Class 5: 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.

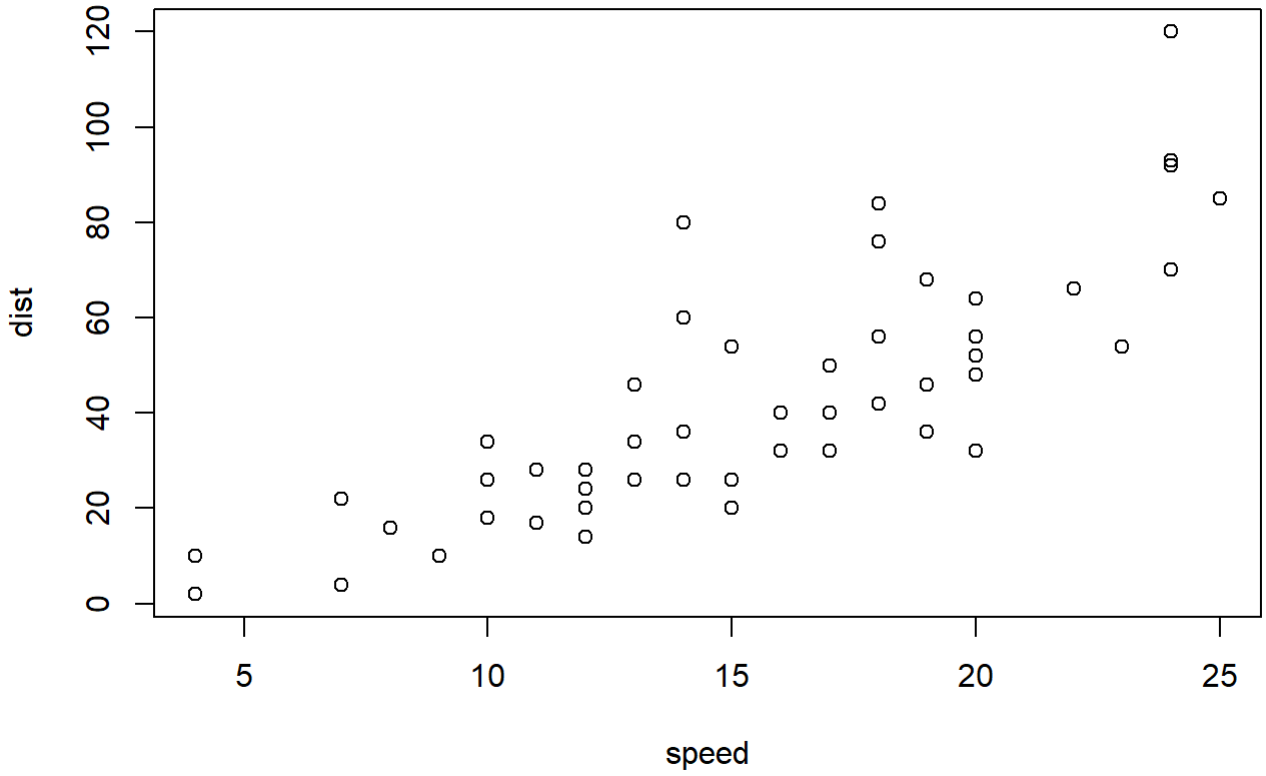
To compare these let's play with the inbuilt `cars` dataset.

```
head(cars)
```

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

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("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...

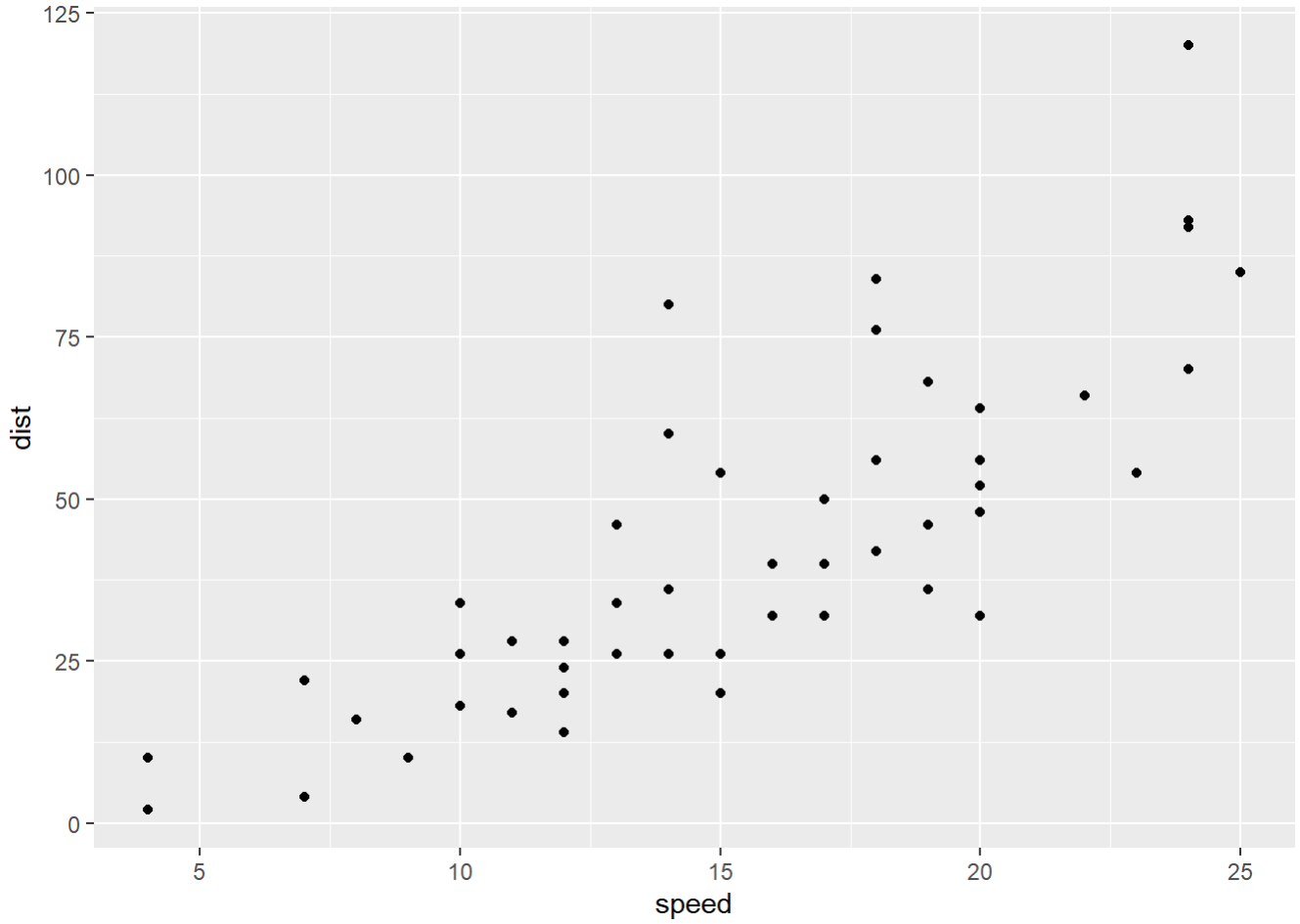
The main function in this package is called `ggplot()`. Can I just call it?

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

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

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

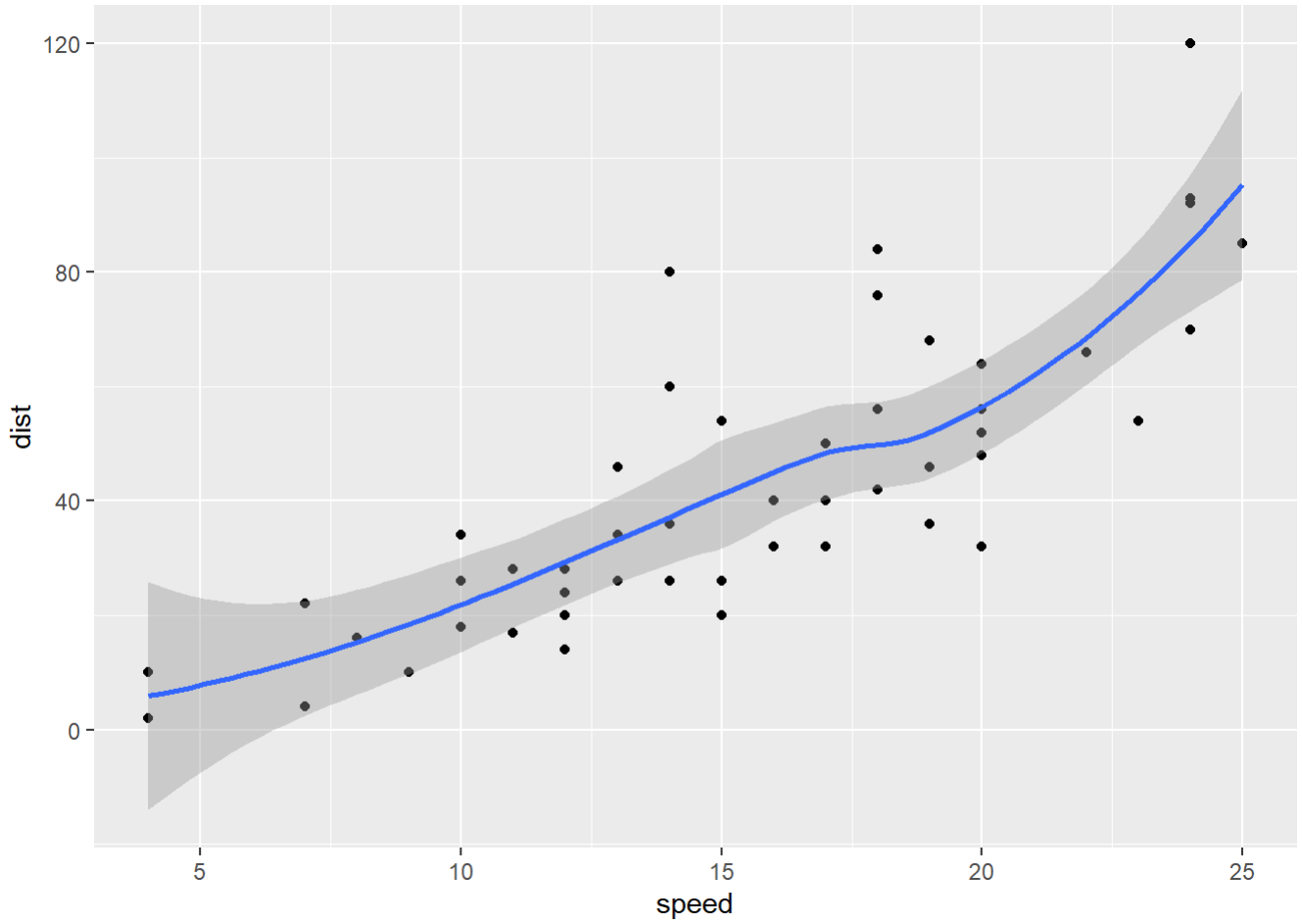
```
ggplot(data = cars) +
  aes(x = speed, y = dist) +
  geom_point()
```



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()
```

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

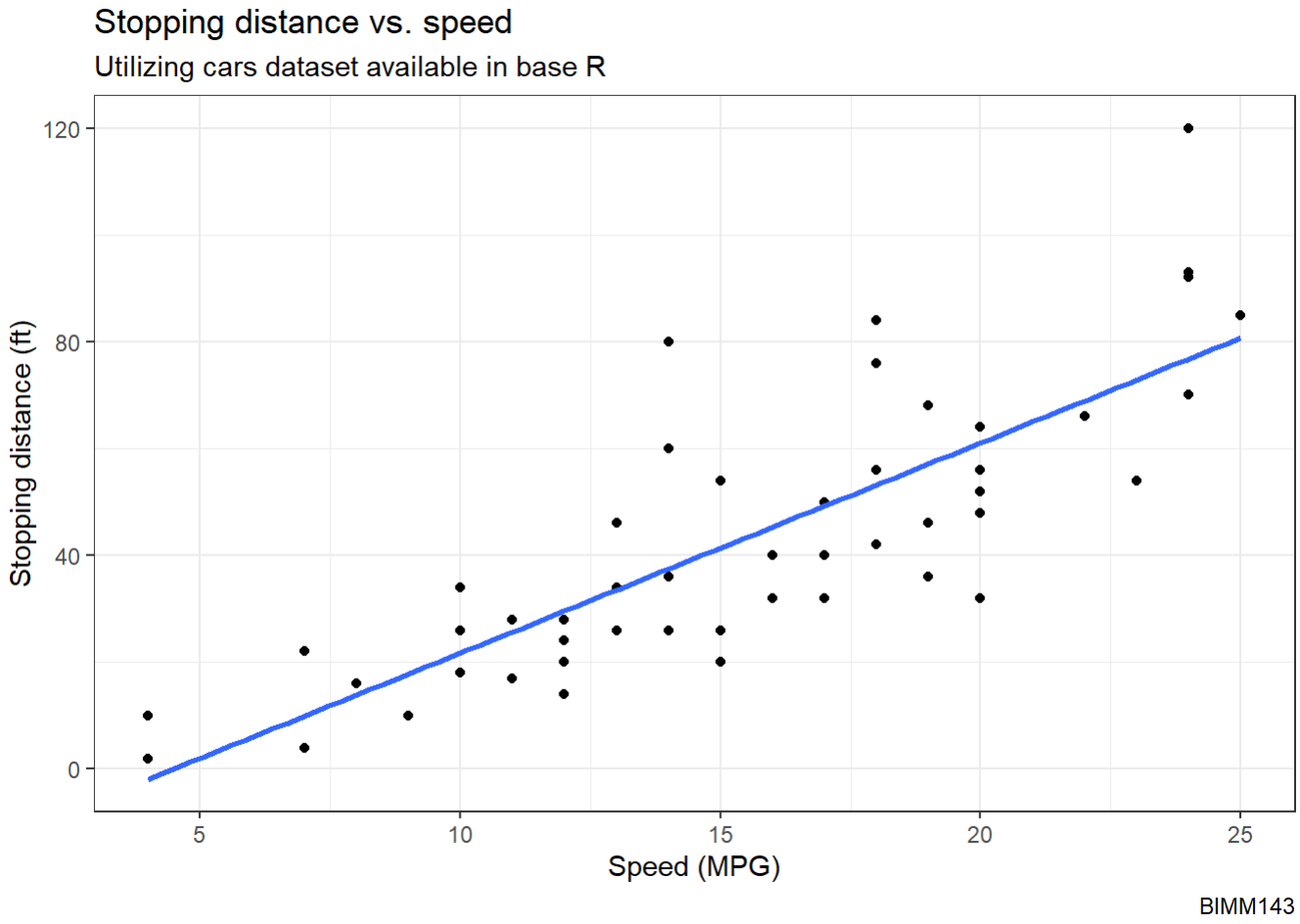


GGplot is much more verbose than base R plots for standard plots but it has a consistent layer system that I can use to make just about any plot.

Let's make a plot with a straight line fit - i.e. a linear model and no standard error shown.

```
ggplot(data = cars) +
  aes(x = speed, y = dist) +
  geom_point() +
  geom_smooth(se = FALSE, method = "lm") +
  labs(title = "Stopping distance vs. speed",
       subtitle = "Utilizing cars dataset available in base R",
       caption = "BIMM143",
       x = "Speed (MPG)",
       y = "Stopping distance (ft)") +
  theme_bw()
```

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



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 that last column - the "State" column? I.e. how many genes are up, down, or unchanging?

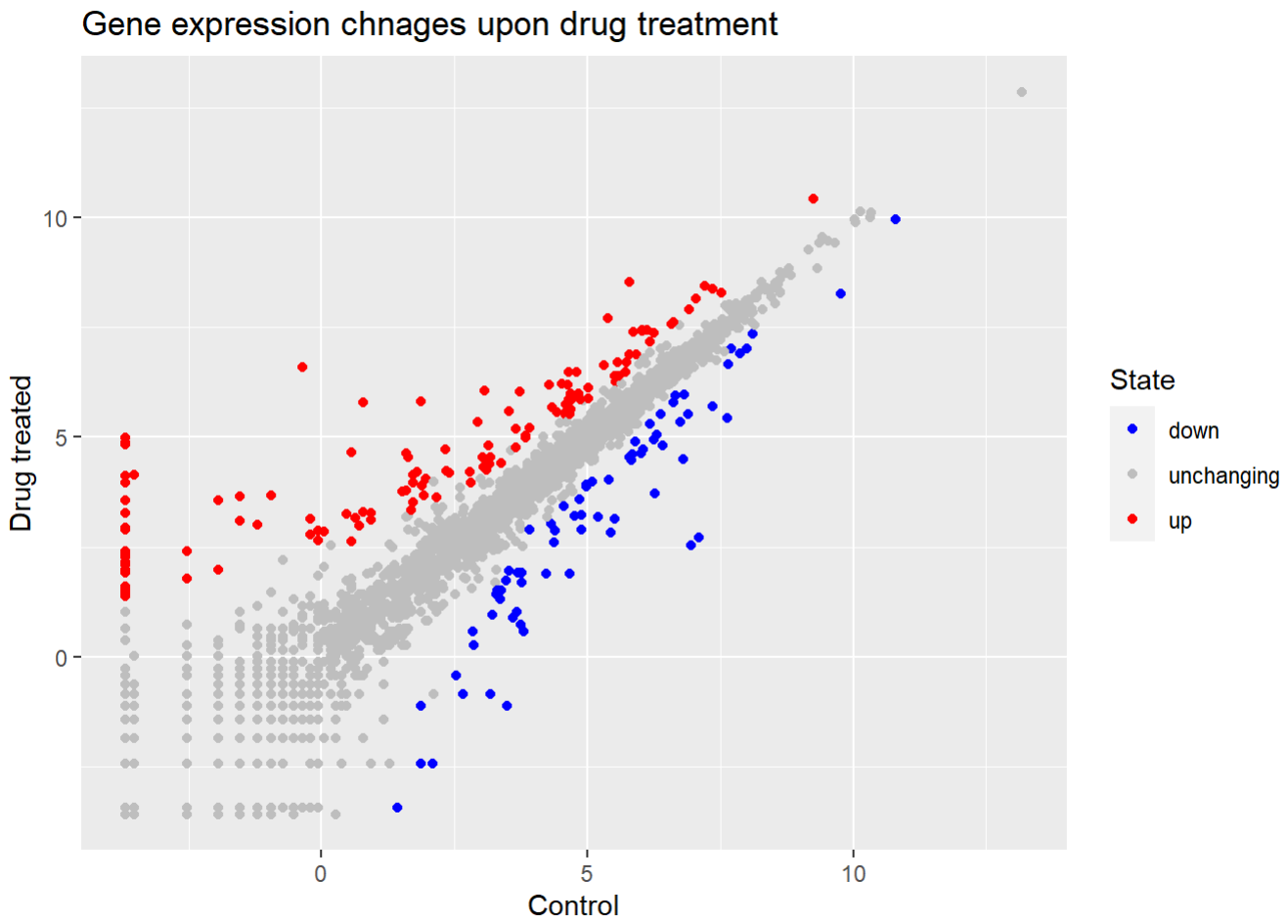
```
table(genes[, "State"])
```

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

```
plot <- ggplot(genes) +
          aes(x = Condition1, y = Condition2, col = State) +
          geom_point() +
          labs(title = "Gene expression chnages upon drug treatment",
               x = "Control", y = "Drug treated")
```

I can now just call `plot` when I want to do things, such as specifying the color scale:

```
plot + scale_color_manual( values = c("blue", "gray", "red"))
```



Going further

Here I read a slightly larger dataset:

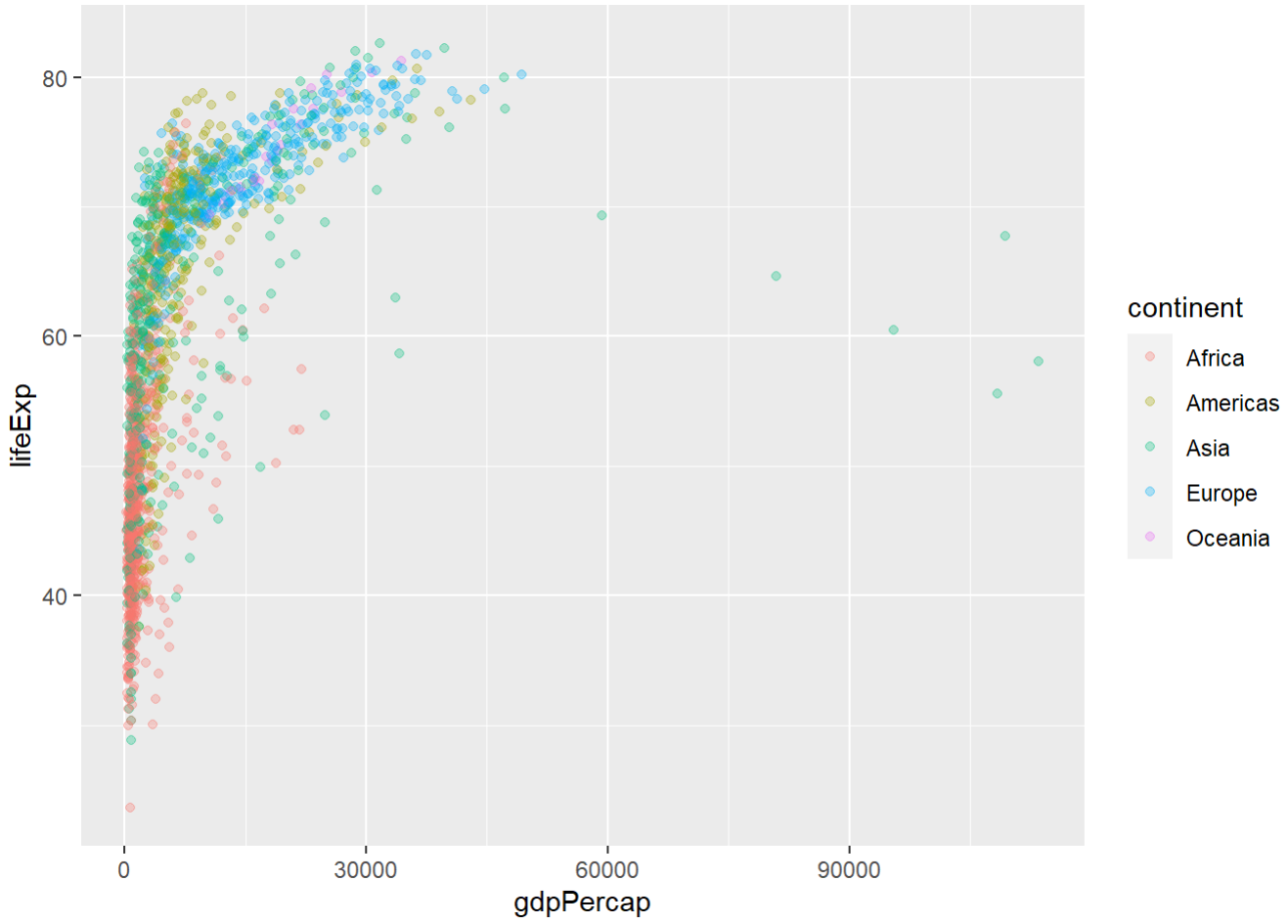
```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"

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
```

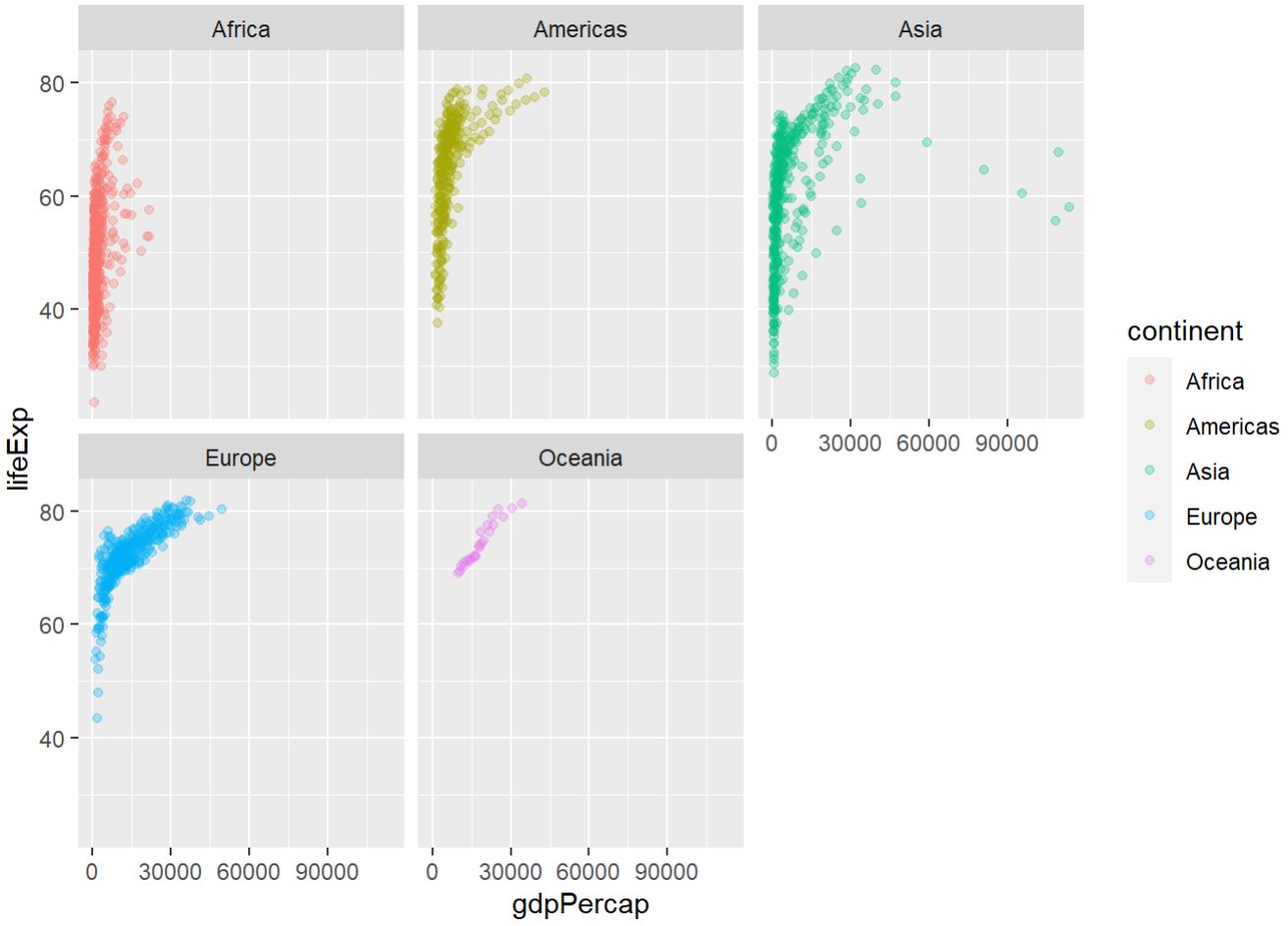
Comparing life expectancy vs gdpPercap:

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



A very useful layer to add sometimes is for “faceting”:

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


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