

Class 5: Data Viz with ggplot

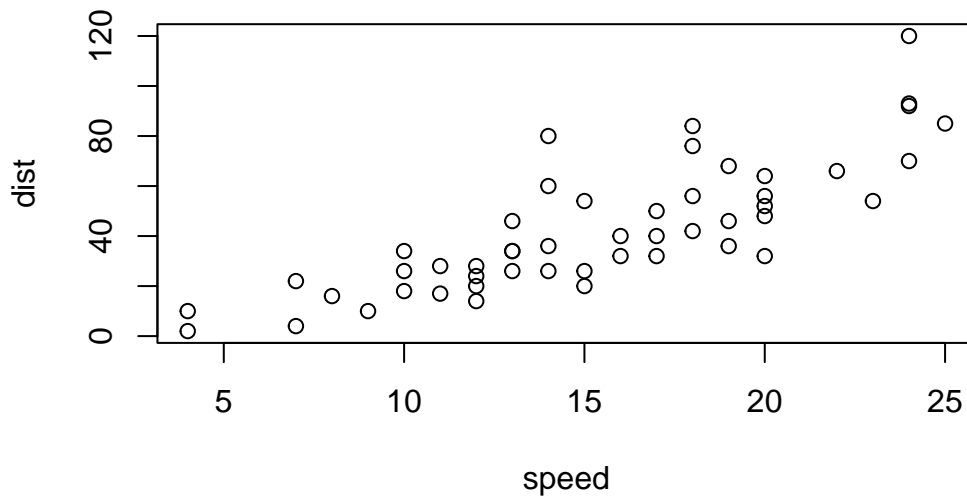
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Graphics system in R

There are many graphics systems in R. These include so-called “*base R*” and those in add-on packages like `ggplot2`.

```
plot(cars)
```



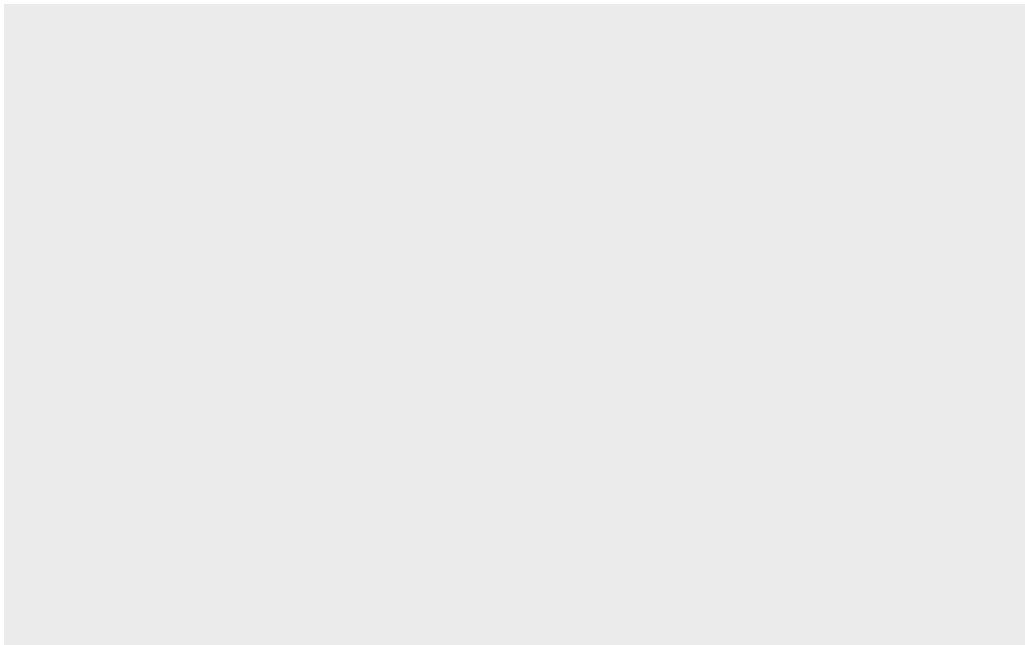
How can we make this with `ggplot2`

This is an odd-on package and I first need to install it on my computer. This install is a one time only deal.

To install any package I use `install.packages()` function.

To use it we need to load up the package from our library of install packages. For this I use `library(ggplot2)`

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



Using ggplot is not as straightforward as base R plot for basic plots. I have some more typing to do.

Every ggplot has at least 3 things (layers):

- data (data.frame)
- aes (how the data map to the plot)
- **geoms** (think of this as the type of plot, eg points, lines, etc)

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

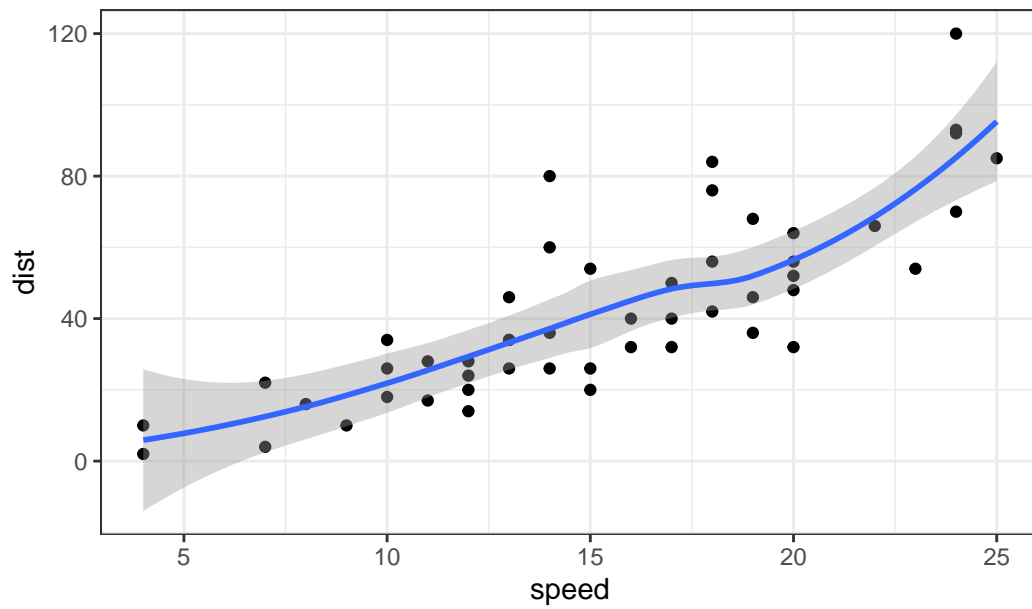


Here ggplot was more verbose - i.e. I had more typing to do - than base R. However, I can add more layers.

```
ggplot(cars) +  
  aes(speed, dist) +  
  geom_point() +  
  geom_smooth() +  
  labs(title = "Stopping Distance of Old Cars") +  
  theme_bw()
```

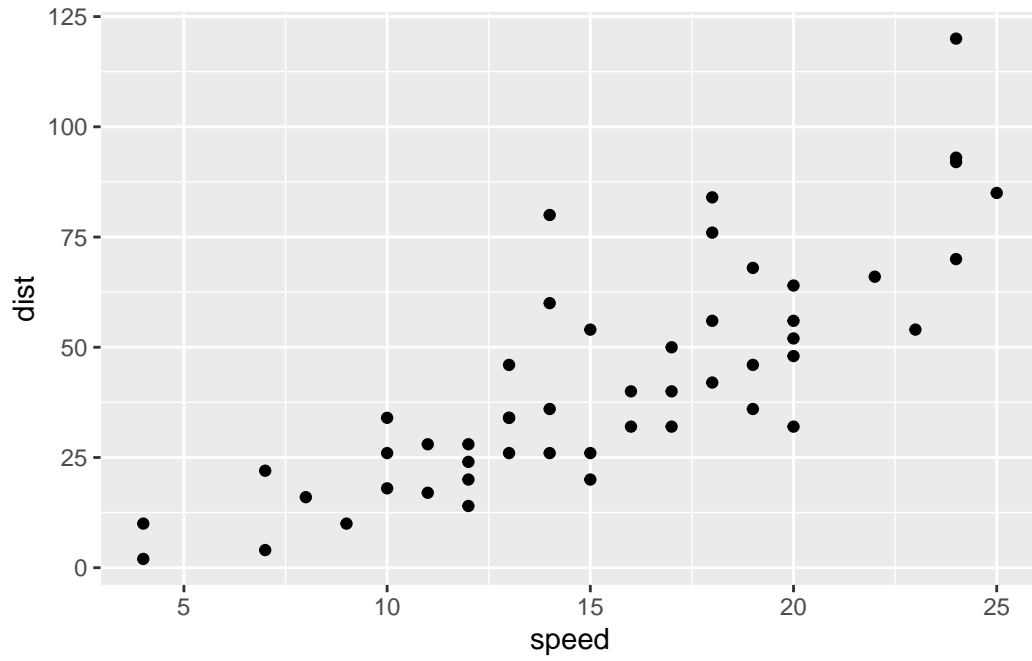
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'

Stopping Distance of Old Cars

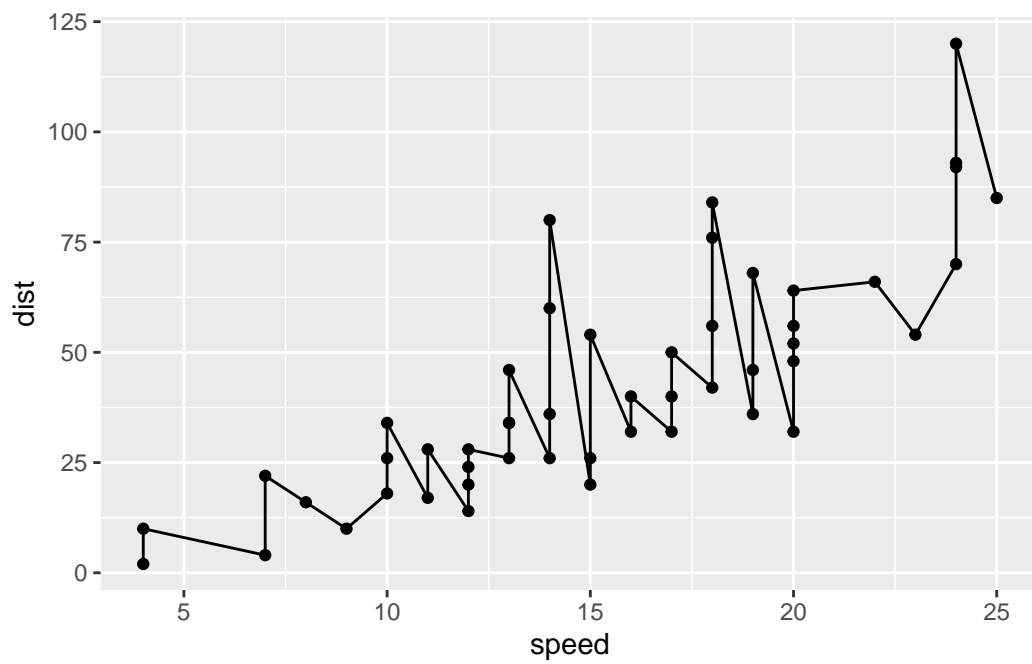


```
p1 <- ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```

```
p1
```

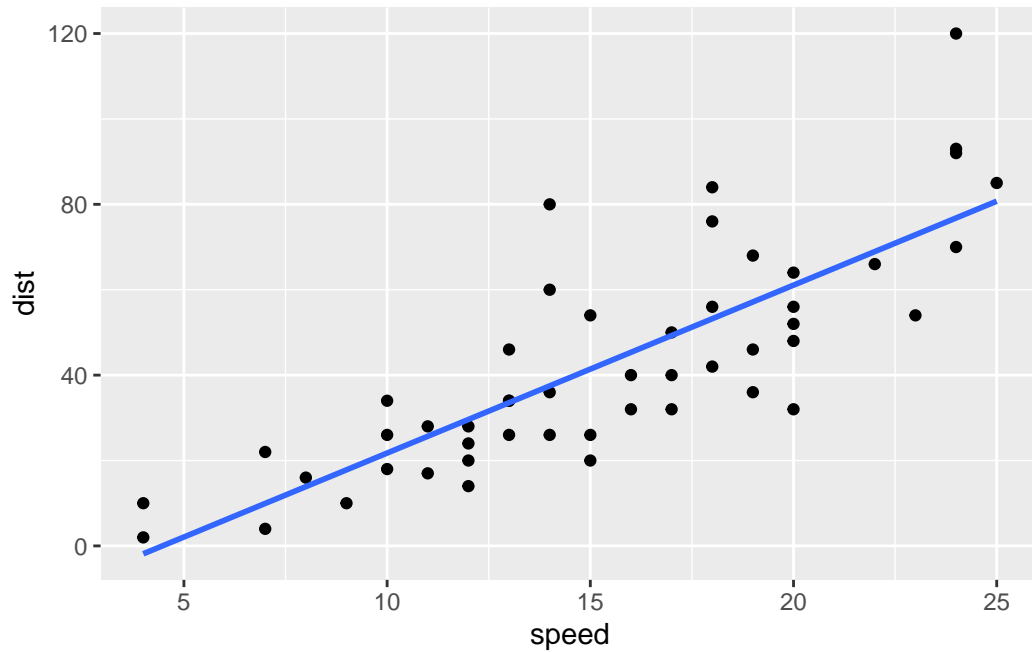


```
p1 + geom_line()
```



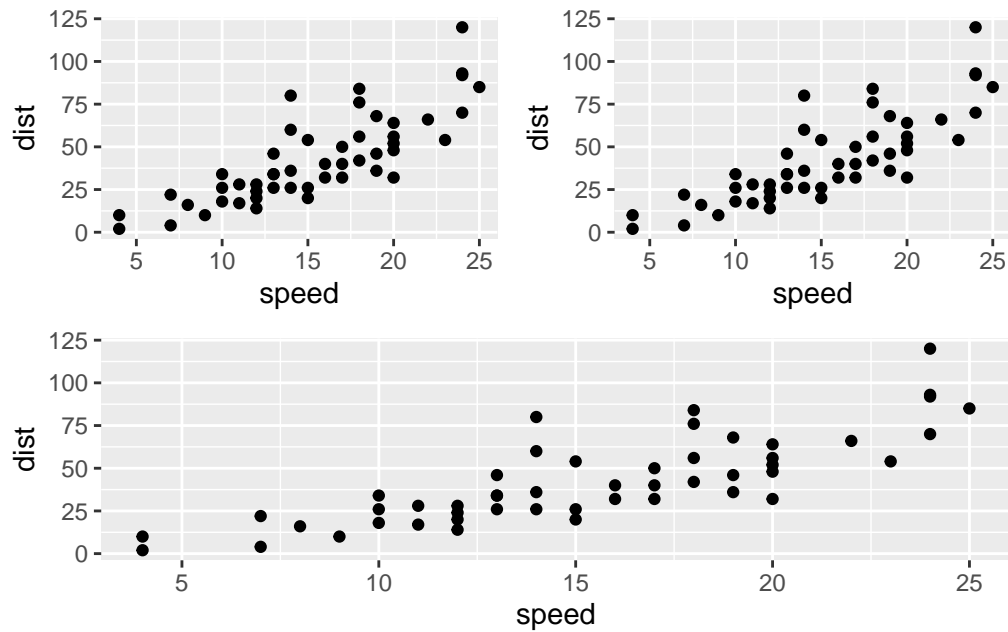
```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE)
```

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



```
library(patchwork)

(pl | pl)/ pl
```



Lab sheet

```
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

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

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

Q. Use the `nrow()` function to find out how many genes are in this dataset. What is your answer?

```
nrow(genes)
```

```
[1] 5196
```

Q. Use the `colnames()` function and the `ncol()` function on the `genes` data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find?

```
ncol(genes)
```

```
[1] 4
```

Q. Use the `table()` function on the `State` column of this `data.frame` to find out how many 'up' regulated genes there are. What is your answer?

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

down	unchanging	up
72	4997	127

Q. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

```
round(table(genes$State) / nrow(genes) * 100, 2)
```

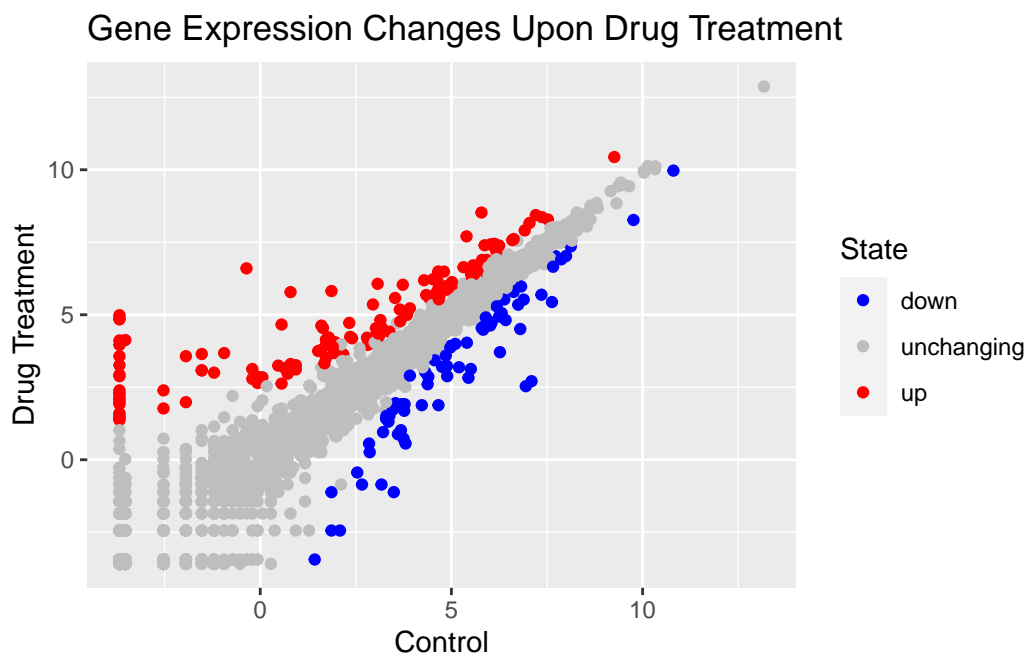
down	unchanging	up
1.39	96.17	2.44

Q. Nice, now add some plot annotations to the `p` object with the `labs()` function so your plot looks like the following:

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



```
scale_colour_manual( values=c("blue","gray","red") ) +
labs(title = "Gene Expression Changes Upon Drug Treatment", x = "Control", y = "Drug Tre
```



```
p2 <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  scale_colour_manual( values=c("blue","gray","red") ) +
  labs(title = "Gene Expression Changes Upon Drug Treatment", x="Control", y="Drug Treatme
```

And an interactive version with plotly

```
library("plotly")
```

Create interactive plots

```
#ggplotly(p2)
```

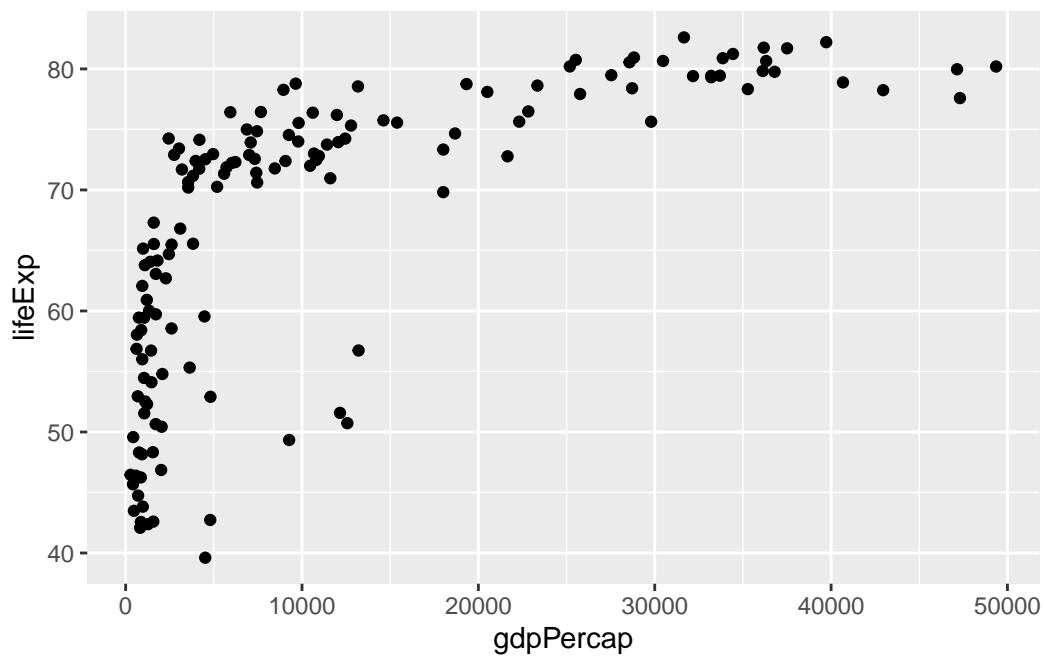
##Another example:

```
library("gapminder")
```

```
library(dplyr)
```

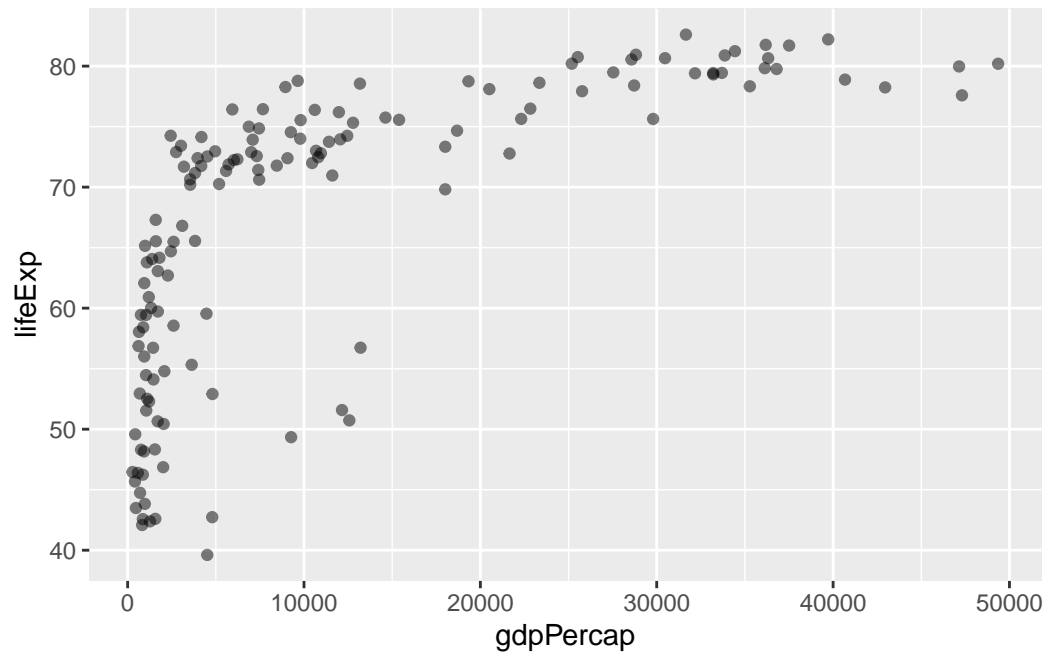
```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

```
ggplot(gapminder_2007) +  
  aes(x=gdpPerCap, y=lifeExp) +  
  geom_point()
```

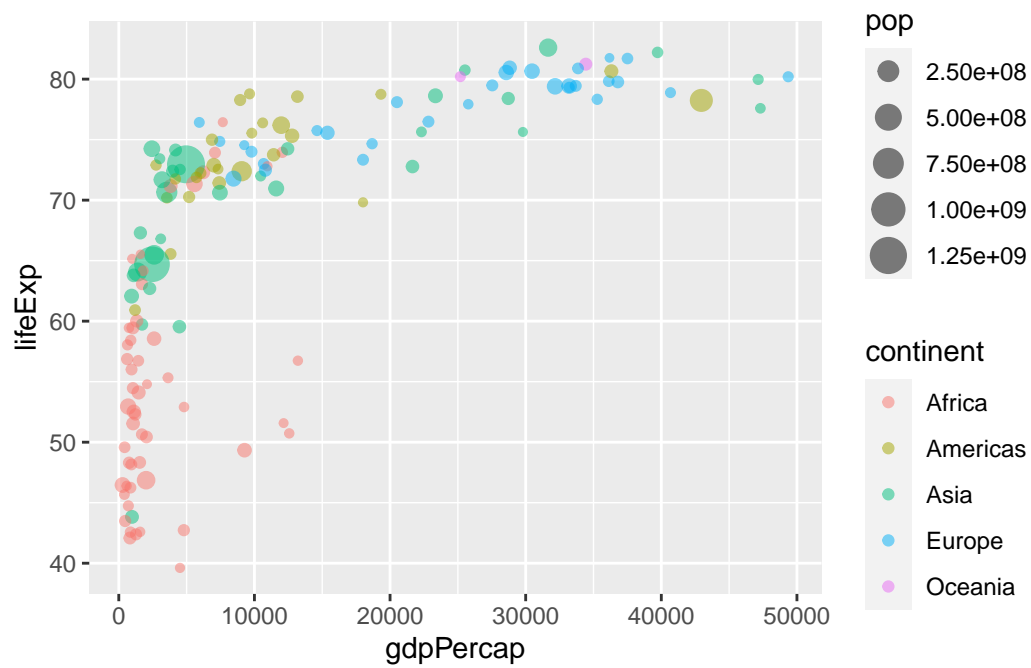


##One useful approach here is to add an `alpha=0.4` argument to your `geom_point()` call to make the points slightly transparent:

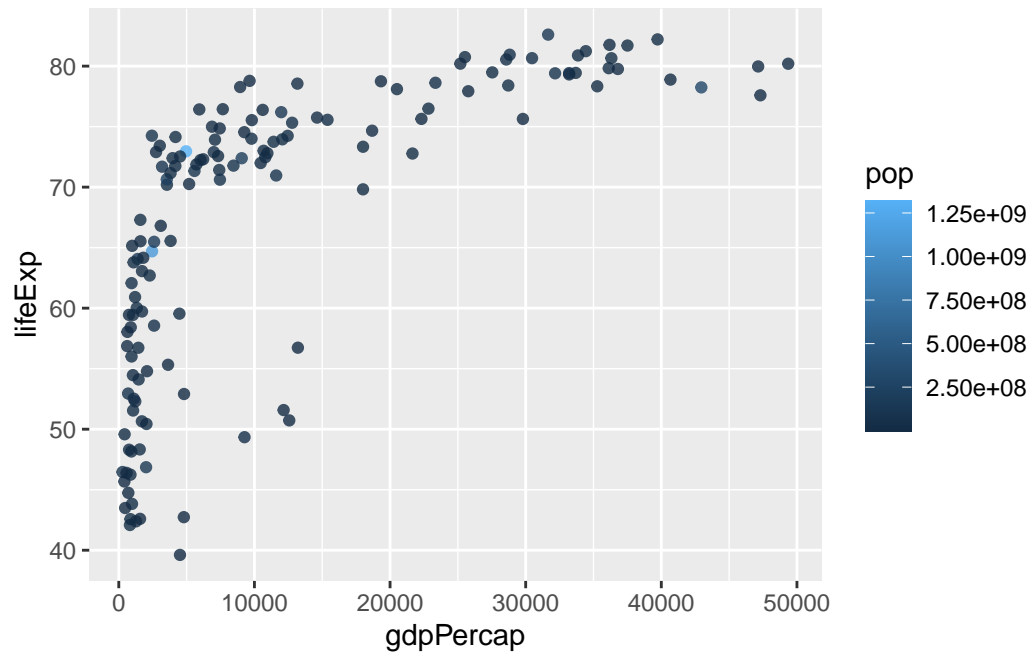
```
ggplot(gapminder_2007) +  
  aes(x=gdpPerCap, y=lifeExp) +  
  geom_point(alpha=0.5)
```



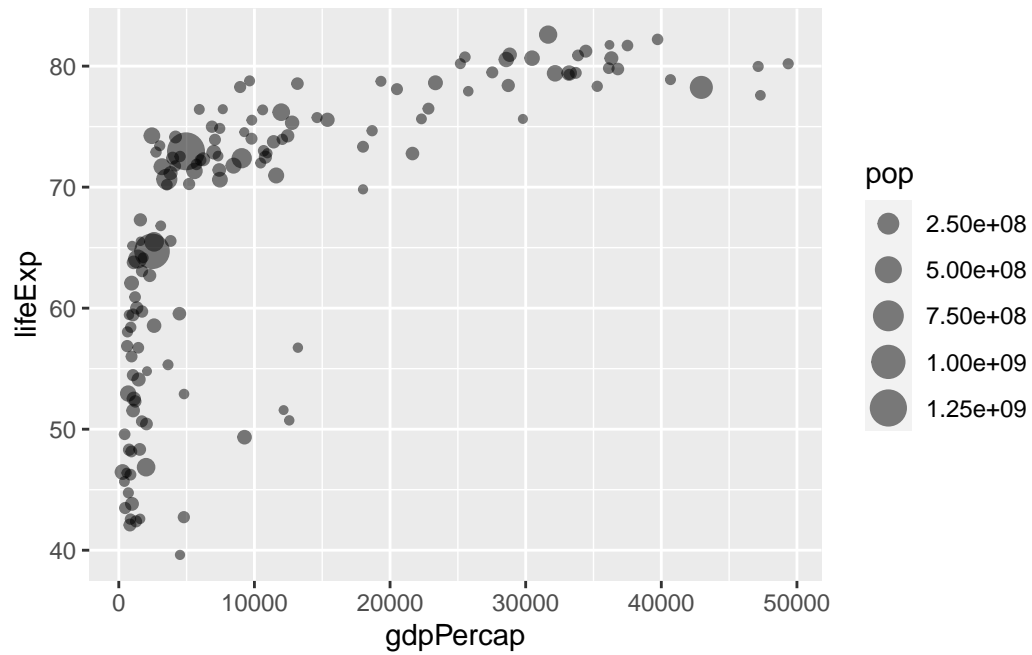
```
ggplot(gapminder_2007) +  
  aes(x=gdpPerCap, y=lifeExp, color=continent, size=pop) +  
  geom_point(alpha=0.5)
```



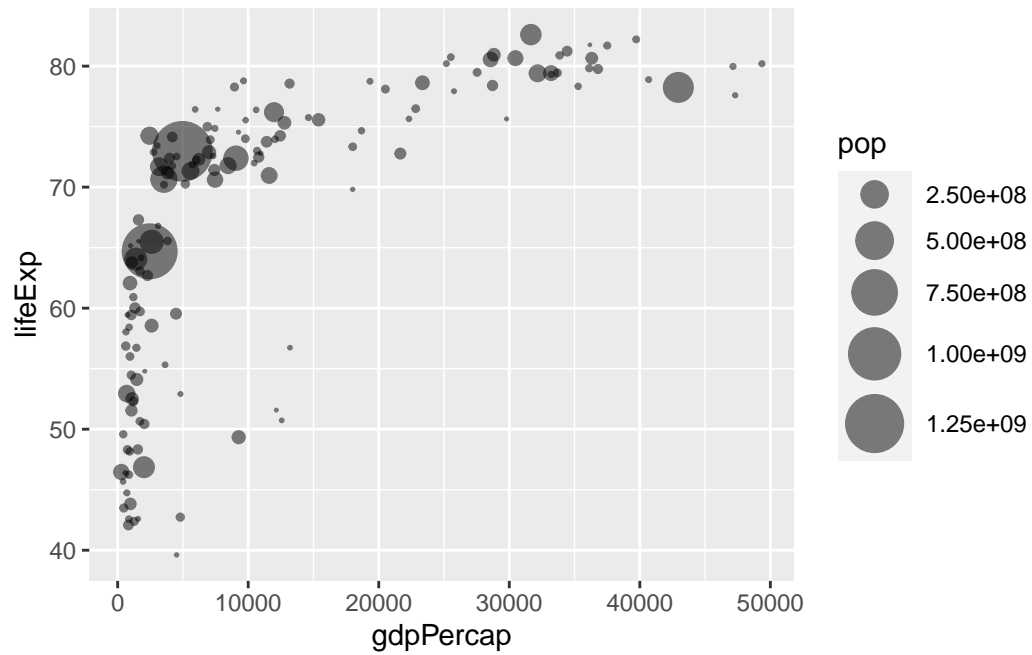
```
ggplot(gapminder_2007) +  
  aes(x = gdpPercap, y = lifeExp, color = pop) +  
  geom_point(alpha=0.8)
```



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

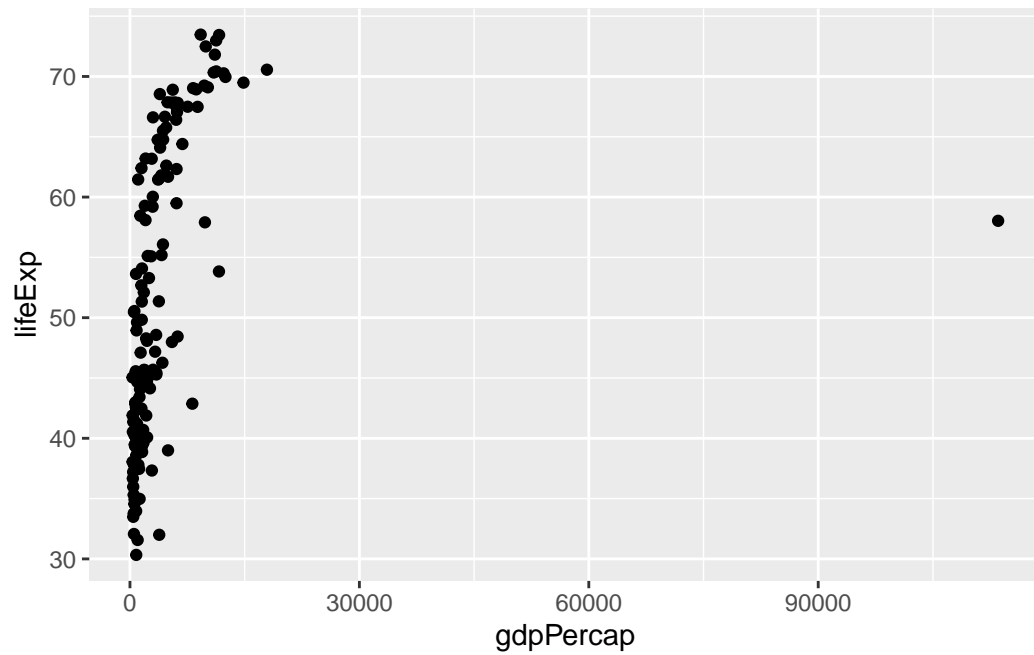


```
ggplot(gapminder_2007) +  
  geom_point(aes(x = gdpPercap, y = lifeExp,  
                 size = pop), alpha=0.5) +  
  scale_size_area(max_size = 10)
```

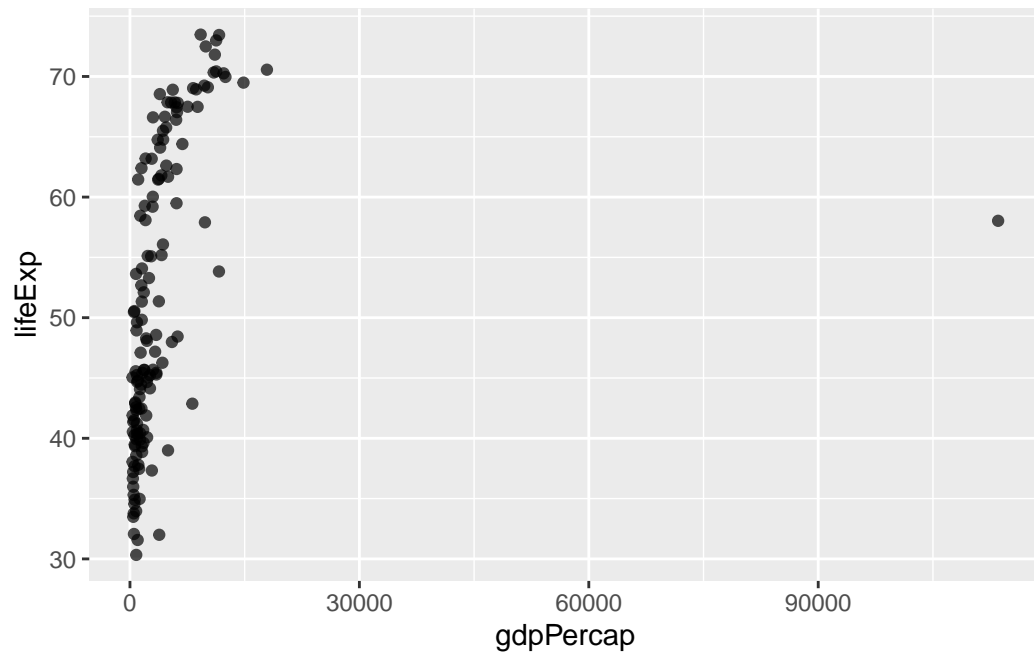


```
gapminder_1957 <- gapminder %>% filter(year==1957)
```

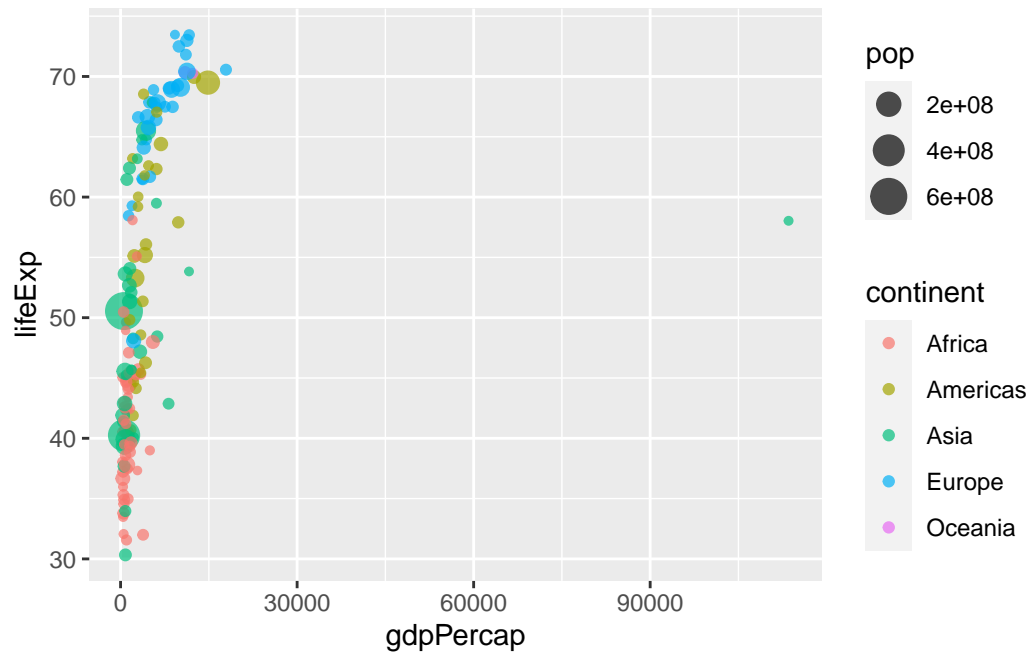
```
ggplot(gapminder_1957) +  
  aes(x = gdpPercap, y = lifeExp) +  
  geom_point()
```



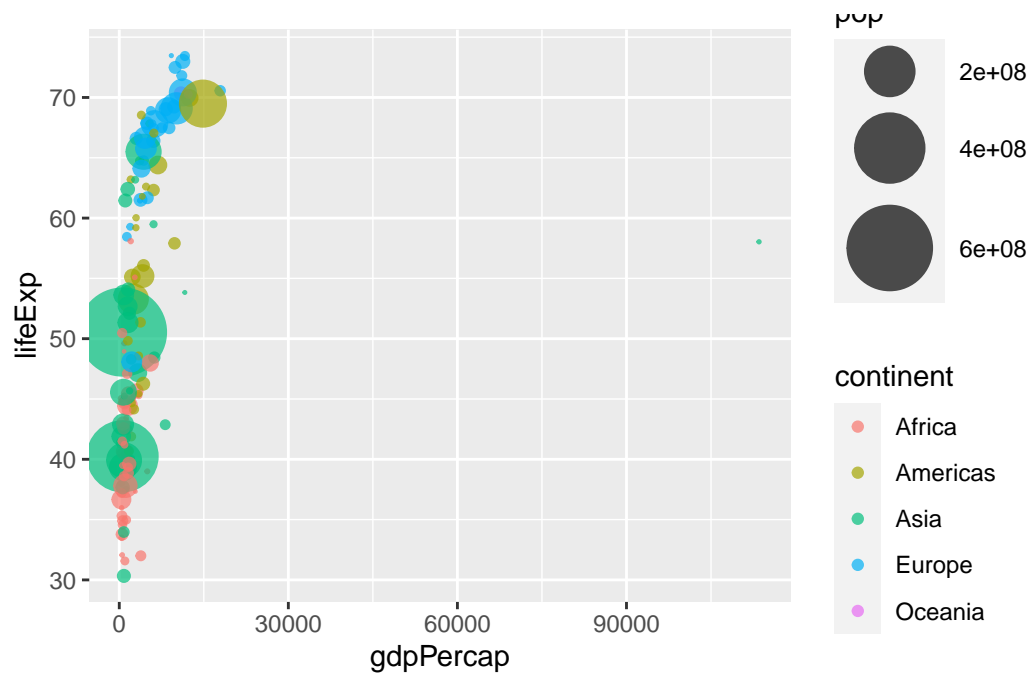
```
ggplot(gapminder_1957) +  
  aes(x = gdpPerCap, y = lifeExp) +  
  geom_point(alpha = 0.7)
```

```
ggplot(gapminder_1957) +  
  aes(x = gdpPercap, y = lifeExp, color = continent, size = pop) +  
  geom_point(alpha = 0.7)
```

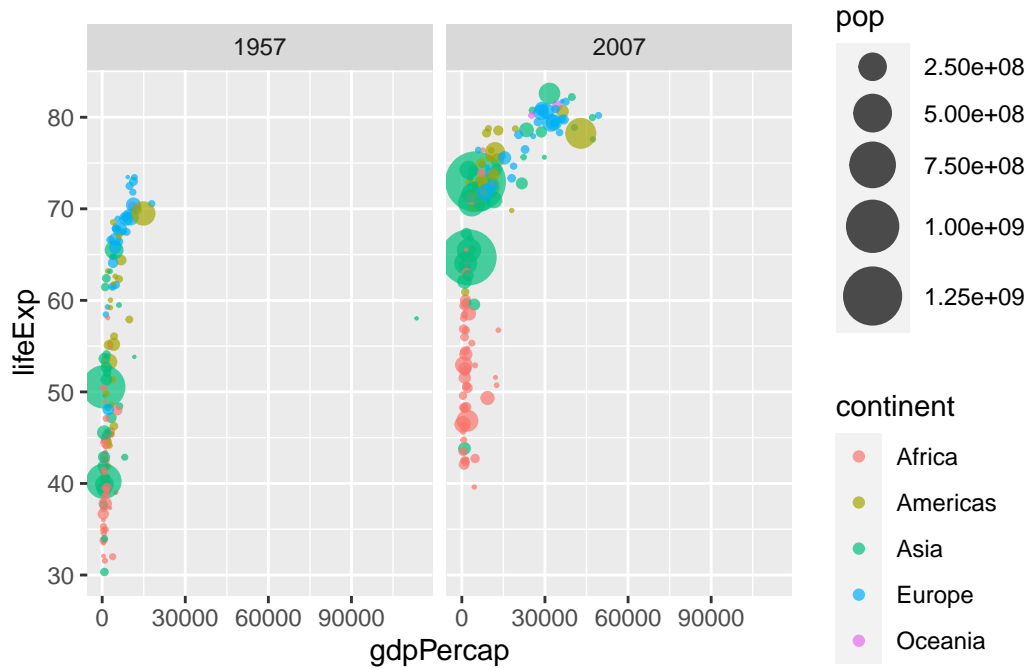


```
ggplot(gapminder_1957) +
  geom_point(aes(x = gdpPerCap, y = lifeExp, color = continent, size = pop), alpha = 0.7)
  scale_size_area(max_size = 15)
```



```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
                 size = pop), alpha=0.7) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```



Introduction to bar charts

```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)
```

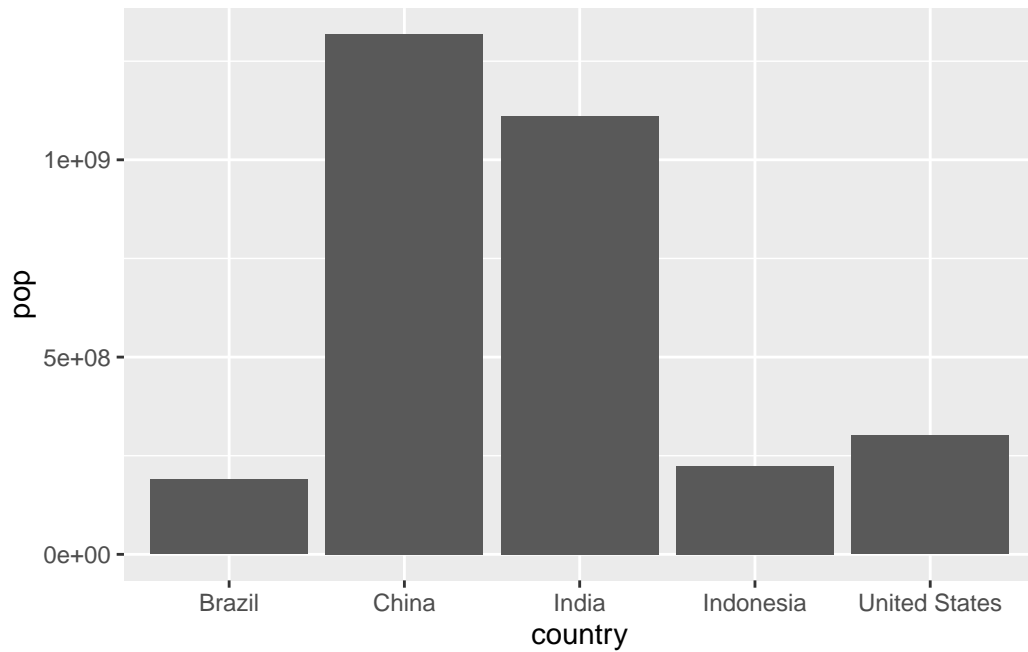
```
gapminder_top5
```

A tibble: 5 x 6

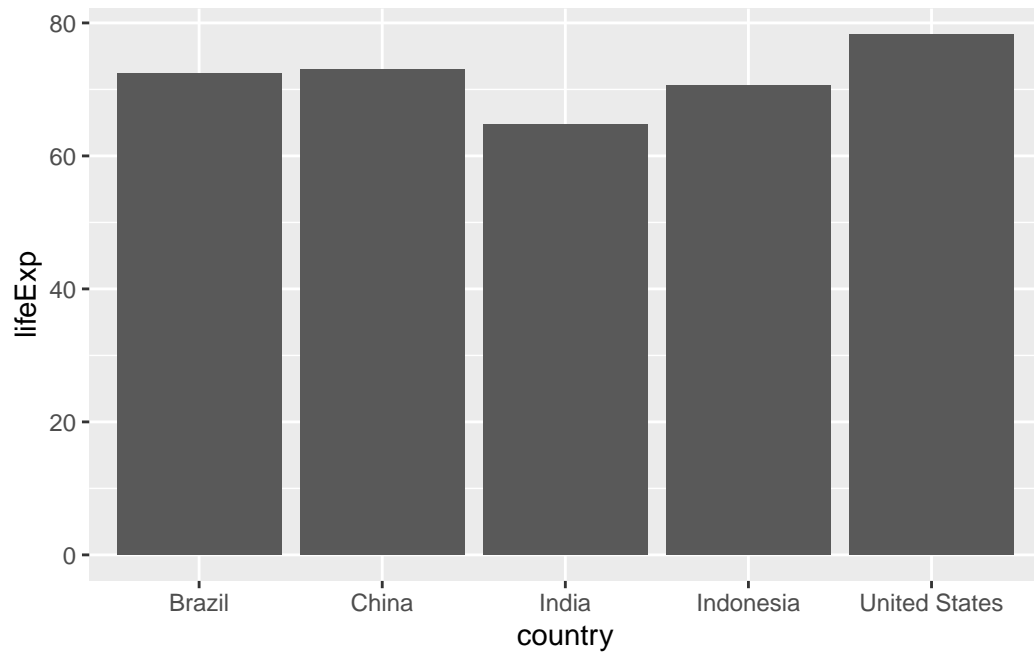
	country	continent	year	lifeExp	pop	gdpPercap
	<fct>	<fct>	<int>	<dbl>	<int>	<dbl>
1	China	Asia	2007	73.0	1318683096	4959.
2	India	Asia	2007	64.7	1110396331	2452.
3	United States	Americas	2007	78.2	301139947	42952.
4	Indonesia	Asia	2007	70.6	223547000	3541.
5	Brazil	Americas	2007	72.4	190010647	9066.

Simple bar

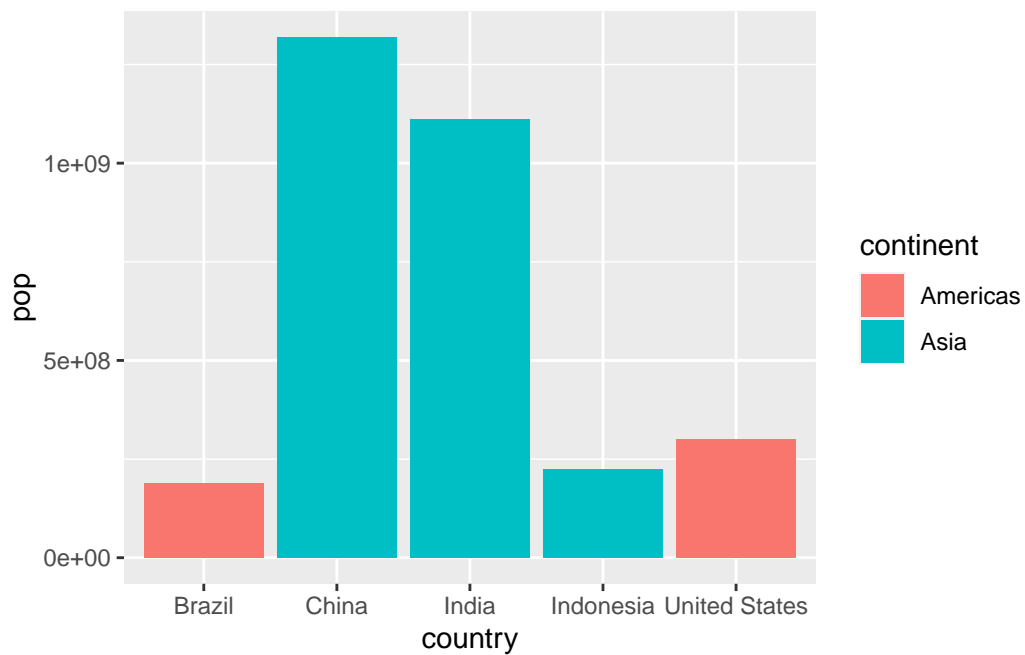
```
ggplot(gapminder_top5) +  
  geom_col(aes(x = country, y = pop))
```



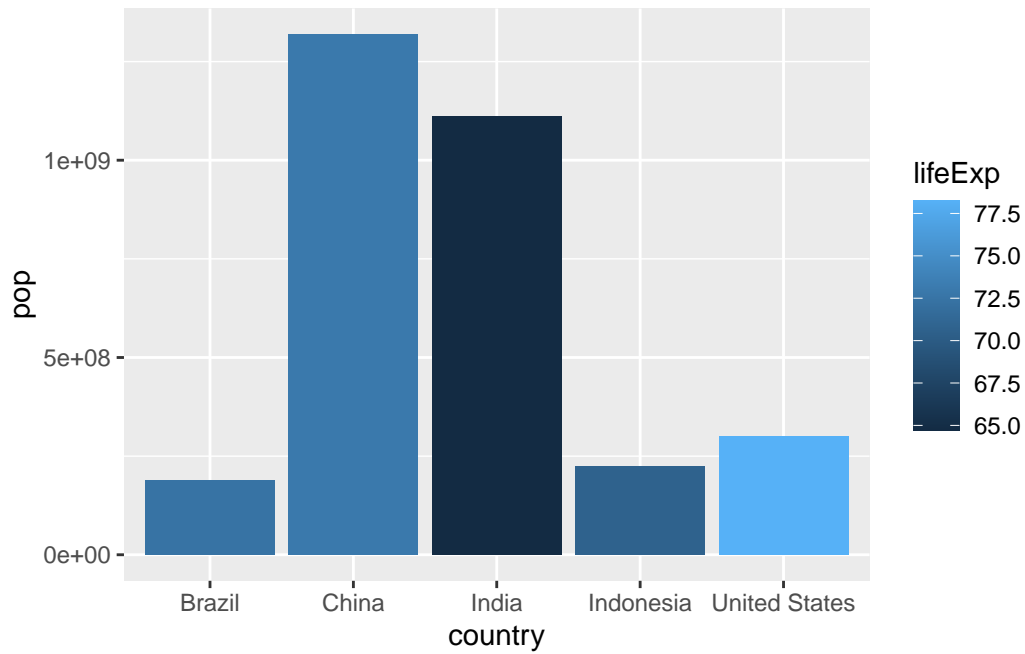
```
ggplot(gapminder_top5) +  
  geom_col(aes(x = country, y = lifeExp))
```



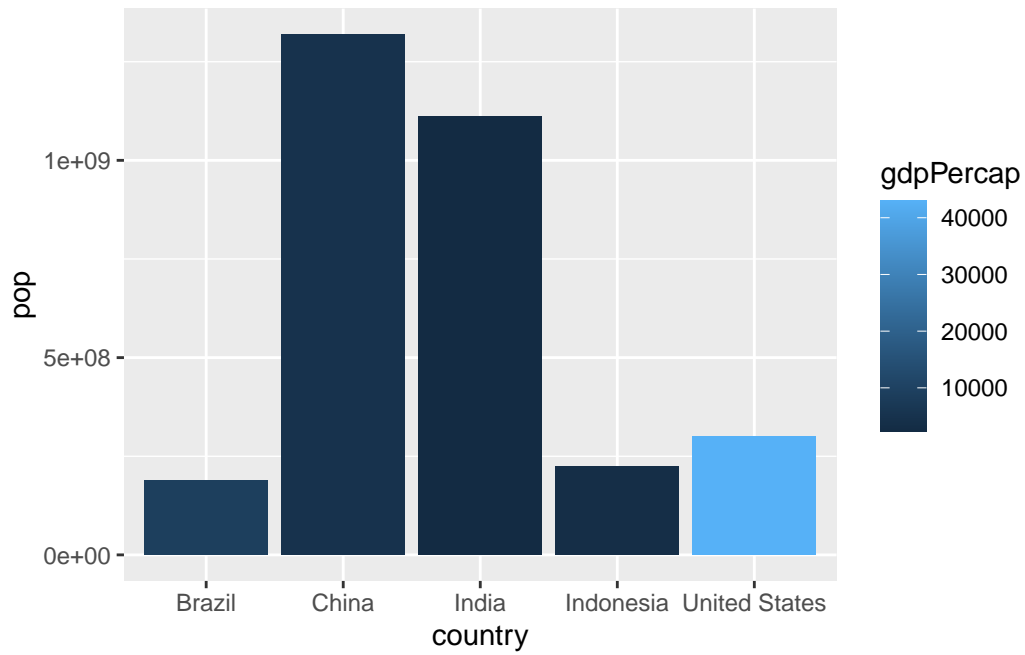
```
ggplot(gapminder_top5) +  
  geom_col(aes(x = country, y = pop, fill = continent))
```



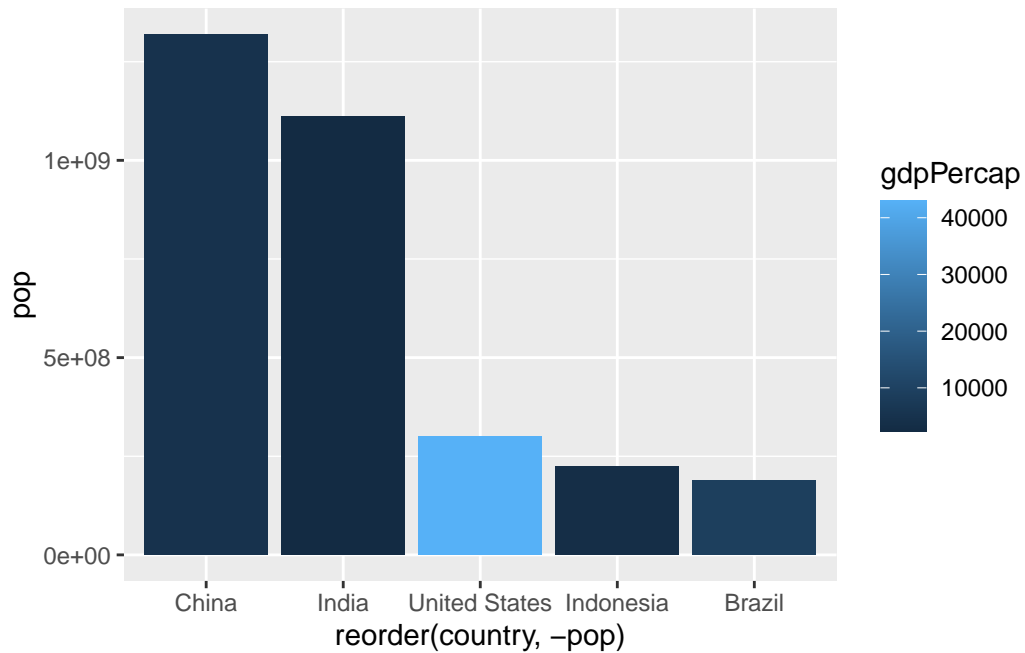
```
ggplot(gapminder_top5) +  
  geom_col(aes(x = country, y = pop, fill = lifeExp))
```



```
ggplot(gapminder_top5) +  
  aes(x = country, y = pop, fill = gdpPercap) +  
  geom_col()
```



```
ggplot(gapminder_top5) +  
  aes(x=reorder(country, -pop), y=pop, fill=gdpPercap) +  
  geom_col()
```

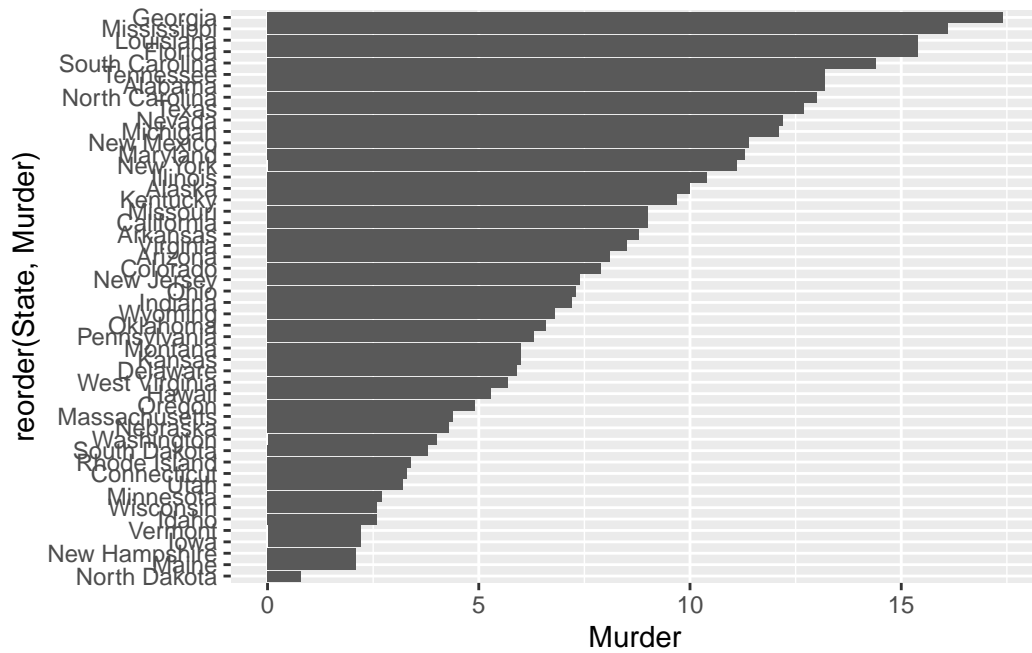



Flipping bar charts

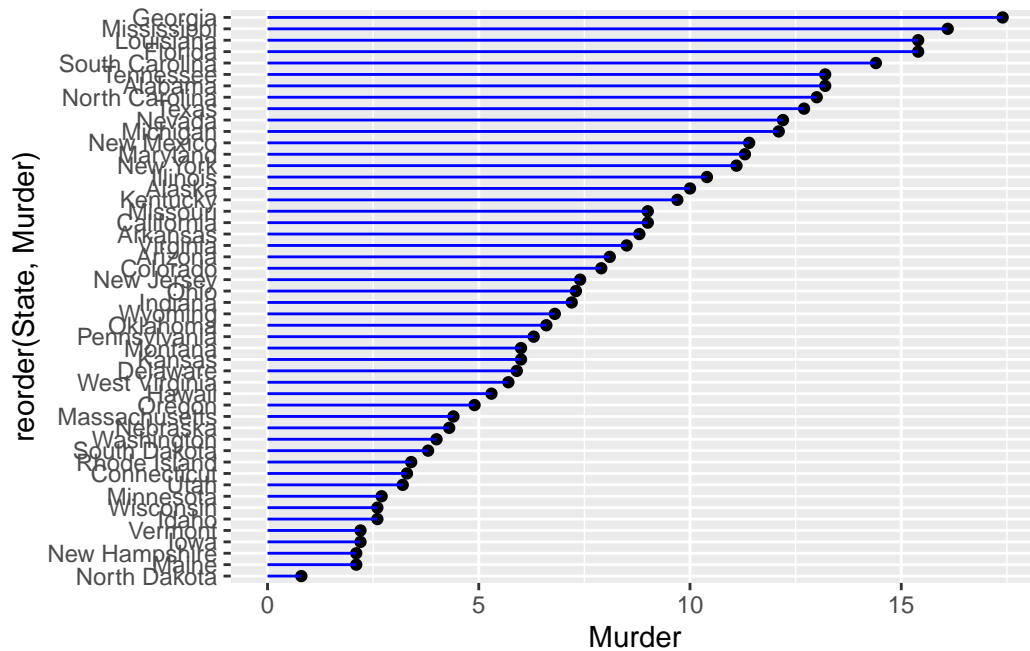
```
head(USArrests)
```

	Murder	Assault	UrbanPop	Rape
Alabama	13.2	236	58	21.2
Alaska	10.0	263	48	44.5
Arizona	8.1	294	80	31.0
Arkansas	8.8	190	50	19.5
California	9.0	276	91	40.6
Colorado	7.9	204	78	38.7

```
USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_col() +
  coord_flip()
```



```
ggplot(USArrests) +
  aes(x = reorder(State, Murder), y = Murder) +
  geom_point() +
  geom_segment(aes(x = State,
                  xend = State,
                  y = 0,
                  yend = Murder), color = "Blue") +
  coord_flip()
```



Combining plots

```
library(patchwork)

# Setup some example plots
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(disp, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

# Use patchwork to combine them here:
(p1 | p2 | p3) /
  p4
```

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

