Lab5__Data__Visualization

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Base R graphics vs ggplot2

There are many graphics systems available in R, including so-called "base" R graphics and the very popular **ggplot2** package.

To compare these let's play with the inbuilt `cars` dataset.

```
head(cars)
```

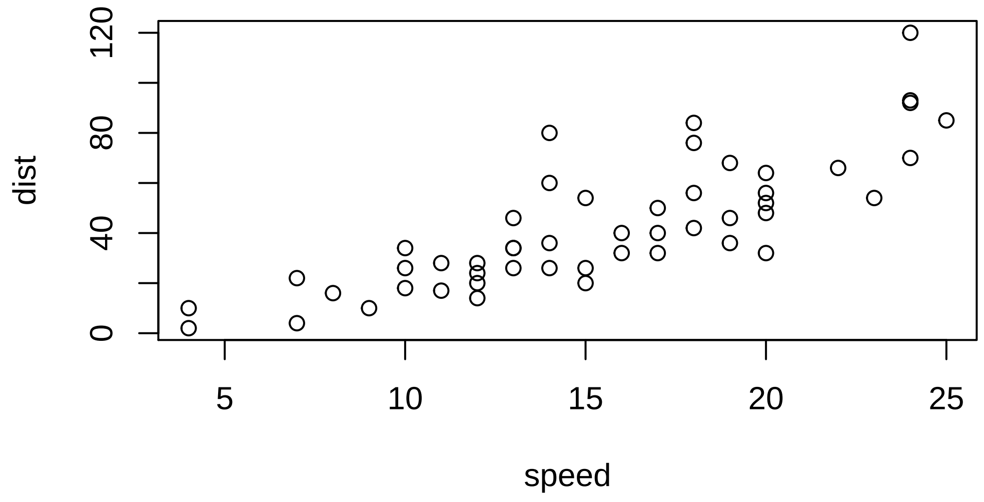
```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

```
head(cars, 3)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
```

To use "base" R I can simply call the `plot()` function:

```
plot(cars)
```

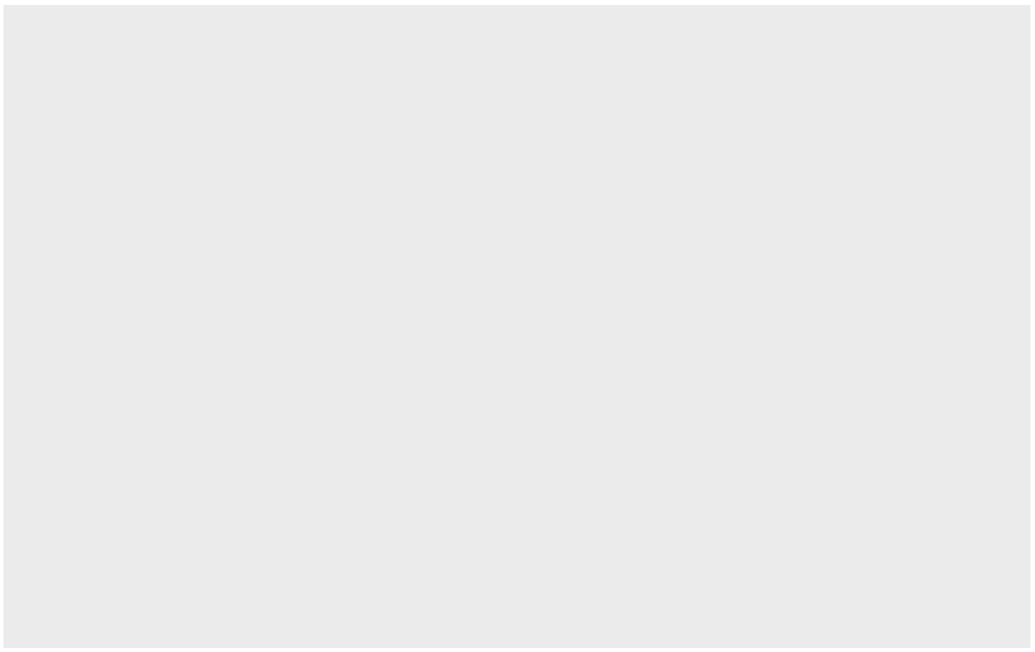


To use `ggplot2` package I first need to install it with the function `install.packages("ggplot")`.

I will run this in my R console (i.e. the R brain) as I do not want to re-install it every time I render my report…

The main function in this package is called `ggplot()`. Can I just call it?

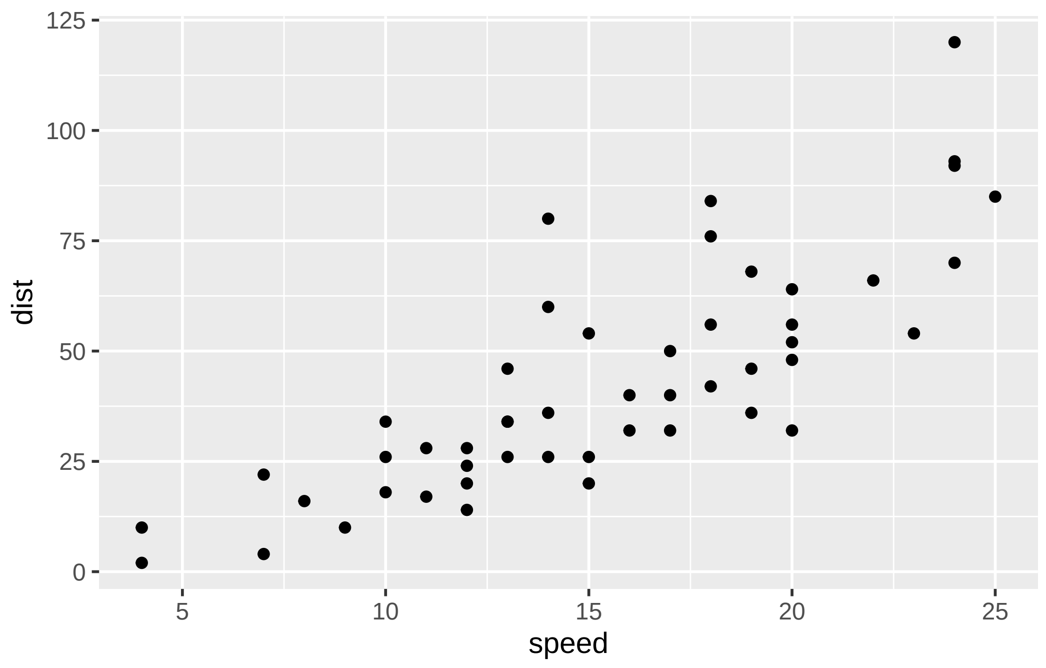
```
library(ggplot2)
ggplot()
```



To make a figure with ggplot I need always at least 3 things:

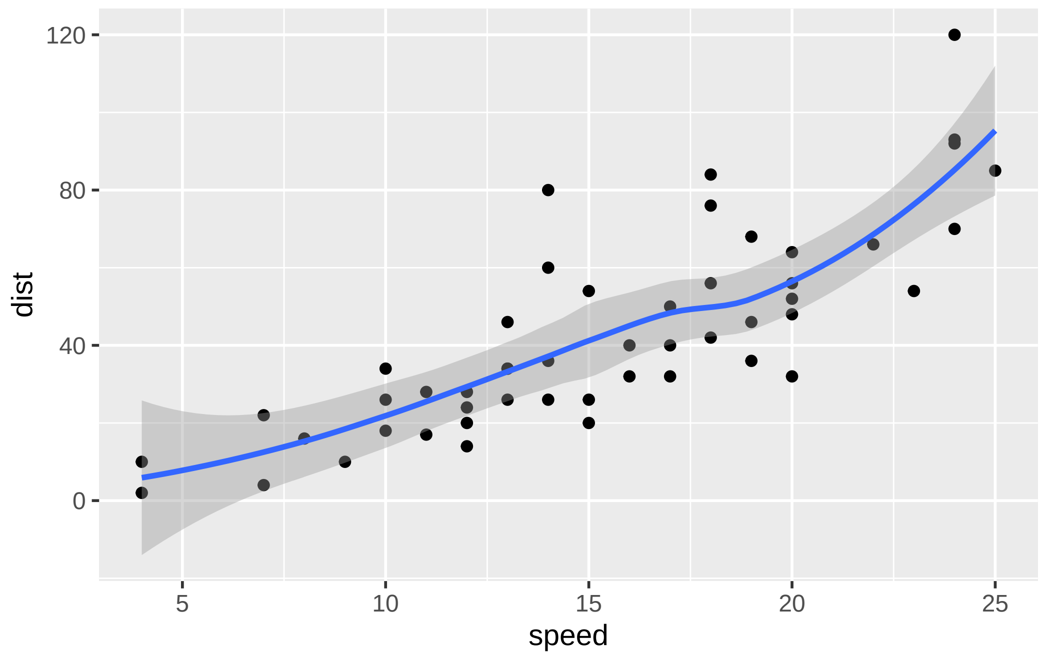
- **data** (i.e. what I want to plot)
- **aes** the aesthetic mapping of the data to the plot I want
- the **geoms** i.e. how I want to plot the data

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



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

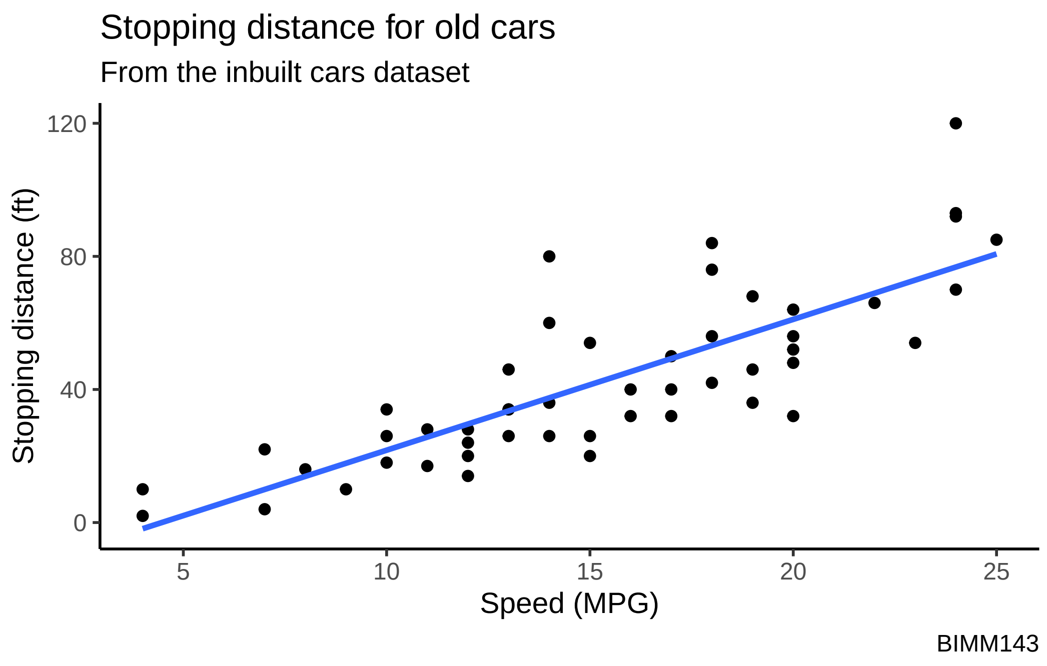
```
`geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



If I want to add more things I can just keep adding layers, e.g.

```
ggplot(data=cars)+
  aes(x=speed, y=dist)+
  geom_point()+
  geom_smooth(se=FALSE, method="lm")+
  labs(title="Stopping distance for old cars",
       subtitle="From the inbuilt cars dataset",
       caption="BIMM143", x="Speed (MPG)", y = "Stopping distance (ft)")+
  theme_classic()
```

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



ggplot is much more verbose than base R plots but it has a consistent layer system that I can use to make just about any plot.

##A more complicated plot Let's plot some gene expression data

```
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
```

> Q. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

```r
colnames(genes)
```

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

Q. How can we summarize the last column - the "State" column?

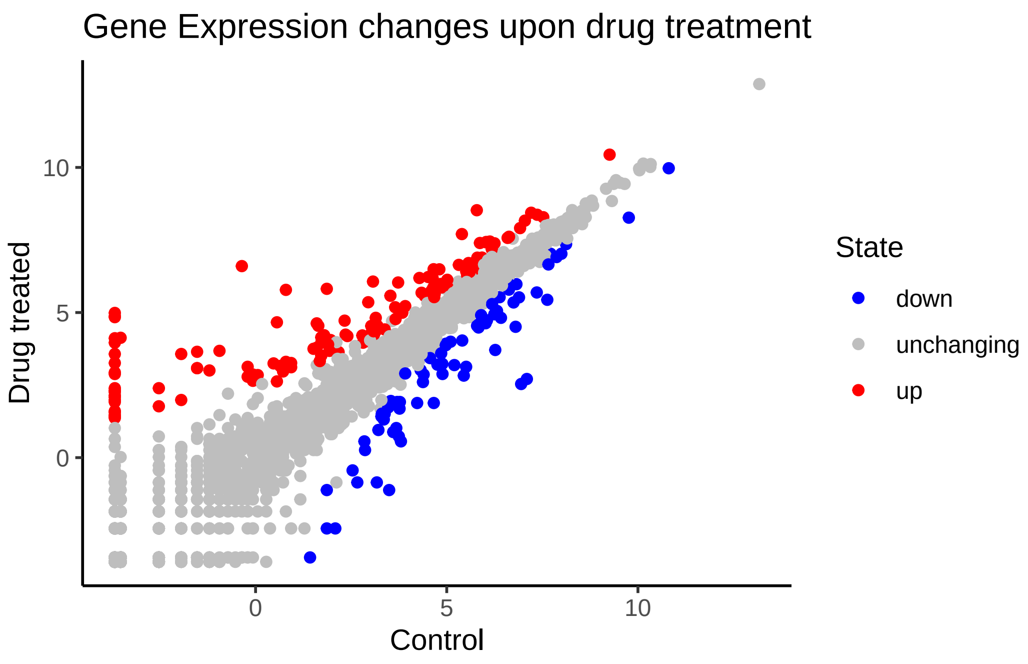
```r
table(genes$State)
```

```

      down unchanging         up 
        72       4997        127 
```

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

I can just call `p` when I want to plot or add to it.

```r
p+ labs(x="Control", y="Drug treated",
        title="Gene Expression changes upon drug treatment")+
  scale_color_manual(values = c("blue","gray","red"))
```



##Going Further

Here I read a slightly larger dataset

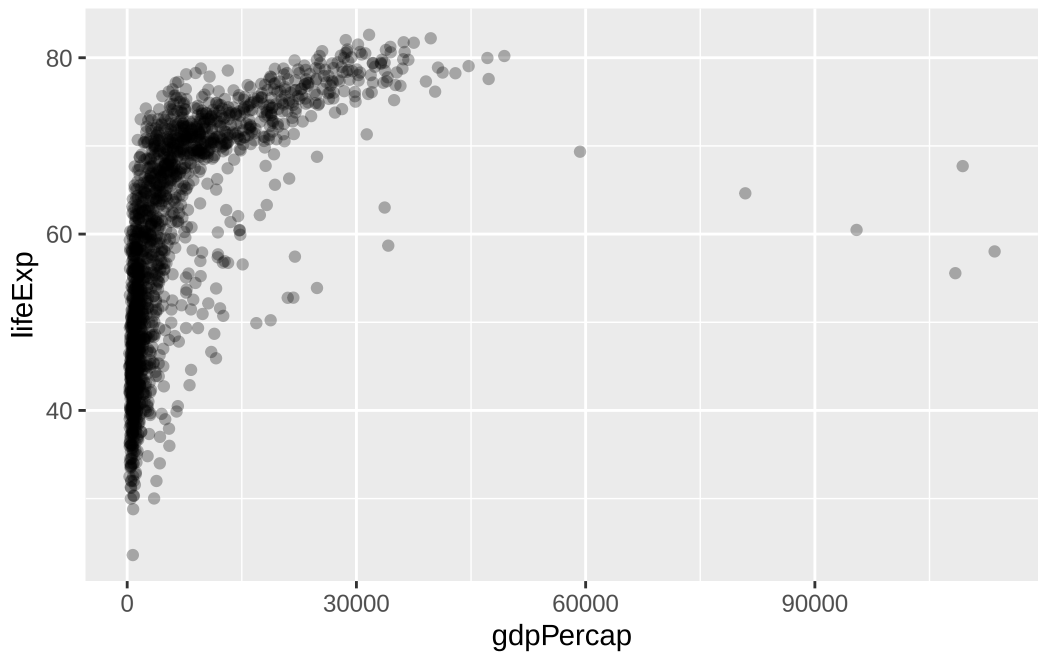
```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.

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

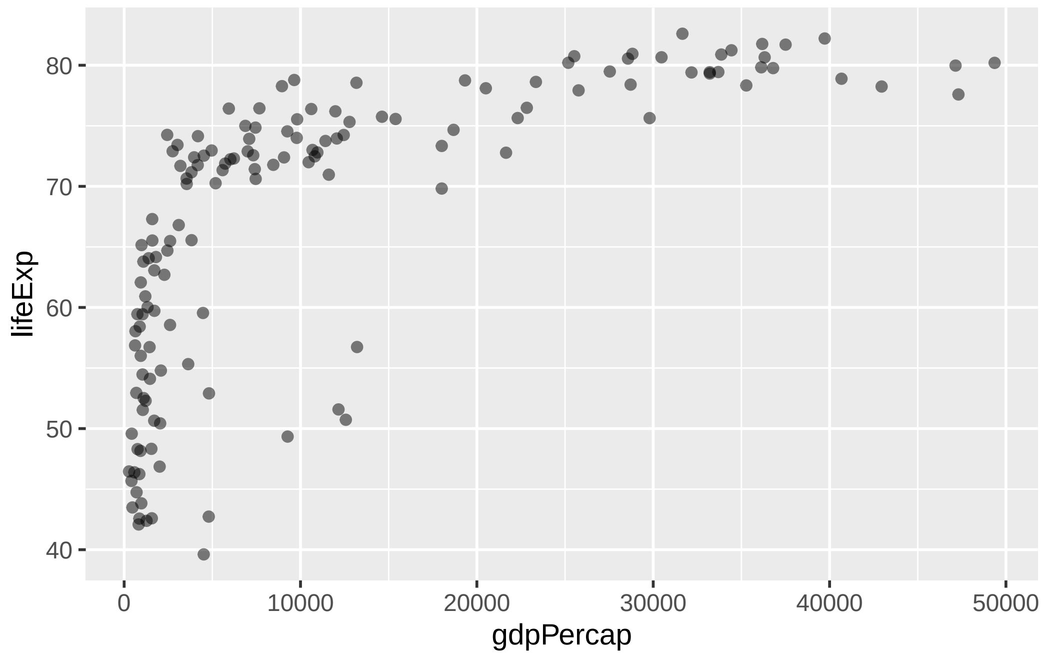
```
library(dplyr)
```

```

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
```

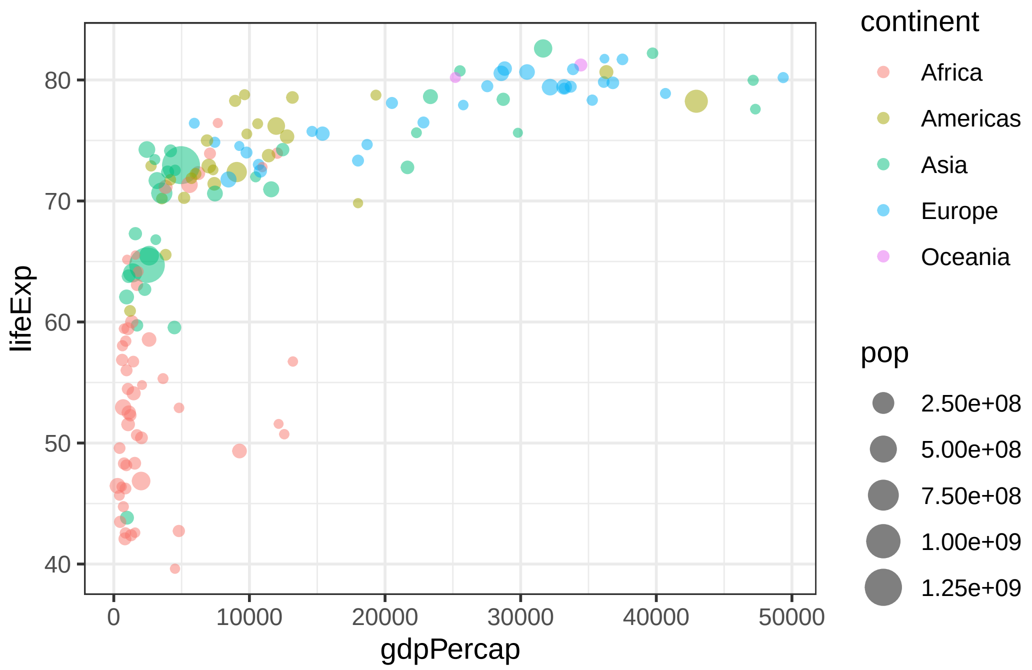
```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.3)
```



```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```

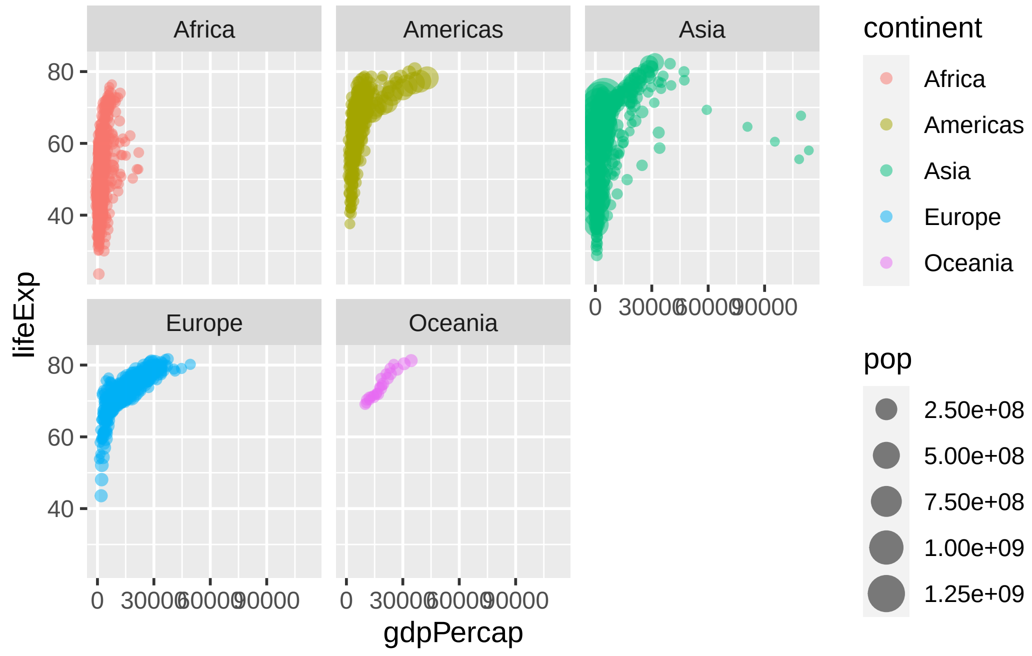


```r
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)+
  theme_bw()
```

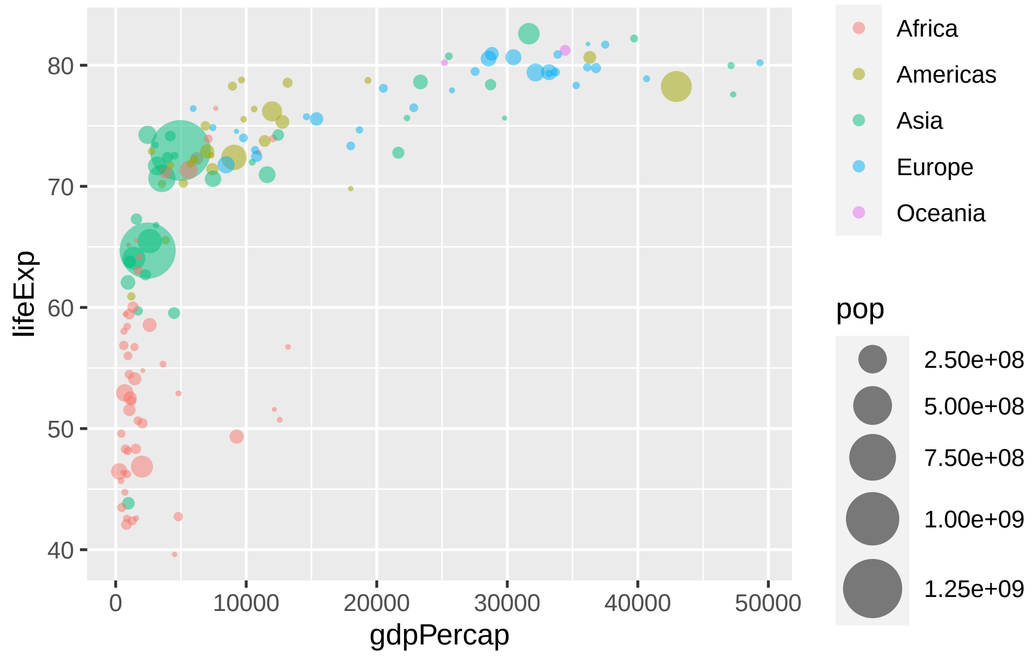


A very useful layer to add sometimes is for "faceting"

```r
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)+
  facet_wrap(~continent)
```



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


lifeExp
gdpPercap
Africa
Americas
Asia
Europe
Oceania
pop
2.50e+08
5.00e+08
7.50e+08
1.00e+09
1.25e+09