# class5.R

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```r
#Class 5 Data Visualization

#Base R plot
plot(1:5)


#for prettier plots, we will use ggplot2 (already installed)
#install.packages("ggplot2")
library(ggplot2)
```
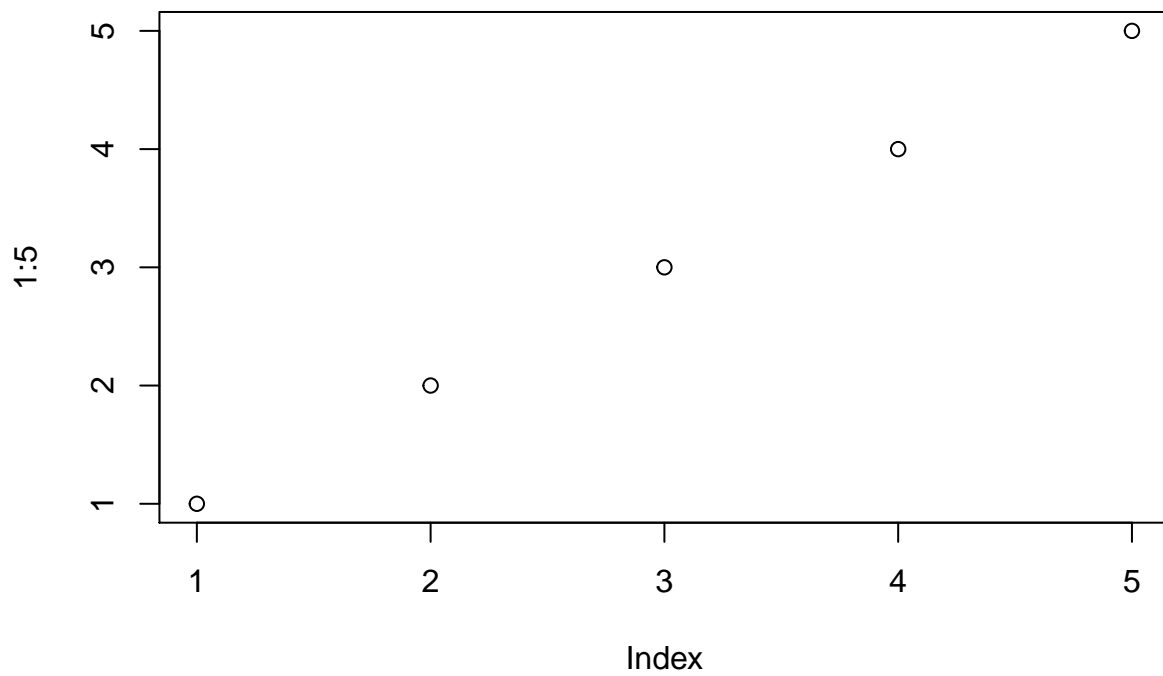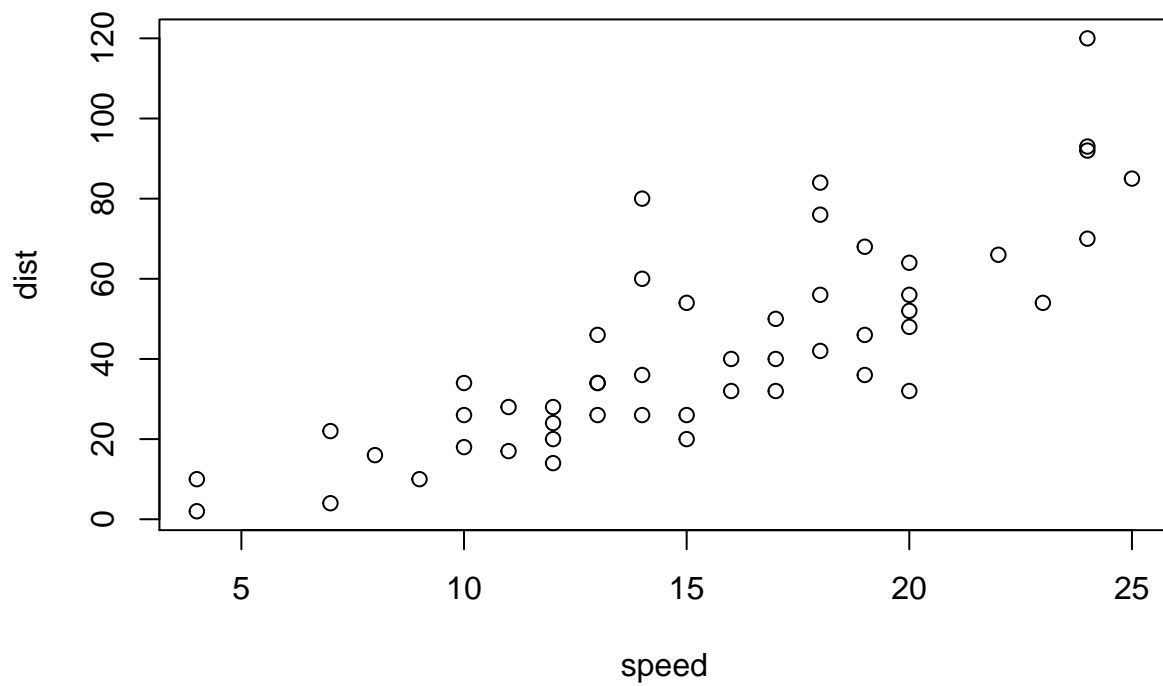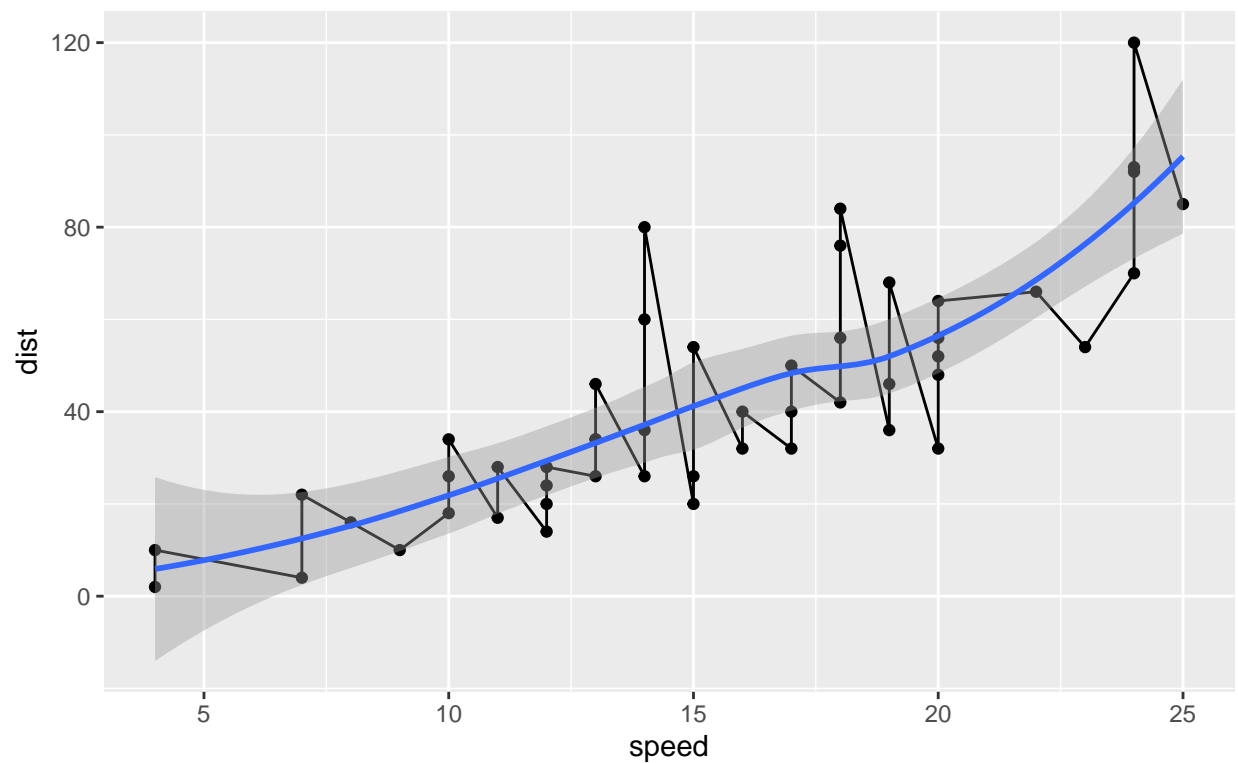


```r
plot(cars)
```

```
p <- ggplot(cars) +
  aes(speed,dist) +
  geom_point() +
  geom_line() +
  geom_smooth() +
  labs(title="distance vs speed", caption = "cars plot")

p
```

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

distance vs speed

cars plot

```
#RNA-seq plot

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
```

```
colnames(genes)
```

```
## [1] "Gene"       "Condition1" "Condition2" "State"
```
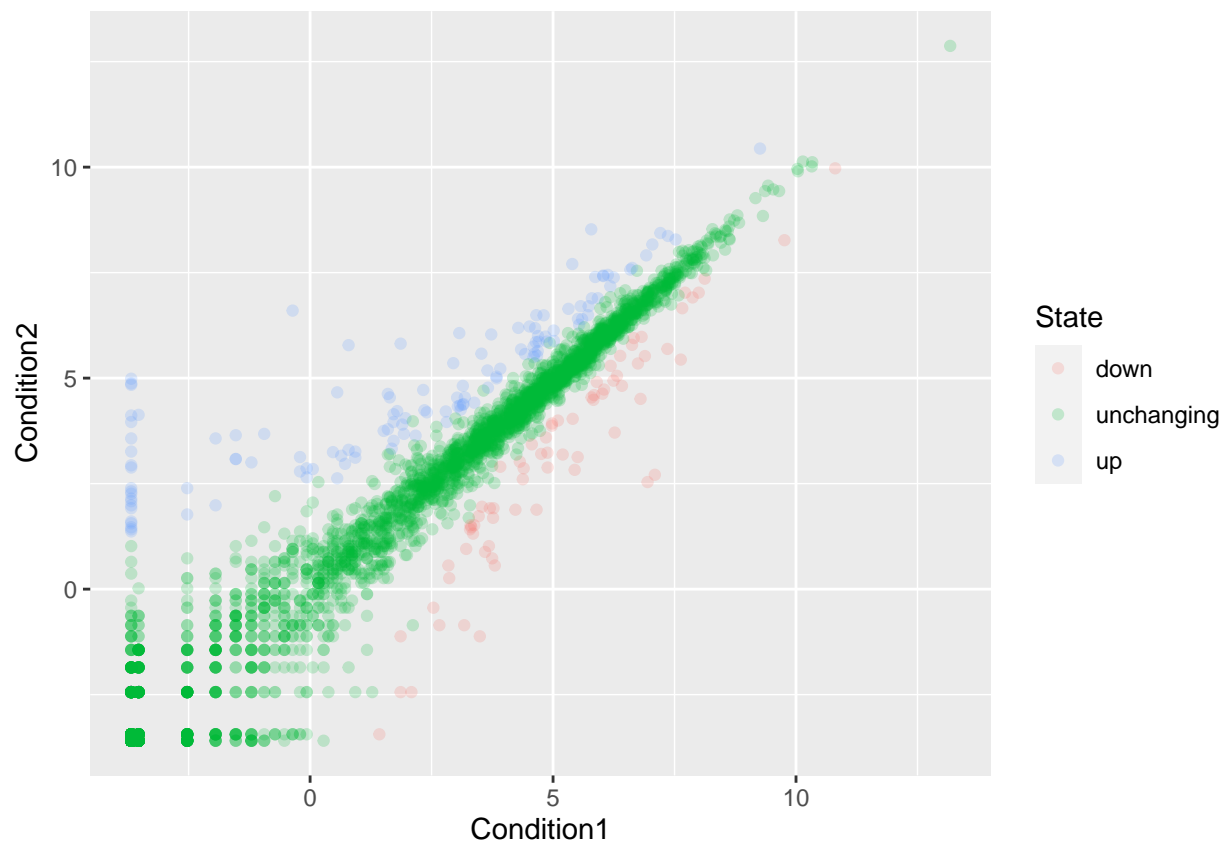
3

```
ncol(genes)
```

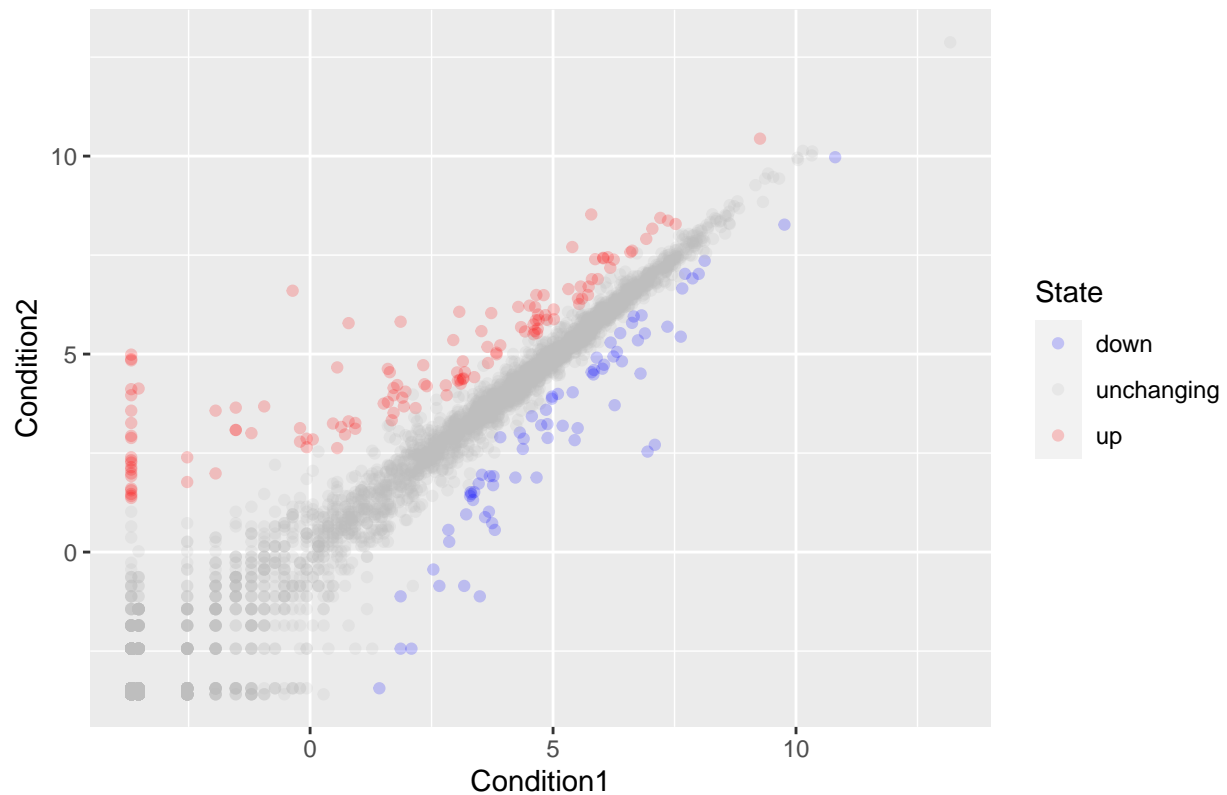```
## [1] 4
```

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

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

```
p <- ggplot(genes,
        aes(Condition1, Condition2, col = State)) +
        geom_point(alpha = 0.2)
p
```



```
p<- p + scale_colour_manual( values=c("blue","gray","red") )+
  labs(title = "Gene Expression Changes Upon Drug Treatment", xlabs = "Control(no drug)", ylabs = "Drug
```

```
p
```

## Gene Expression Changes Upon Drug Treatment



```
#gapminder optional part
#install("gapminder")
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 %>% filter(year==2007)
```

```
ggplot(gapminder_2007,aes(gdpPercap, lifeExp, color=continent, size = pop))+
  geom_point(alpha=0.5)
```
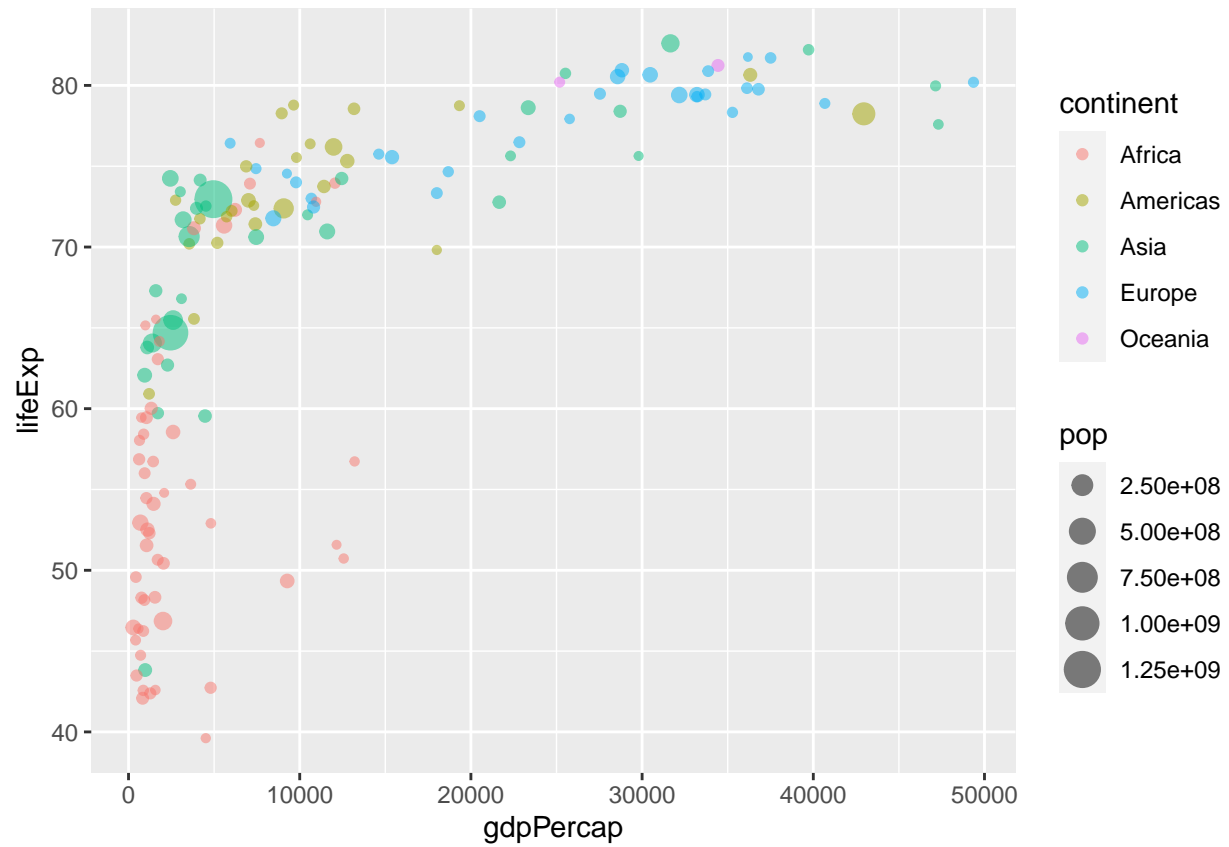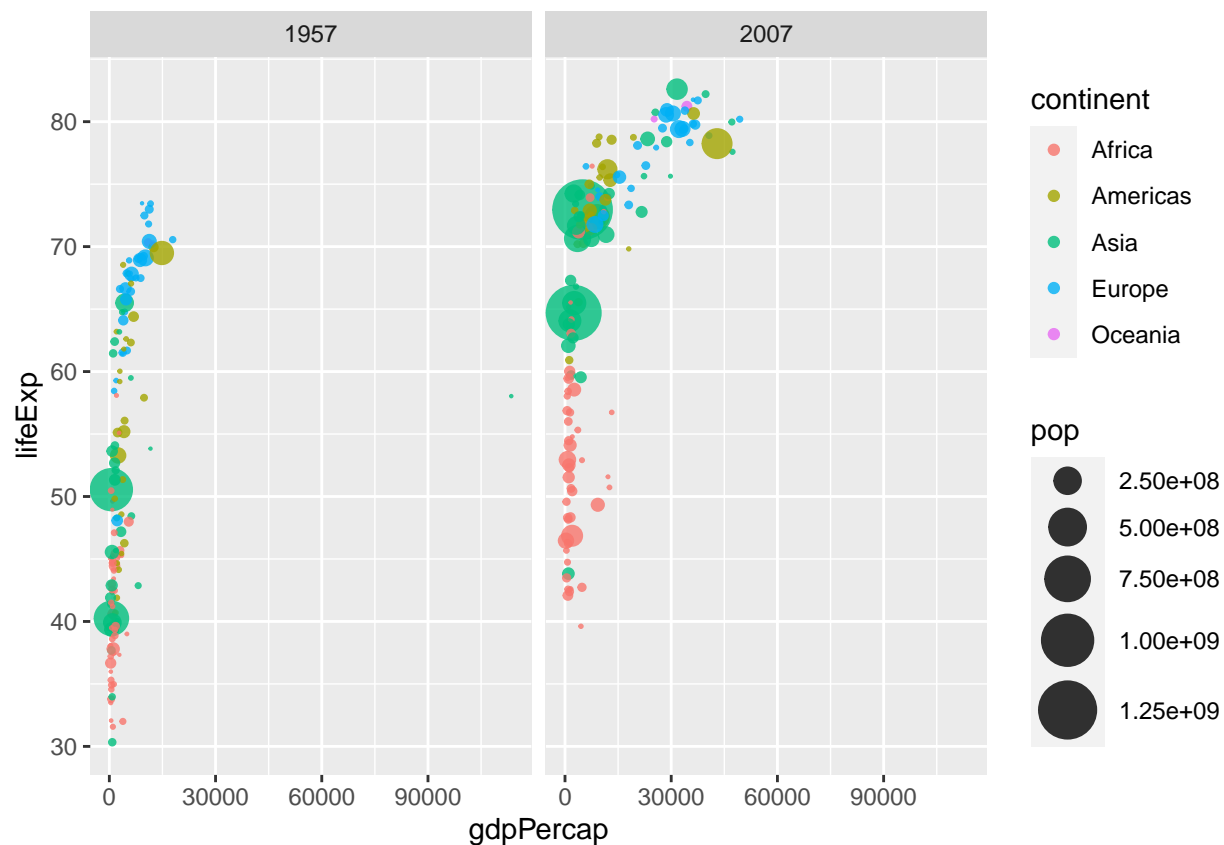
```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = pop) +
  geom_point(alpha=0.8) +
  scale_size_area(max_size = 10)
```
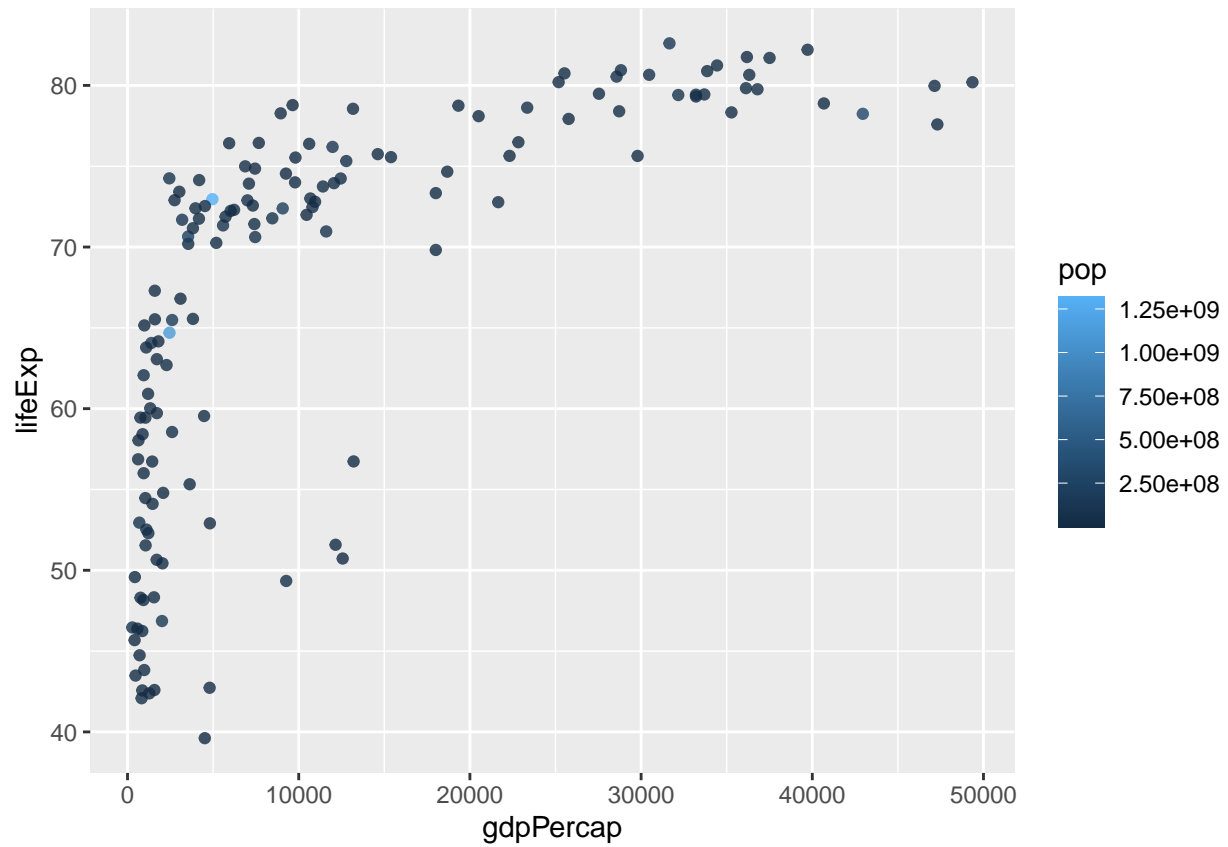
```
gapminder_1957 <- gapminder %>% filter(year==1957 | year ==2007)

ggplot(gapminder_1957) +
  aes(x = gdpPercap, y = lifeExp, color = continent, size = pop) +
  geom_point(alpha=0.8) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```

```r
#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.
```

```r
p1 <- ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill = continent))

p2 <- ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill = lifeExp))


p3 <- ggplot(gapminder_top5) +
```
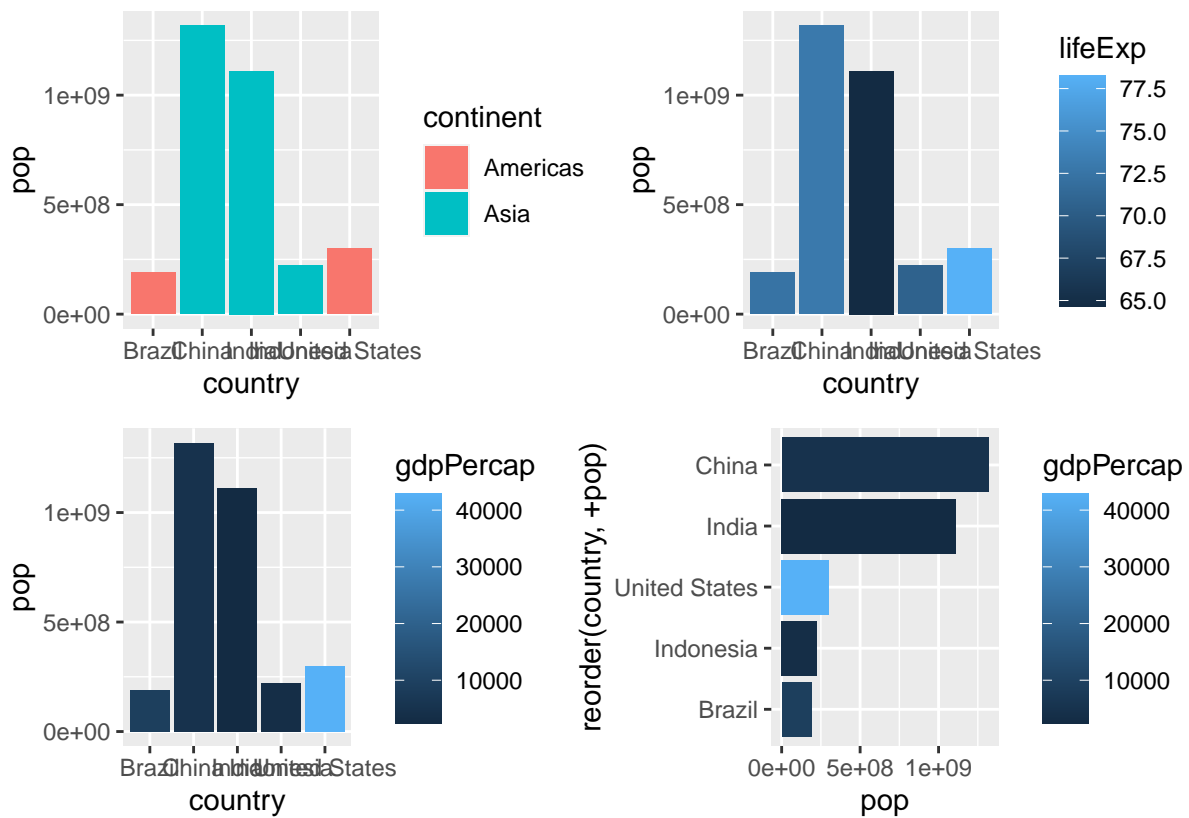
```
  geom_col(aes(x = country, y = pop, fill = gdpPercap))


p4 <- ggplot(gapminder_top5) +
  geom_col(aes(x = reorder(country, +pop), y = pop, fill = gdpPercap))+
  coord_flip()

#load package patchwork to arrange multiple plots together
library(patchwork)
(p1 | p2 )/ ( p3 | p4)
```



```
# for making pdf report
#install.packages("tinytex")
#library(tinytex)
#install_tinytex()
```