Class 5: Data Visualization with ggplot

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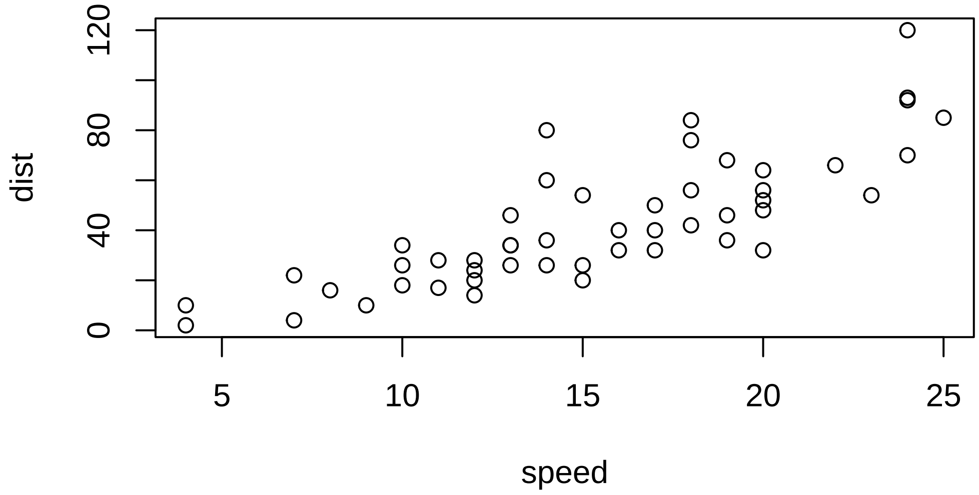
Today we will have our first play with the **ggplot2** package - one of the most popular graphics packages on the planet.

There are many plotting systems in R. These include so-called *"base"* plotting/graphics.

```r
plot(cars)
```



Based plot is generally short code and somewhat dull plots - but it is always there for you and is really fast for big datasets.

If I want to use **ggplot2** it takes some more work

```
# ggplot(cars)
```

I need to install the package first to my computer. To do this I can use the function `install.packages("ggplot2")`

Every time I want to use a package I need to load it up with a `library()`

```
library(ggplot2)
```

Now finally I can use ggplot

```
ggplot(cars)
```

Every ggplot has at least 3 things:

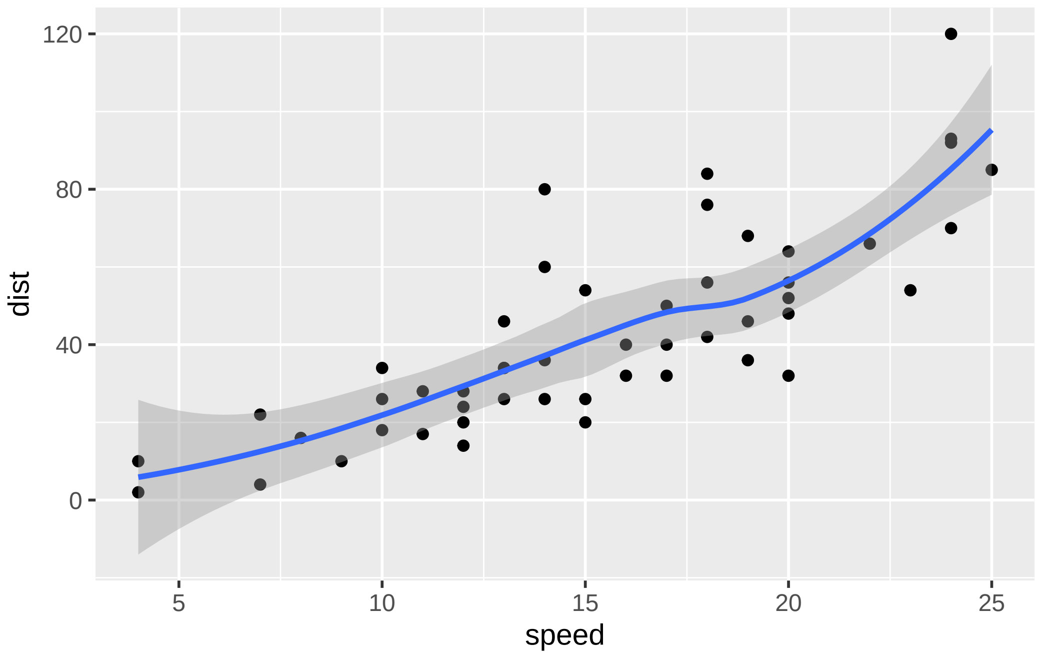
- **data** (the data.frame with the data you want to plot)
- **aes** (the aesthetics mapping of the data to the plot)
- **geom** (how do you want the plot to look, points, lines, etc.)

```
head(cars)
```

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

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

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

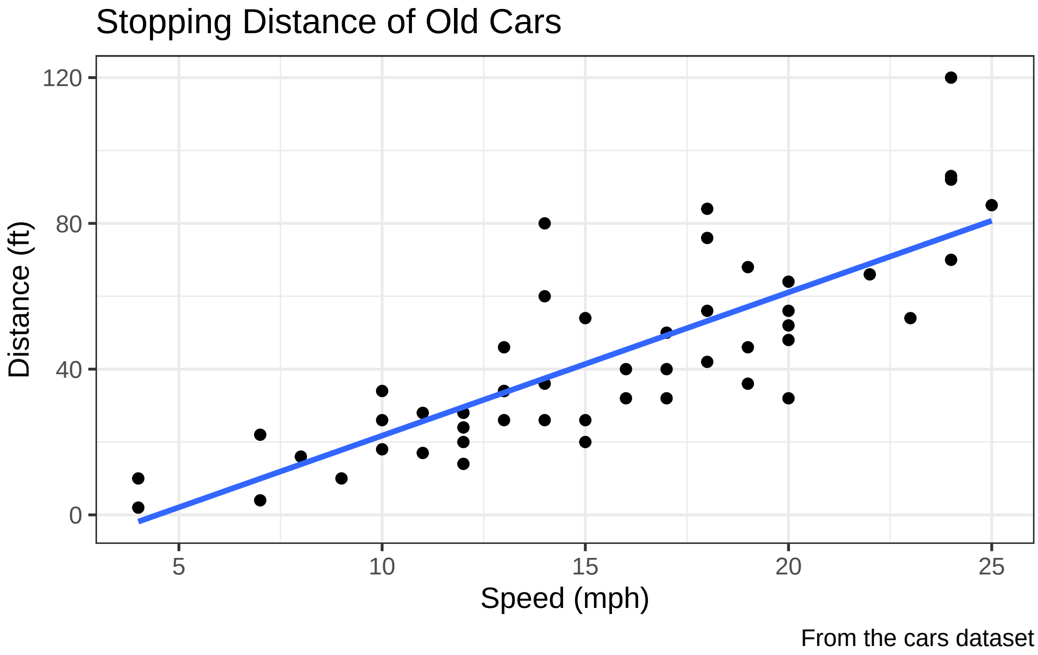


I want a linear model and no standard error bounnds shown on my plot. I also want nicer axis labs, a title, etc.

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

```r
bp + geom_smooth(method = 'lm', se=FALSE) +
  labs(title="Stopping Distance of Old Cars",
       x="Speed (mph)",
       y="Distance (ft)",
       caption="From the cars dataset") +
  theme_bw()
```

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



A more complicated scatter plot

Here we make a plot of gene expression data

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

```r
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
```

```r
nrow(genes)
```

```
[1] 5196
```

```r
colnames(genes)
```

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

```r
ncol(genes)
```

```
[1] 4
```

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

```

      down unchanging         up
        72       4997        127
```

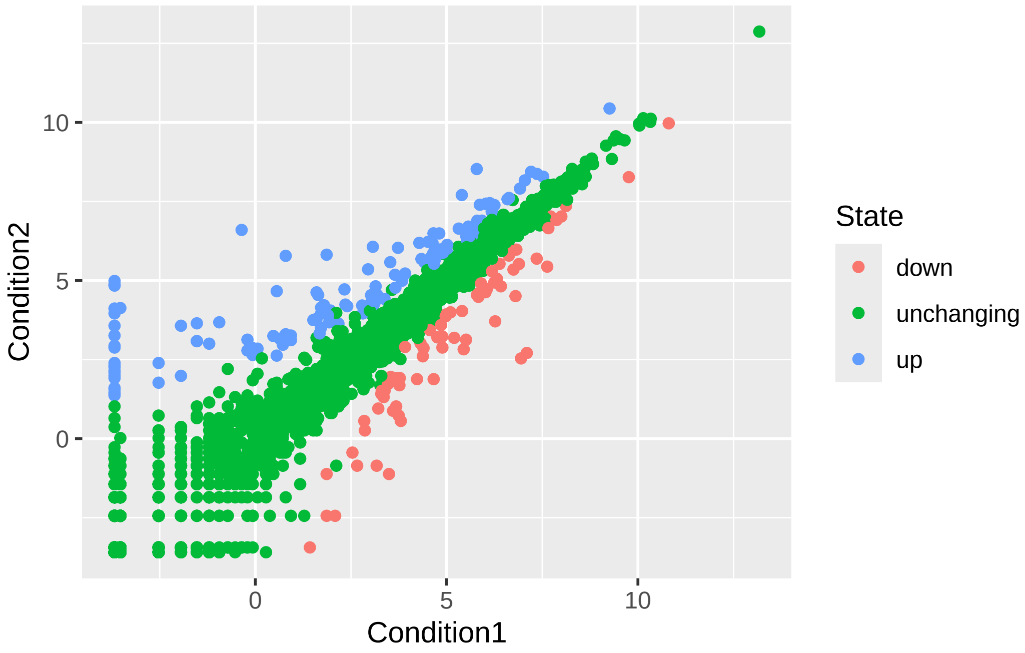
```r
round(sum(genes$State=="up") / nrow(genes) * 100, 2)
```

```
[1] 2.44
```

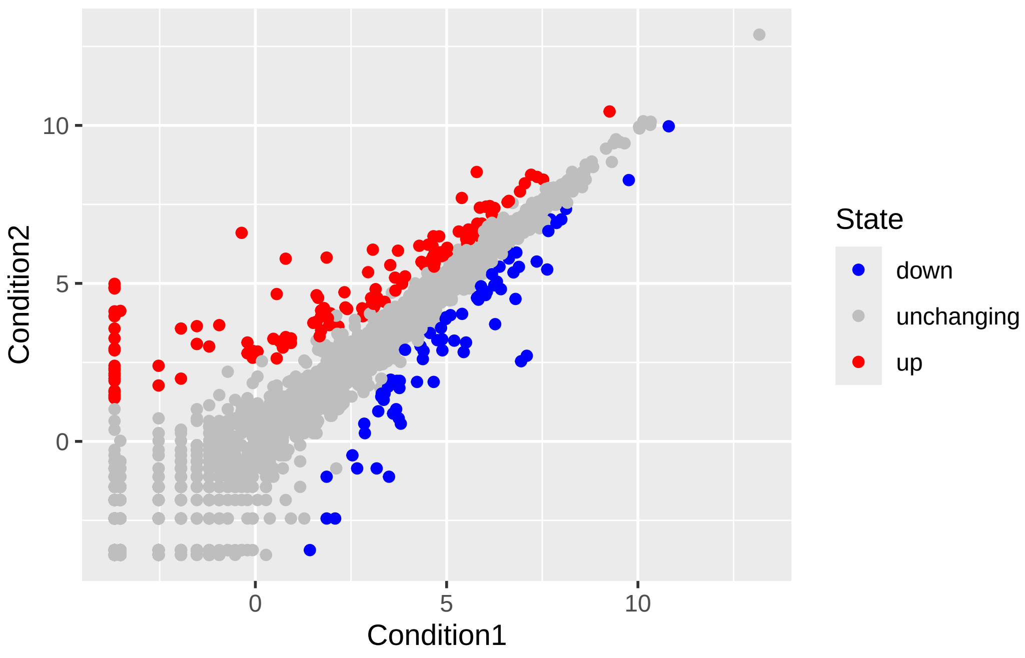
```r
head(genes, 2)
```

```
   Gene Condition1 Condition2      State
1 A4GNT  -3.680861  -3.440135 unchanging
2  AAAS   4.547958   4.386413 unchanging
```

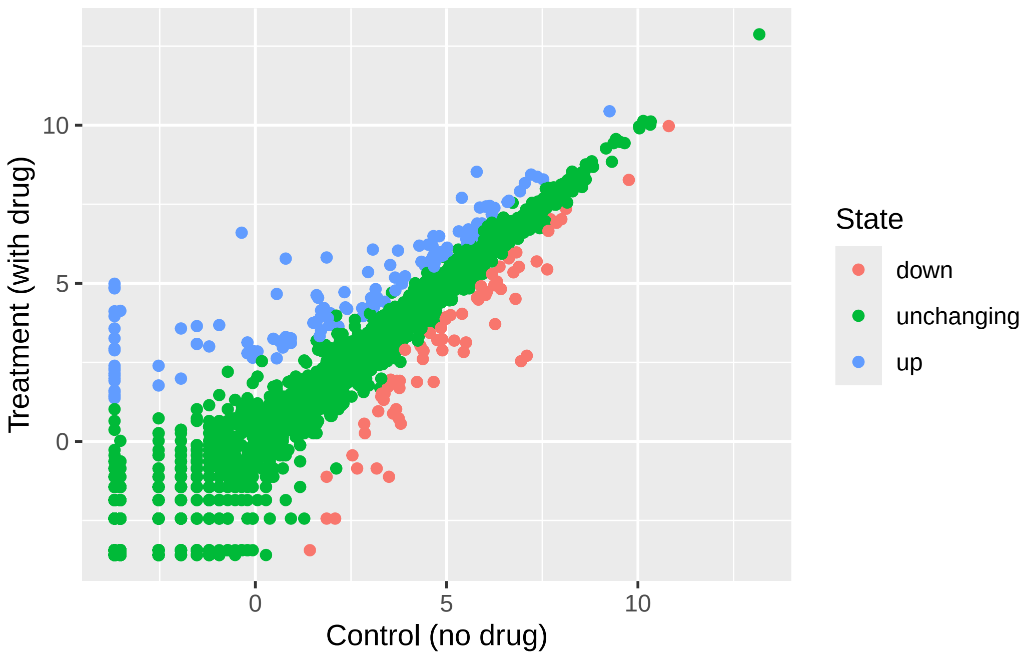
```
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
p
```



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



```
p + labs(Title="Drug Data", x="Control (no drug)", y="Treatment (with drug)")
```



Exploring the gapminder dataset

Here we will load up the gapminder dataset

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.

gapminder <- read.delim(url)
```

> Q. How many entries rows are in this dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

> Q. How many columns?

```
ncol(gapminder)
```

```
[1] 6
```

```
head(gapminder)
```

```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
4 Afghanistan      Asia 1967  34.020 11537966  836.1971
5 Afghanistan      Asia 1972  36.088 13079460  739.9811
6 Afghanistan      Asia 1977  38.438 14880372  786.1134
```

```
table(gapminder$year)
```

```
1952 1957 1962 1967 1972 1977 1982 1987 1992 1997 2002 2007
 142  142  142  142  142  142  142  142  142  142  142  142
```

> Q. How many continents?

```
table(gapminder$continent)
```

```
  Africa Americas      Asia    Europe   Oceania 
     624       300       396       360        24 
```

I could use the `unique()` function…

```r
length(unique(gapminder$continent))
```

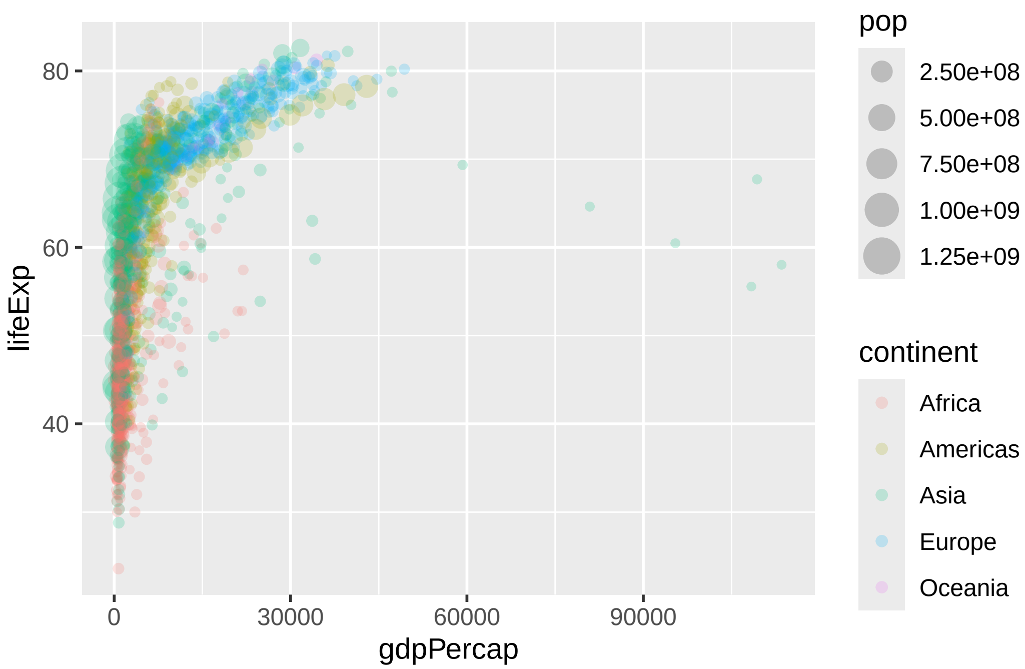
```
[1] 5
```

> Q. HOw man countries are there in this dataset?

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

```
[1] 142
```

```r
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent, size=pop) +
  geom_point(alpha=0.2)
```



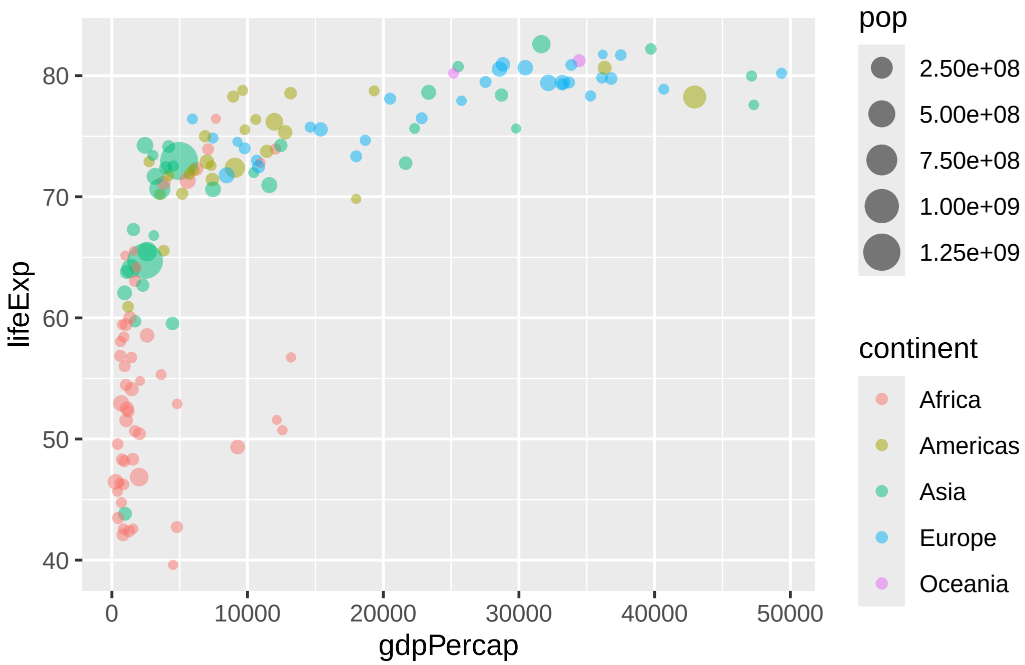
```r
library(dplyr)
```

```

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
```

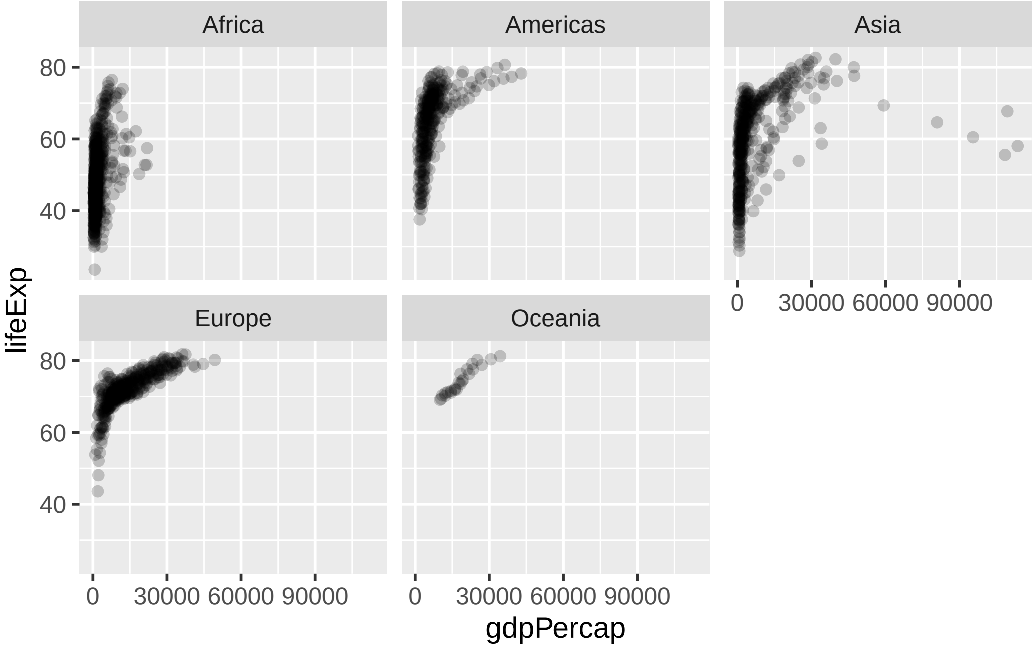
```r
gapminder_2007 <- gapminder %>% filter(year==2007)
head(gapminder_2007)
```

```
      country continent year lifeExp      pop  gdpPercap
1 Afghanistan      Asia 2007  43.828 31889923   974.5803
2     Albania    Europe 2007  76.423  3600523  5937.0295
3     Algeria    Africa 2007  72.301 33333216  6223.3675
4      Angola    Africa 2007  42.731 12420476  4797.2313
5   Argentina  Americas 2007  75.320 40301927 12779.3796
6   Australia   Oceania 2007  81.235 20434176 34435.3674
```

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



```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.2) +
  facet_wrap(~continent)
```


Africa
Americas
Asia
Europe
Oceania
lifeExp
80
60
40
0
30000
60000
90000
gdpPercap