Class 05 Data Visualization

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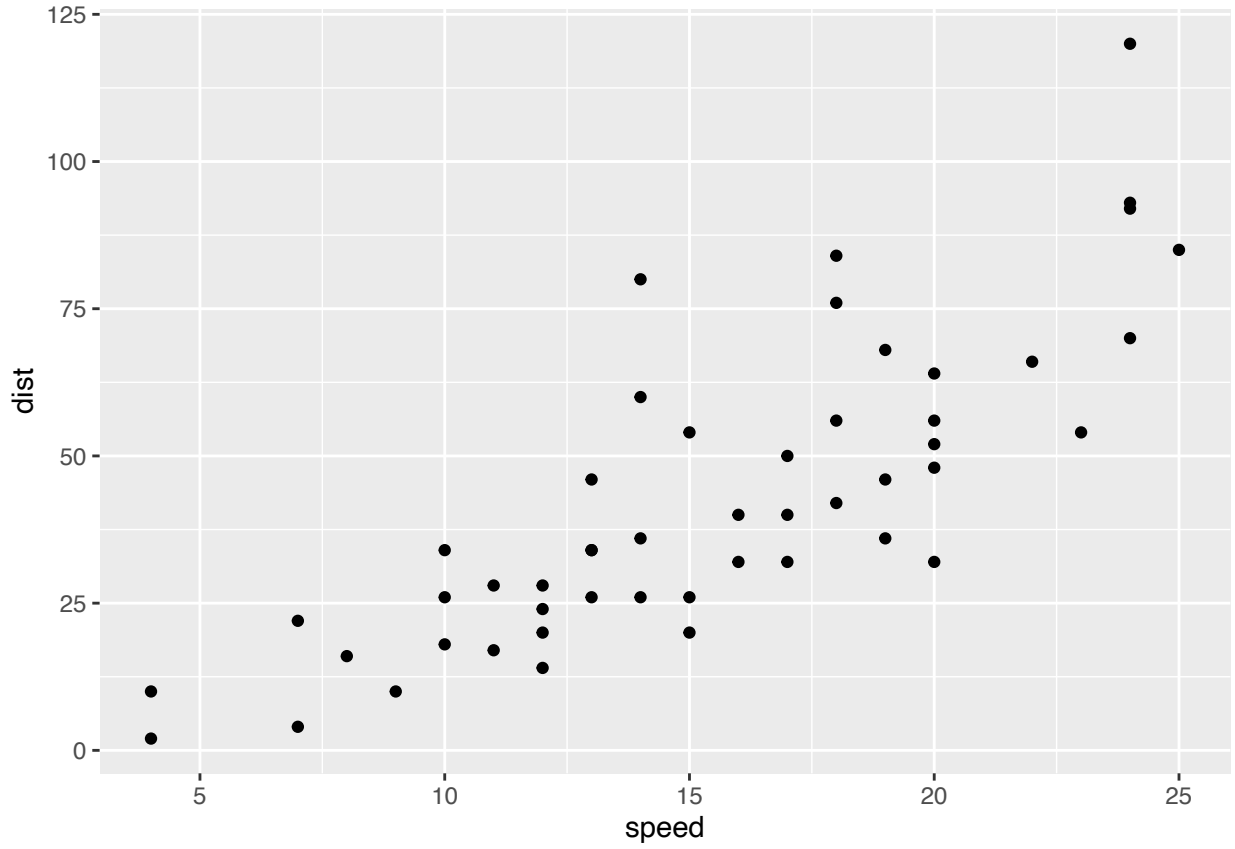
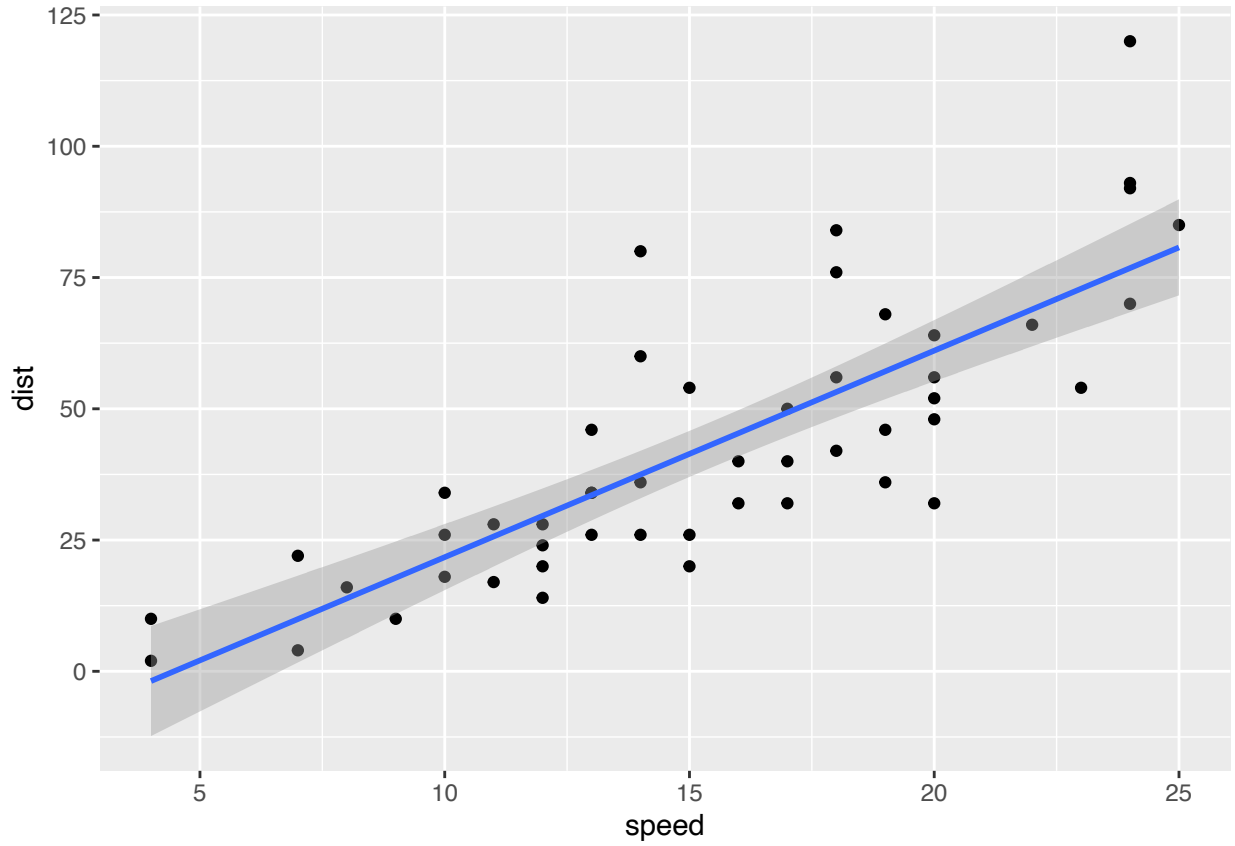
```
# SCATTERPLOTS

# Install, then load ggplot.
library (ggplot2)

# Every ggplot has data + aes + geom.
# **First geom_point() plot of cars data:
ggplot(data=cars)  +
  aes(x=speed, y=dist) +
  geom_point()
```




```
# Change to a linear model.
# **Plot with 2 or more geoms:
```

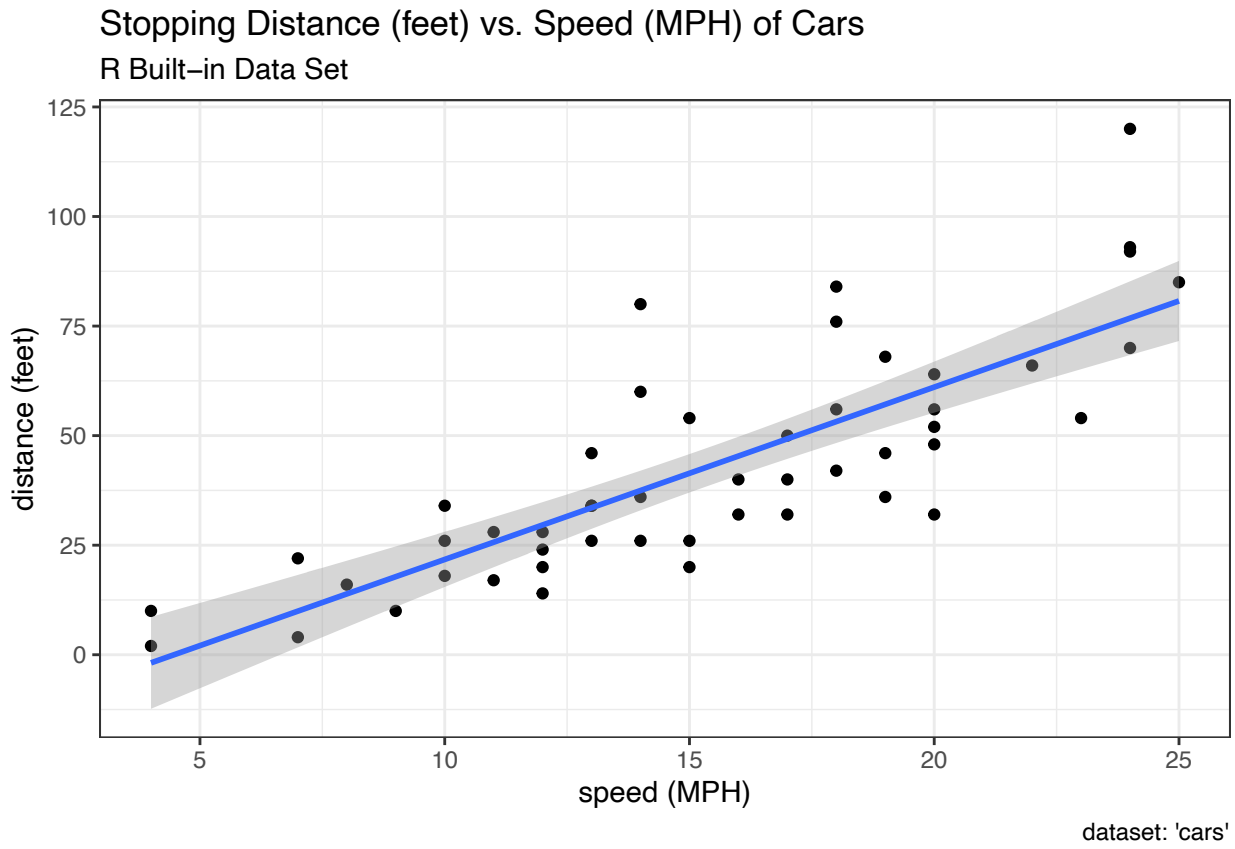
```
p <- ggplot(data=cars)  +
  aes(x=speed, y=dist)+
  geom_point() +
  geom_smooth(method="lm")
p
```

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




```
# Adjusting labels & theme.
p + labs(title="Stopping Distance (feet) vs. Speed (MPH) of Cars",
         x=("speed (MPH)"),
         y=("distance (feet)"),
         subtitle=("R Built-in Data Set"),
         caption=("dataset: 'cars'")) +
  theme_bw()
```

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




```
# New data set...
# **Read an input file

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 there in the data set?
nrow(genes)
```

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

```
# Q. What are the column names?
colnames(genes)
```

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

```
# Q. How many columns are there?
ncol(genes)
```

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

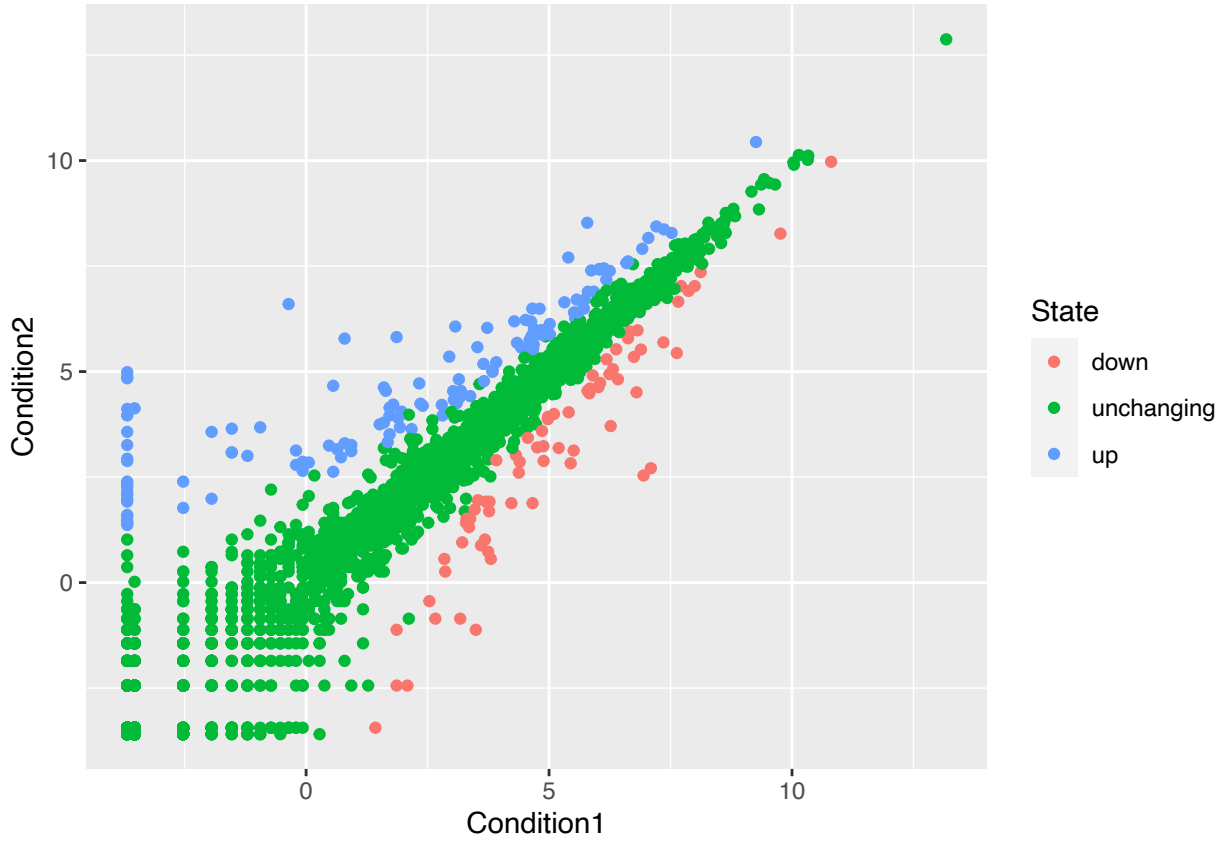
```
# Q. How many 'up' regulated genes are there?
table(genes$State)
```

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

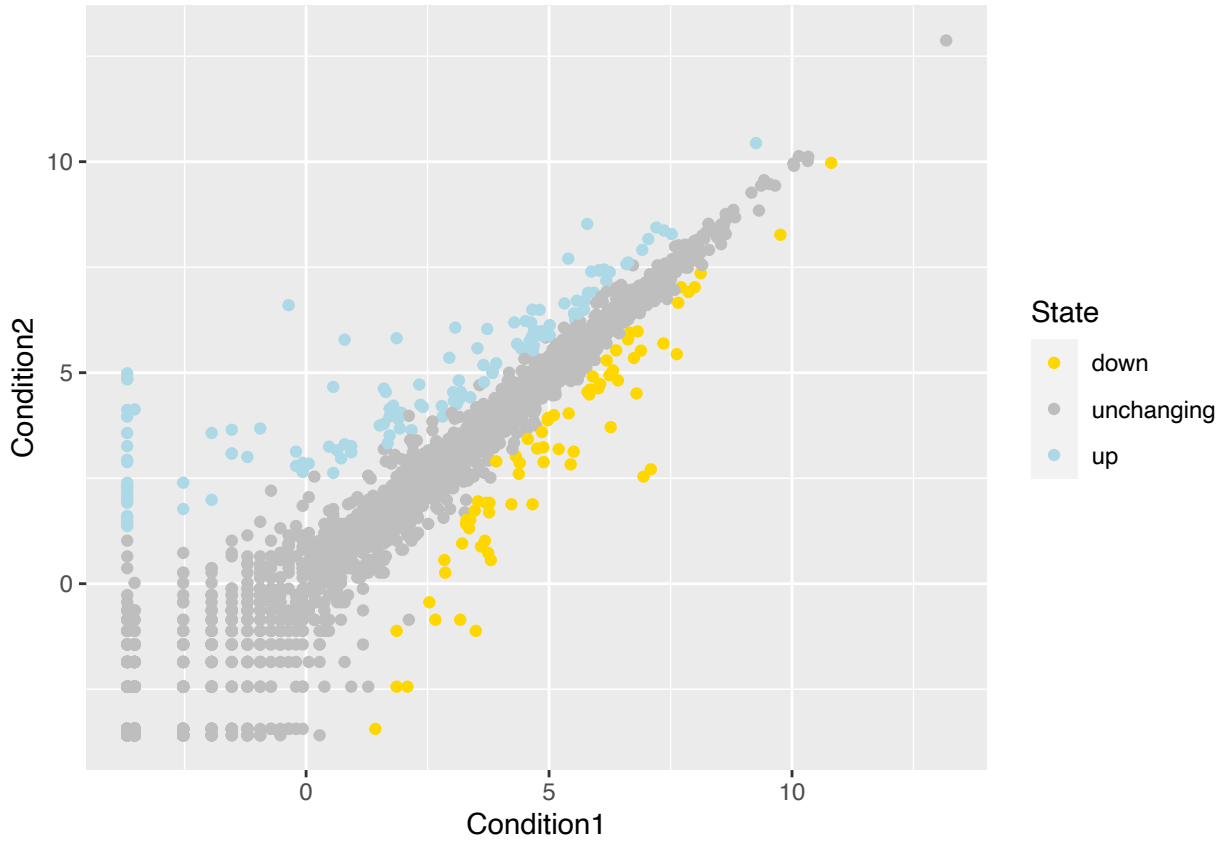
```
#Q. What fraction of total genes is up-regulated in this dataset? (2 sig figs)
prec <- table(genes$State) / nrow(genes) * 100
round (prec, 2)
```

```
##
##       down unchanging         up
##       1.39      96.17       2.44
```

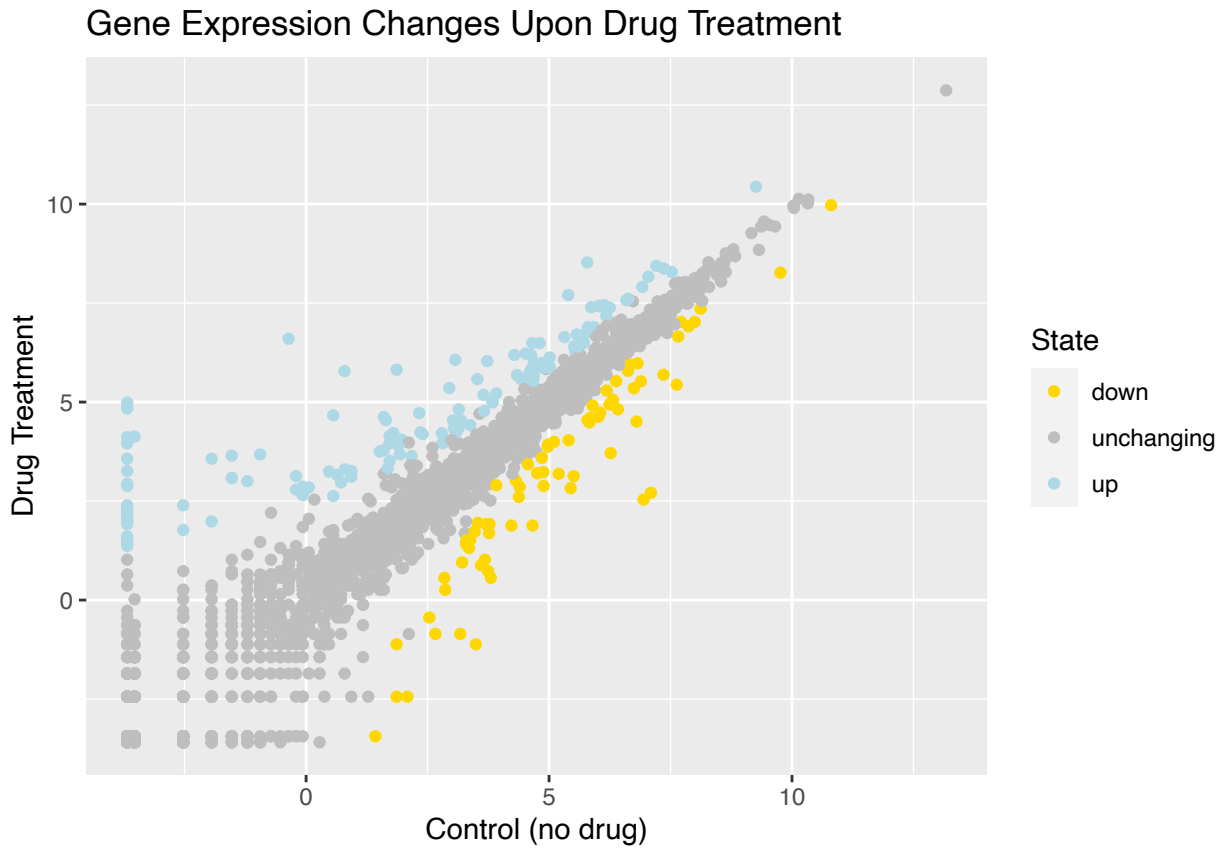
```
# Q. Make plot
q <- ggplot(data=genes)  +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
q
```



```
# **Plot with custom settings.
q + scale_color_manual(values=c("gold", "gray", "lightblue"))
```



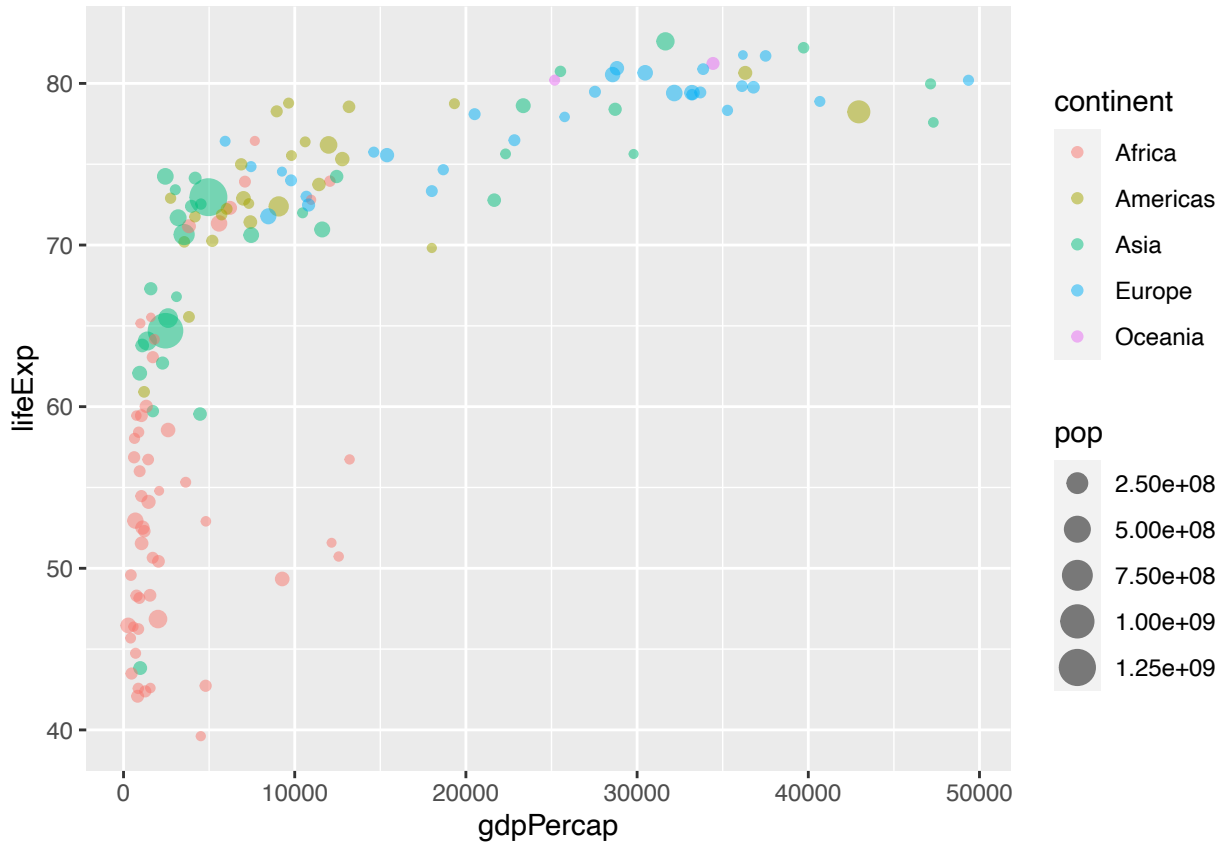

```
# **Plot with labs settings.
q + scale_color_manual(values=c("gold", "gray", "lightblue")) +
  labs (title="Gene Expression Changes Upon Drug Treatment",
        x=("Control (no drug)"),
        y=("Drug Treatment"))
```



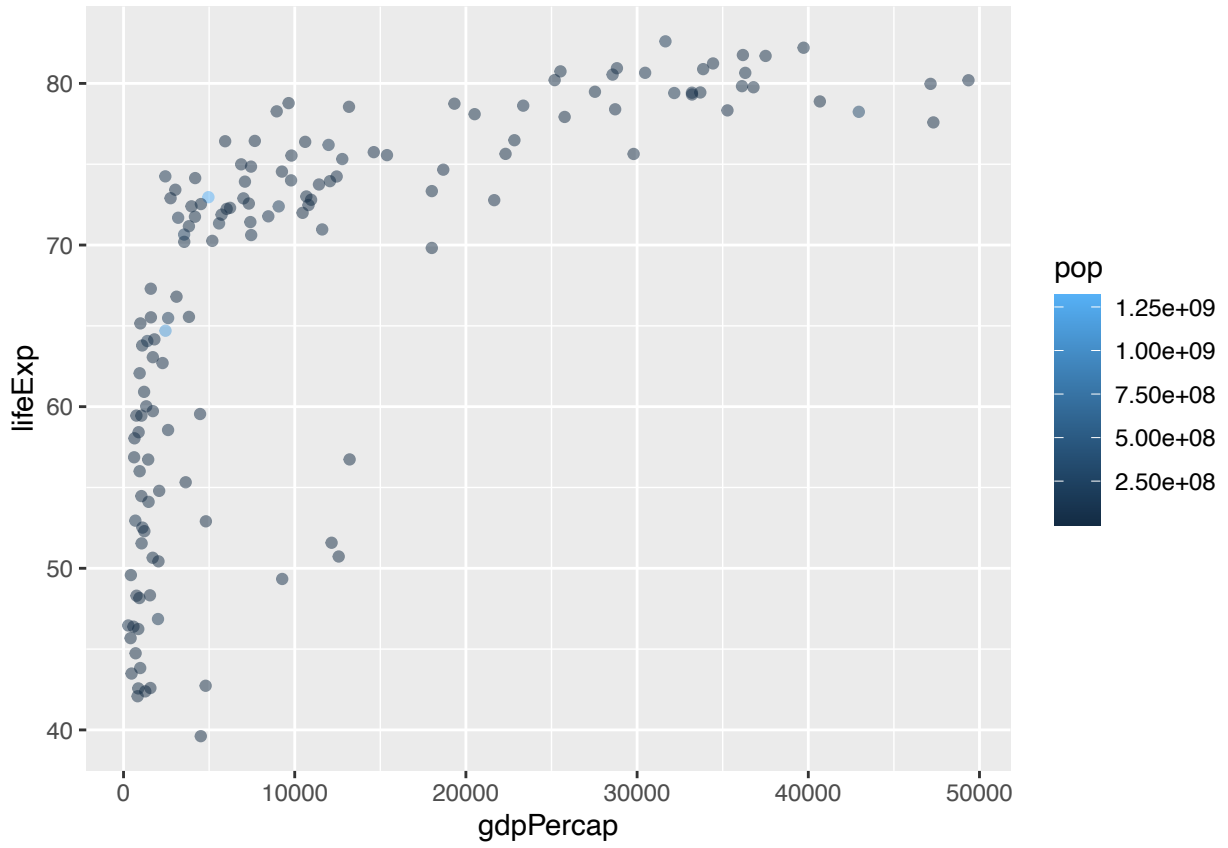

```
# New data set...

# **Install, then load gapminder.
library (gapminder)

# Install, then load dplyr.
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
```

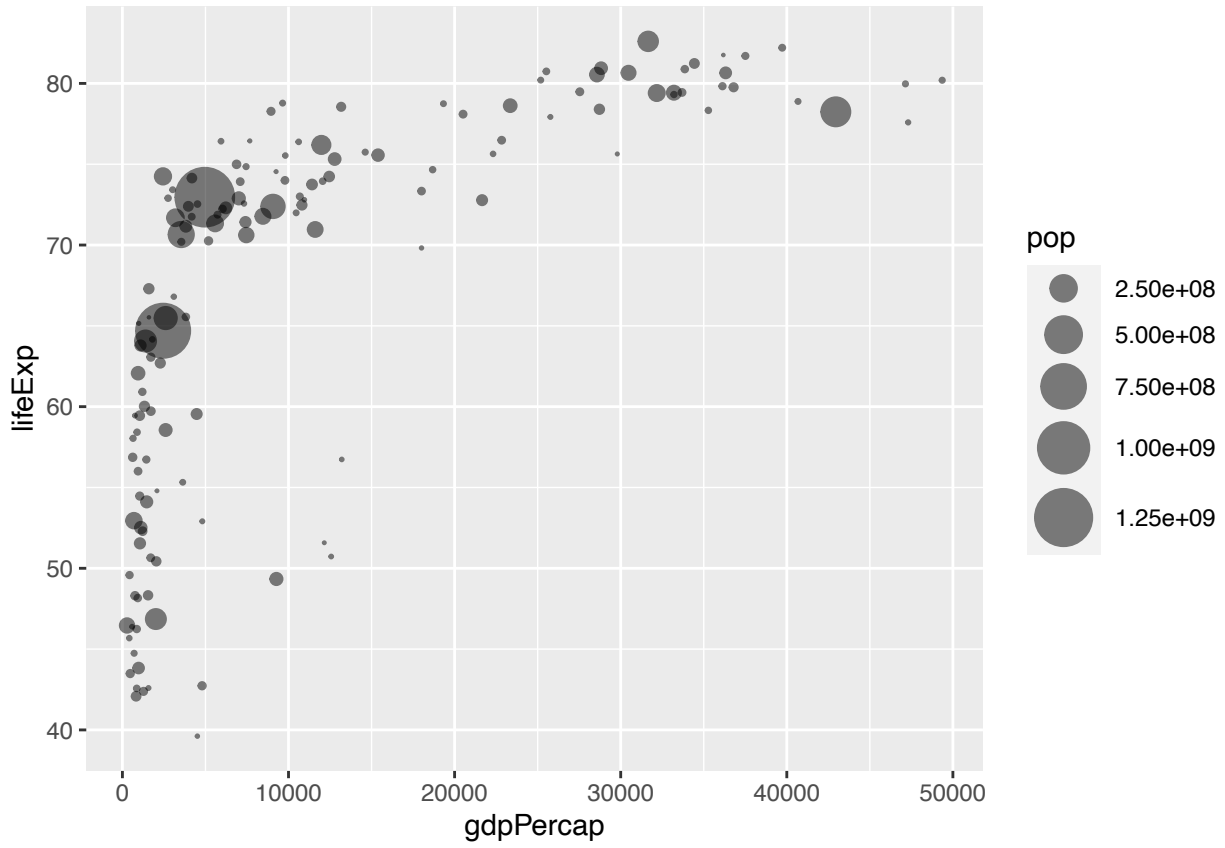
```
# Filter to year 2007.
gapminder_2007 <- gapminder %>% filter(year==2007)

# Q. Scatter plot of gapminder_2007.
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



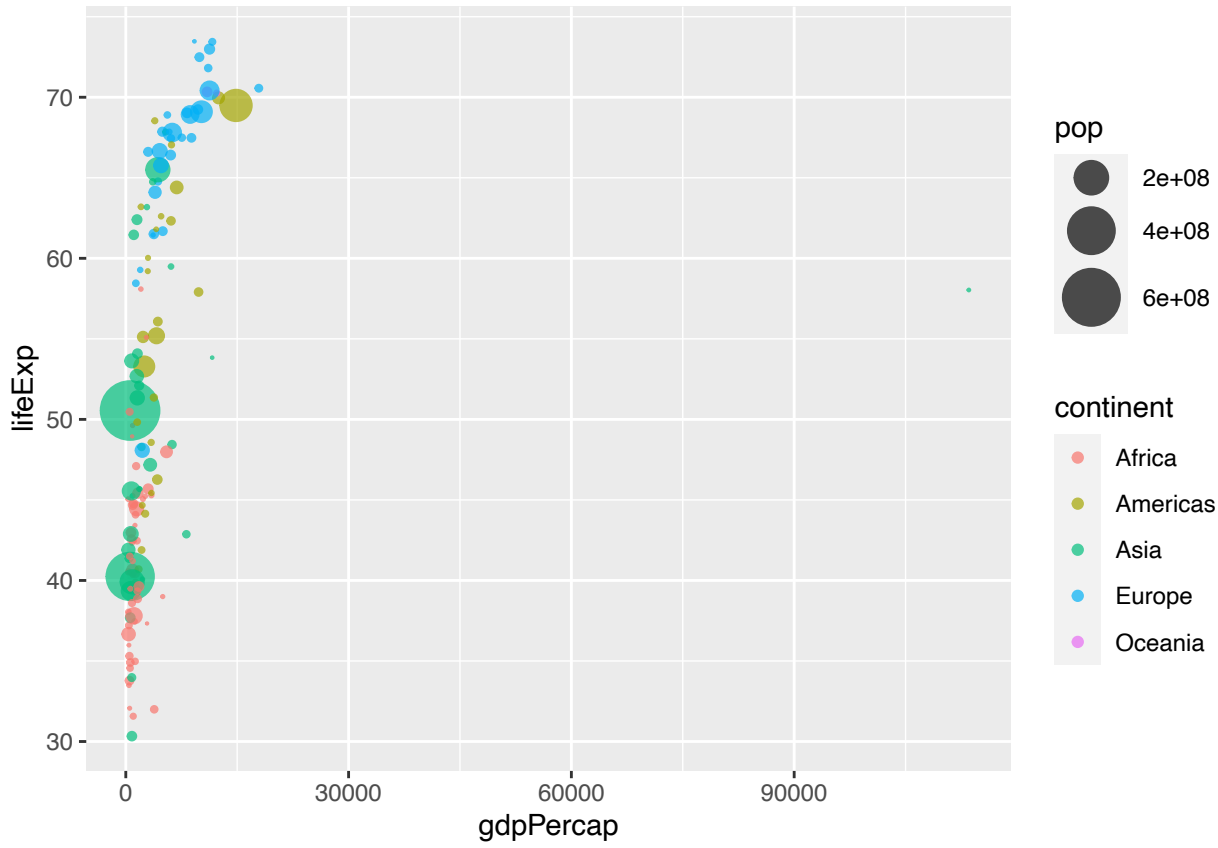

```
# Another version: points colored by popultion size.
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=pop) +
  geom_point(alpha=0.5)
```



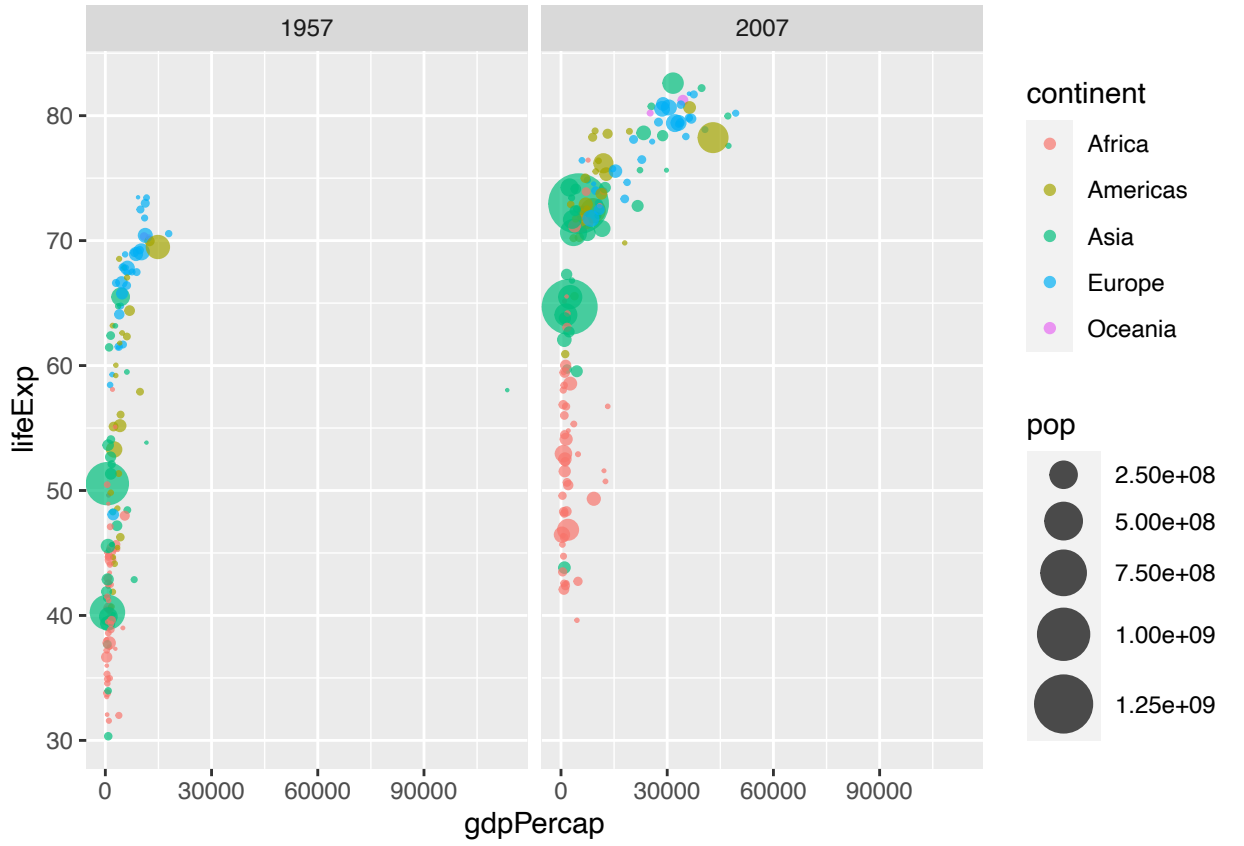

```
# Another version: adjusting point size based on population size.
ggplot(gapminder_2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp,
                 size = pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```




```
# Q. For the year 1957:

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

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



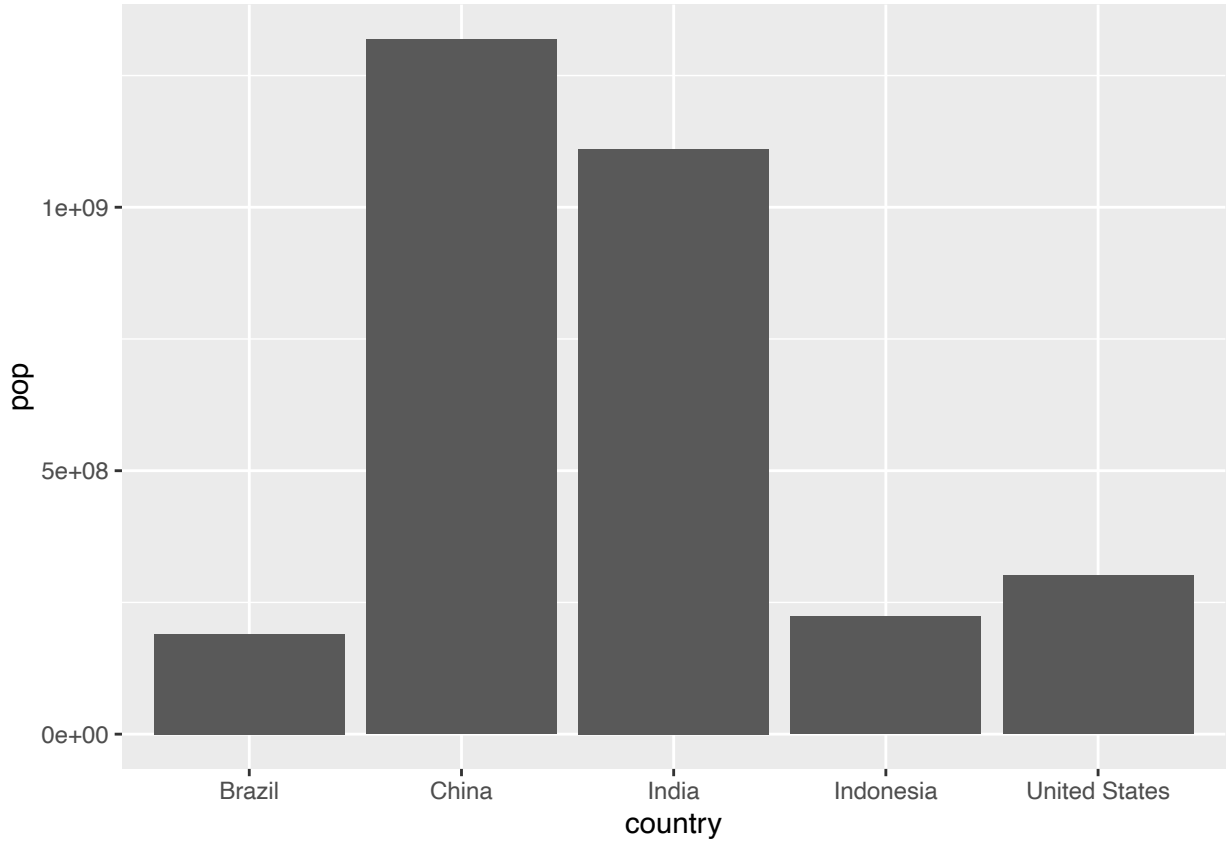

```
# Q. For the years 1957 AND 2007"

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

ggplot(gapminder_1957.2007) +
  aes(x=gdpPercap, y=lifeExp,
      color=continent,
      size=pop)+
  geom_point(alpha=0.7)+
  scale_size_area(max_size=10) +
  facet_wrap(~year)
```



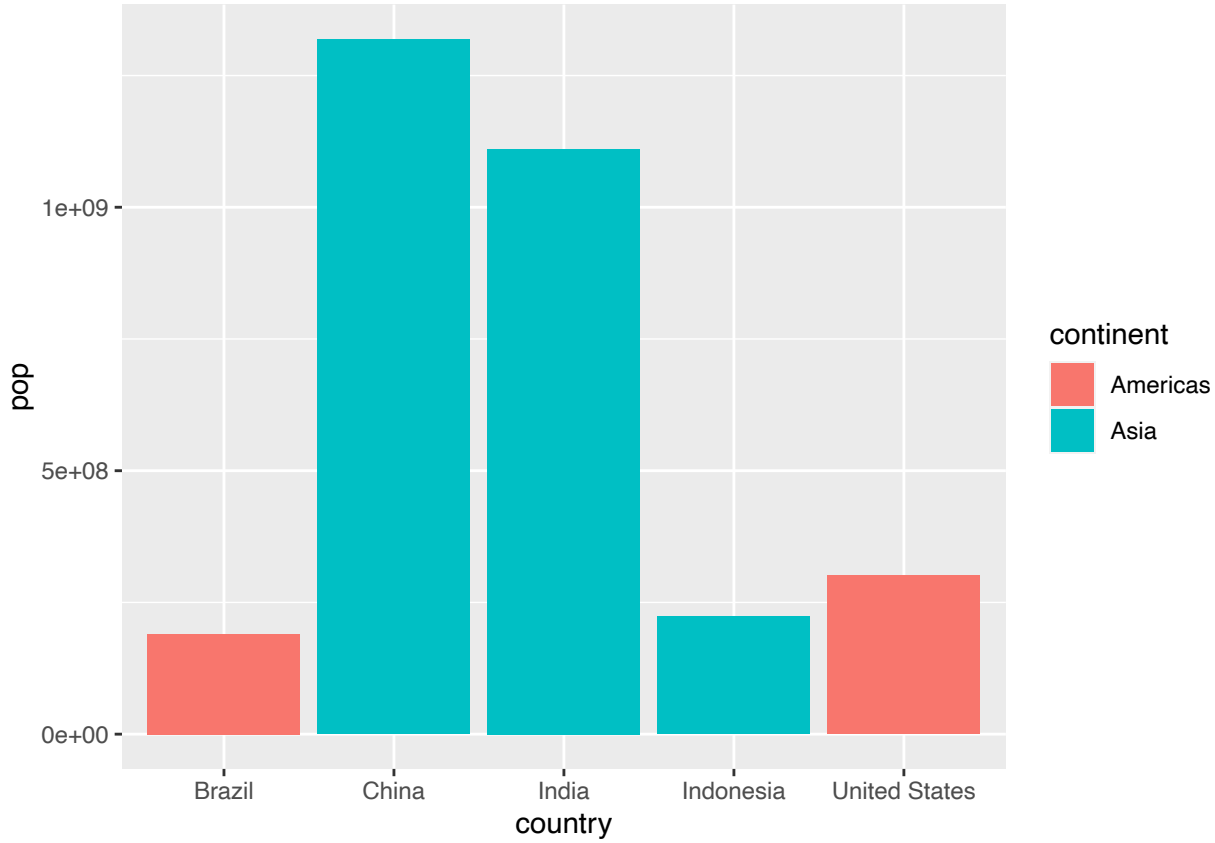

```
# BAR CHARTS

# Data for 5 biggest countries:
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.
```

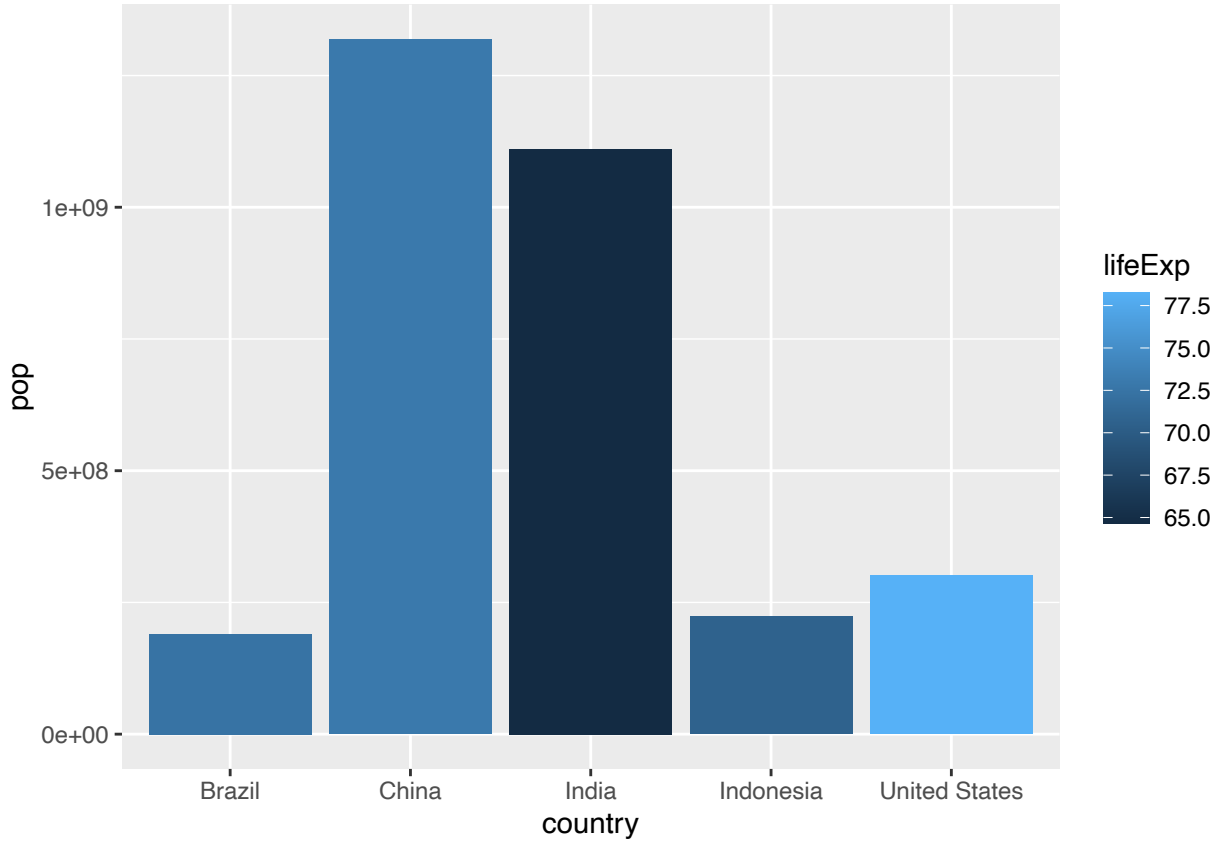
```
# A simple bar chart:
ggplot(gapminder_top5) +
  geom_col(aes(x=country,y=pop))
```



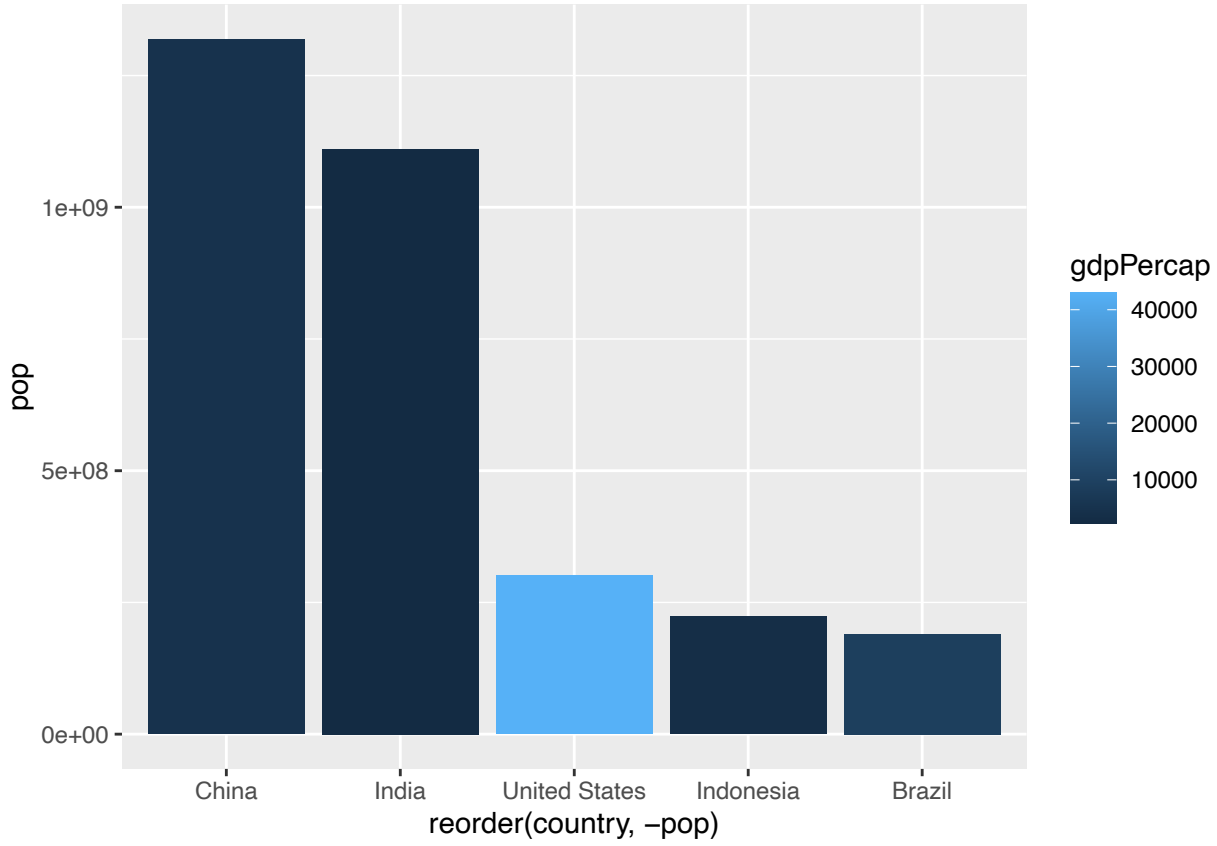

```
# Fill by continent:
ggplot(gapminder_top5) +
  geom_col(aes(x=country,y=pop,
           fill=continent) )
```




```
# Fill by life expectancy:
ggplot(gapminder_top5) +
  geom_col(aes(x=country,y=pop,
               fill=lifeExp) )
```

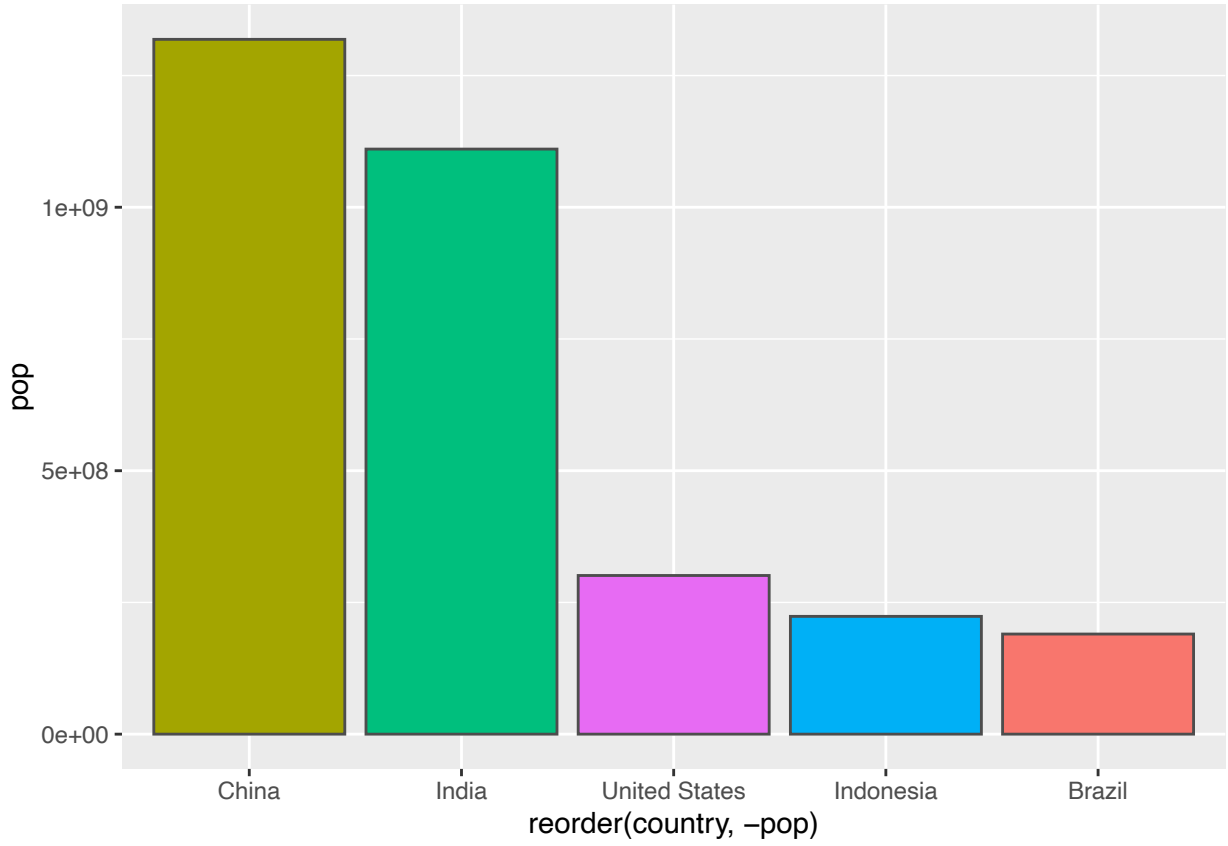



```
# Fill by GDP per capita, change the order of bars:
ggplot(gapminder_top5) +
  aes(x=reorder(country,-pop),y=pop, fill=gdpPercap)+
  geom_col()
```




```
# Just fill by country
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=country) +
  geom_col(col="gray30") +
  guides(fill=FALSE)
```

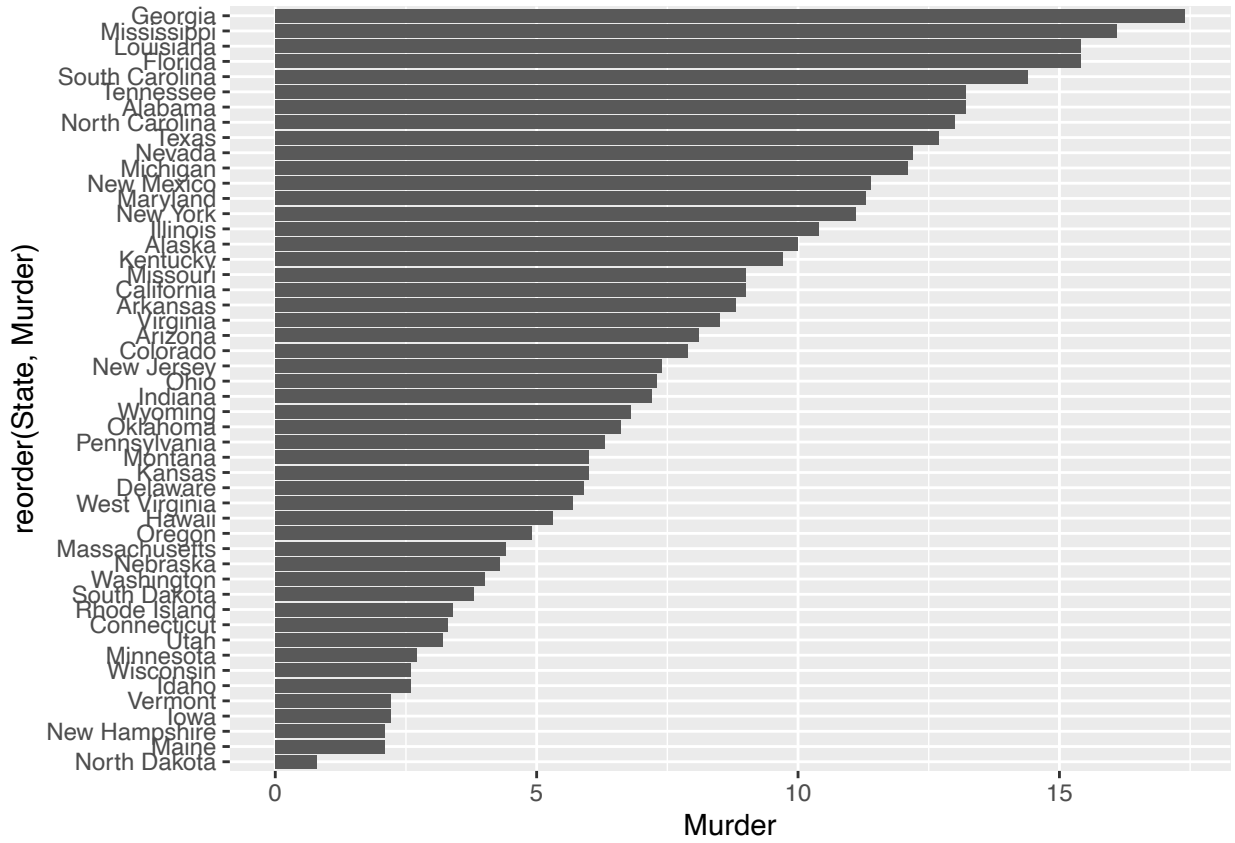
```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```



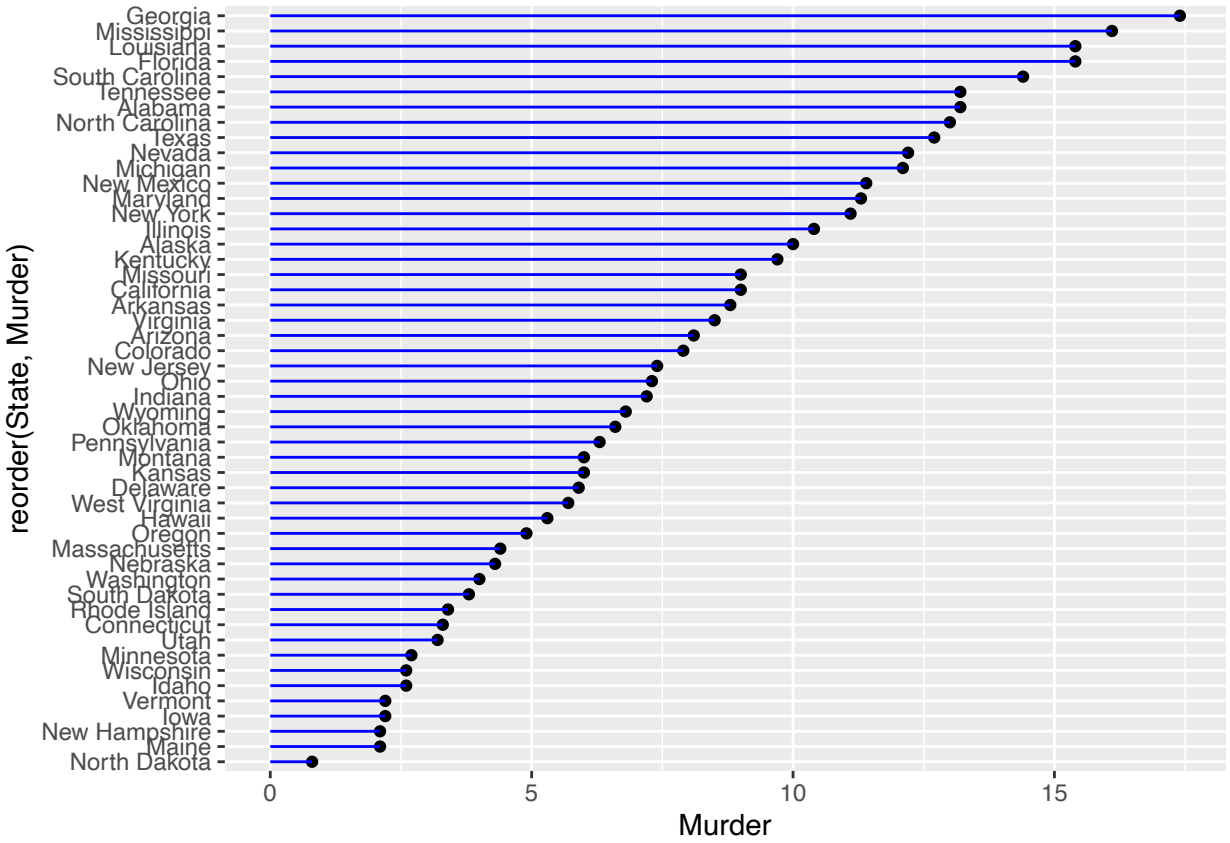

```
# New data set...

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
```

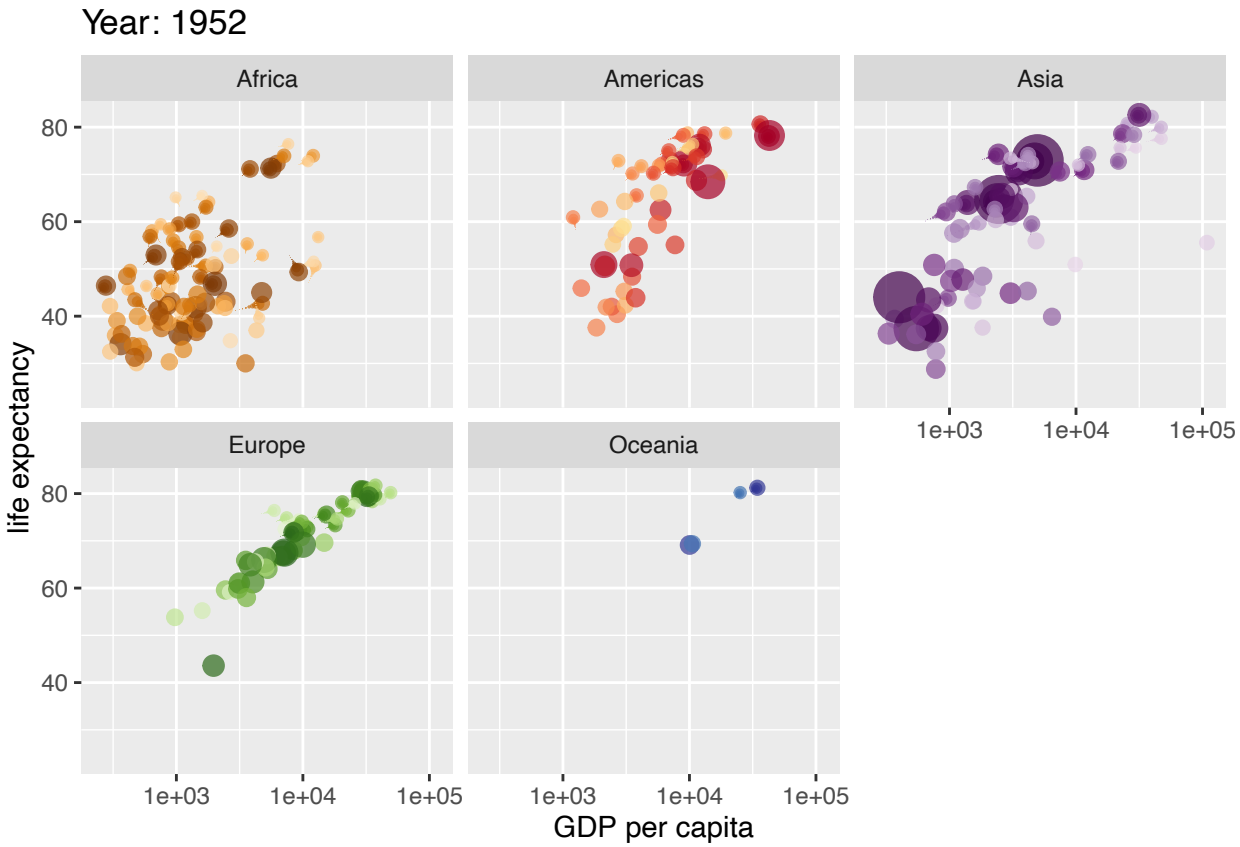
```
# Flipped bar chart:
USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder),y=Murder) +
  geom_col() +
  coord_flip()
```

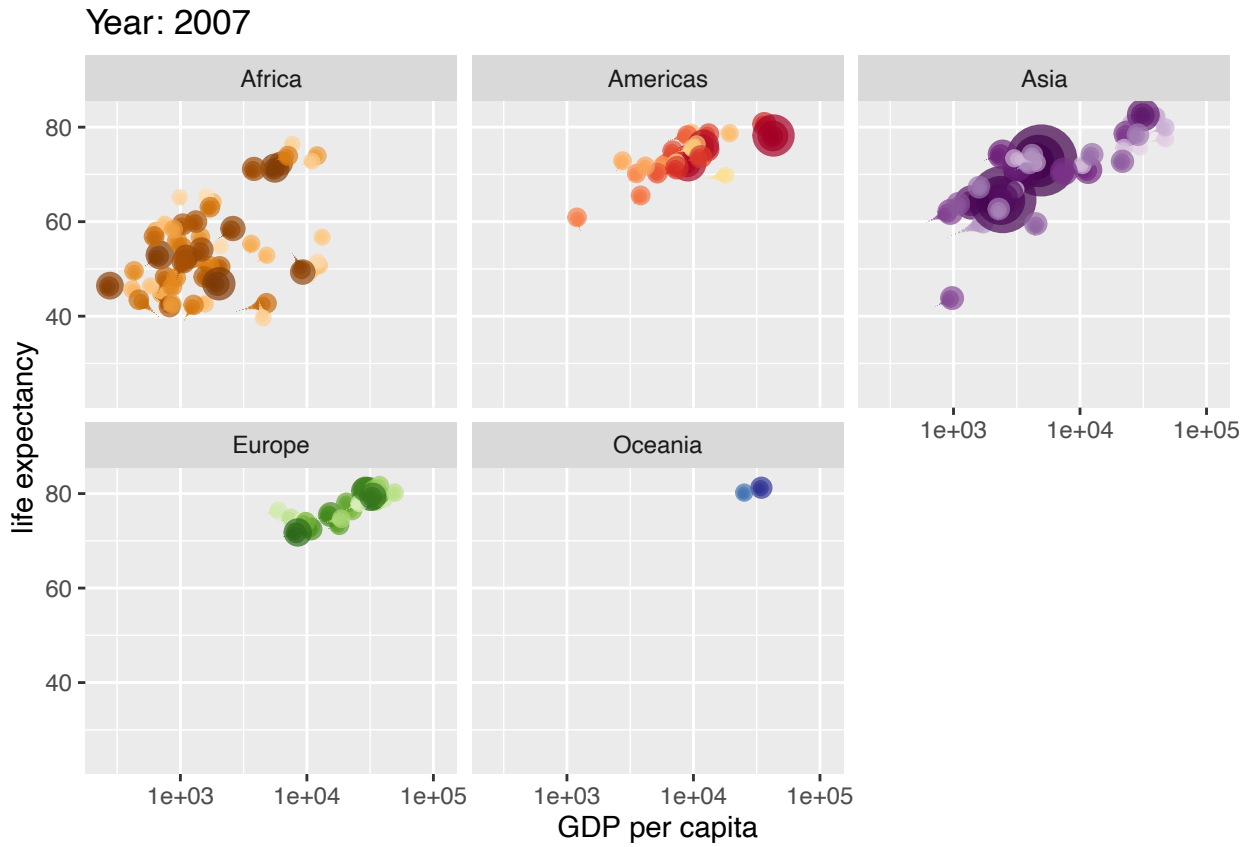



```
# New format:
USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_point() +
  geom_segment(aes(x=State,
                   xend=State,
                   y=0,
                   yend=Murder), color="blue") +
  coord_flip()
```



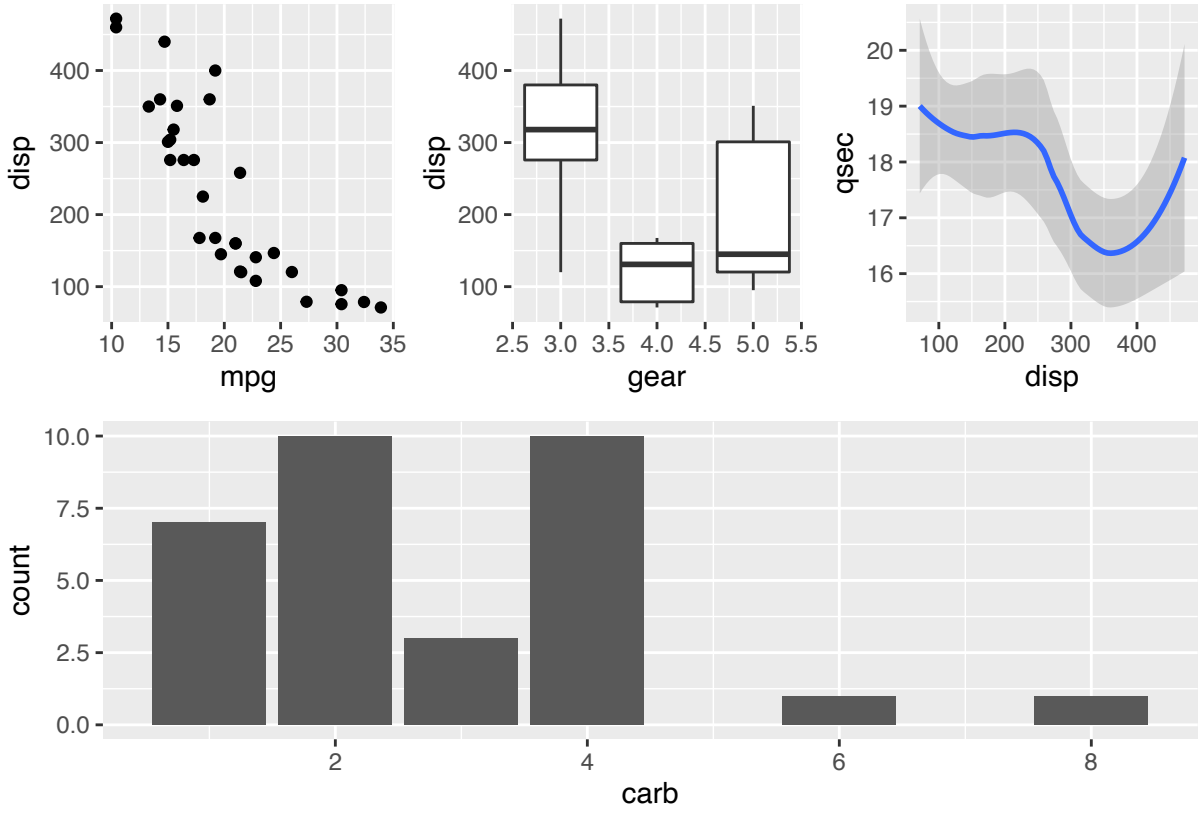

```
# PLOT ANIMATION

# Install, then load gifski & gganimate.
library (gganimate)
library (gifski)

# Normal ggplot of gapminder data:
ggplot (gapminder, aes(gdpPercap, lifeExp, size=pop, color=country))+
  geom_point(alpha=0.7, show.legend=FALSE) +
  scale_color_manual(values=country_colors) +
  scale_size(range= c(2,12)) +
  scale_x_log10()+
  # Facet by continent
  facet_wrap (~continent) +
  # Animations :-)
  labs(title = 'Year: {frame_time}', x = 'GDP per capita', y = 'life expectancy') +
  transition_time(year) +
  shadow_wake(wake_length = 0.1, alpha = FALSE)
```


Year: 1952
Africa
Americas
Asia
Europe
Oceania
life expectancy
80
60
40
1e+03
1e+04
1e+05
GDP per capita




```
# Combining plots

# Install, then load patchwork:
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'
```


disp
400
300
200
100
10
15
20
25
30
35
mpg
disp
400
300
200
100
2.5
3.0
3.5
4.0
4.5
5.0
5.5
gear
qsec
20
19
18
17
16
100
200
300
400
disp
count
10.0
7.5
5.0
2.5
0.0
2
4
6
8
carb