Class 5: Data Visualization

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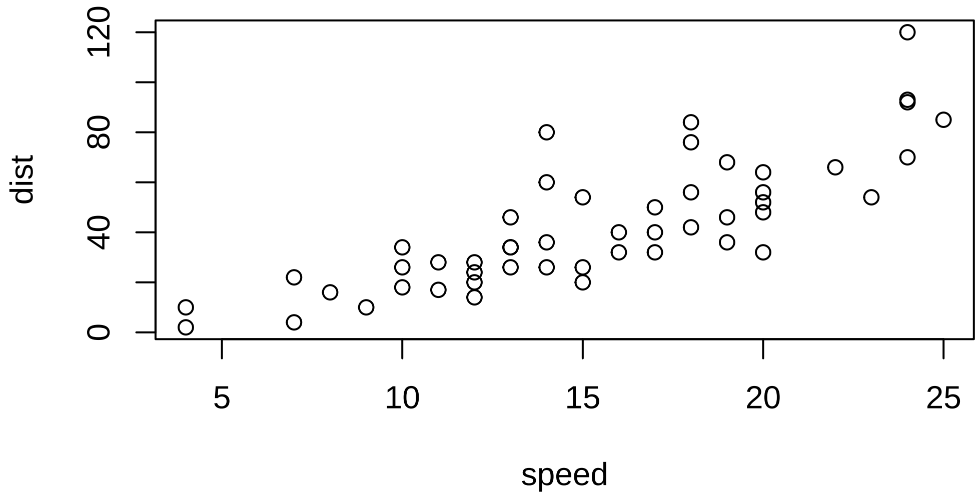
Plotting in R

R has many plotting and visualization systems, including “base” R.

```
head(cars, n = 10)
```

```
   speed dist
1      4    2
2      4   10
3      7    4
4      7   22
5      8   16
6      9   10
7     10   18
8     10   26
9     10   34
10    11   17
```

```
plot(cars)
```

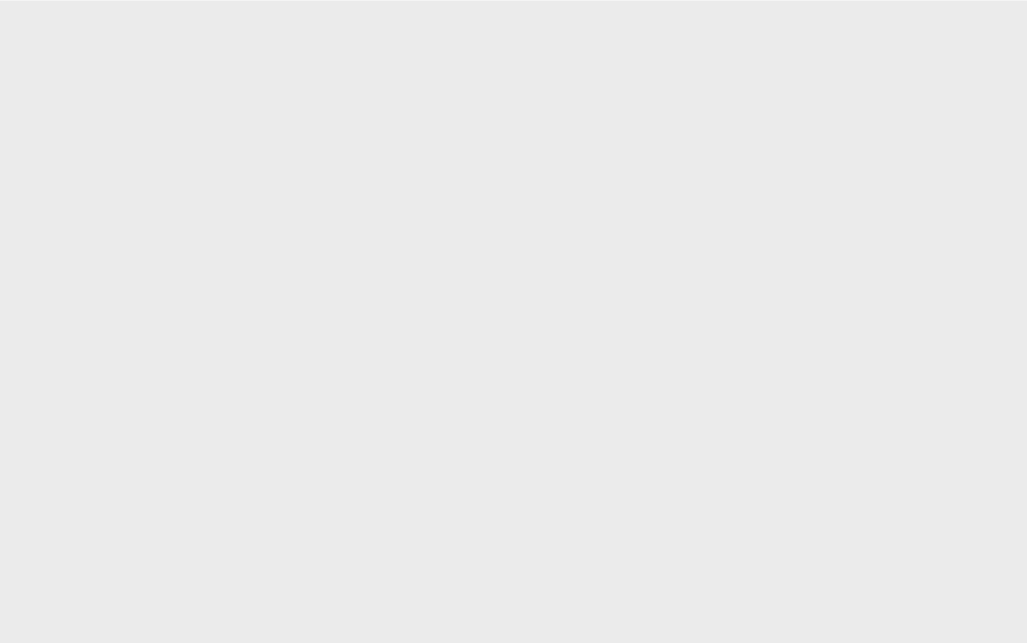


ggplot is great for more complex plots.

```
#ggplot(cars)
```

To use an add-on, it must first be installed using the function `install.packages()` with the name of the desired package in parenthesis. After downloading the package, it needs to be loaded using the `library` function

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

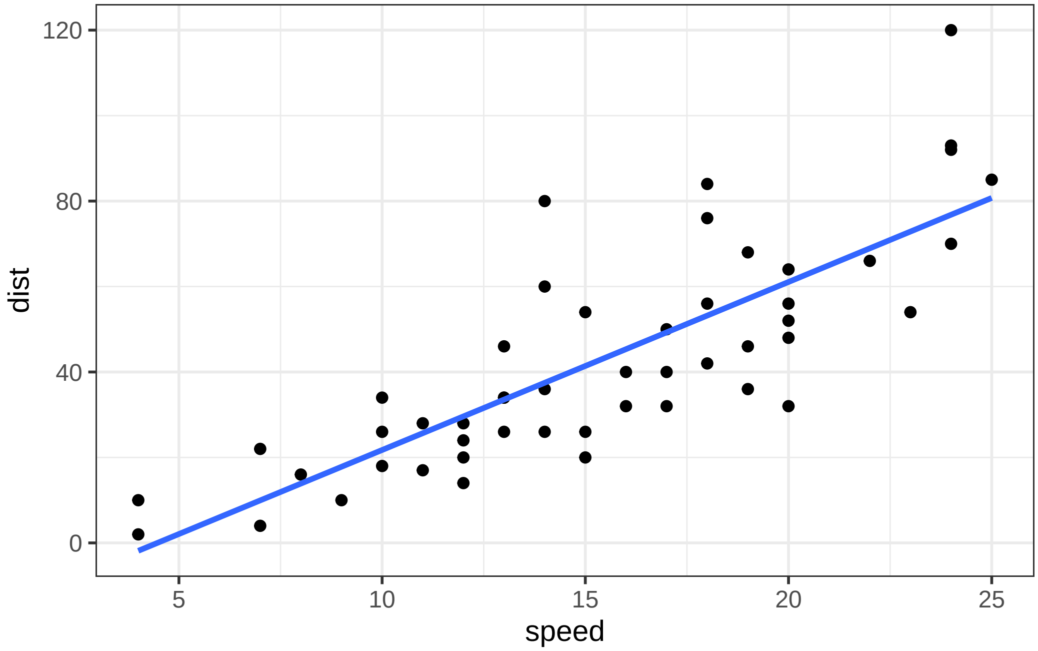


ggplot is highly verbose and each ggplot needs at least three things:

- Data: the dataframe of interest
- aesthetics (aes): how the data is mapped to the plot (x axis, y axis, etc)
- geometries (geom_*type*): plot type (ex: geom_point, geom_line, etc)

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

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



A plot of some genes

```
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
```

How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

There are 5196 genes in this dataset.

> How many genes are upregulated?

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

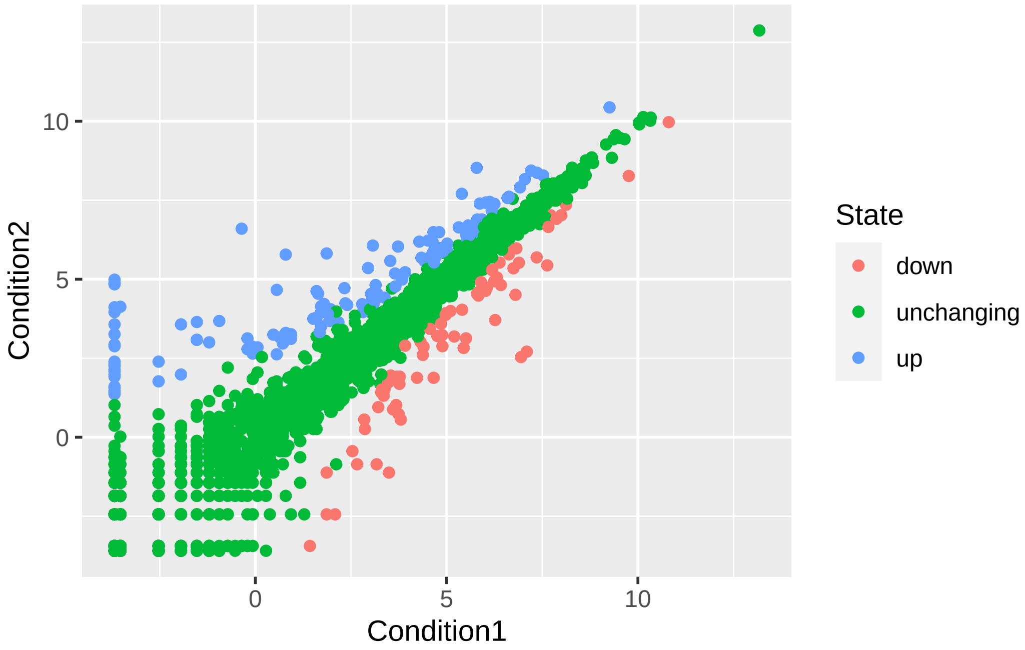
```
      down unchanging         up
        72       4997        127
```

or

```
sum(genes$State == "up")
```

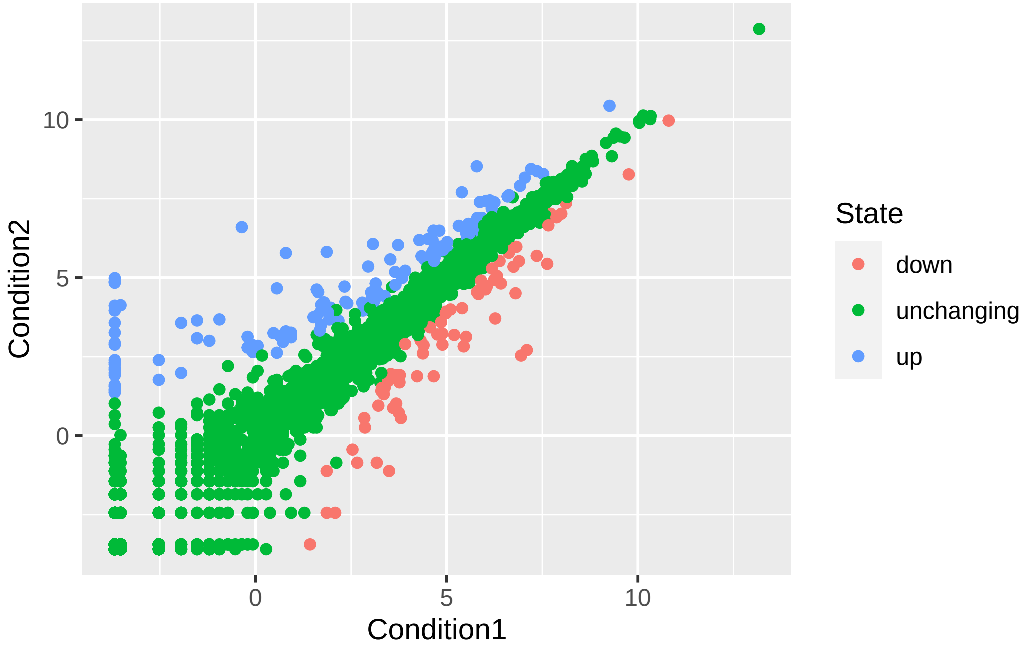
```
[1] 127
```

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



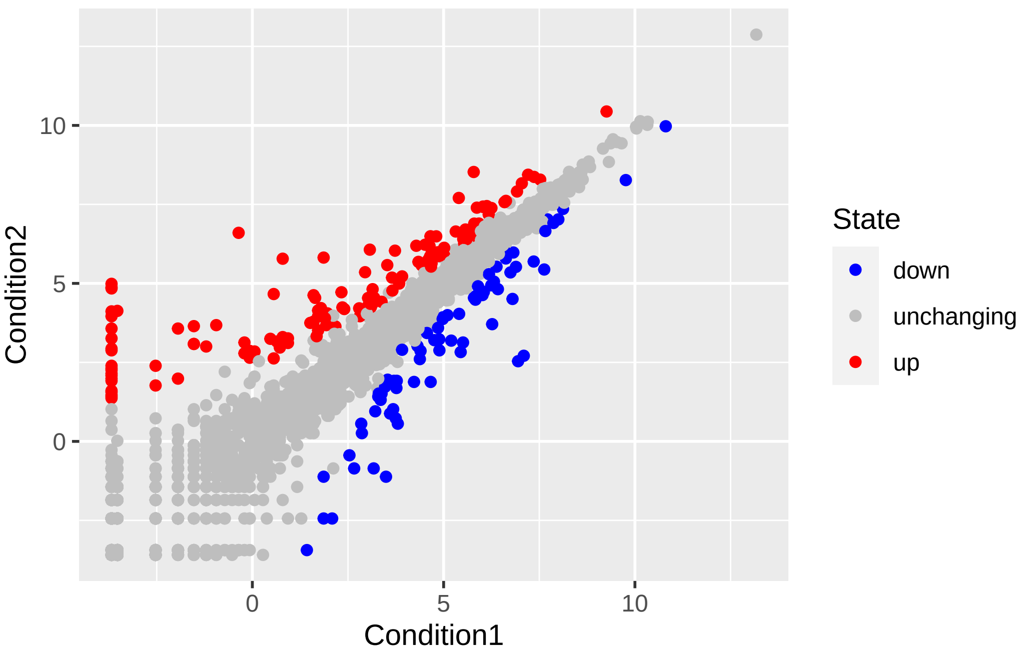
assign plot to a value so it can easily be edited or layered on later and then call the value

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

p
```



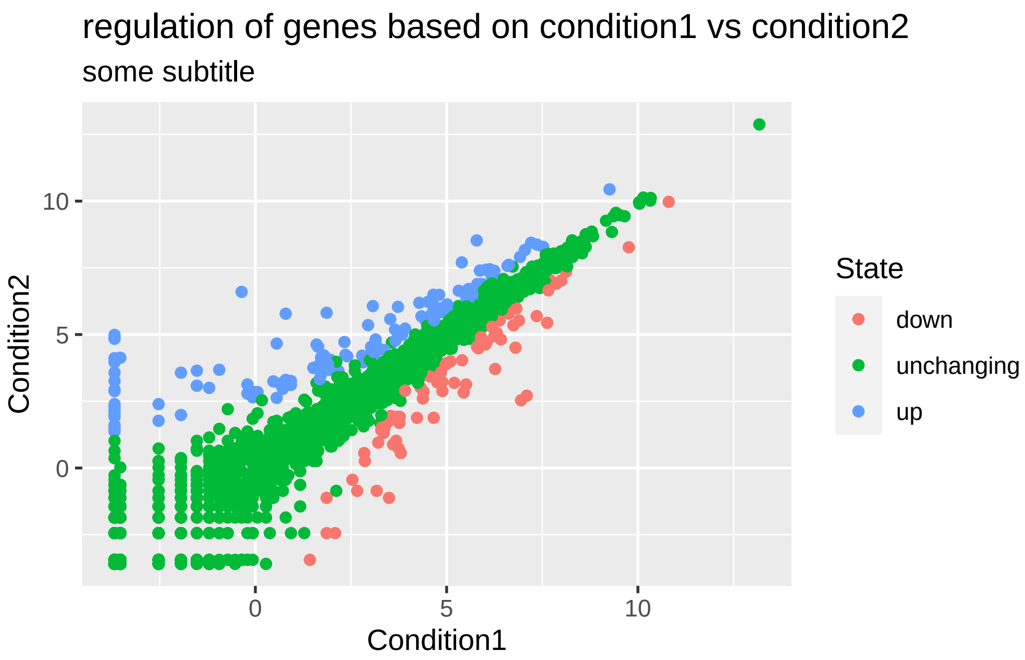
change the legend values of p

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



give labels using `labs()` (x and y labels, title, etc)

```
p + labs(title = "regulation of genes based on condition1 vs condition2", subtitle = "some
```



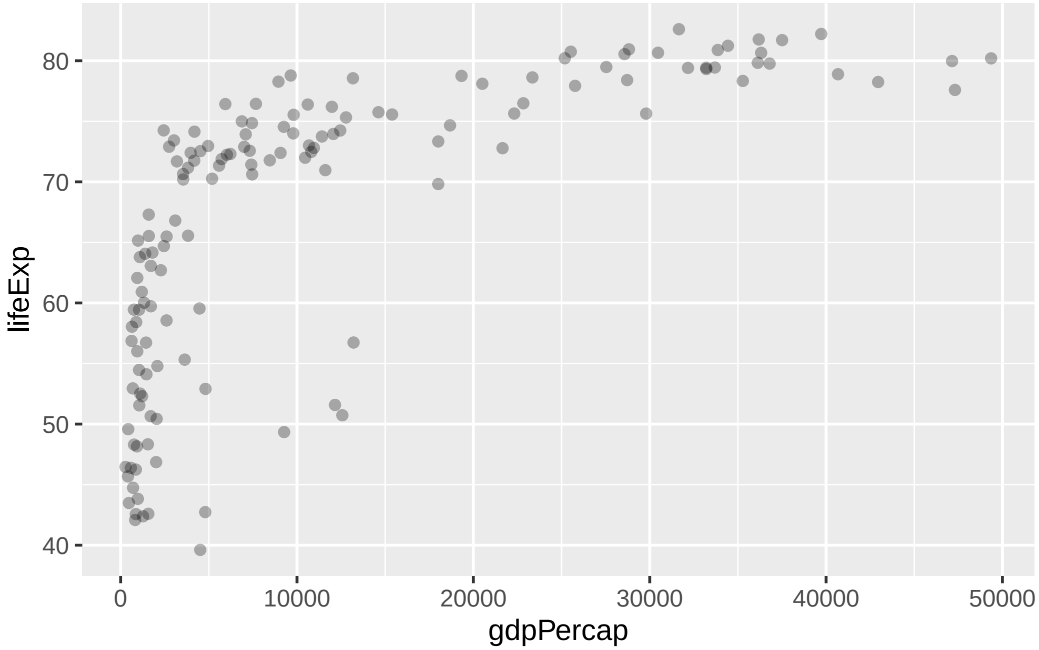
Gapminder

```
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)
```

```
q <- ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp) +
  geom_point(alpha= 0.3)

q
```



Q. How many countries are in this dataset?

```
length( unique(gapminder$country))
```

```
[1] 142
```

Q. How many years does this dataset span?

```
length( unique(gapminder$year))
```

```
[1] 12
```

or

```r
range(gapminder$year)
```

```
[1] 1952 2007
```

> Q. Which country has the smallest population?

first, where is this min value located in the pop vector?

```r
ind <- which.min(gapminder$pop)

ind
```

```
[1] 1297
```

which.min (which.max) for the arg min, i.e., the location where an extreme value occurs.

now use this to access the $country value for this position

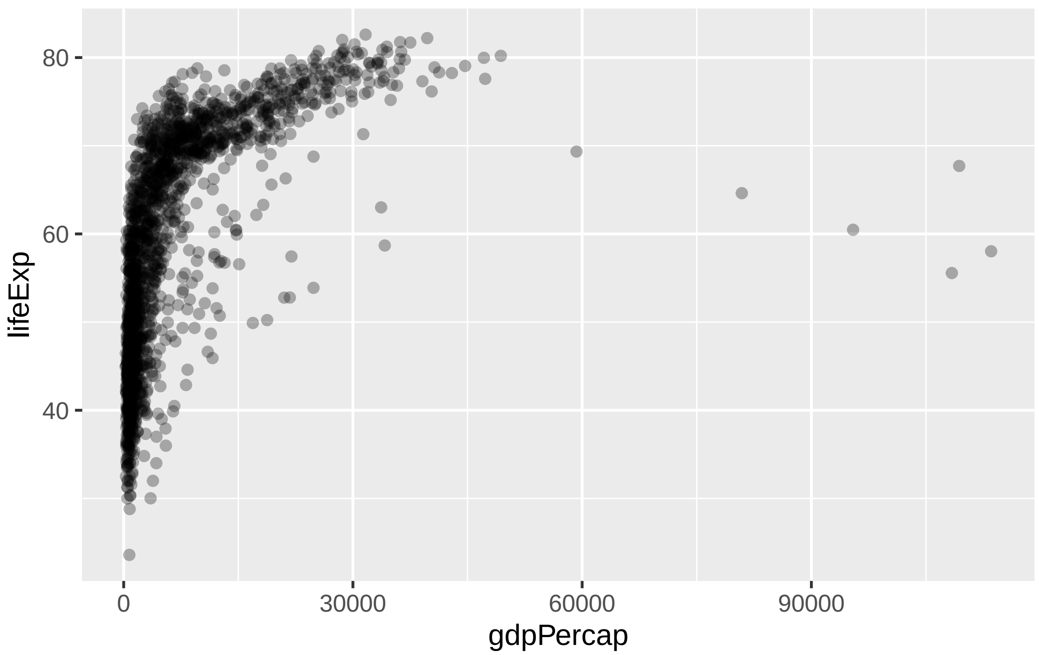
```r
gapminder$country[ind]
```

```
[1] Sao Tome and Principe
142 Levels: Afghanistan Albania Algeria Angola Argentina Australia ... Zimbabwe
```

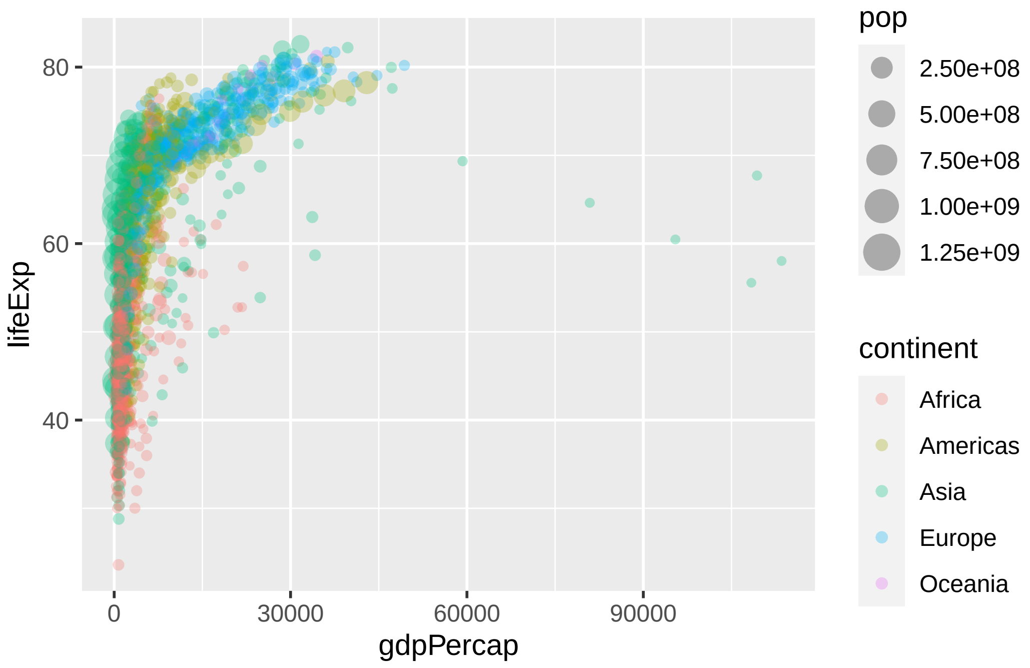
```r
gapminder[ind,]
```

```
# A tibble: 1 x 6
  country               continent  year lifeExp   pop gdpPercap
  <fct>                 <fct>     <int>   <dbl> <int>     <dbl>
1 Sao Tome and Principe Africa     1952    46.5 60011      880.
```

```r
a <- ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.3)

a
```

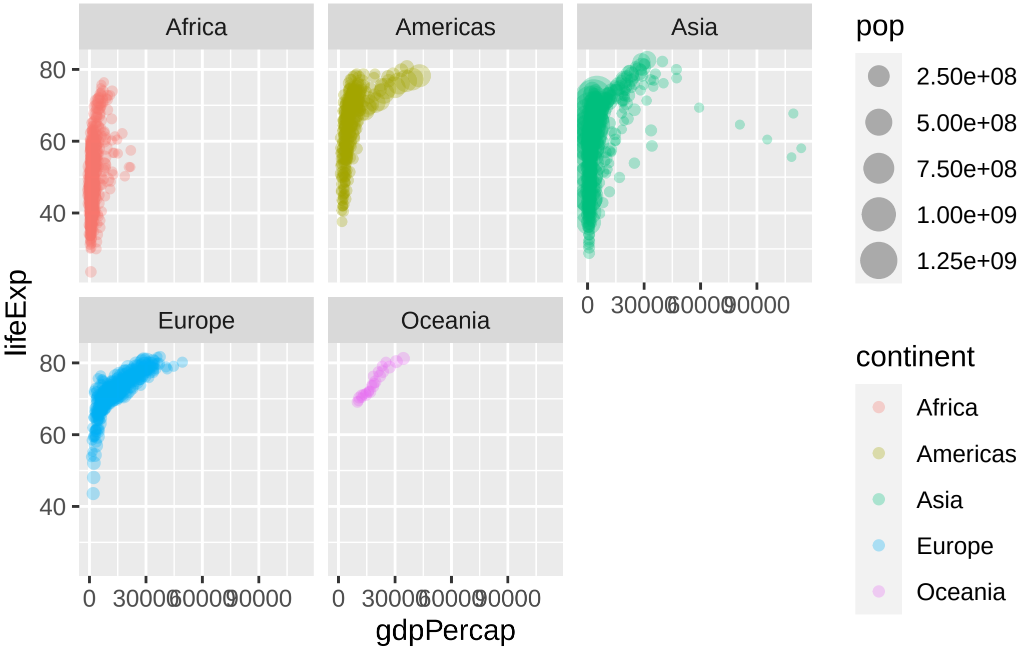


```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color = continent, size = pop) +
  geom_point(alpha=0.3)
```



facet by continent

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color = continent, size = pop) +
  geom_point(alpha=0.3) +
  facet_wrap(~continent)
```


Africa
Americas
Asia
Europe
Oceania
lifeExp
80
60
40
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