

# Class 05: Data Visualization

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## Basic R graphics vs ggplot2

There are many graphics systems available in R, including so-called “base” R graphics and the so-called **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 **ggplot2** package I first need to install it with the function `install.packages("ggplot2")`.

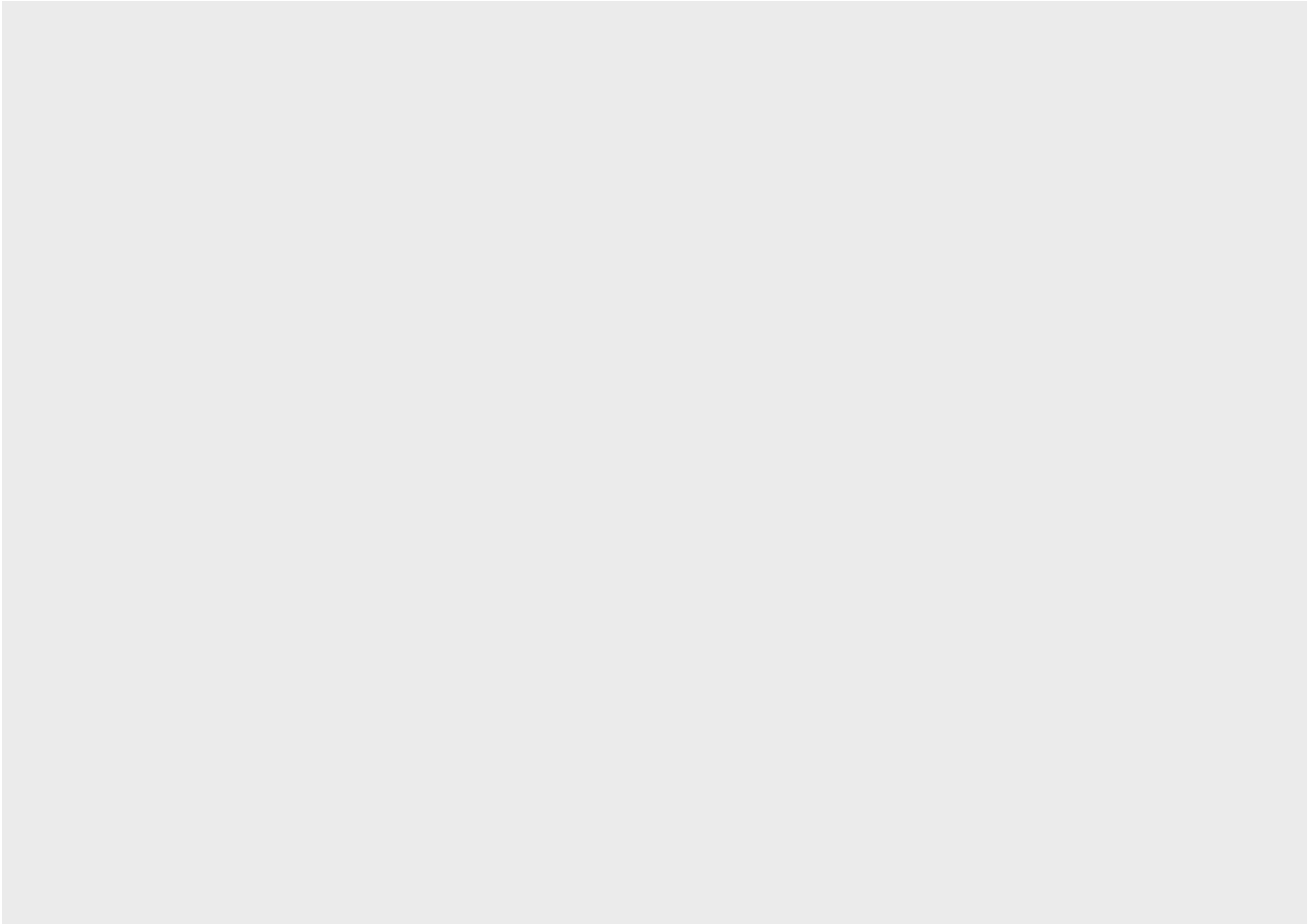
I will run this in my R console (i.e. the R brain) as I do not want to re-install it every time I render my report

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

```
library(ggplot2)
```

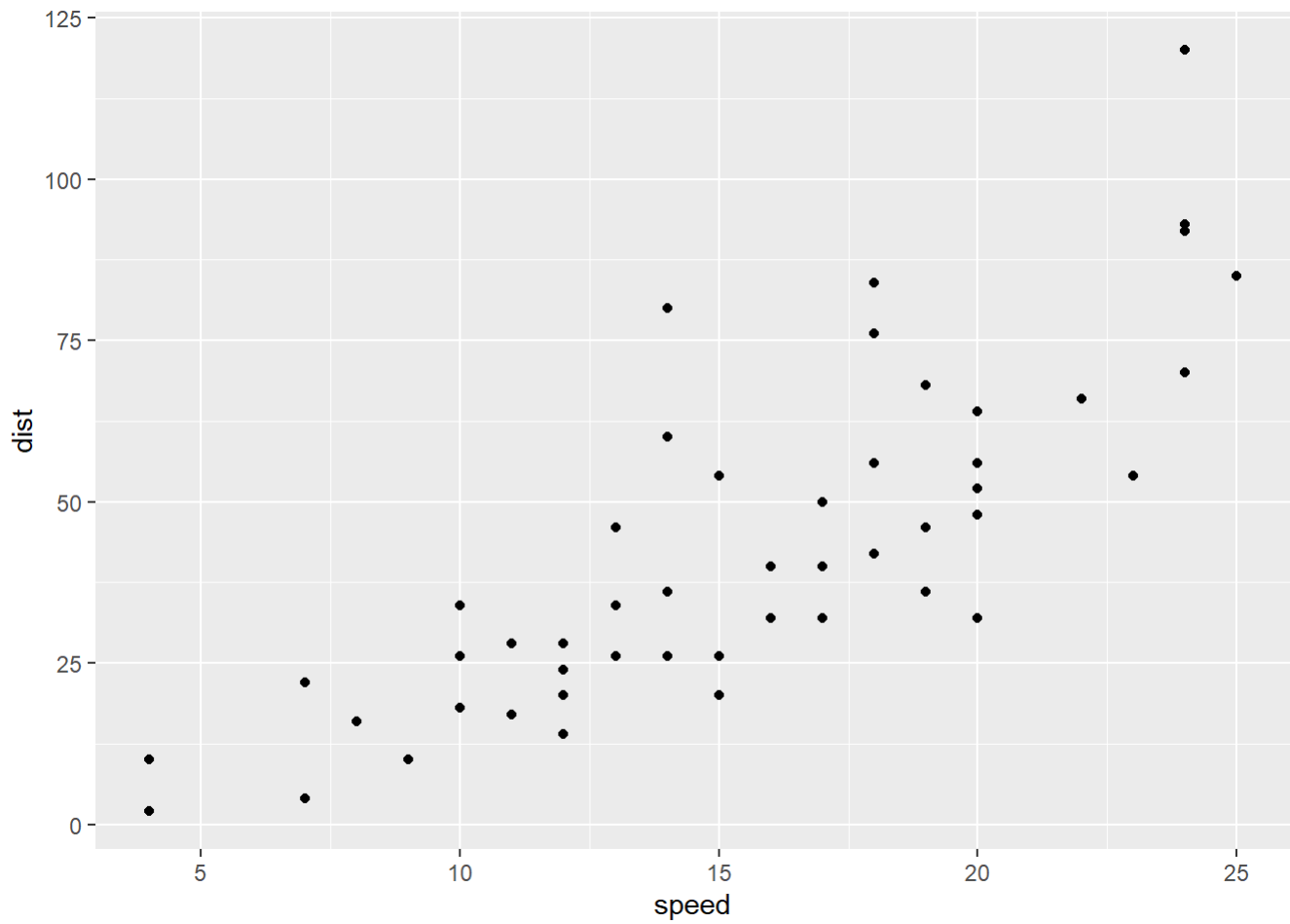
Warning: package 'ggplot2' was built under R version 4.2.3

```
ggplot()
```



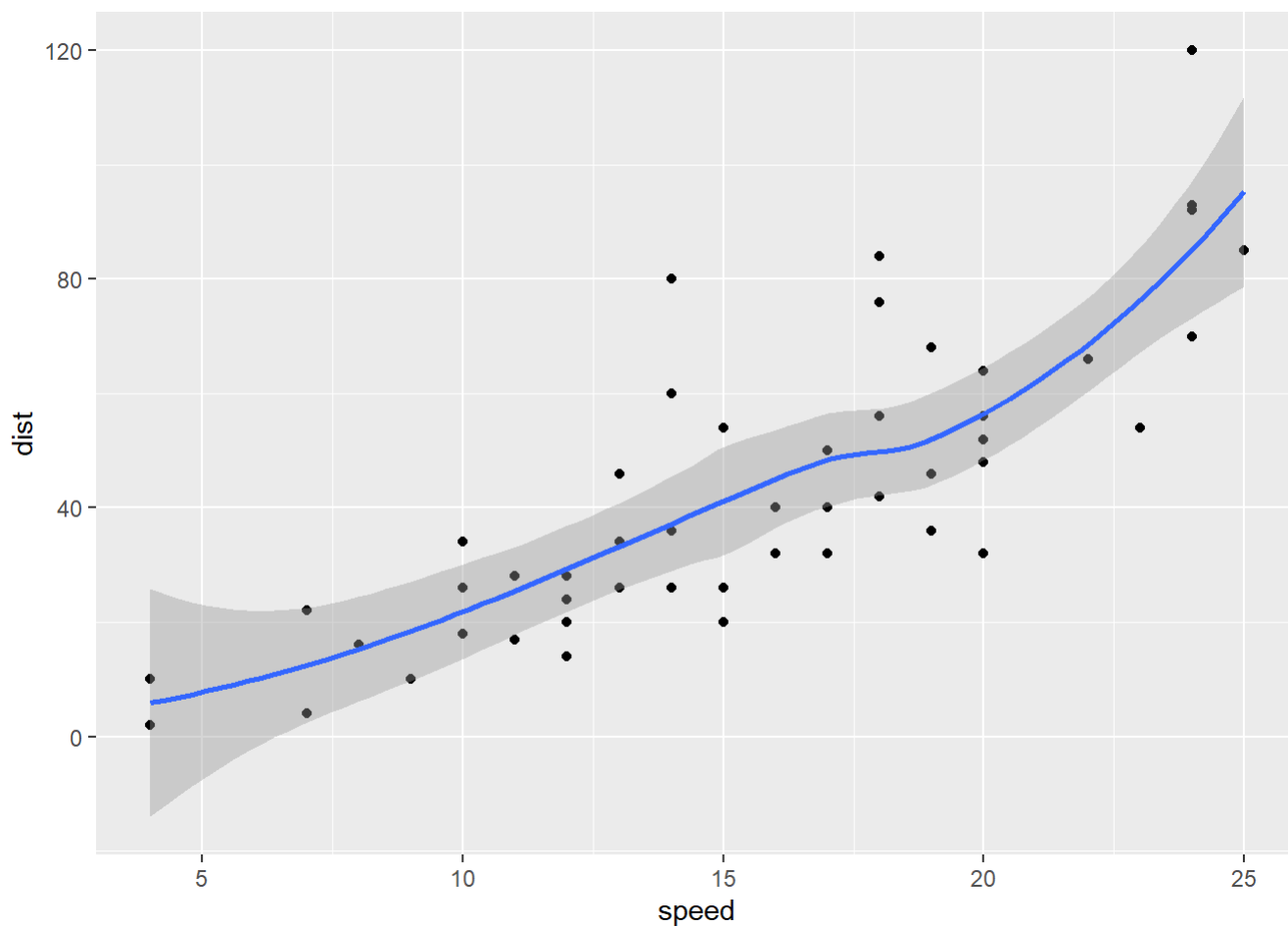
To make a figure with ggplot I need always at least 3 things: - data (i.e. what I want to plot) - aes: the aesthetic mapping of the data I want to plot - the geoms (i.e. how I want to plot the data)

```
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'



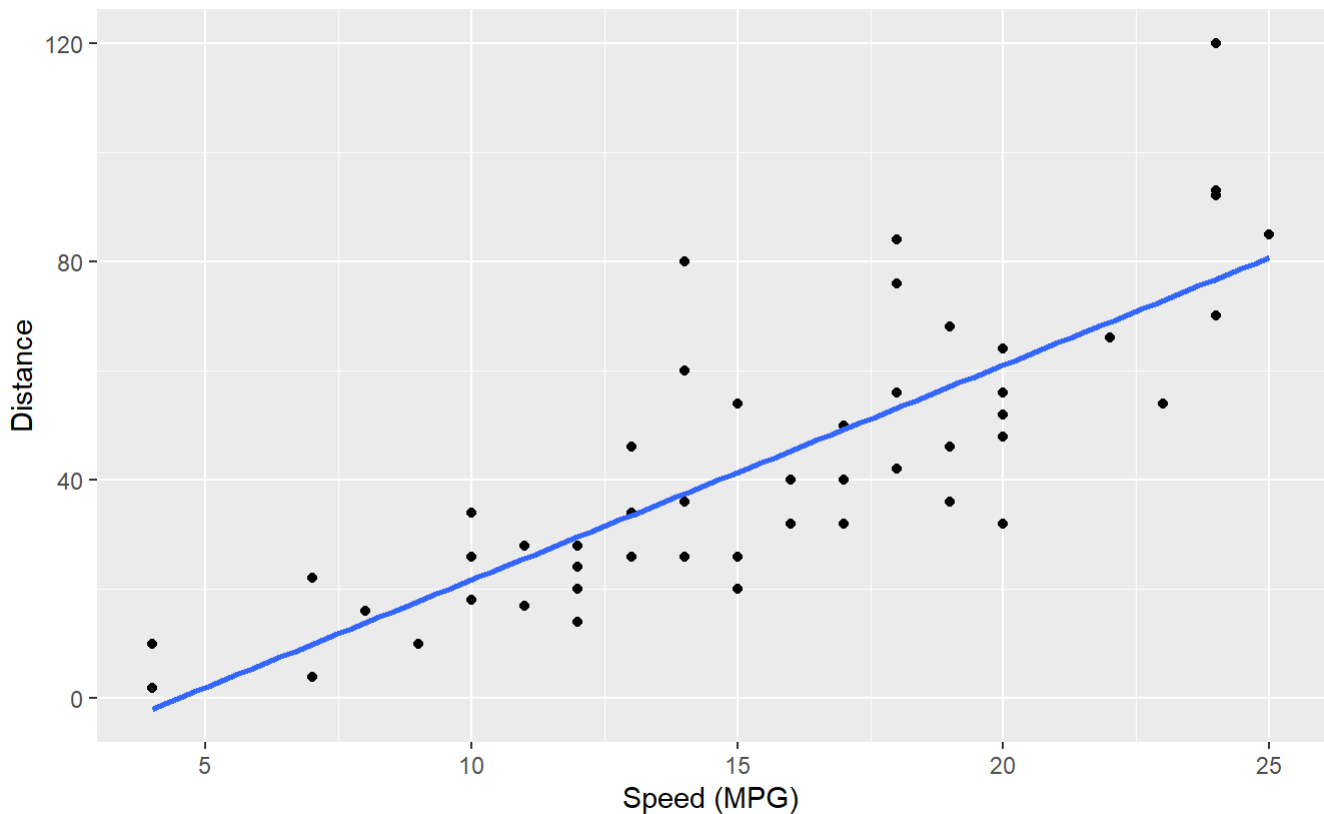
If I want to add more stuff, I can just keep adding layers such as

```
ggplot(data=cars)+  
  aes (x=speed, y=dist)+  
  geom_point()+  
  geom_smooth(se=FALSE, method="lm")+  
  labs(title="stopping distance for all cars", subtitle="From the inbuilt cars dataset", caption=
```

`geom\_smooth()` using formula = 'y ~ x'

## stopping distance for all cars

From the inbuilt cars dataset



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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
```

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

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

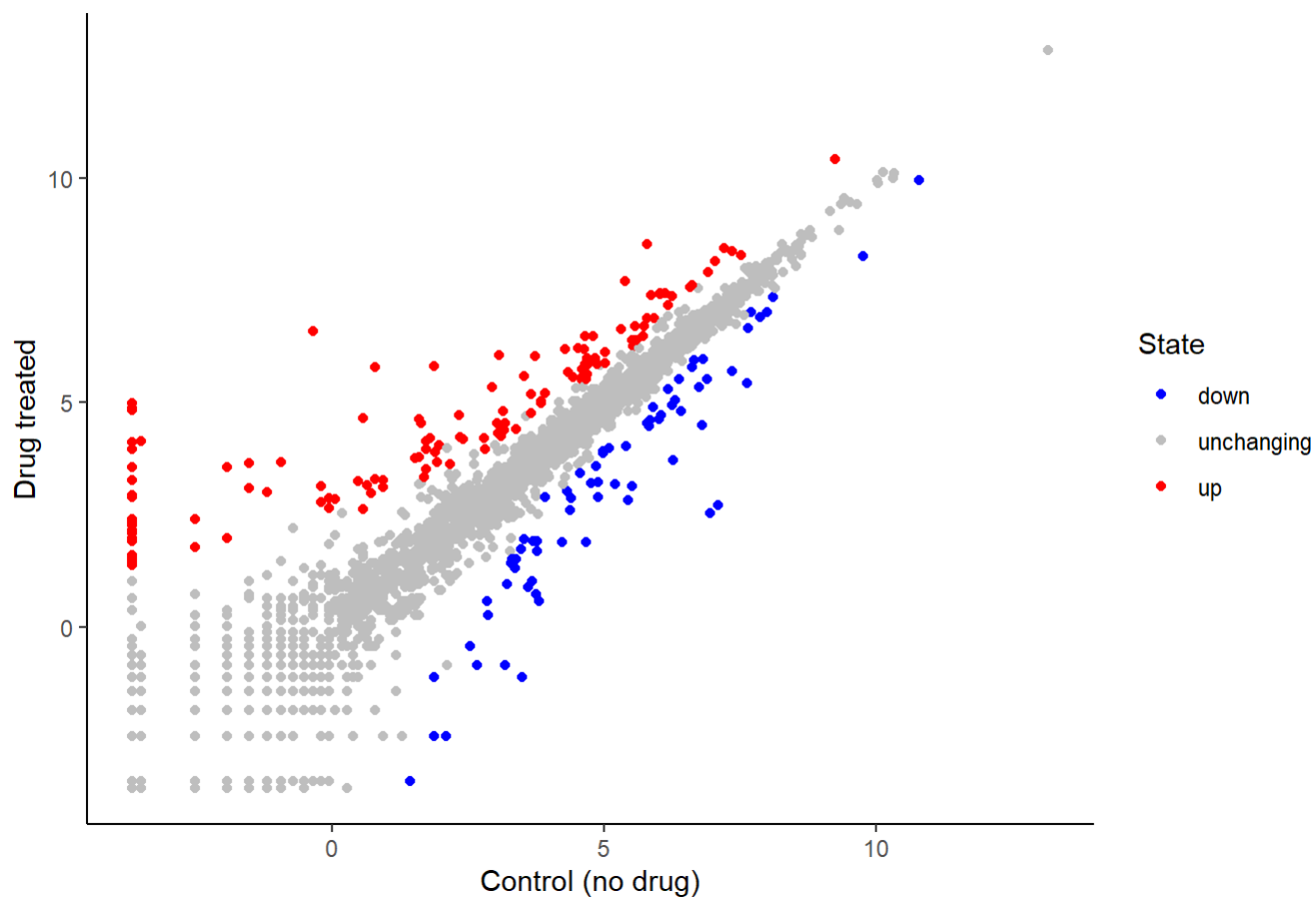
down	unchanging	up
72	4997	127

```
library(ggplot2)
p <- ggplot(genes)+
  aes(x=Condition1, y=Condition2, color=State)+
  geom_point()+
  theme_classic()
```

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

```
p + labs(title="Gene Expression changes upon drug treatment", x="Control (no drug)", y="Drug treatment") +
  scale_colour_manual(values=c("blue", "gray", "red"))
```

## Gene Expression changes upon drug treatment



## ##Going Further

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

gapminder <- read.delim(url)

library(dplyr)
```

Warning: package 'dplyr' was built under R version 4.2.3

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

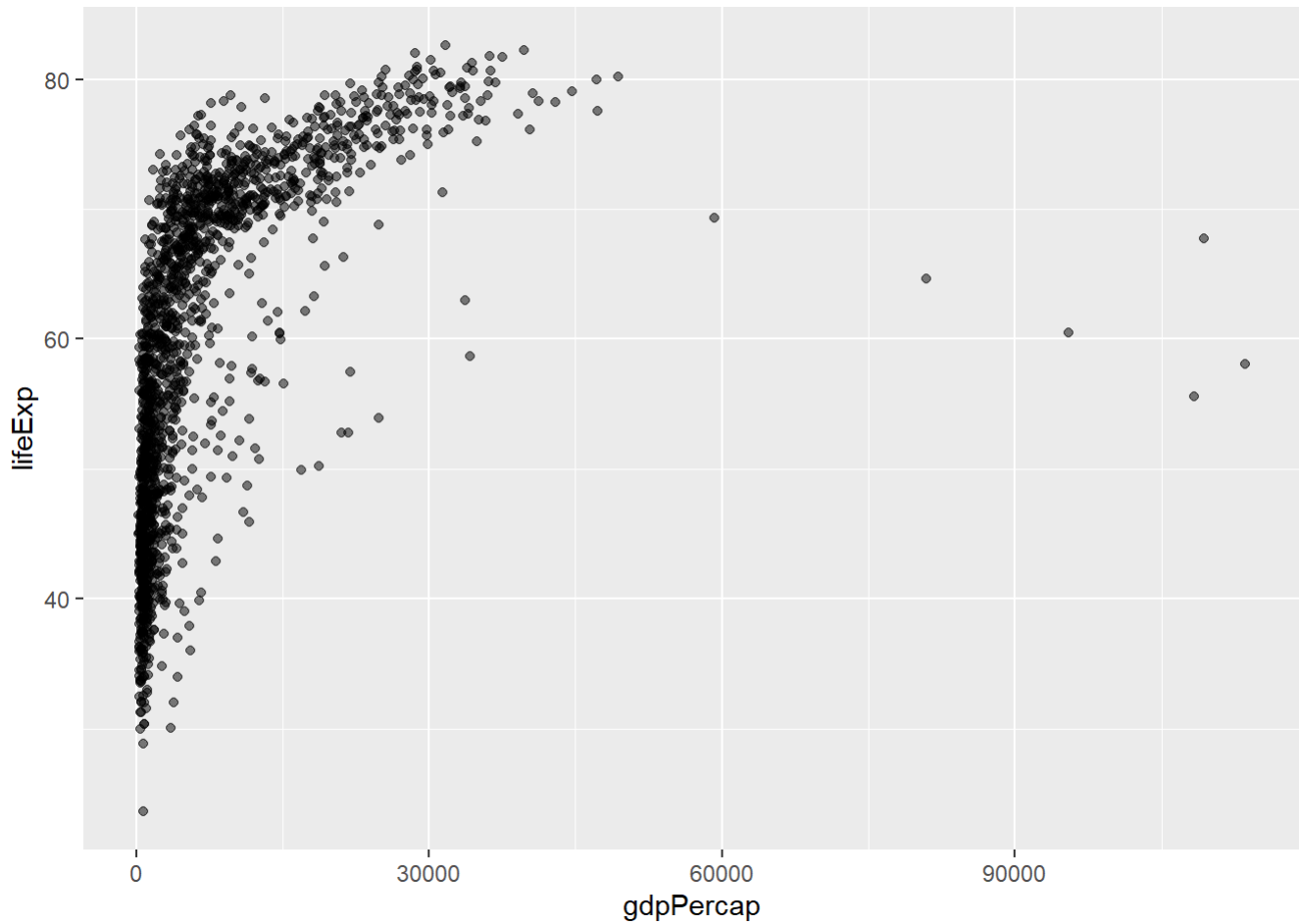
filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

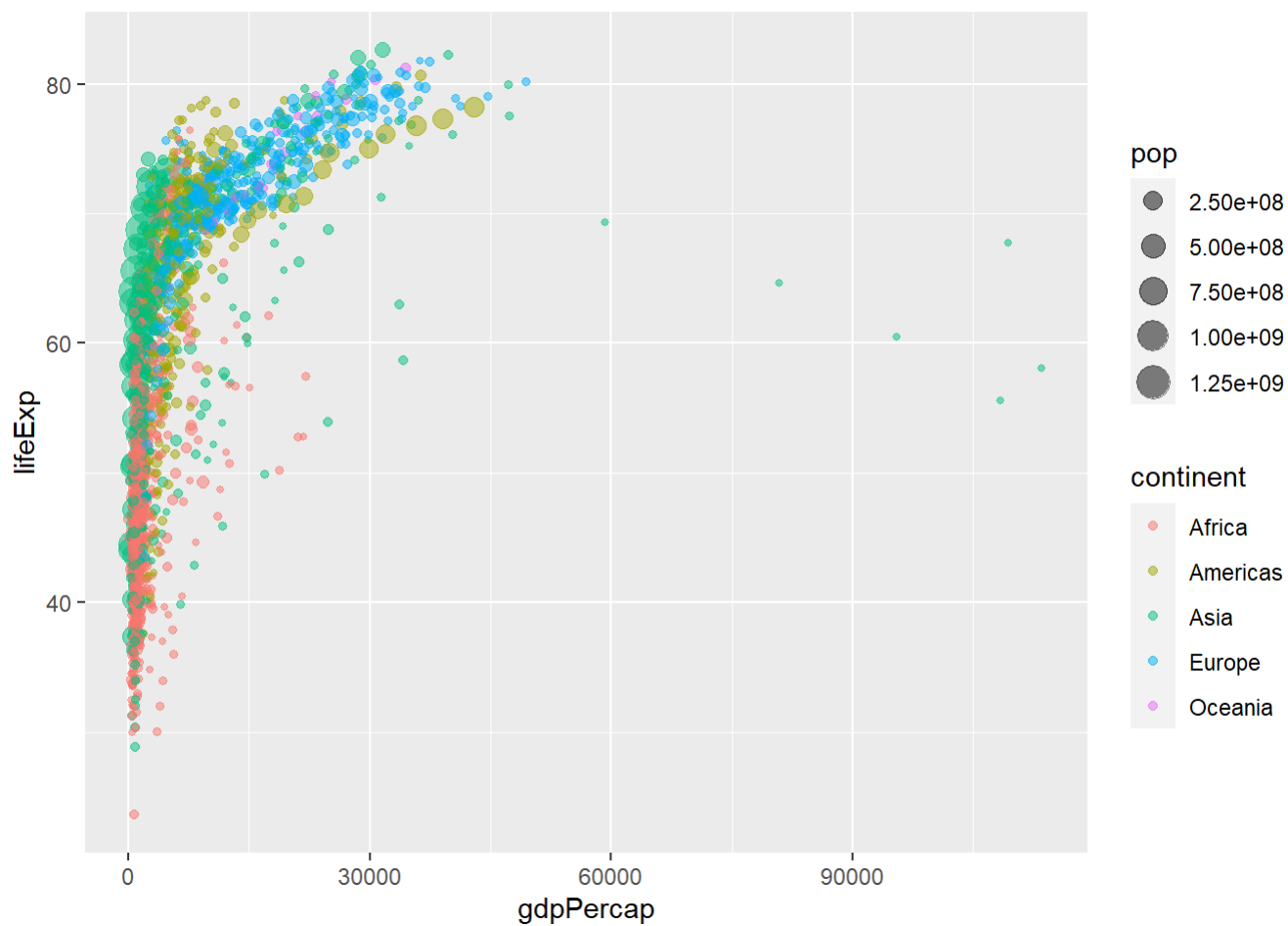
```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
```

```
geom_point(alpha=0.5)
```



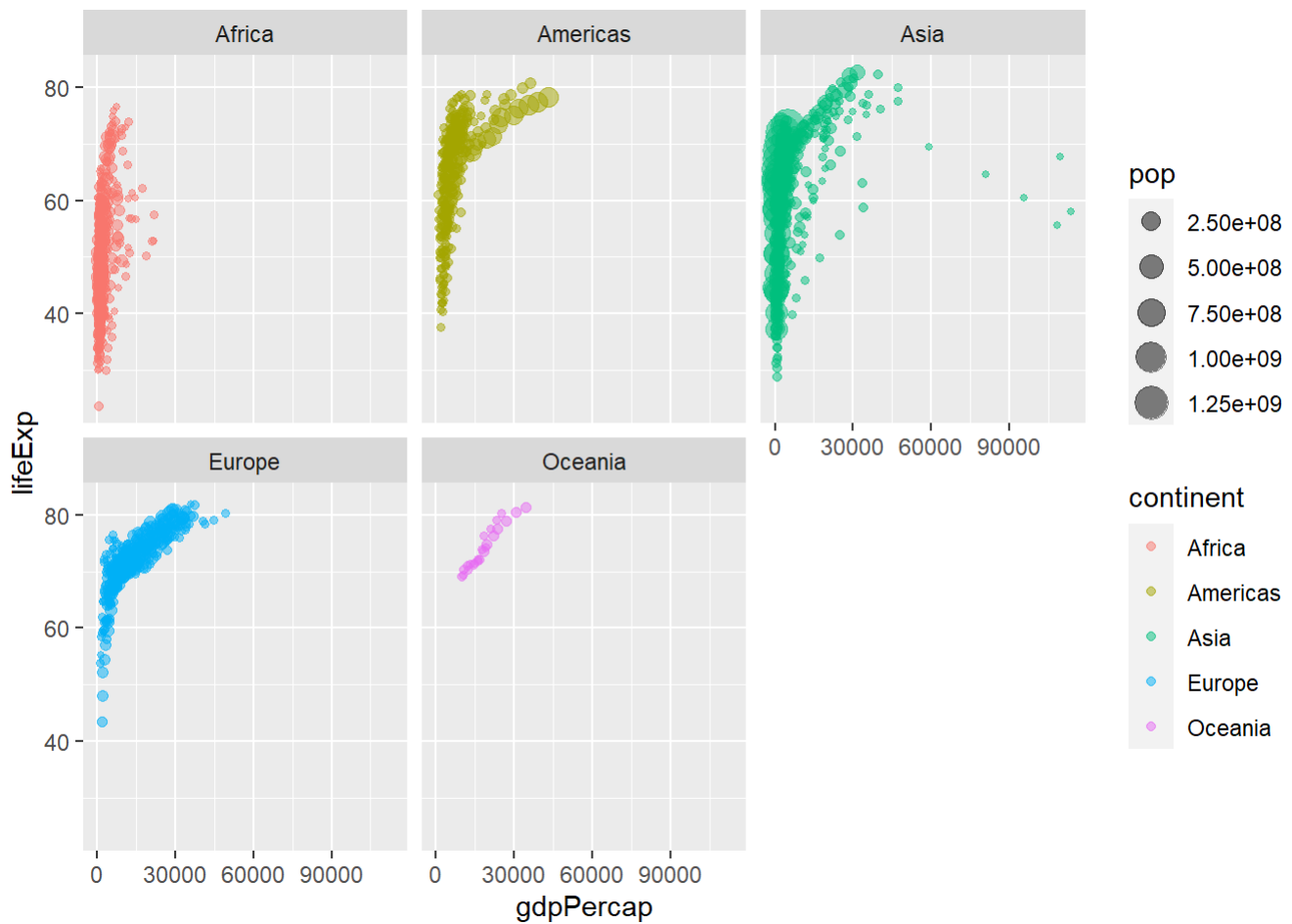
```
ggplot(gapminder) +  
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +  
  geom_point(alpha=0.5)
```





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

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



Let's see how the plot looks like if we color the points by the numeric variable population `pop`

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

