

class05.R

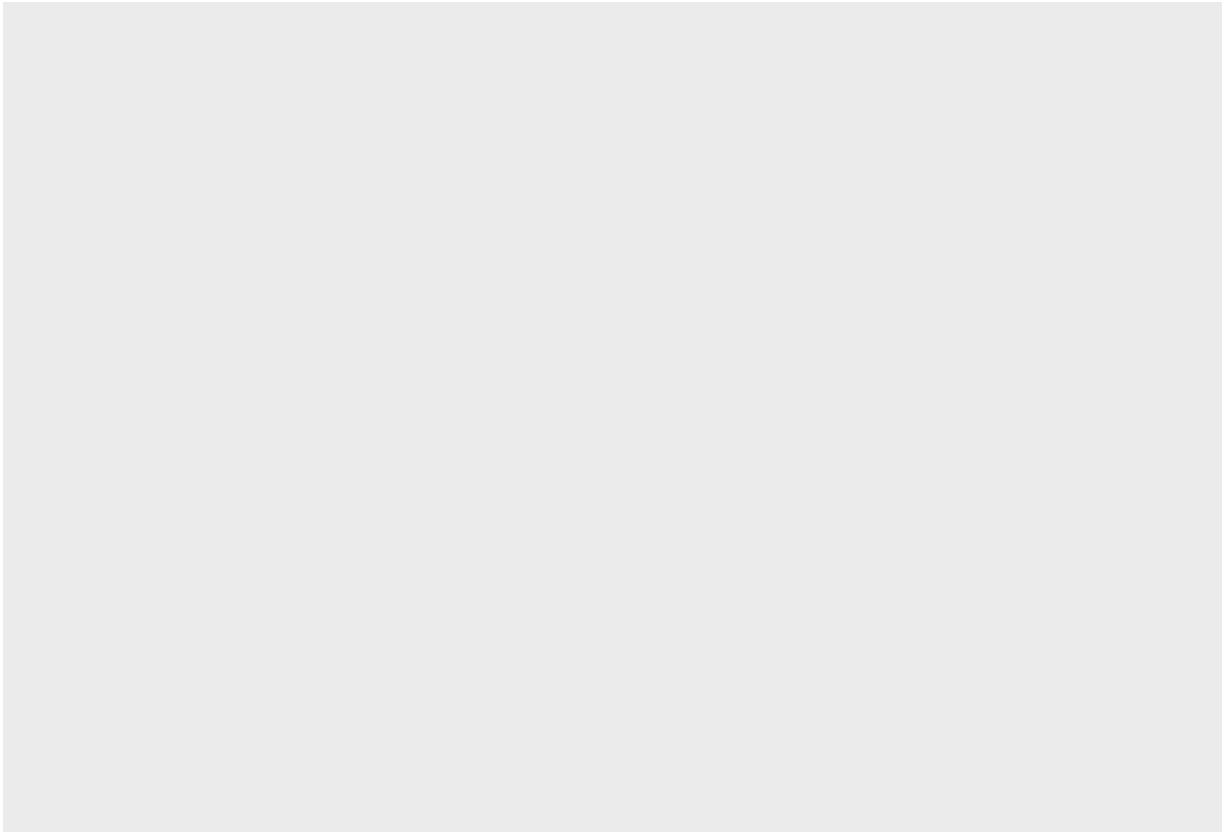
katybrown

2022-02-03

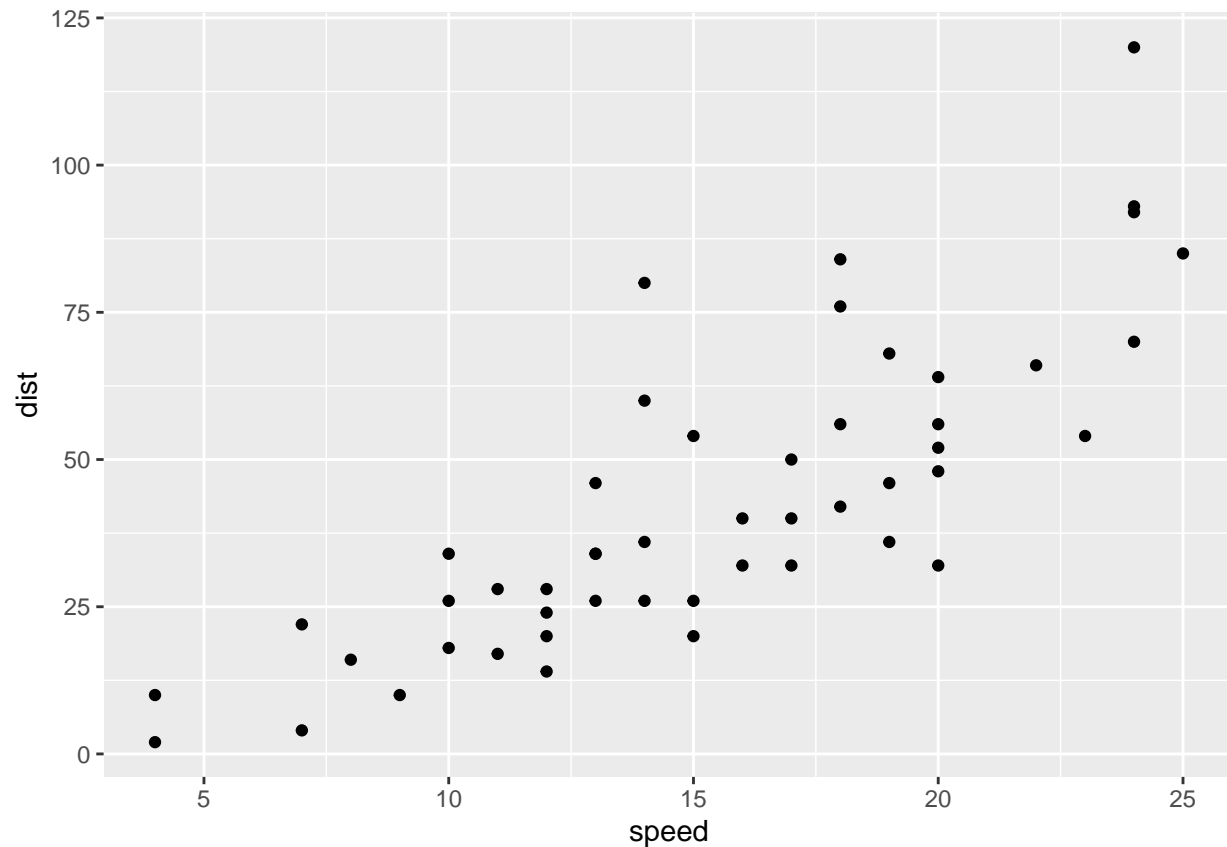
```
# Installed ggplot  
library(ggplot2)
```

```
## Warning in register(): Can't find generic 'scale_type' in package ggplot2 to  
## register S3 method.
```

```
ggplot(cars)
```



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



```
# Genes 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
```

```
nrow(genes)
```

```
## [1] 5196
```

```
ncol(genes)
```

```
## [1] 4
```

```
colnames(genes)
```

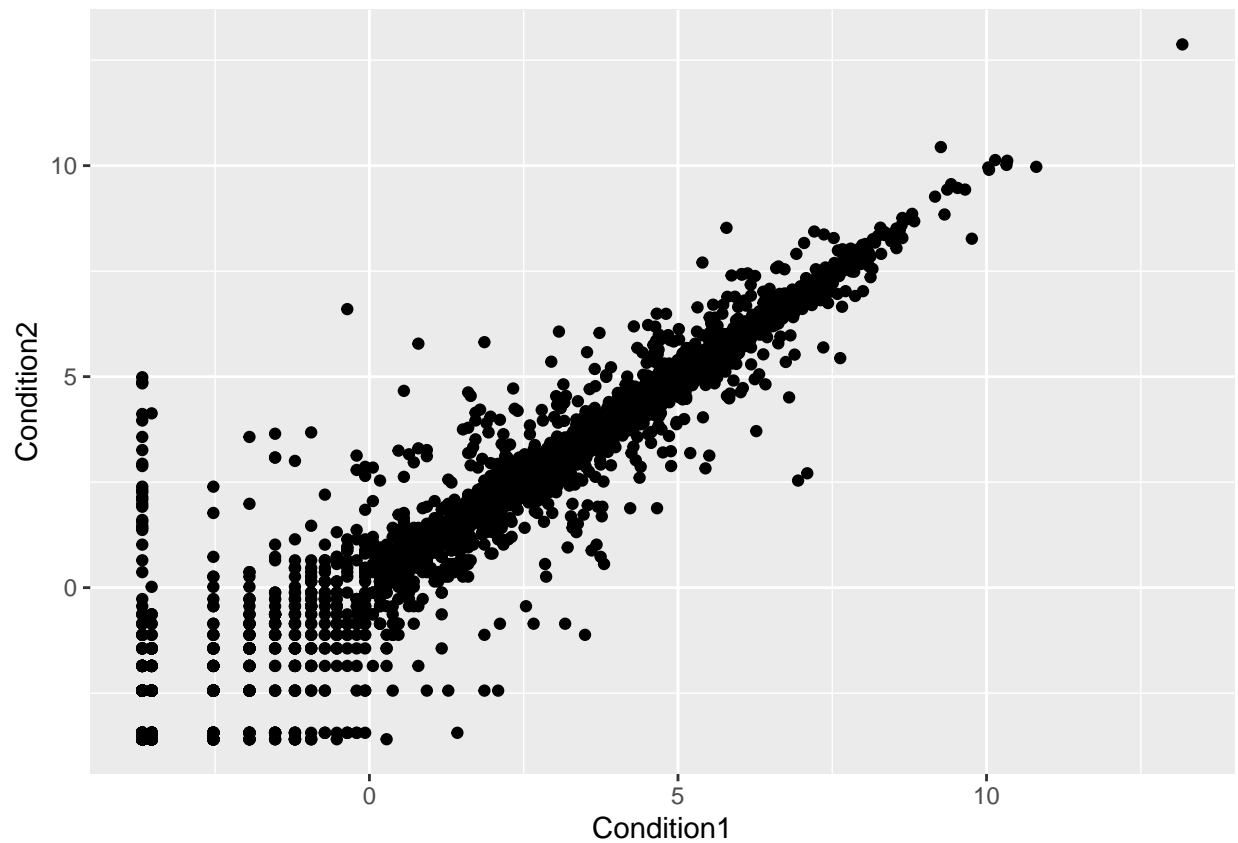
```
## [1] "Gene"      "Condition1" "Condition2" "State"
```

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

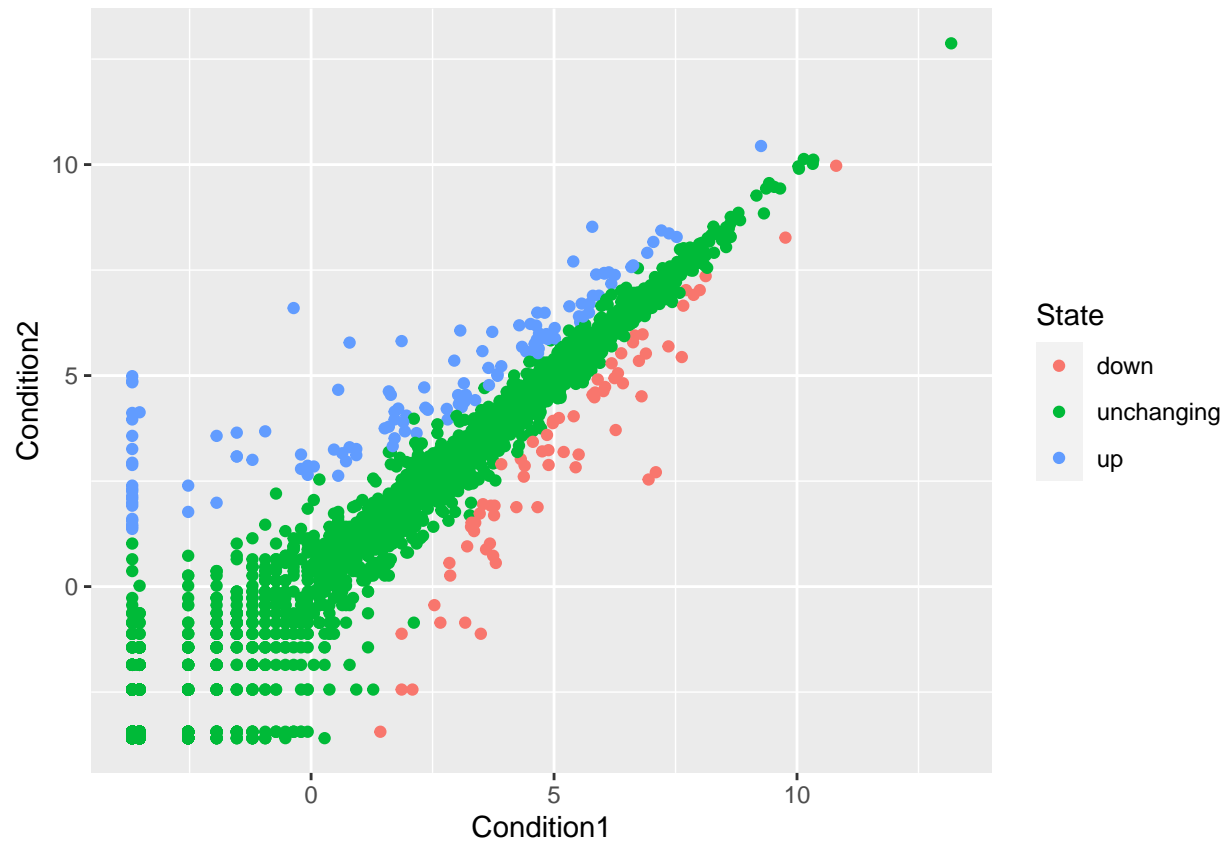
```
##  
##      down  unchanged      up  
##      72      4997      127
```

```
# Genes plots
```

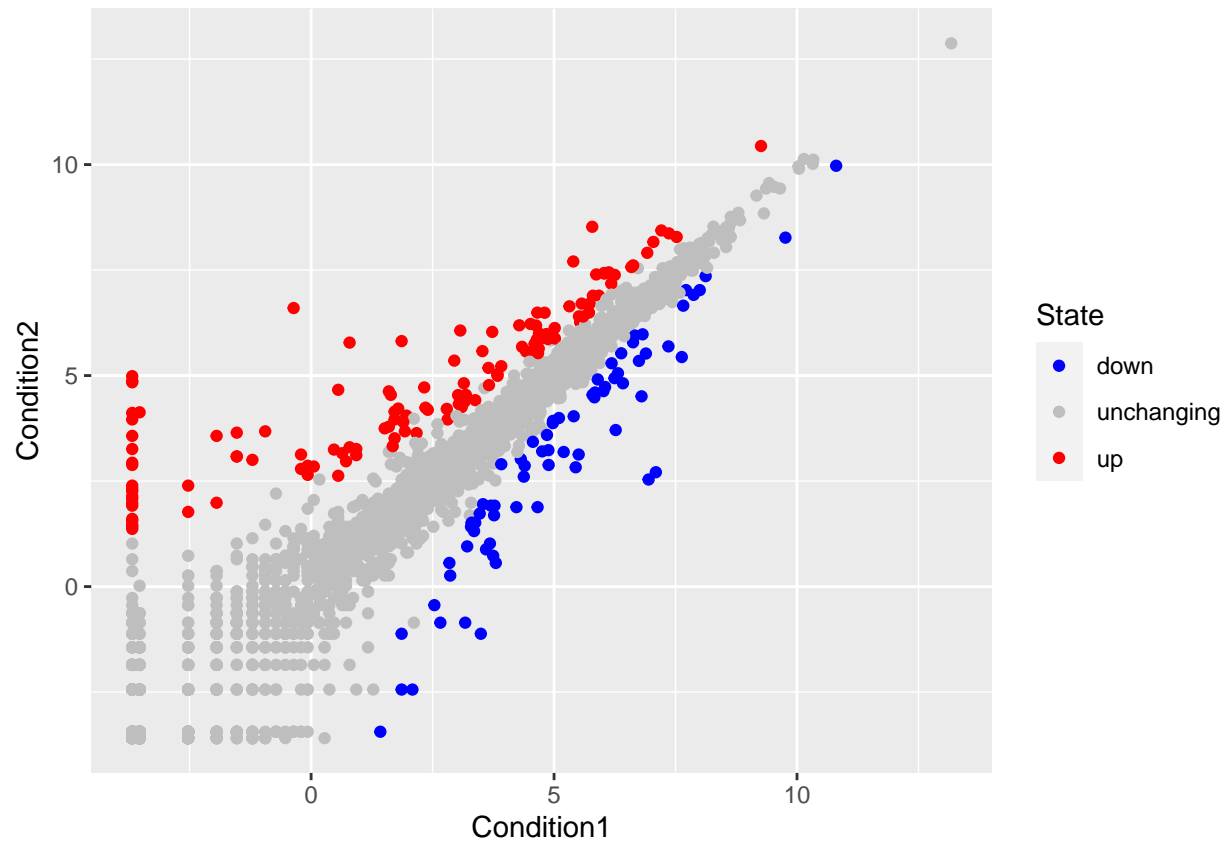
```
ggplot(genes) + aes(x = Condition1, y = Condition2) + geom_point()
```



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

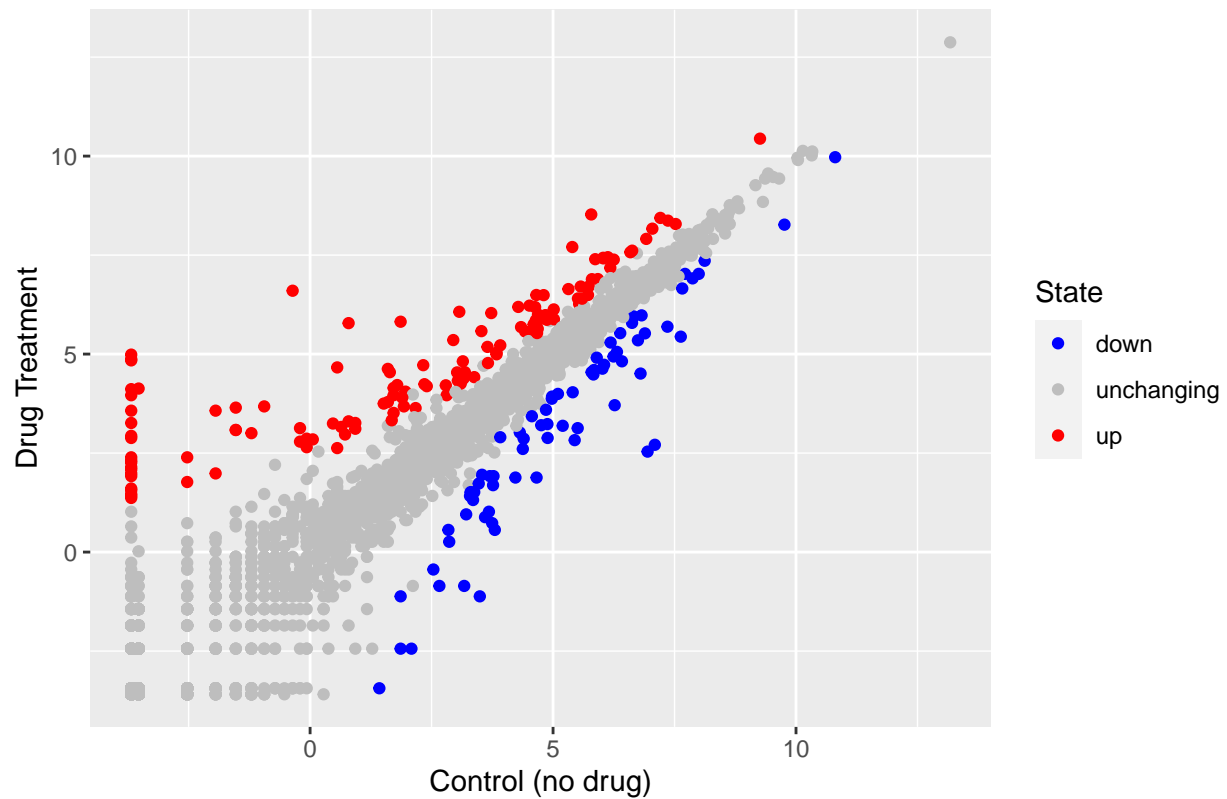


```
p <- ggplot(genes) + aes(x = Condition1, y = Condition2, col = State) + geom_point()
p + scale_colour_manual(values = c("blue", "gray", "red"))
```



```
p + scale_colour_manual(values = c("blue", "gray", "red")) + labs(title = "Gene Expression Changes Upon
```

Gene Expression Changes Upon Drug Treatment



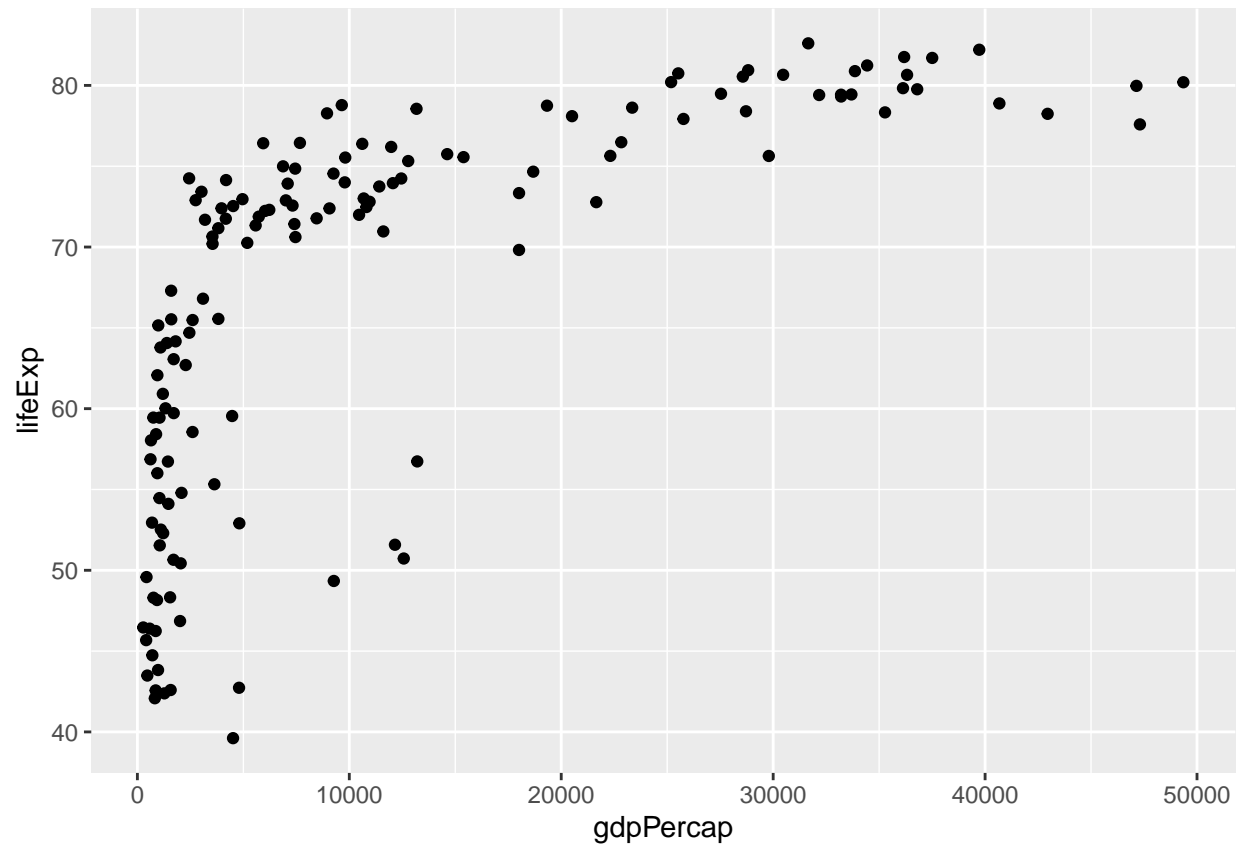
```
# Installed gapminder, dplyr
library(gapminder)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

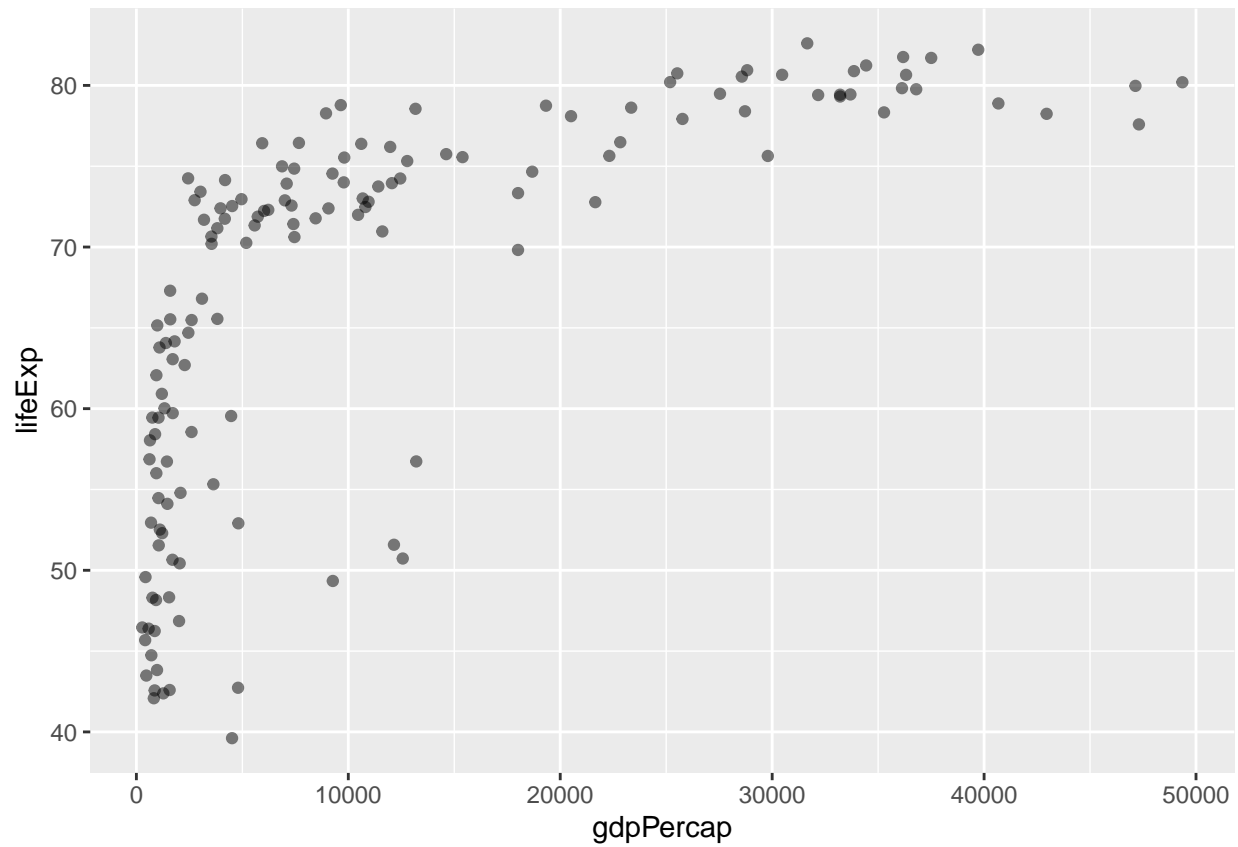
## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

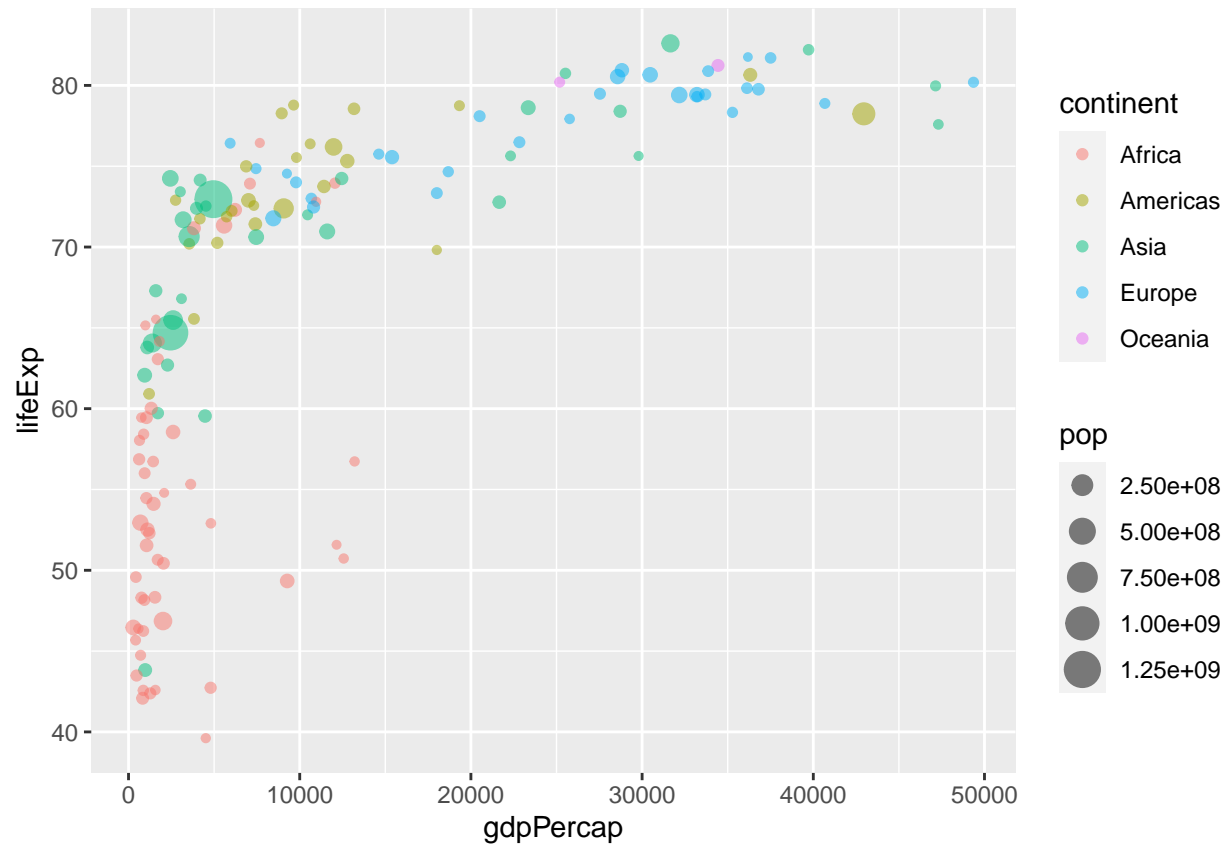
```
# Gapminder 2007
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) + aes(x = gdpPercap, y = lifeExp) + geom_point()
```



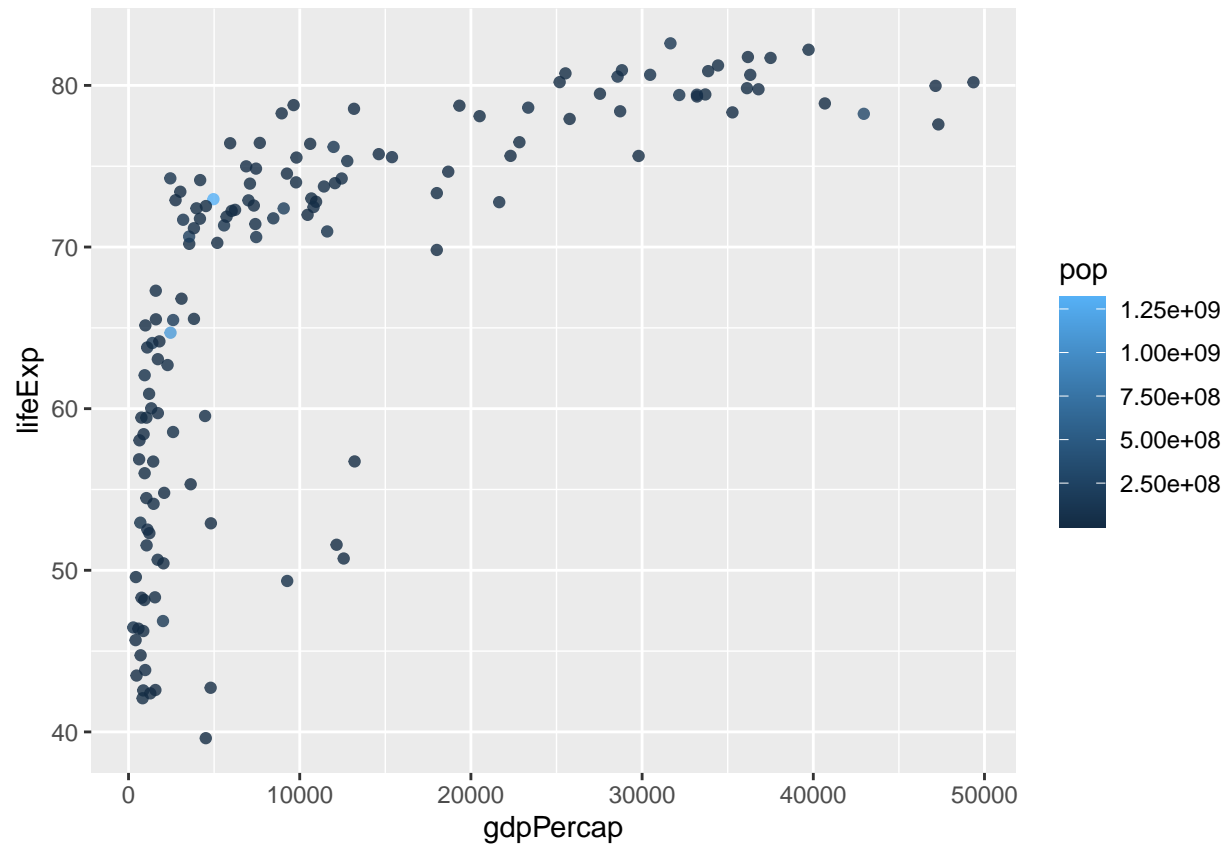
```
ggplot(gapminder_2007) + aes(x = gdpPercap, y = lifeExp) + geom_point(alpha = 0.5)
```



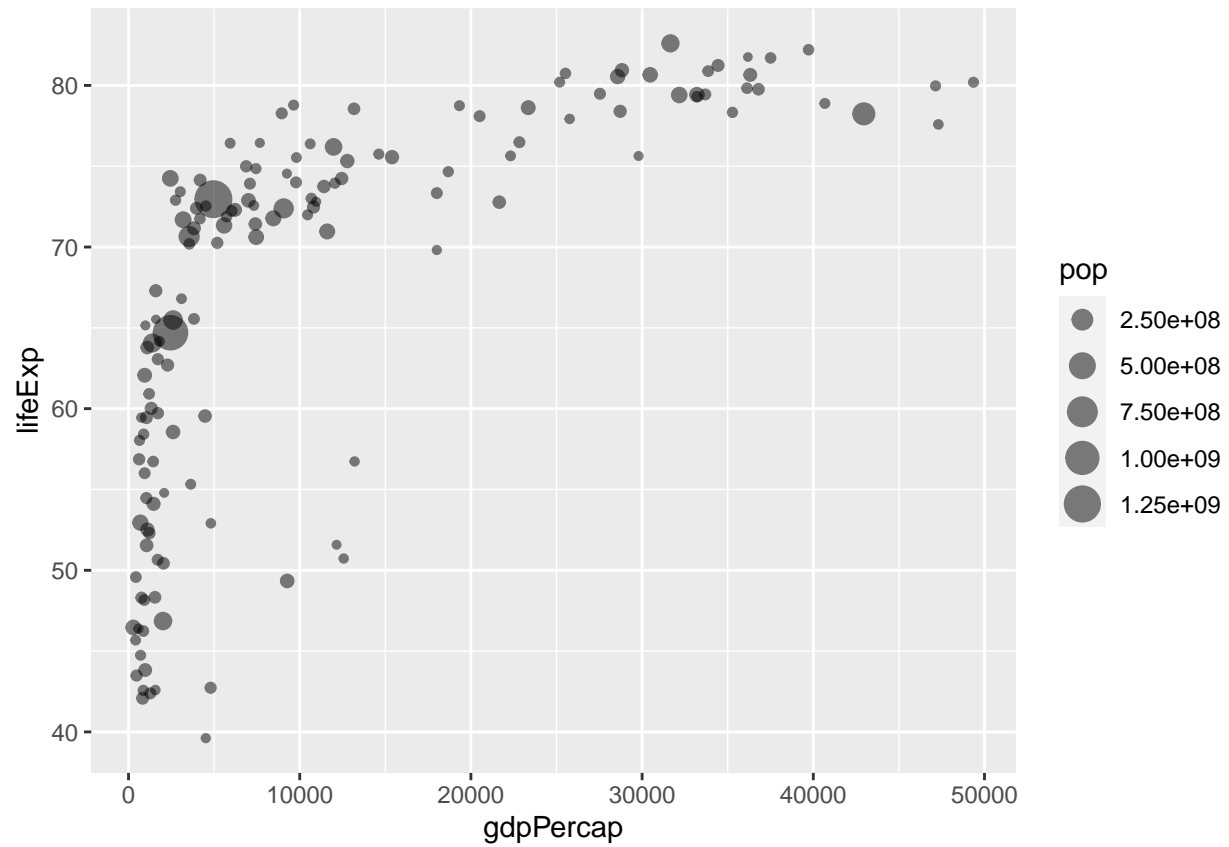
```
ggplot(gapminder_2007) + aes(x = gdpPercap, y = lifeExp, color = continent, size = pop) + geom_point(alpha = 0.5)
```

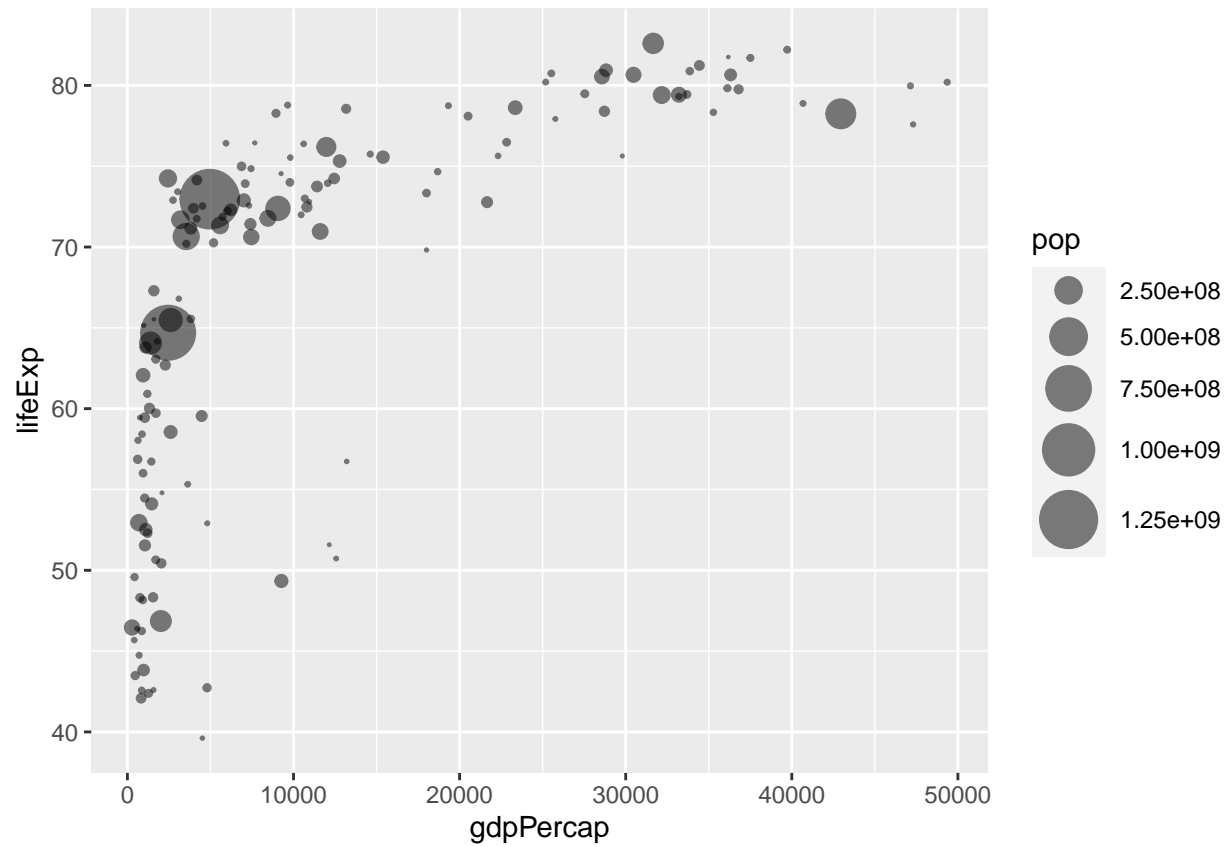
```
ggplot(gapminder_2007) + aes(x = gdpPercap, y = lifeExp, color = pop) + geom_point(alpha = 0.8)
```



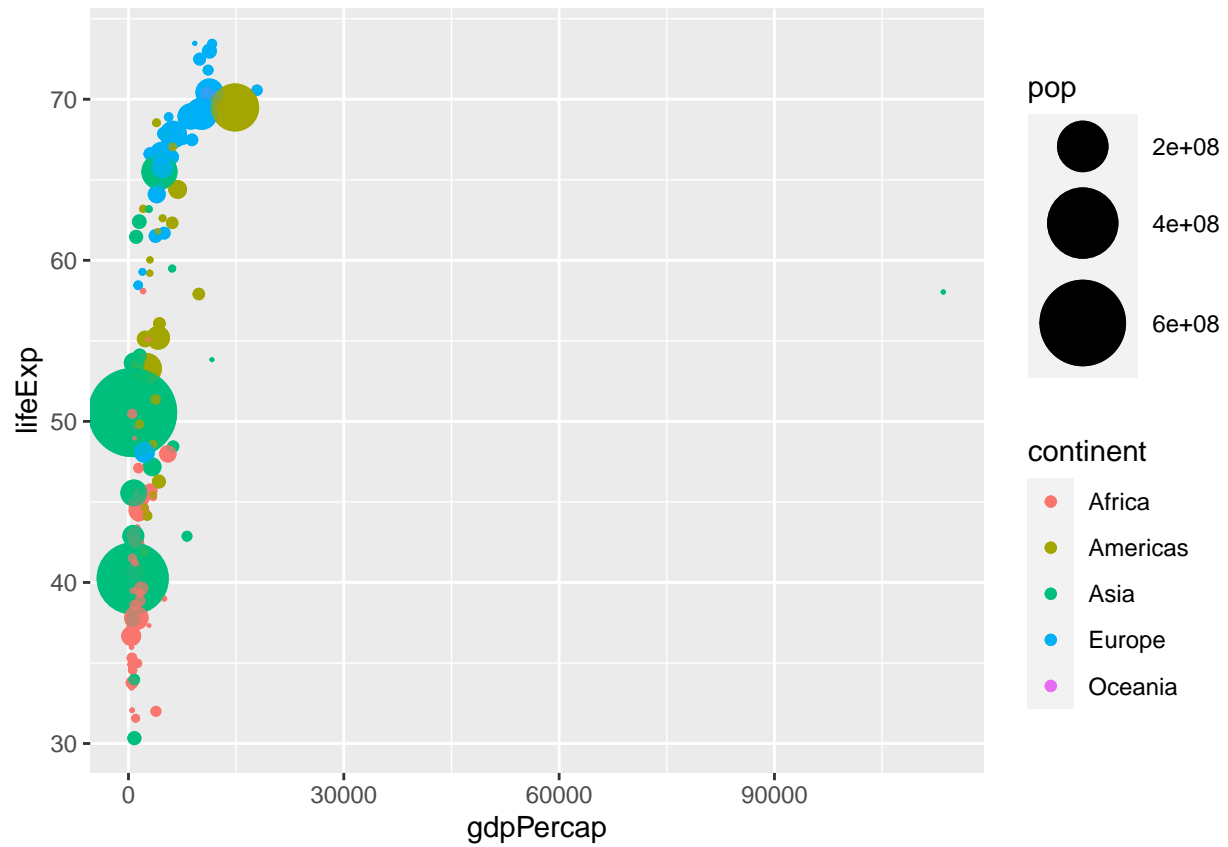
```
ggplot(gapminder_2007) + aes(x = gdpPercap, y = lifeExp, size = pop) + geom_point(alpha = 0.5)
```



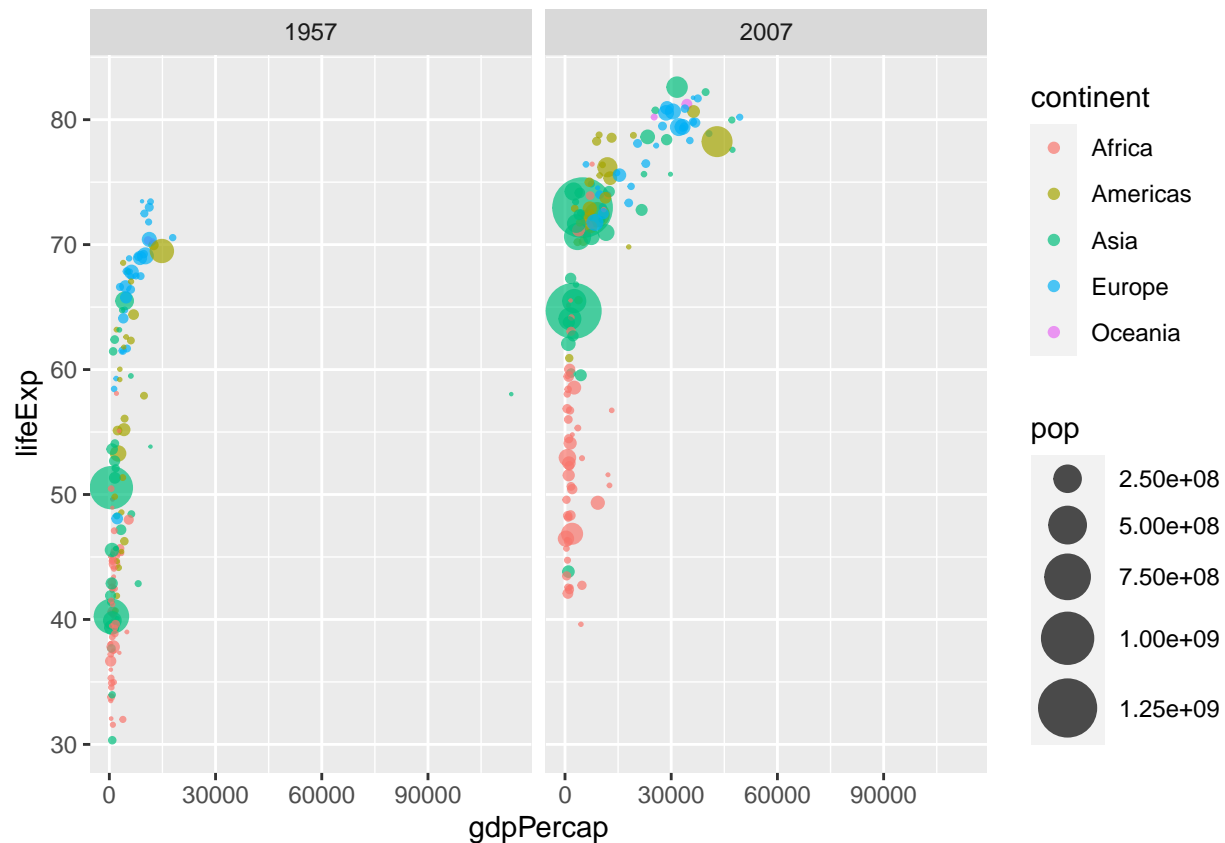
```
ggplot(gapminder_2007) + aes(x = gdpPercap, y = lifeExp, size = pop) + geom_point(alpha = 0.5) + scale_
```



```
# Gapminder 1957
gapminder_1957 <- gapminder %>% filter(year == 1957)
gm1957 <- ggplot(gapminder_1957) + aes(x = gdpPercap, y = lifeExp) + geom_point()
gm1957 + aes(color = continent, size = pop) + scale_size_area(max_size = 15) + geom_point(alpha = 0.7)
```



```
gapminder_1957 <- gapminder %>% filter(year == 1957 | year == 2007)
ggplot(gapminder_1957) + geom_point(aes(x = gdpPercap, y = lifeExp, color = continent, size = pop), alpha = 0.5)
```



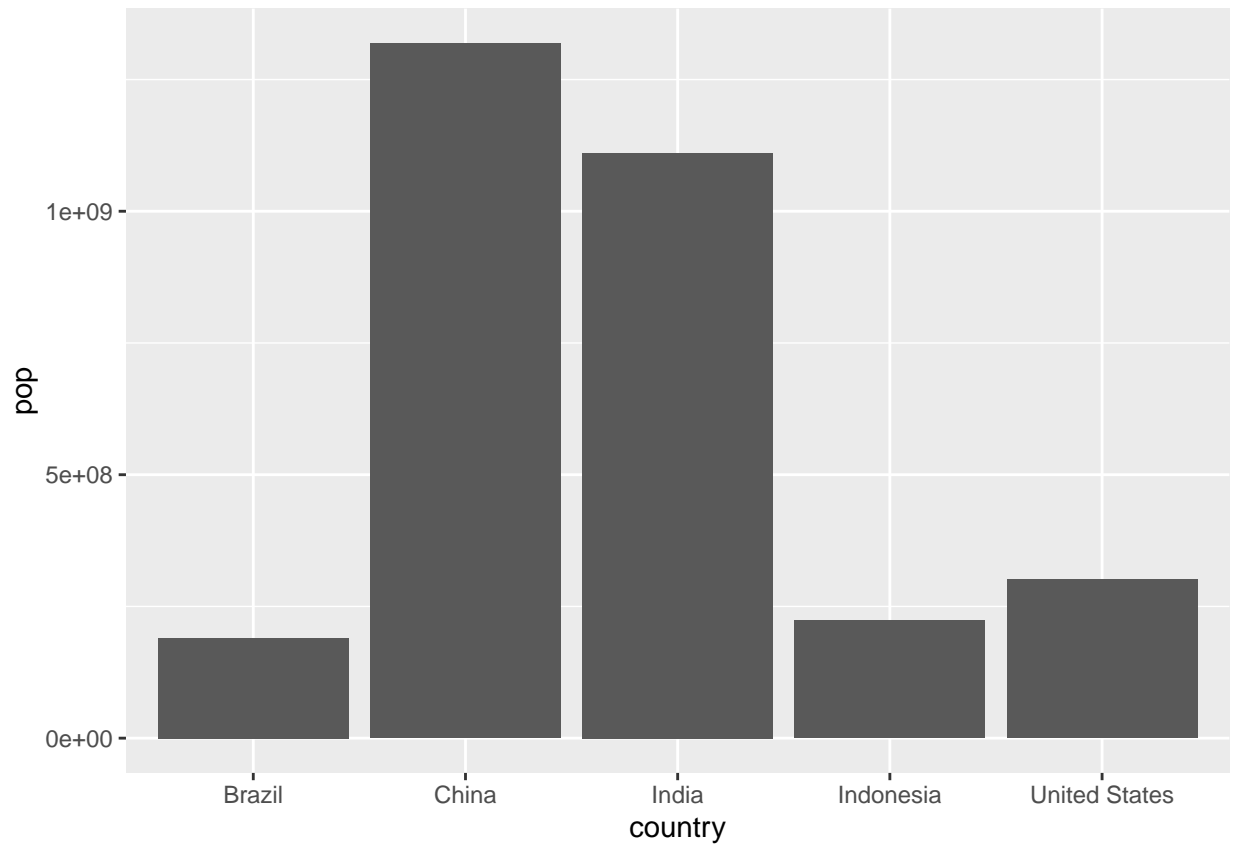
Bar charts

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

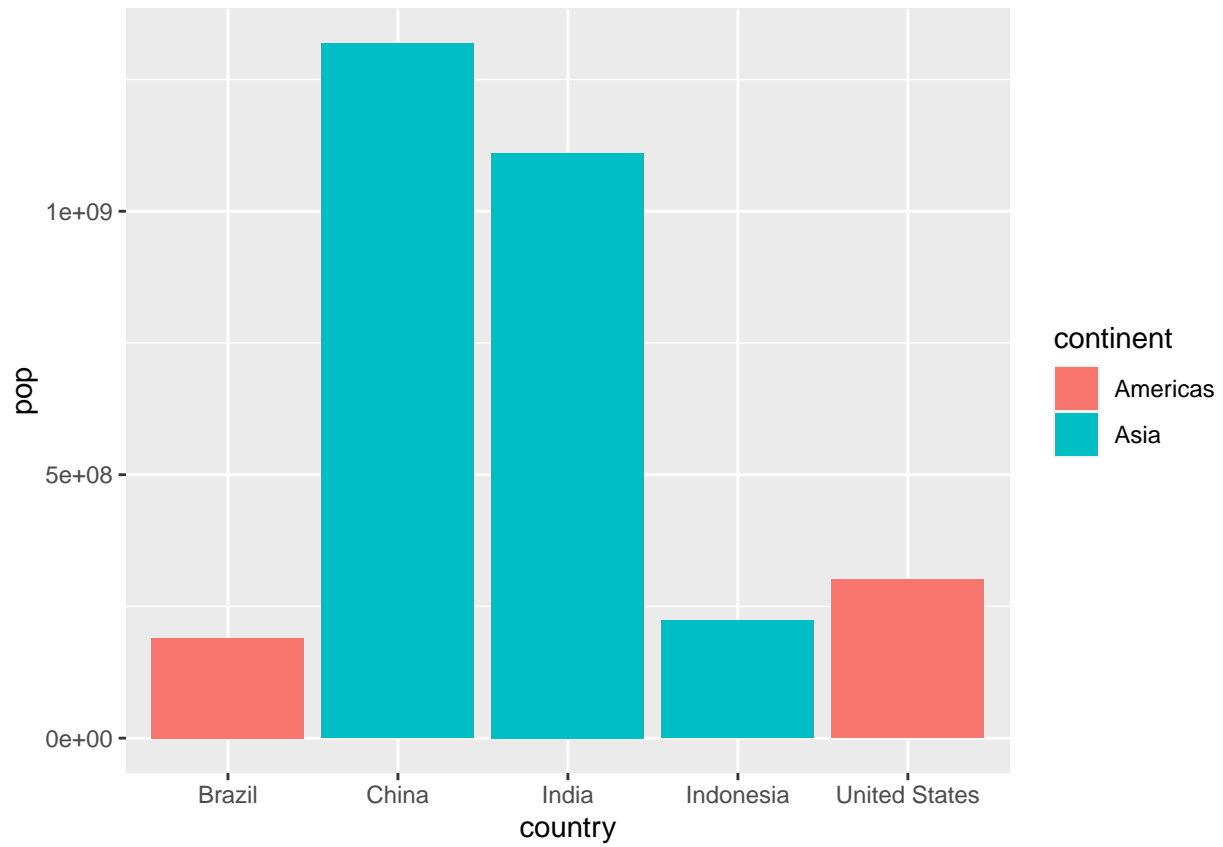
A tibble: 5 x 6

##	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.

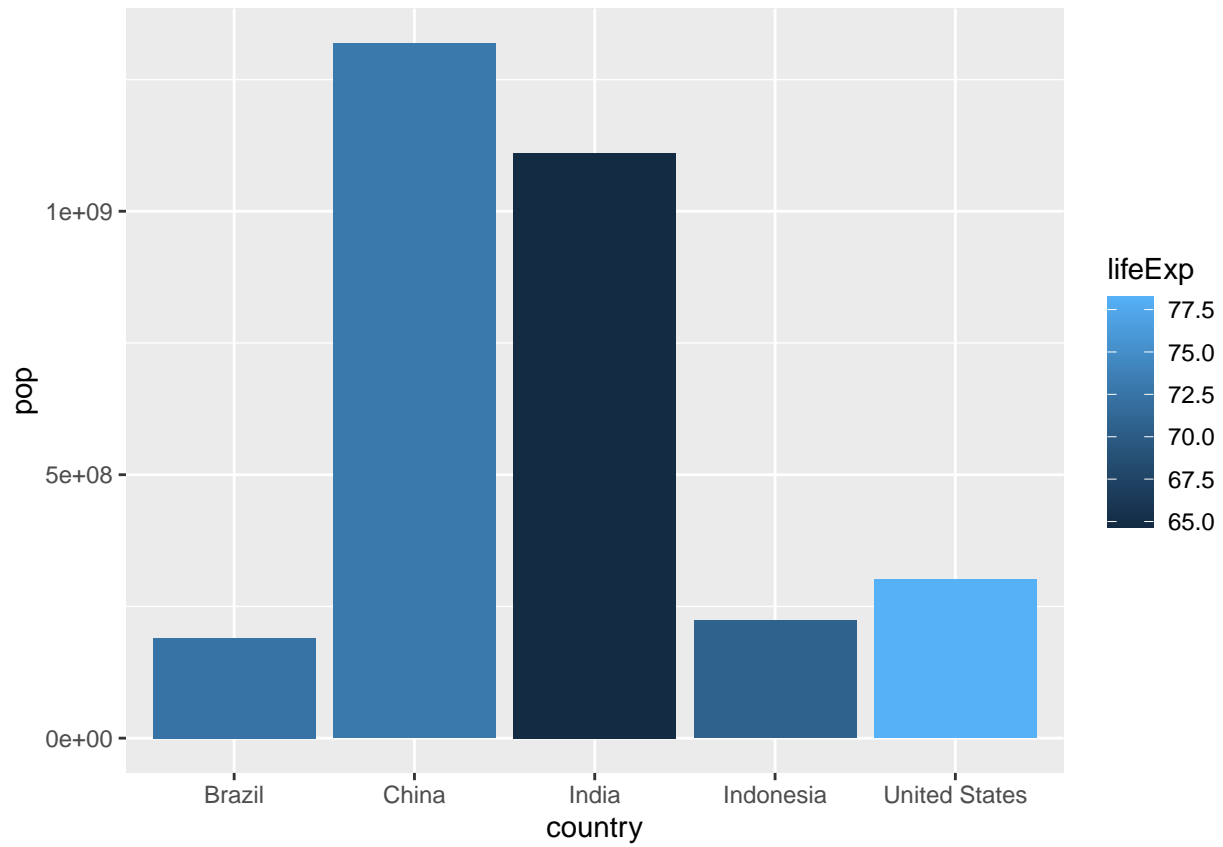
```
ggplot(gapminder_top5) + geom_col(aes(x = country, y = pop))
```



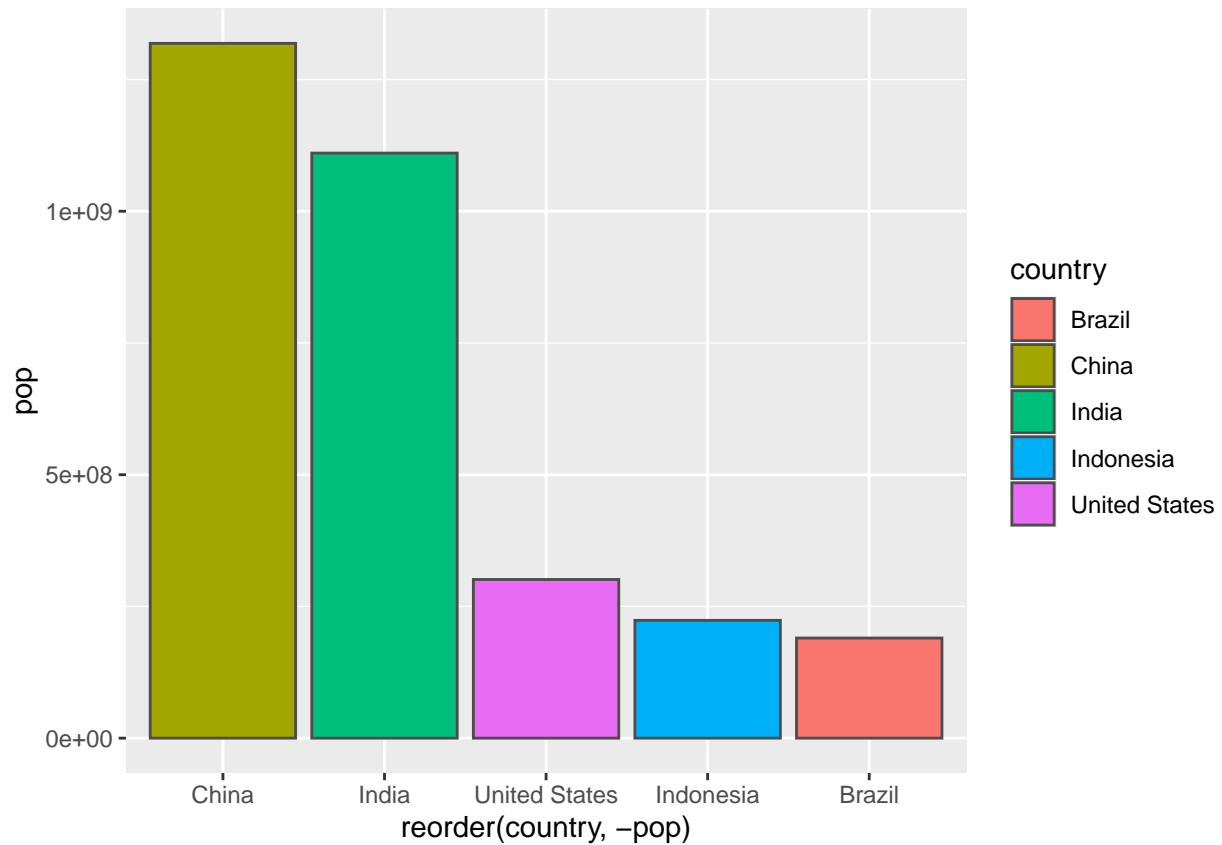
```
ggplot(gapminder_top5) + geom_col(aes(x = country, y = pop, fill = continent))
```



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

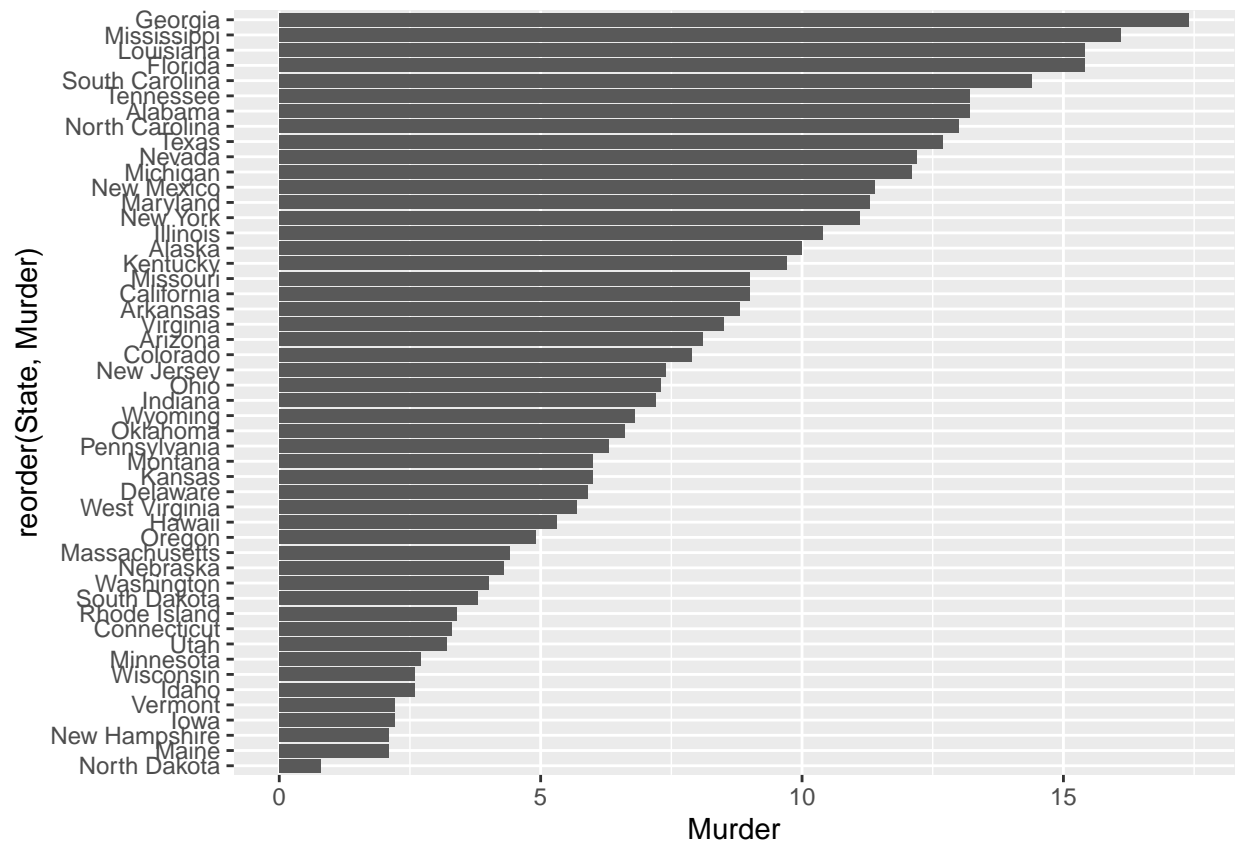
```
ggplot(gapminder_top5) + aes(x = reorder(country, -pop), y = pop, fill = country) + geom_col(col = "gray")
```



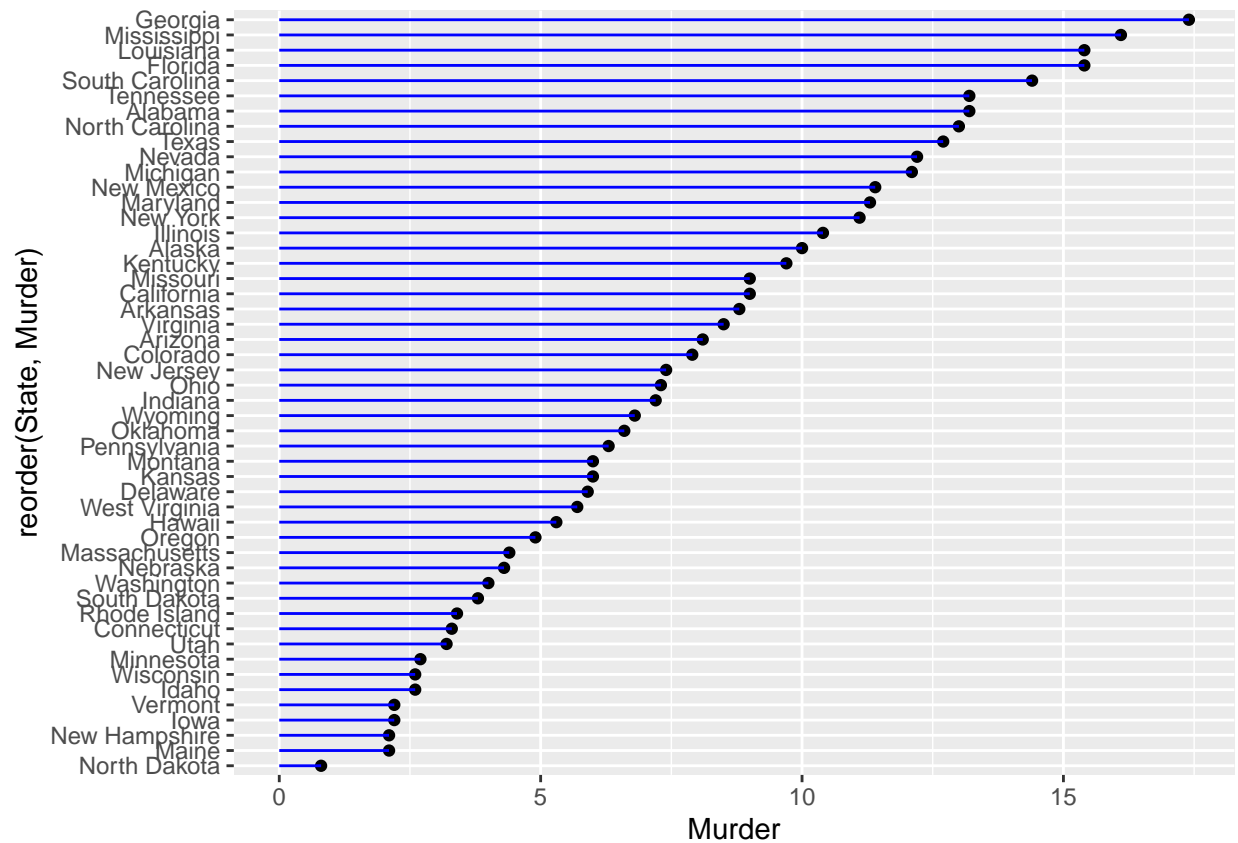
```
# Flipping bar charts
head(USArrests)
```

```
##      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 = S
```



```
# Animating plots
# Installed gifski, gganimate
library(gapminder)
library(gganimate)
# Plot was animated, but will not show in final report

# Combining plots
# Installed patchwork
library(patchwork)
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))

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

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

