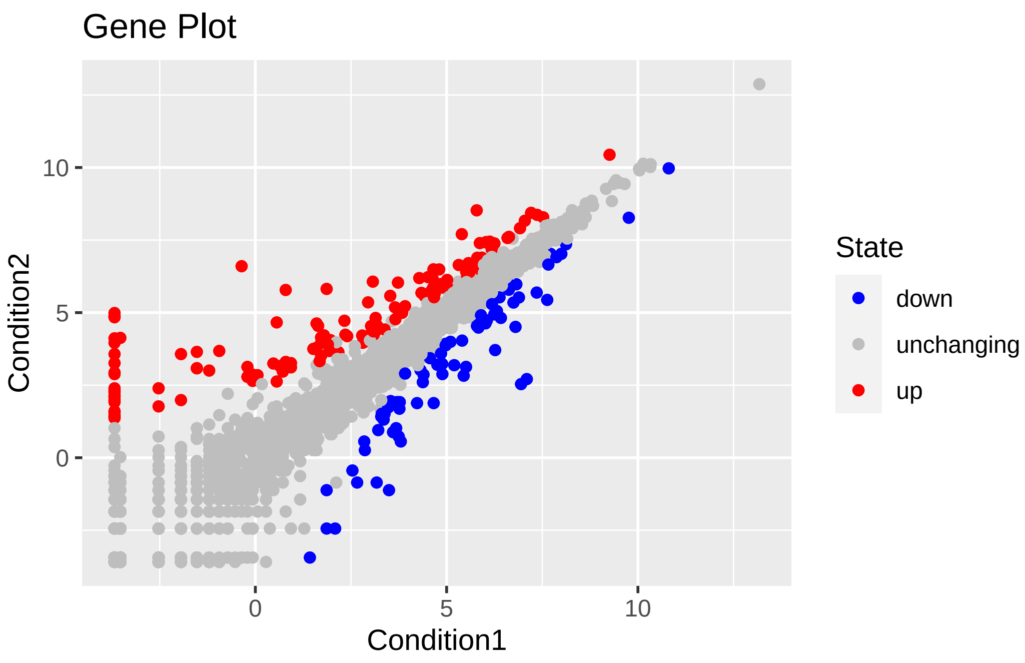
```
p <- ggplot(genes) +
  aes(Condition1,Condition2, color = State) +
  geom_point() +
  labs(title = "Gene Plot")
```

```
p
```



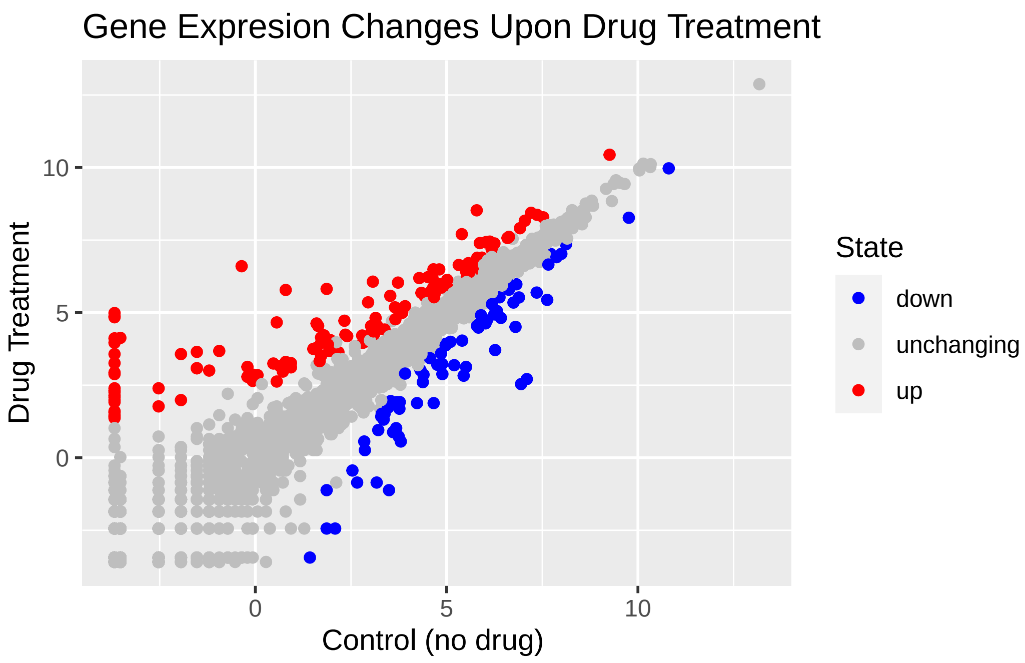
Change the colors of p

```
p + scale_colour_manual( values=c("blue","gray","red") )
```



Add Plot Annotations

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



Gapminder 2007

```
#install.packages("gapminder")
#install.packages("dplyr")
library(gapminder)
library(dplyr)
```

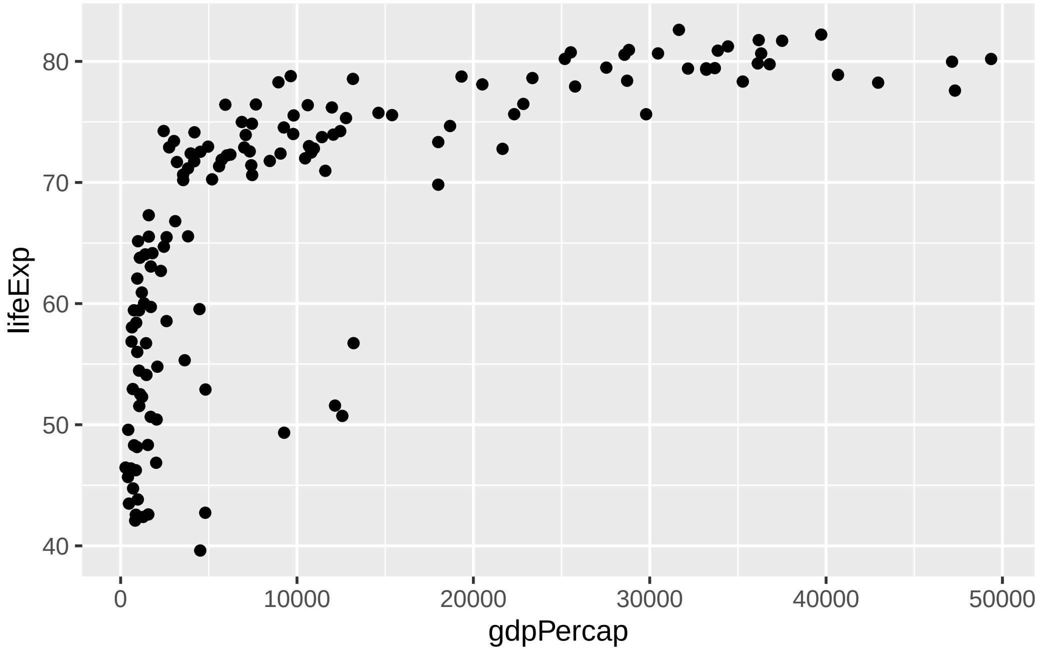
```

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
```

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

```
head(gapminder_2007)
```

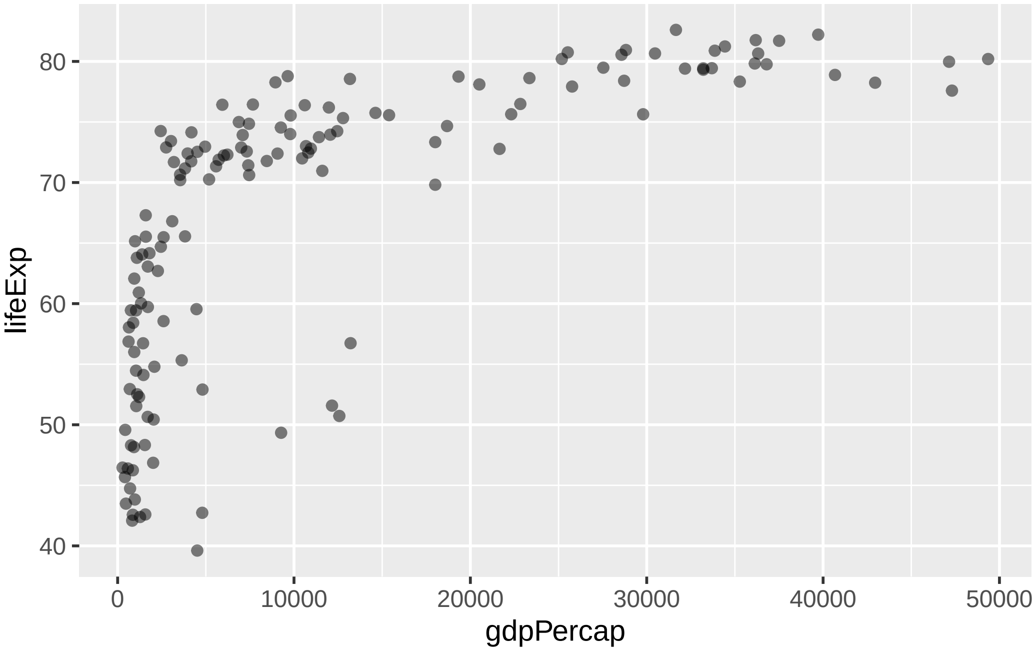
```
# A tibble: 6 x 6
  country     continent  year lifeExp      pop gdpPercap
  <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
1 Afghanistan Asia       2007    43.8 31889923      975.
2 Albania     Europe     2007    76.4  3600523     5937.
3 Algeria     Africa     2007    72.3 33333216     6223.
4 Angola      Africa     2007    42.7 12420476     4797.
5 Argentina   Americas   2007    75.3 40301927    12779.
6 Australia   Oceania    2007    81.2 20434176    34435.
```

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



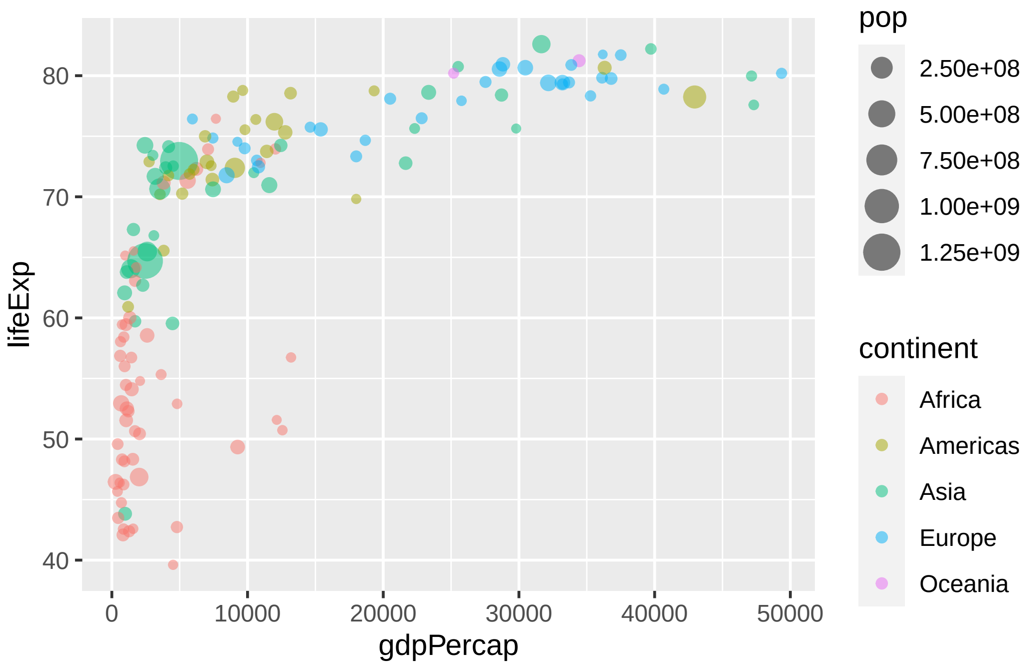
Changing the transparency

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



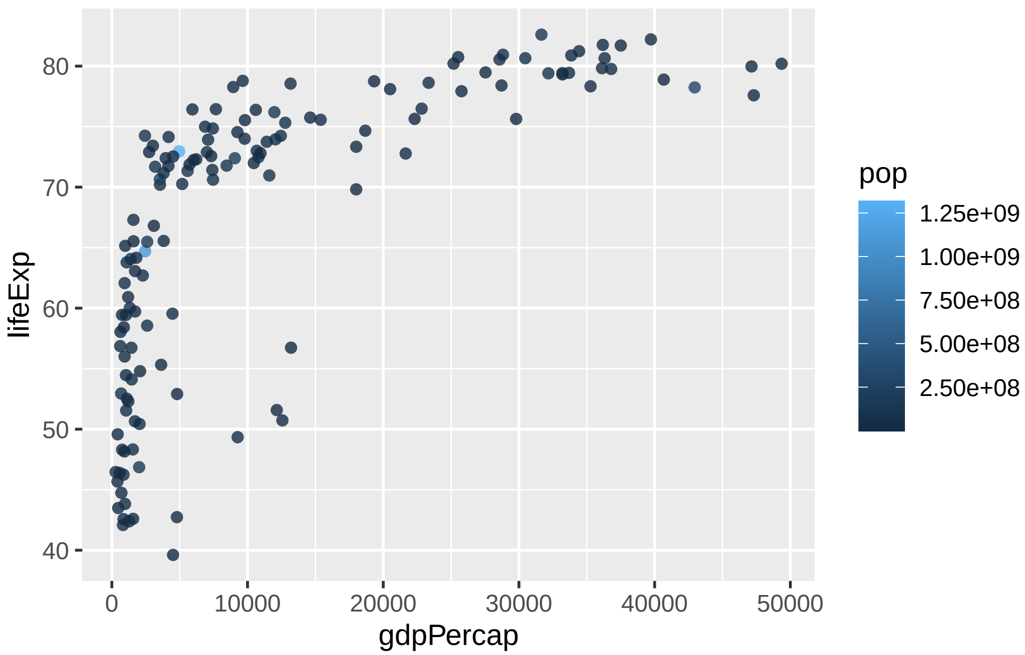
Adding more variables to aes

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



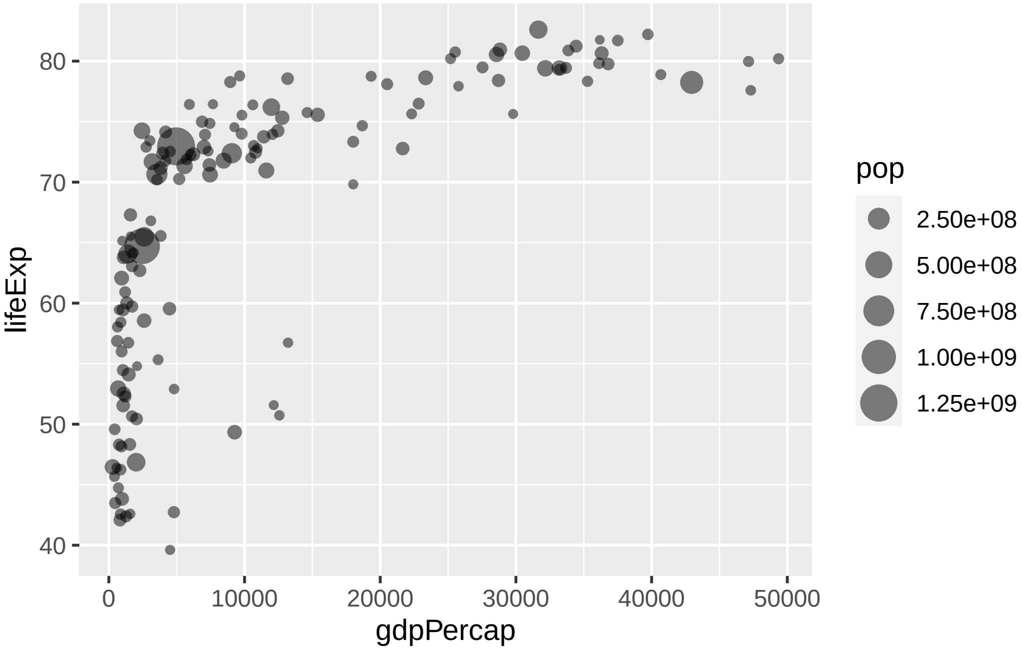
Numeric Pop Points

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



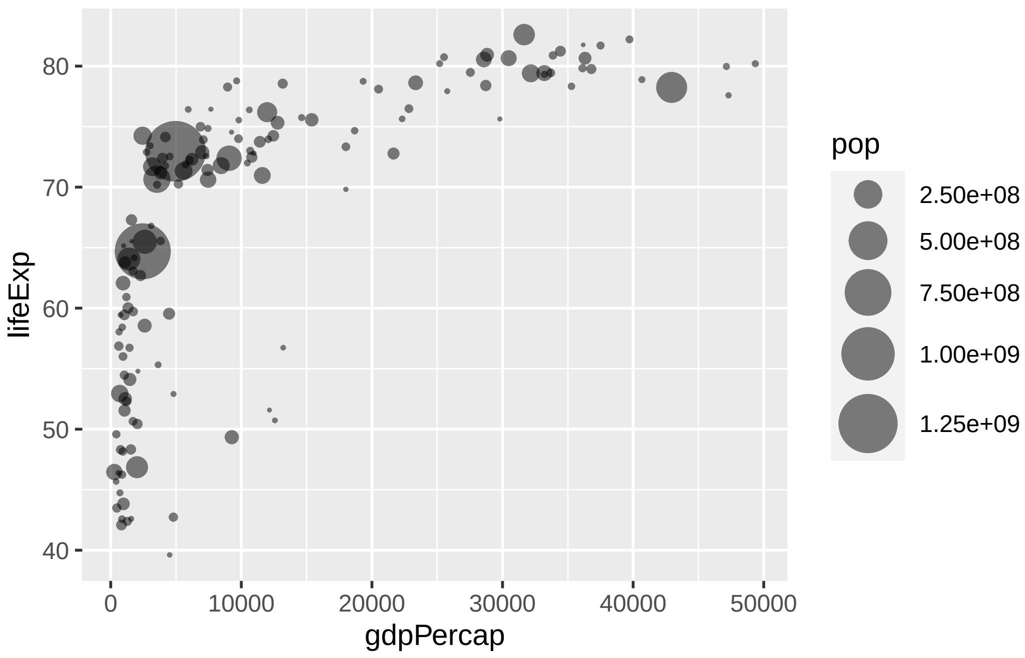
Adjusting Point Size

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



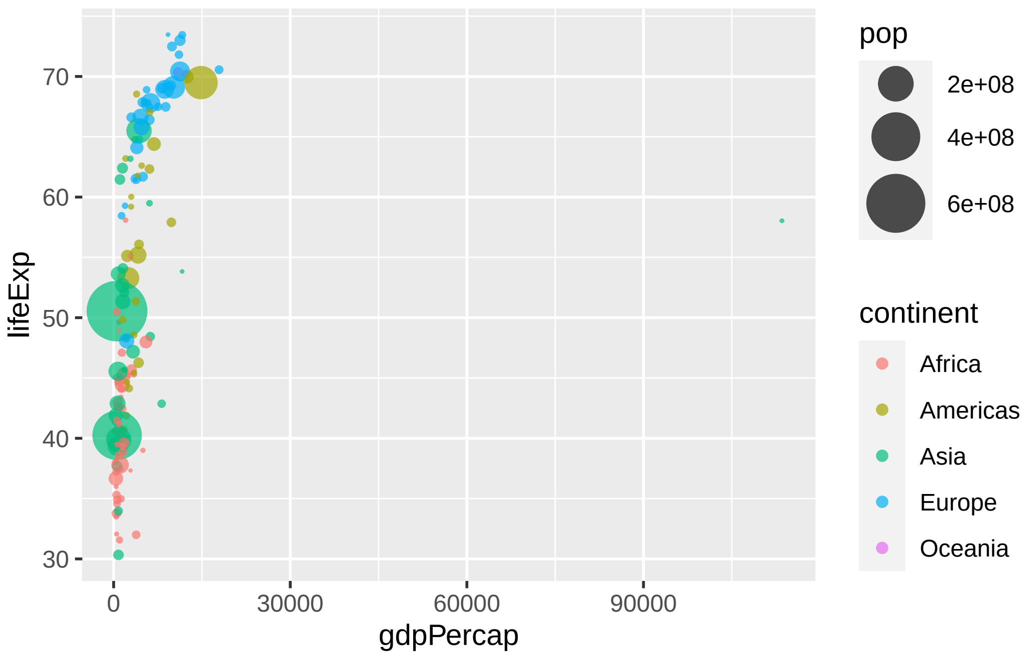
Scaling

```
ggplot(gapminder_2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp,
                 size = pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```



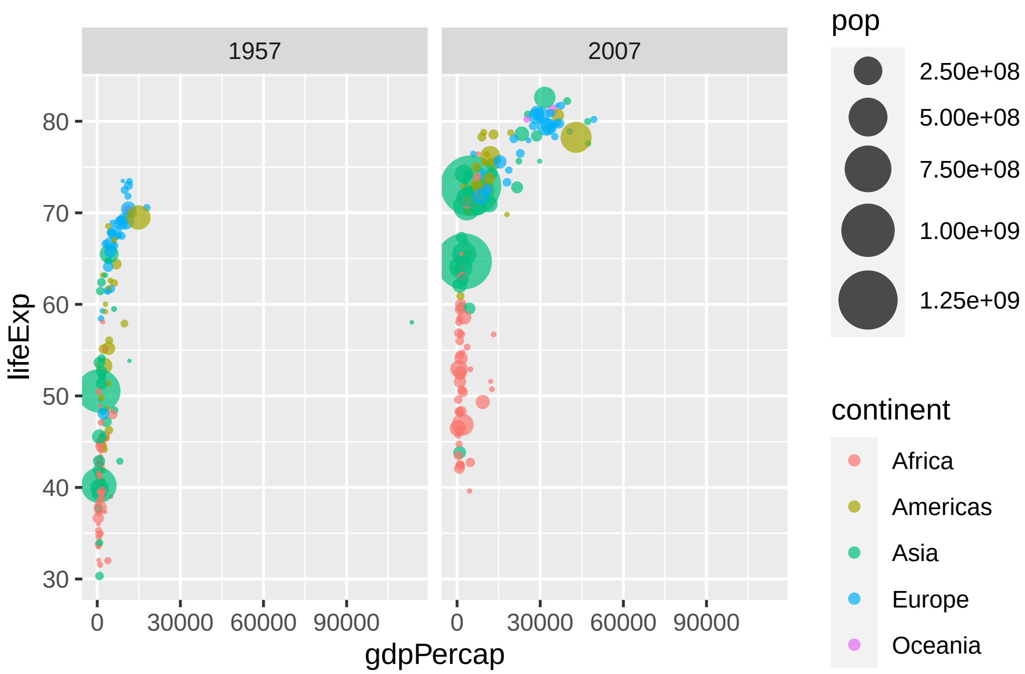
Gapminder 1957

```
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)
```



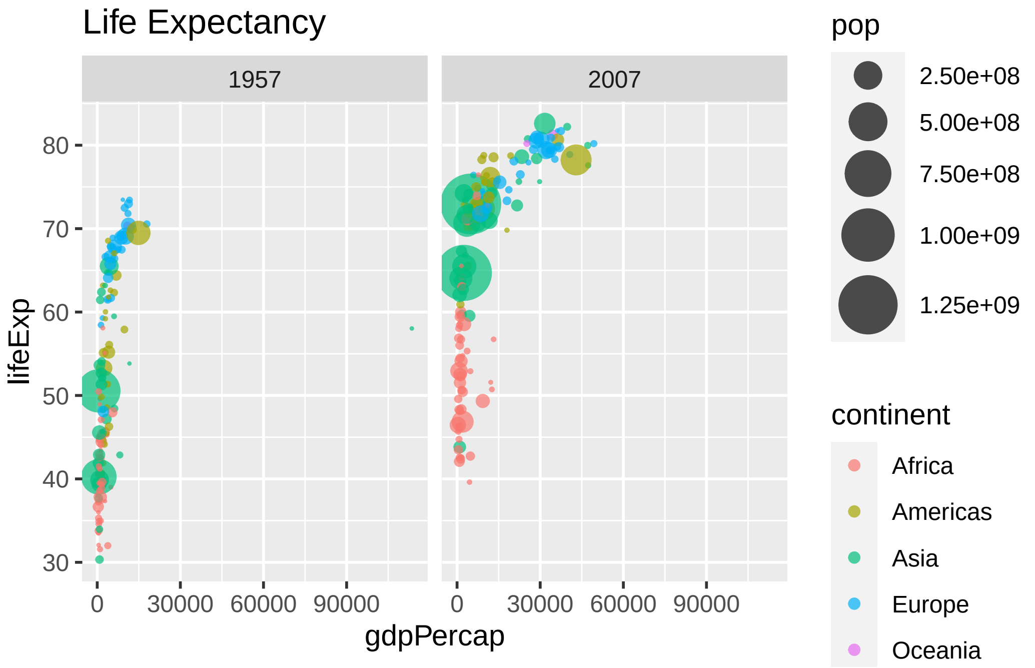
Gapminder 1957 and 2007

```
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 = 10) +
  facet_wrap(~year)
```



Final Graph

```
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 = 10) +
  facet_wrap(~year) +labs(title = "Life Expectancy")
```


Life Expectancy
1957
2007
lifeExp
80
70
60
50
40
30
0
30000
60000
90000
gdpPercap
pop
2.50e+08
5.00e+08
7.50e+08
1.00e+09
1.25e+09
continent
Africa
Americas
Asia
Europe
Oceania