

Class 5: Data Vis with ggplot

Dalena (PID: A17327787)

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Background

There are many graphic systems available in R. These include “base” R and tons of add on packages like **ggplot2**.

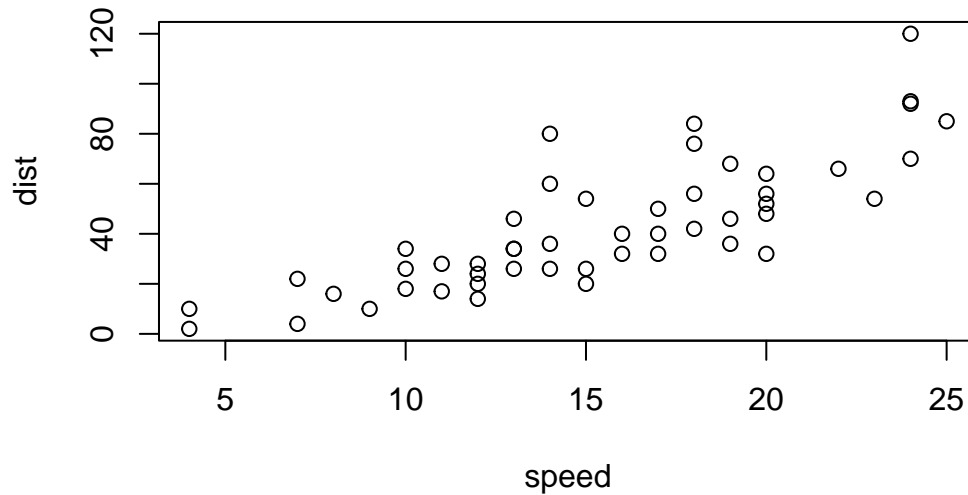
Let’s compare “base” and **ggplot2** briefly. We can use some example data that is built-in with R called `cars`:

```
head(cars)
```

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

In base R I can just call `plot()`

```
plot(cars)
```



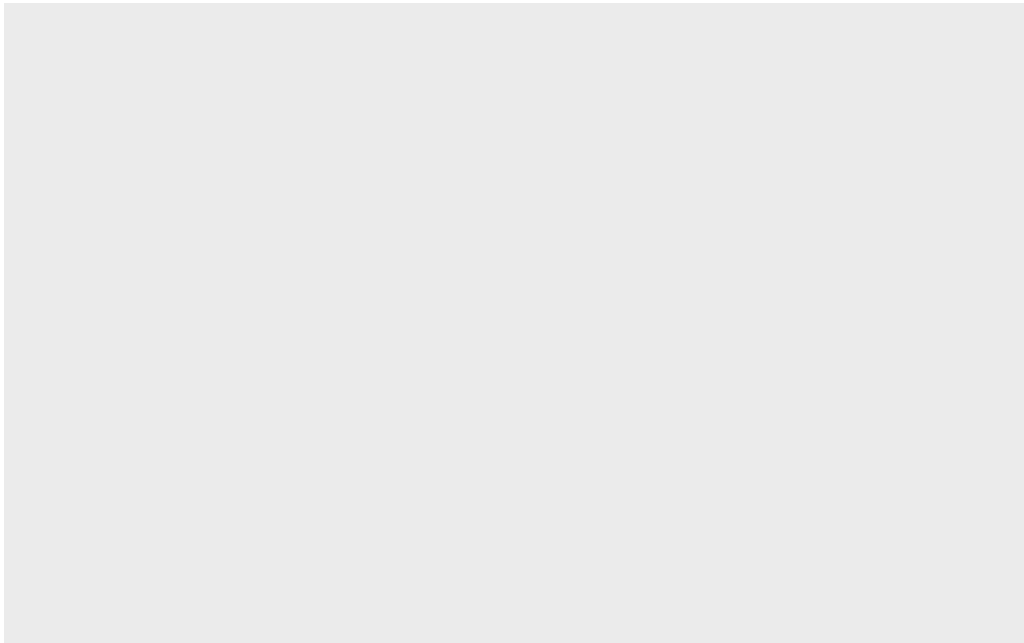
How can we do this with **ggplot2**?

First we need to install the package. We do this `install.packages("ggplot2")`. I only need to do this once and then it will be available on my computer from then on.

Key point: I only install packages in the R console not within quarto docs or Rscripts.

Before I use any add-on package I must load it up with a call to `library()`

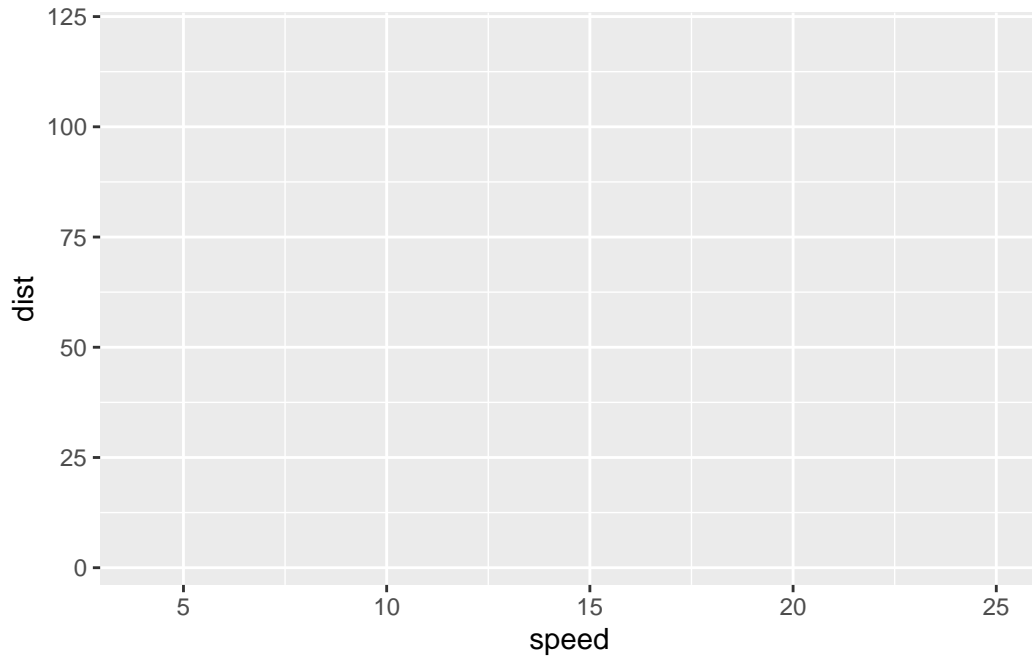
```
library(ggplot2)
ggplot(cars)
```



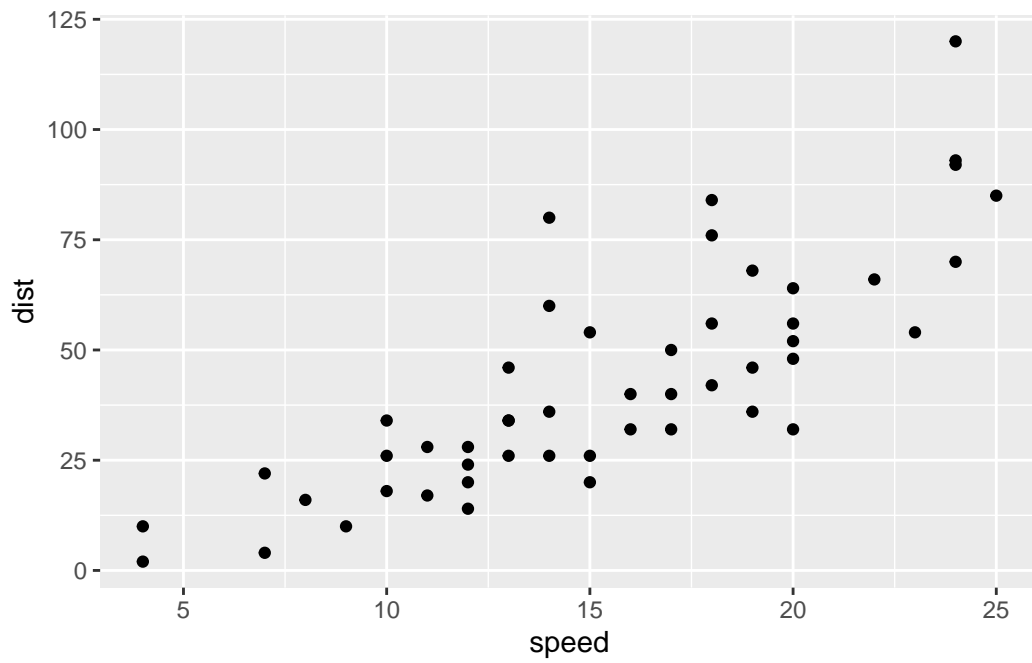
Every ggplot has/needs at least 3 things:

- the **data** (in our case **cars**)
- the **aesthetics** (how the data map to the plot)
- the **geoms** that determine how the plot is drawn (lines, points, columns, boxplots, densities, etc.)

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



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



For “simple” plots ggplot is much more verbose than base R but the defaults are nicer and for complicated plots it becomes much more efficient and structured.

Using different aes and geoms

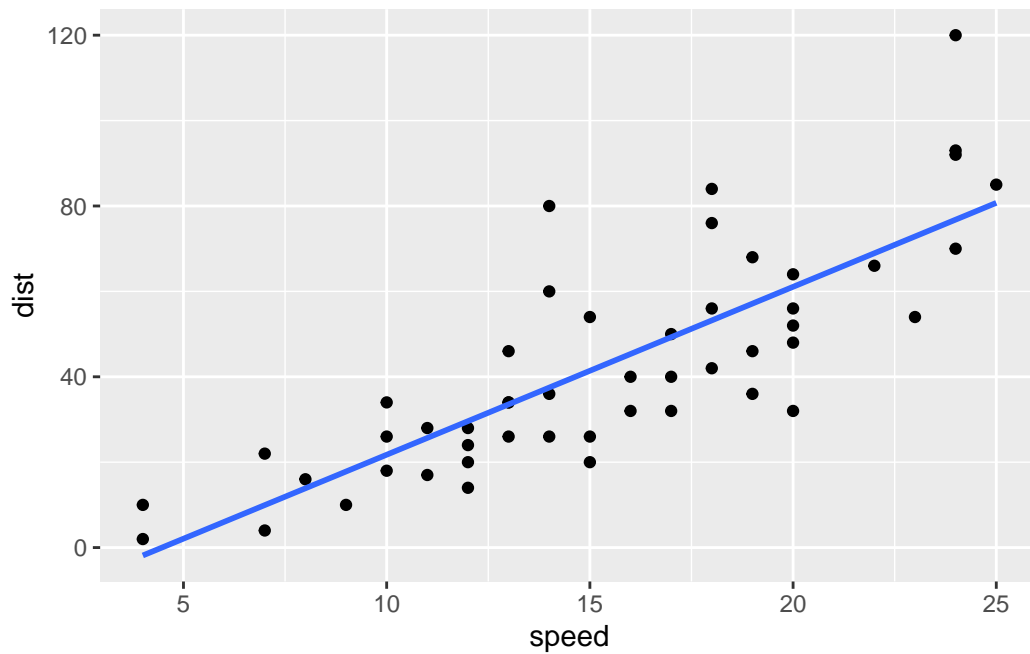
Q. Add a line to show the relationship of speed to stopping distance (i.e. add another “layer”)

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

I can always save any ggplot object (i.e. plot) and then use it later for adding more layers. Geom_smooth (se=FALSE) removes the StDev area.

p

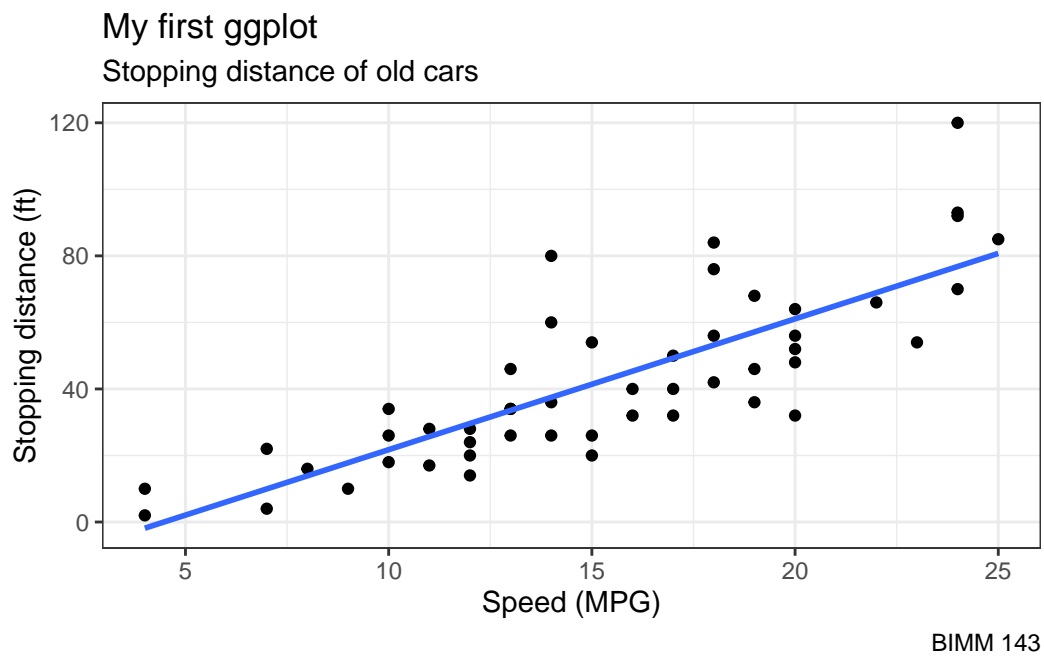
`geom_smooth()` using formula = 'y ~ x'



Q. How to add a title and subtitle to the plot?

```
p+
  labs(title="My first ggplot",
        subtitle = "Stopping distance of old cars",
        caption = "BIMM 143",
        x = "Speed (MPG)",
        y="Stopping distance (ft)")+
  theme_bw()
```

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



Gene expression plot

Read input data into R

```
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
```

Q. How many columns are there?

```
ncol(genes)
```

```
[1] 4
```

Q. What are the column names?

```
colnames(genes)
```

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

Q. How many “up” and “down” regulated genes are there?

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

```

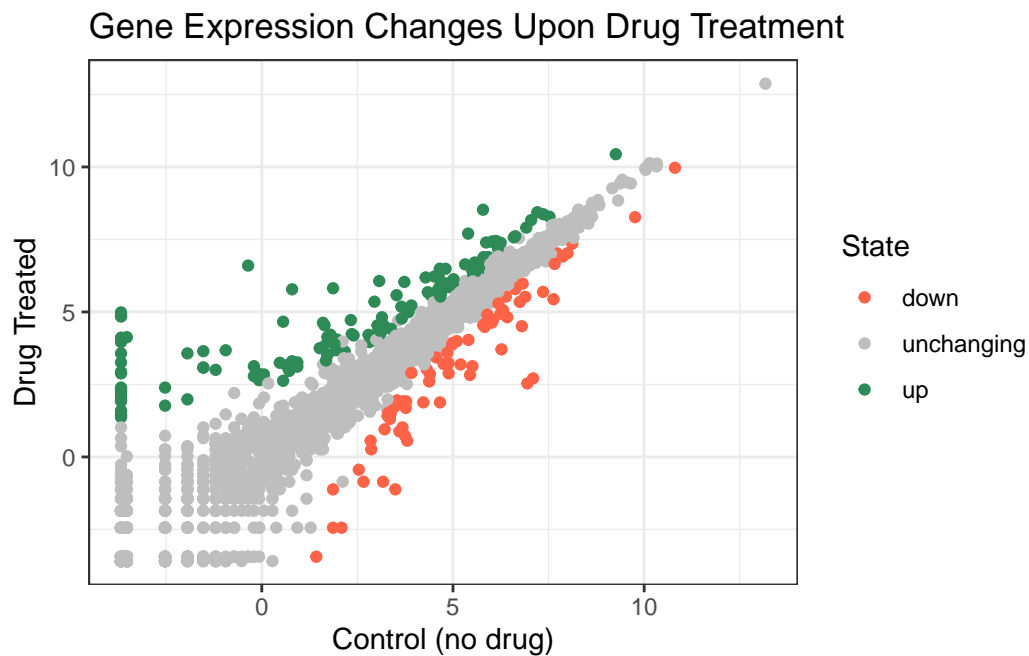
down  unchanging      up
   72      4997     127

```

Custom color plot

Q. Make a first plot of this data

```
ggplot(genes)+
  aes(x=Condition1,y=Condition2,col=State)+
  scale_color_manual(values=c("tomato","gray","seagreen"))+
  labs(title="Gene Expression Changes Upon Drug Treatment",x="Control (no drug)",y= "Drug Tr
  geom_point()+
  theme_bw()
```



Using different geoms

Let's plot some aspects of the in-built `mtcars` dataset

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1

Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

Q. Scatter plot of mpg vs disp

```
p1<-ggplot(mtcars)+
  aes(mpg,disp)+
  geom_point(color="chartreuse")+
  labs(title="MPG vs Displacement",x="Displacement",y="MPG")
```

Q. Box plot of gear vs disp

```
p2<-ggplot(mtcars)+
  aes(gear,disp,group=gear)+
  geom_boxplot()
```

Q. Bar plot of carb

```
p3<-ggplot(mtcars)+
  geom_bar()+
  aes(carb)
```

Smooth of disp vs qsec

```
p4<-ggplot(mtcars)+
  aes(disp,qsec)+
  geom_smooth()
```

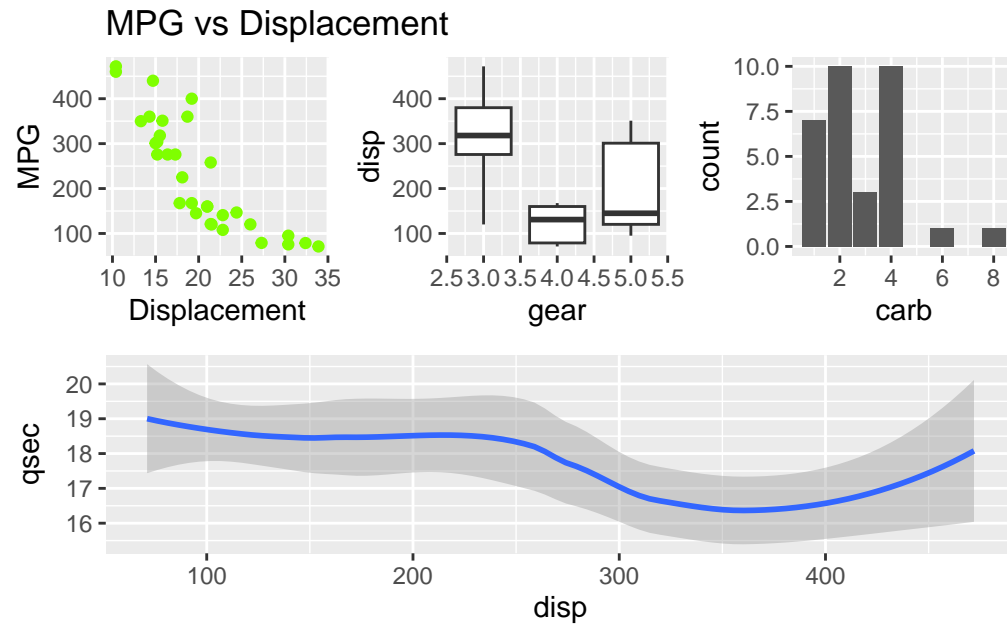
I want to combine all these plots into one figure with multiple panels.

We can use the **patchwork** package to do this.

```
library(patchwork)

((p1|p2|p3)/p4)
```

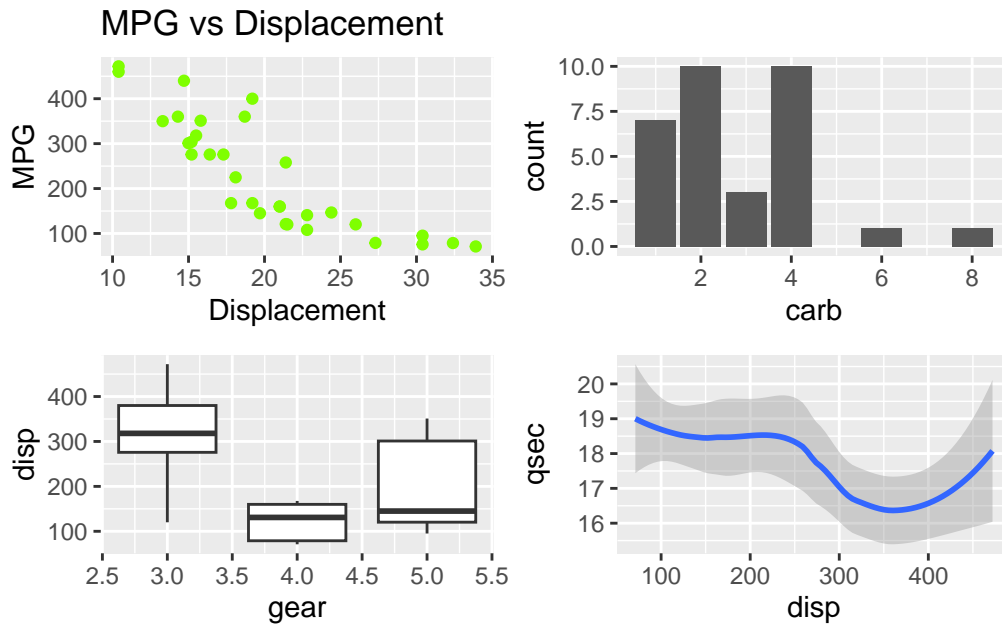
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'



```
library(patchwork)
```

```
((p1/p2|p3/p4))
```

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



```
ggsave(filename="myplot2.png",width=5,height=3)
```

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

Faceting

```
# File location online
url<- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"

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

Q. How many countries are in this dataset?

```
length(table(gapminder$country))
```

[1] 142

Q. Plot gdpPercap vs lifeExp color by continent

```
ggplot(gapminder)+  
  aes(gdpPercap, lifeExp, col= continent)+  
  geom_point(alpha=0.3)+  
  facet_wrap(~continent)+  
  theme_bw()
```

