Class 05: Data Visualization with GGPLOT
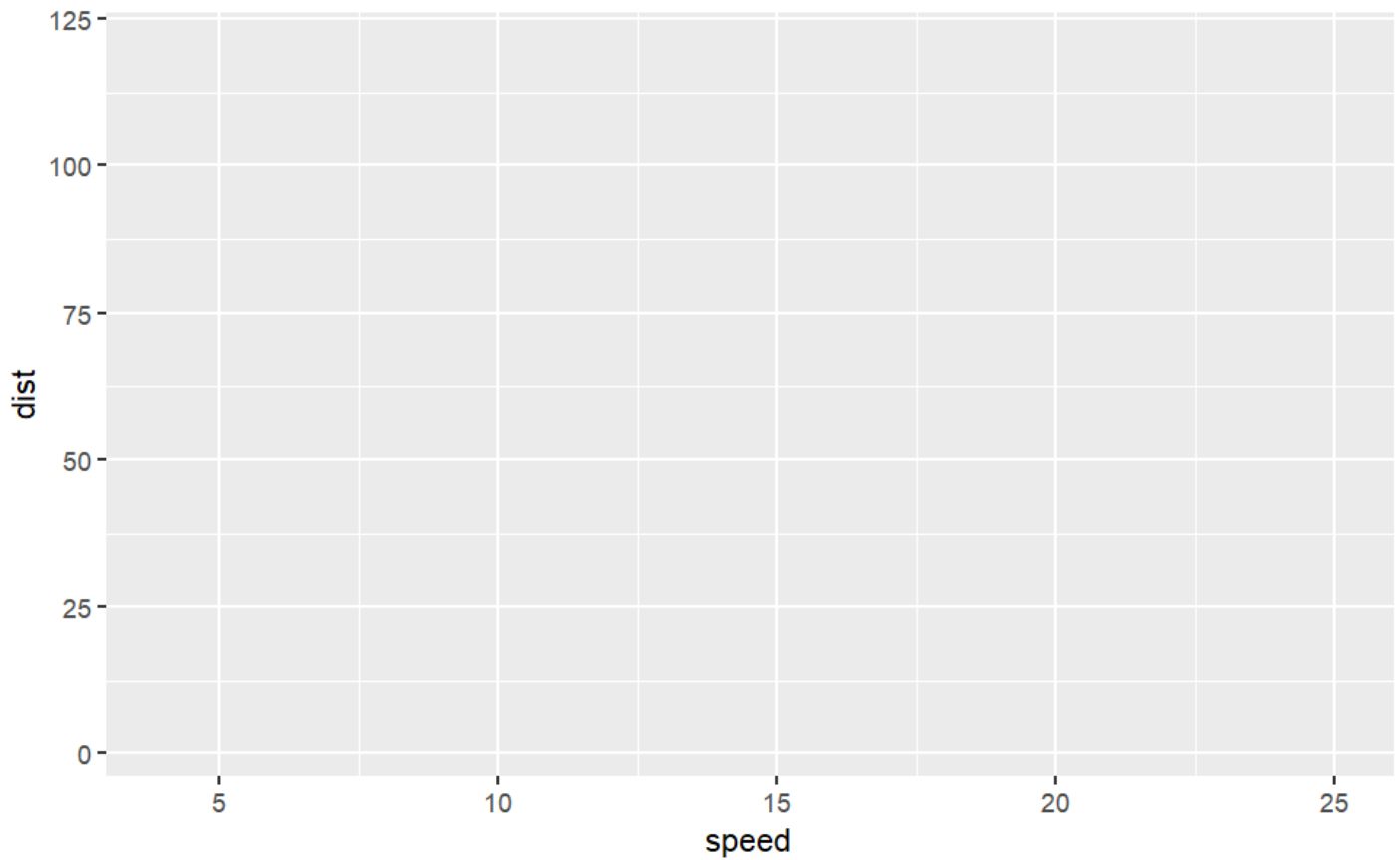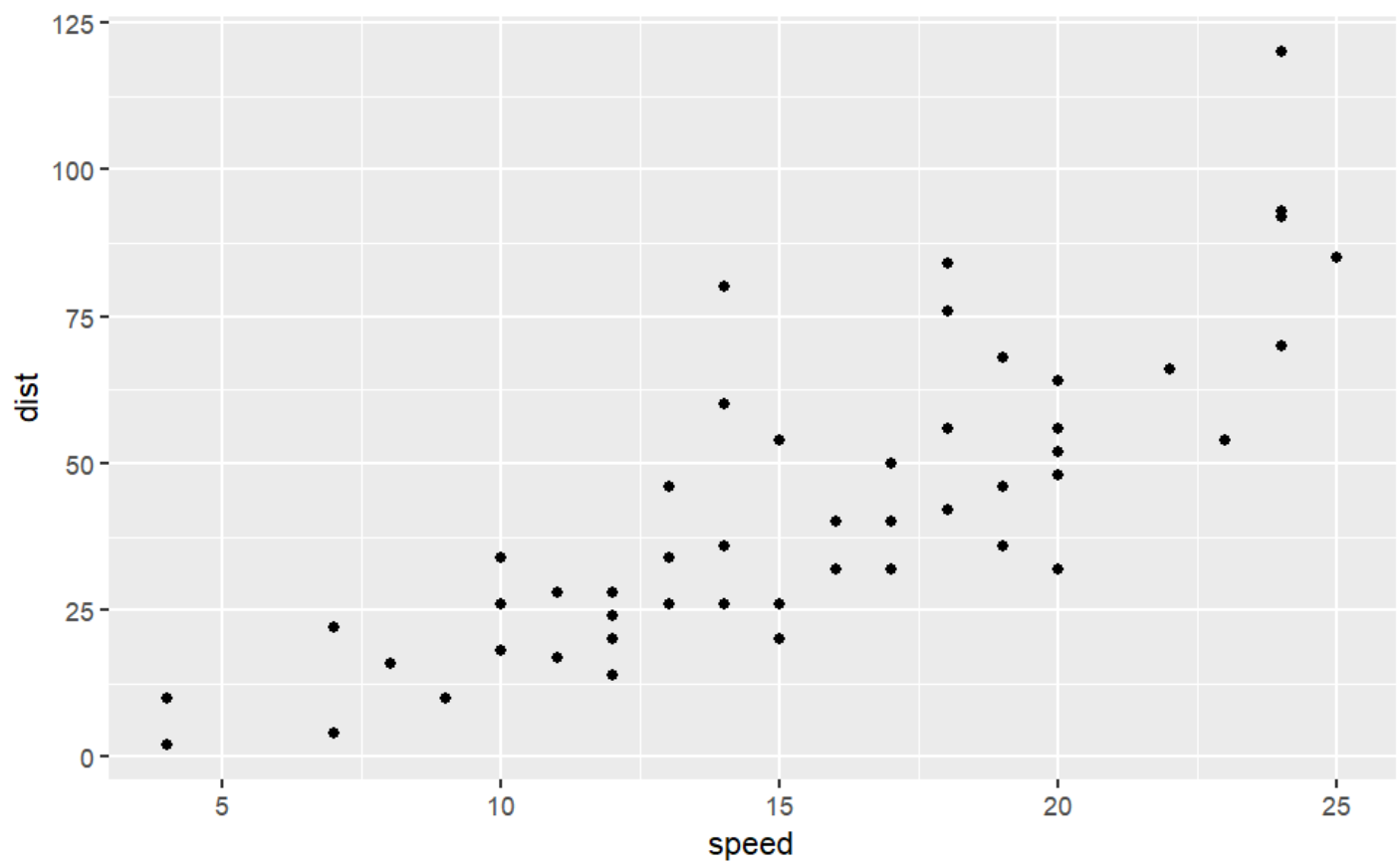
Yufei Zhang

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```
#install.packages("ggplot2")
library(ggplot2)
```

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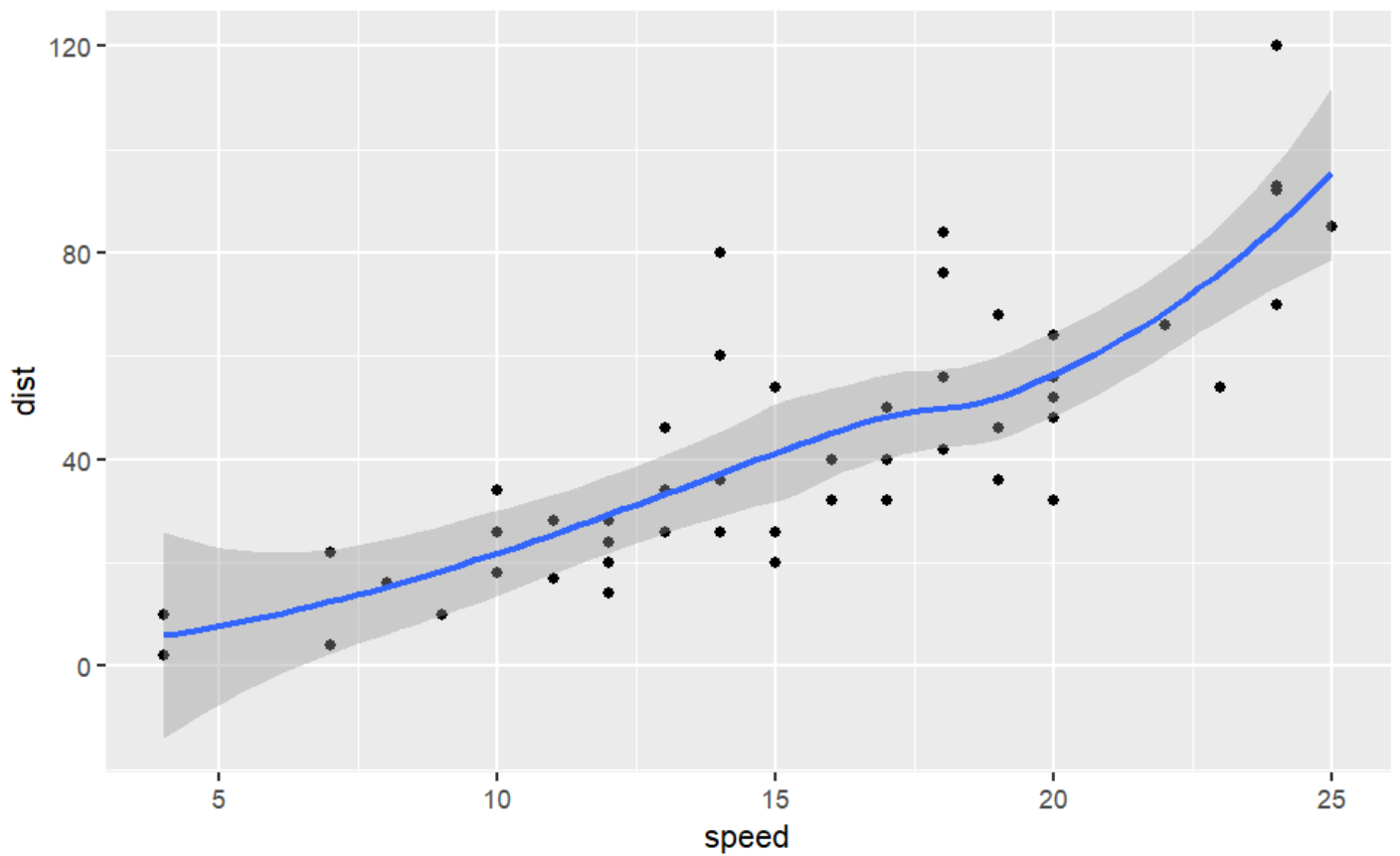

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```
#plotting speed vs distance and plot as points and smooth line
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```

```
#plotting speed vs distance and plot as points
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()+geom_smooth()
```

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```
#read delim file from an url
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```
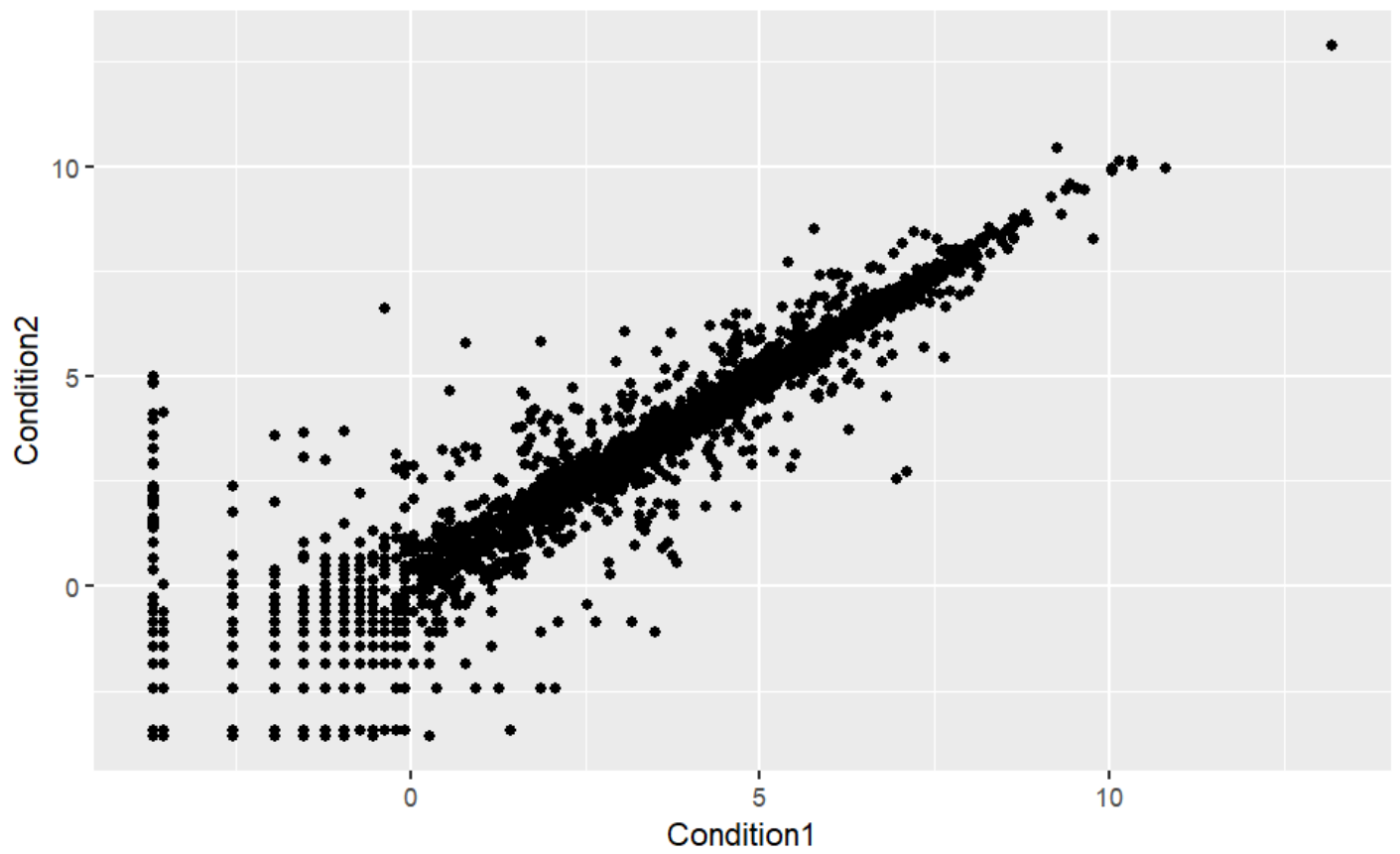
|	Gene <chr>	Condition1 <dbl>	Condition2 <dbl>	State <chr>
1	A4GNT	-3.6808610	-3.4401355	unchanging
2	AAAS	4.5479580	4.3864126	unchanging
3	AASDH	3.7190695	3.4787276	unchanging
4	AATF	5.0784720	5.0151916	unchanging
5	AATK	0.4711421	0.5598642	unchanging
6	AB015752.4	-3.6808610	-3.5921390	unchanging

6 rows

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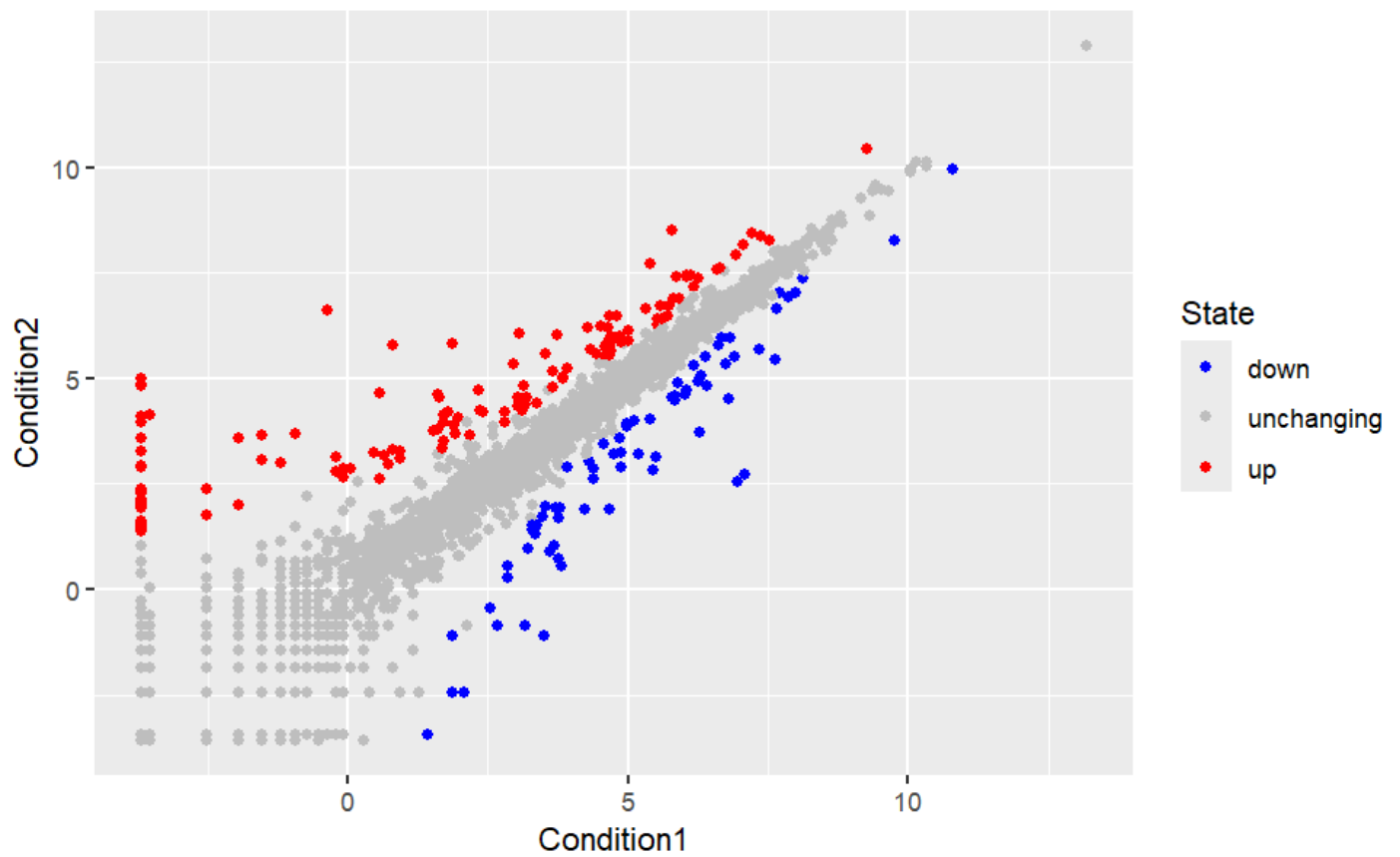
```
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
p
```
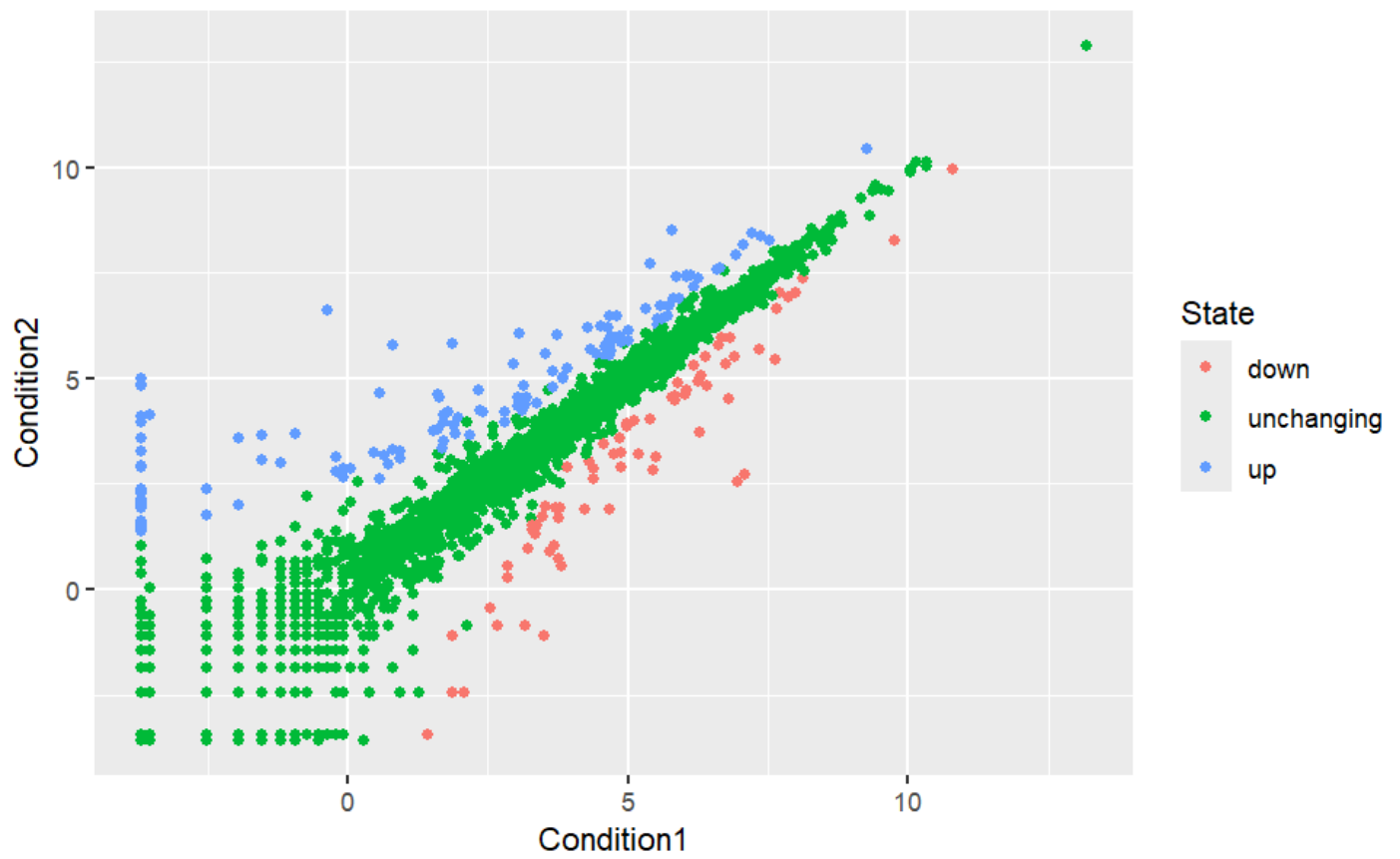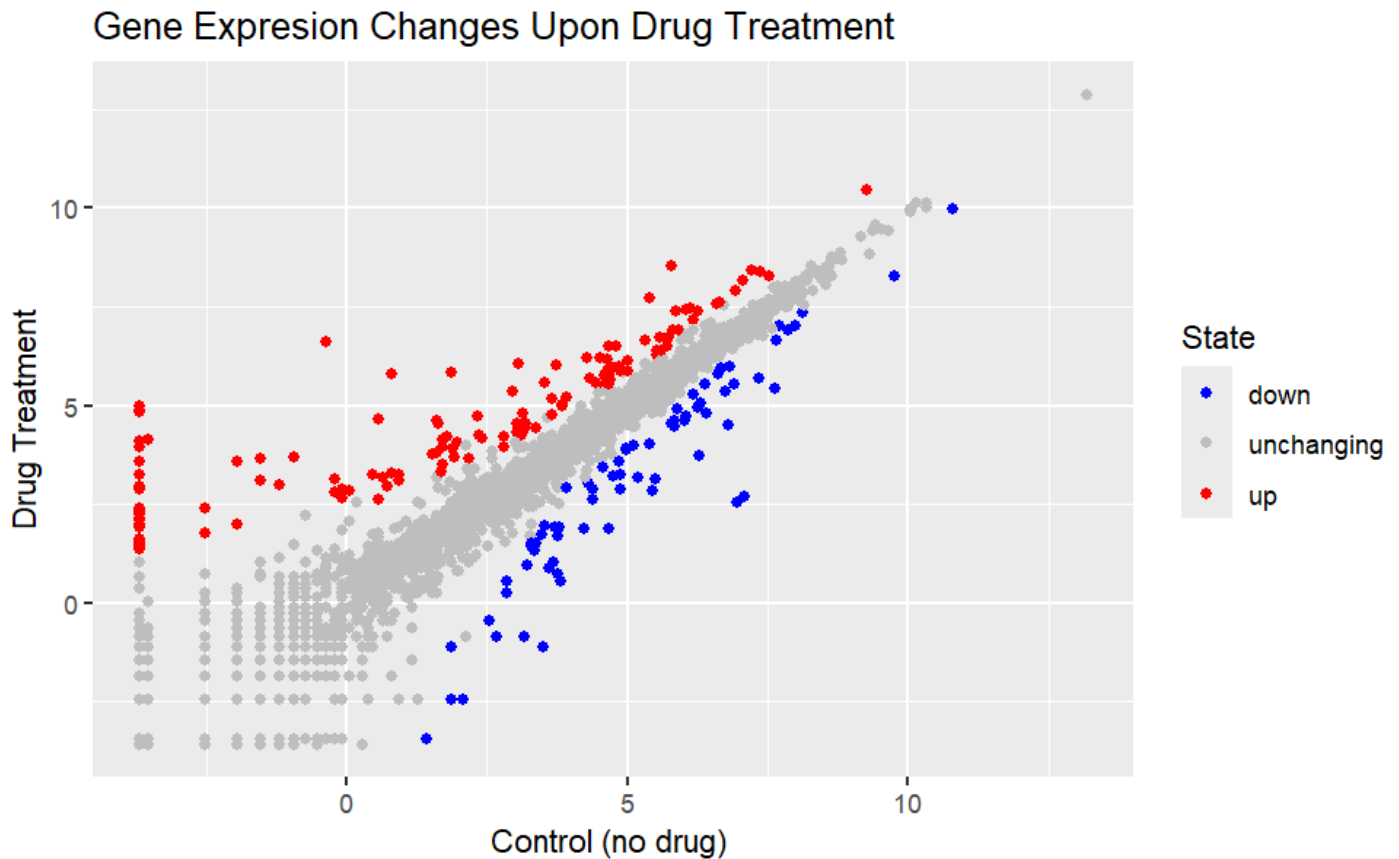
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```
p + scale_colour_manual( values=c("blue","gray","red") )
```

```
p + scale_colour_manual(values=c("blue","gray","red")) +
    labs(title="Gene Expresion Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment")
```


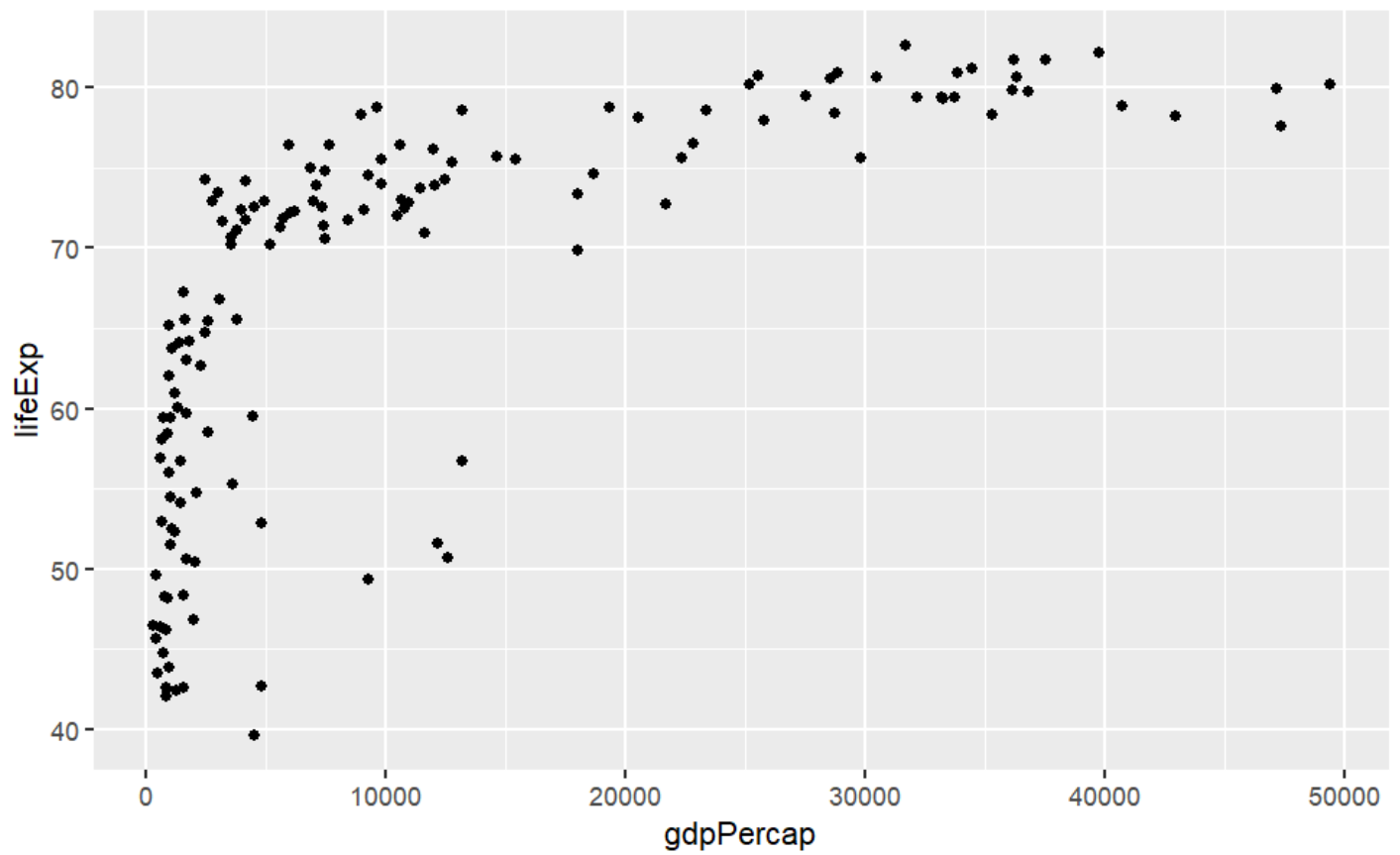Gene Expresion Changes Upon Drug Treatment

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

gapminder <- read.delim(url)
```

```
#install.packages("dplyr")   ## un-comment to install if needed
library(dplyr)

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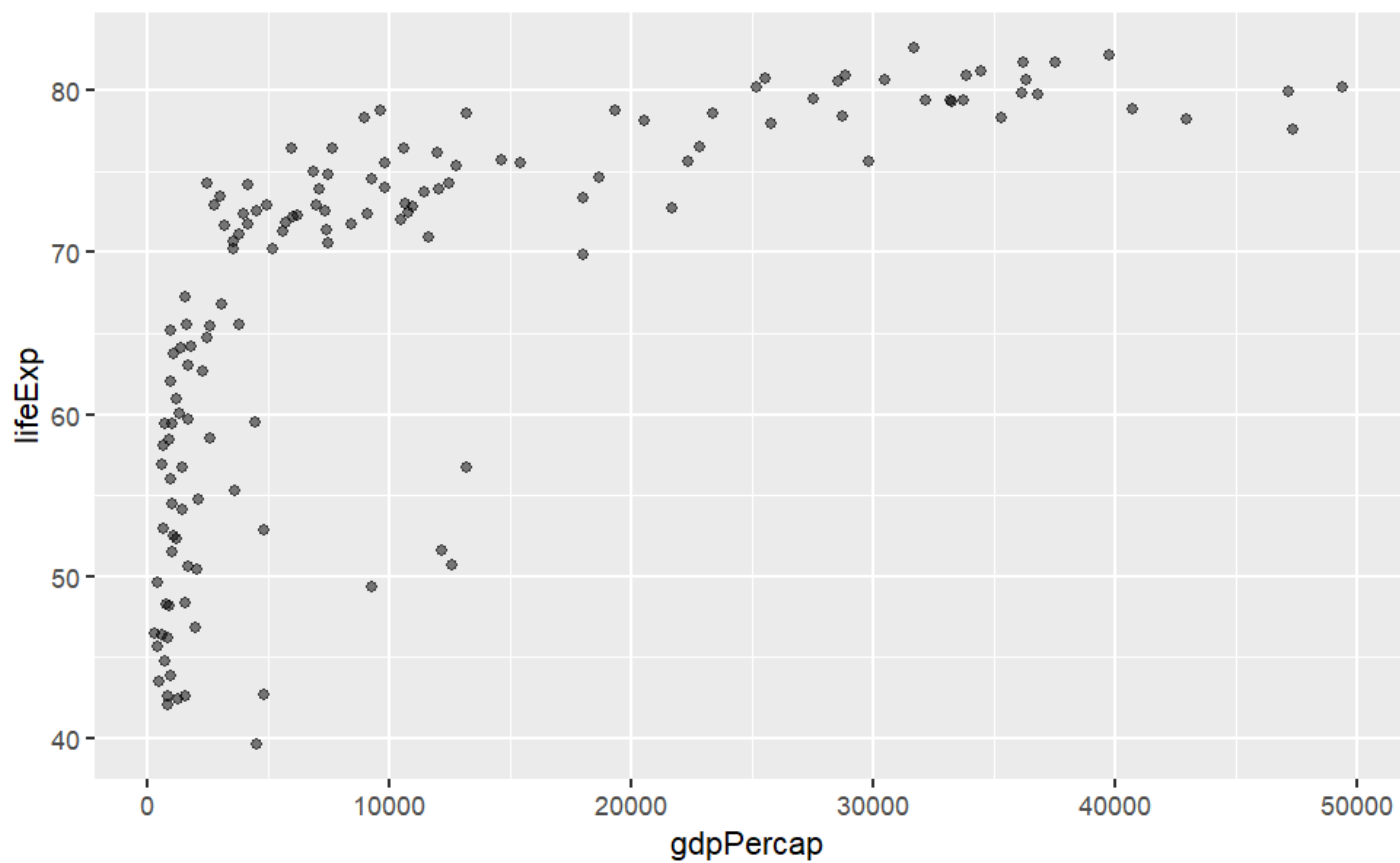
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point()
```
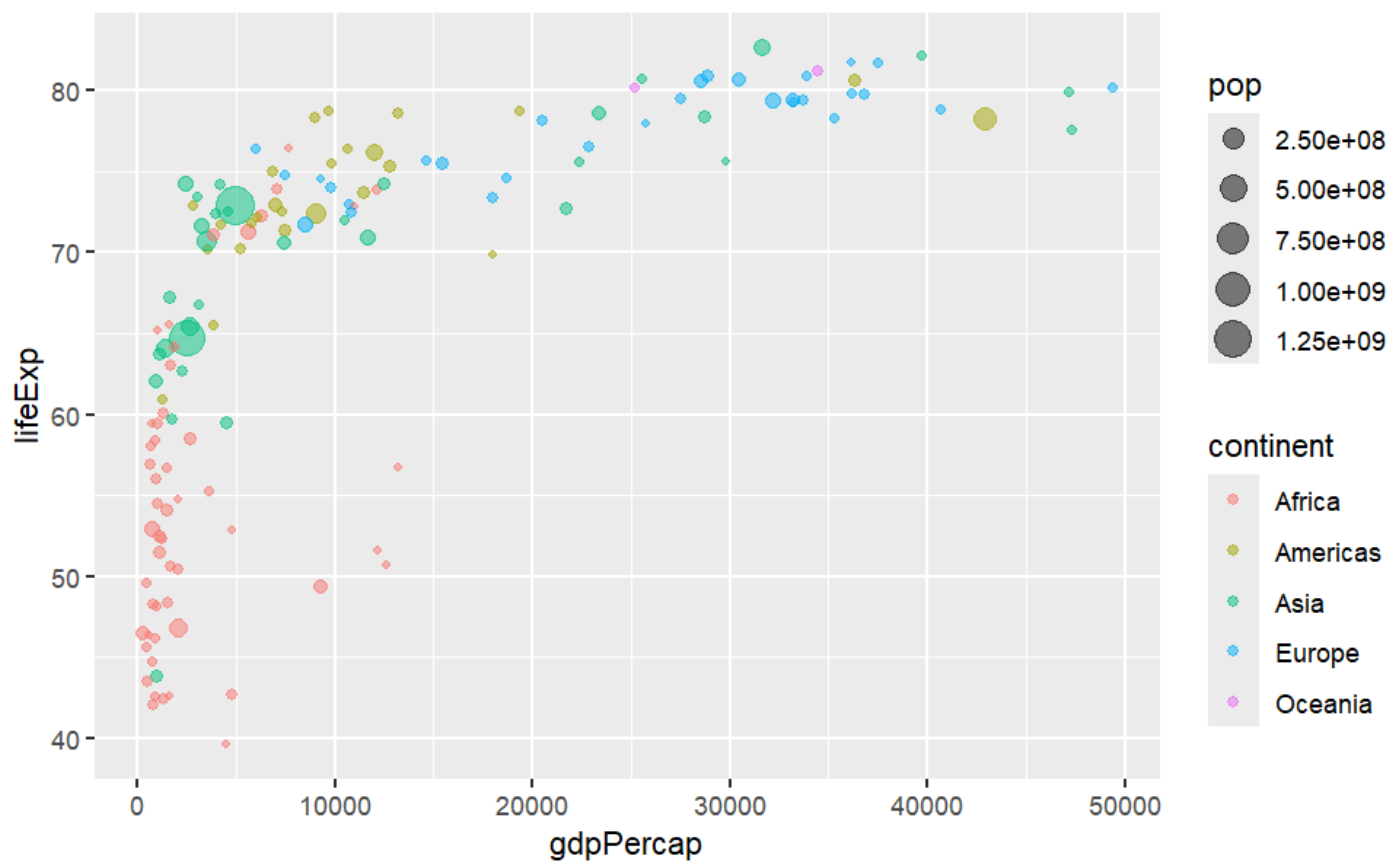
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```
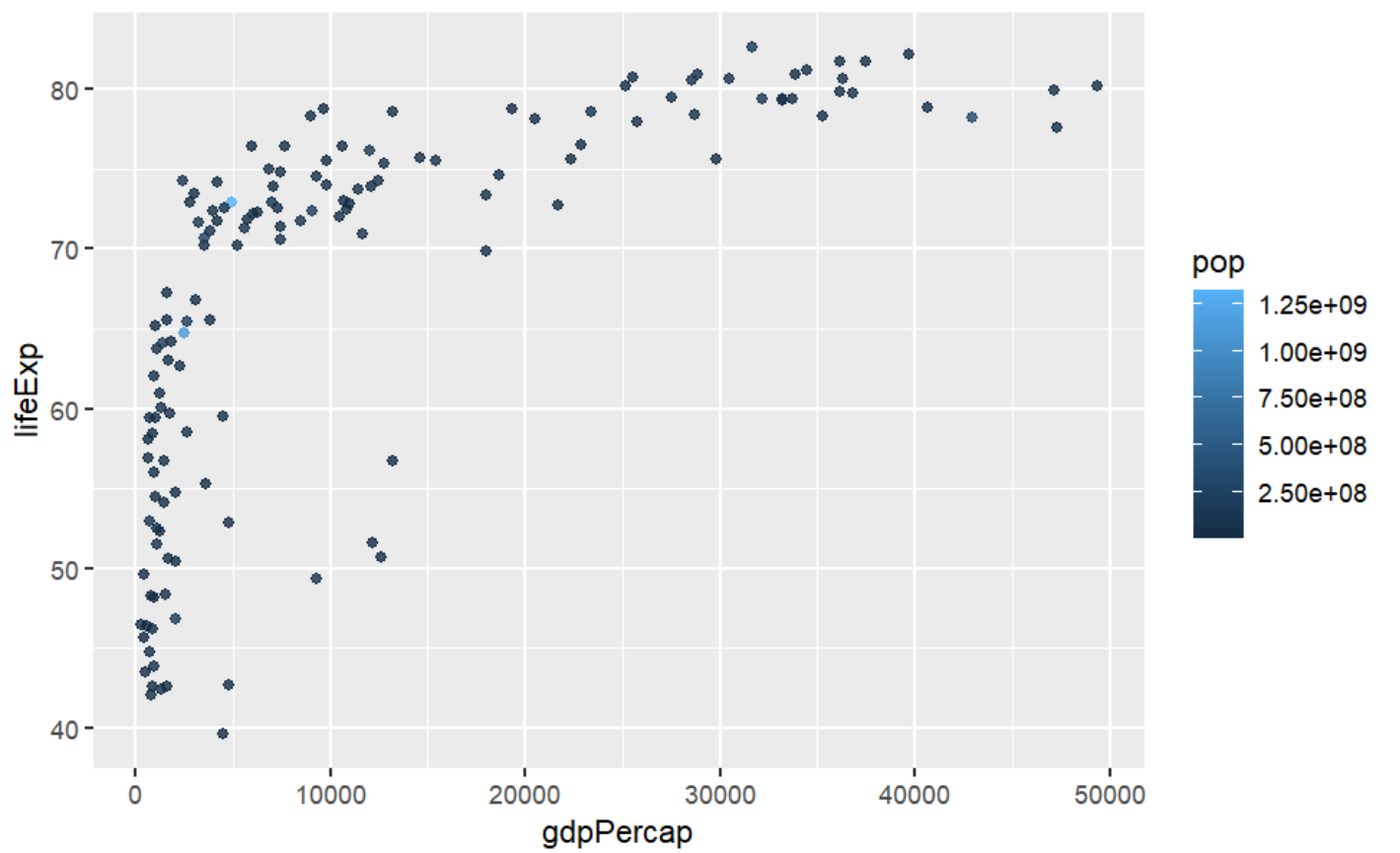
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```
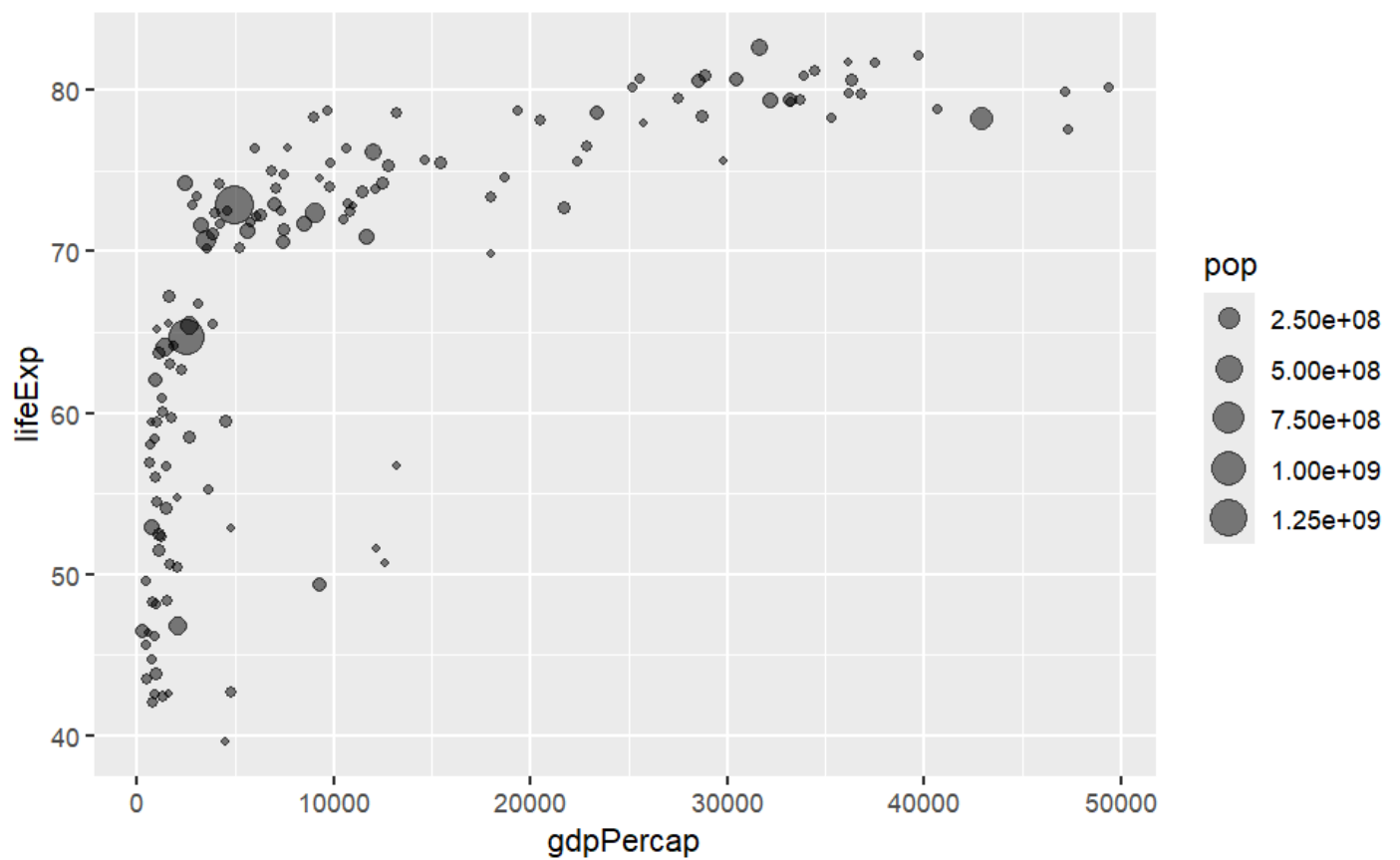
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```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = pop) +
  geom_point(alpha=0.8)
```
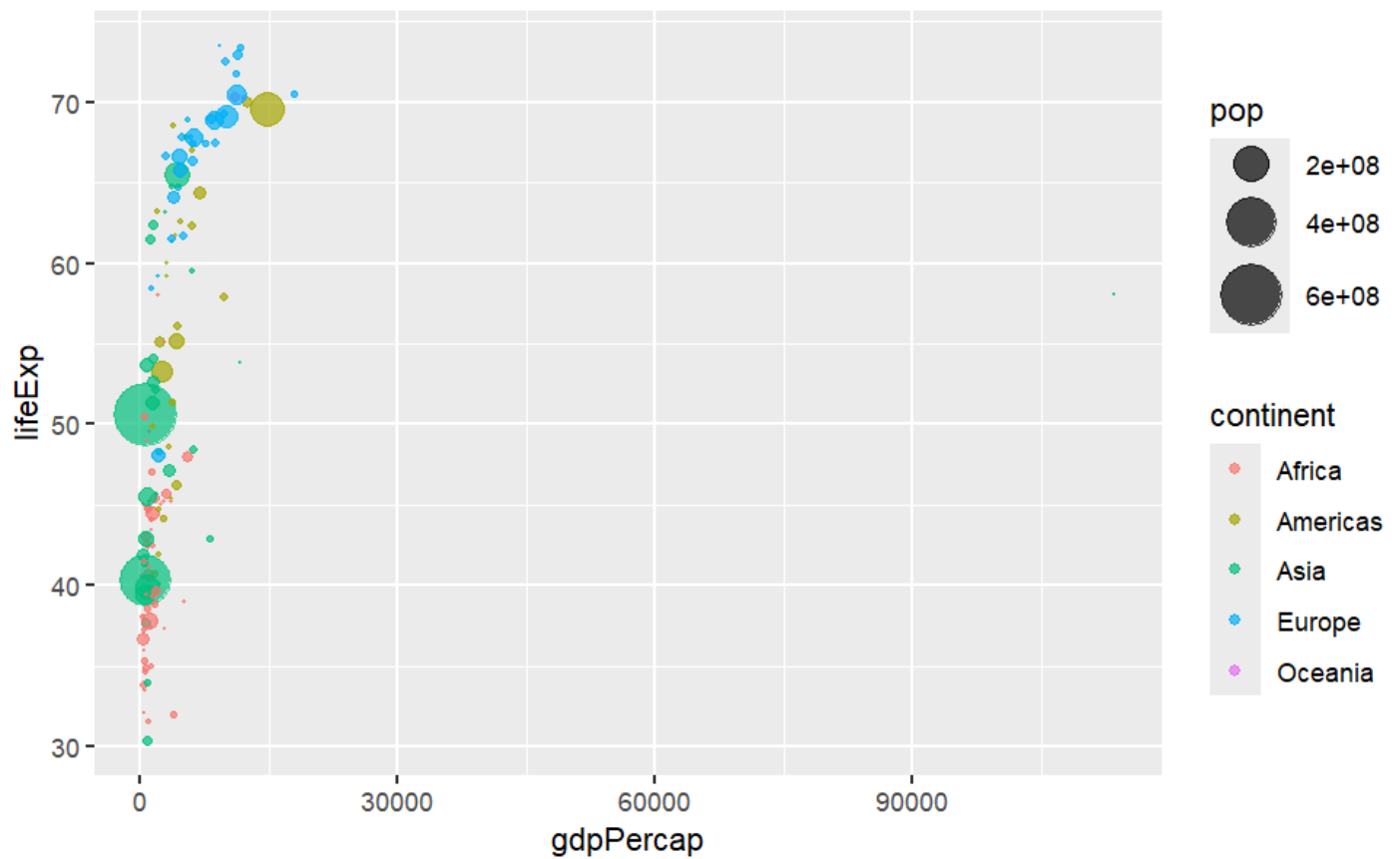
```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, size = pop) +
  geom_point(alpha=0.5)
```

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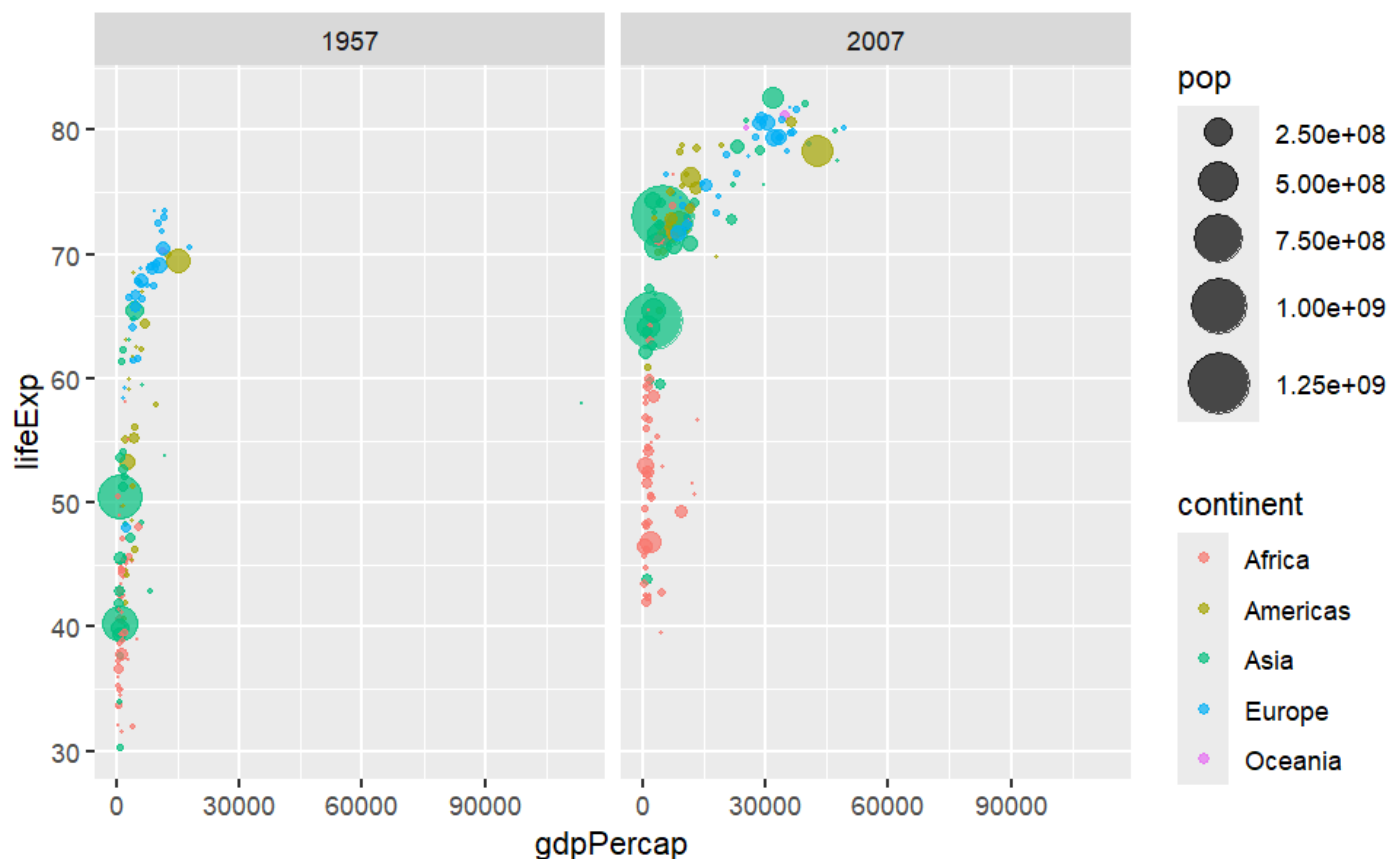
```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

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)
```

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.