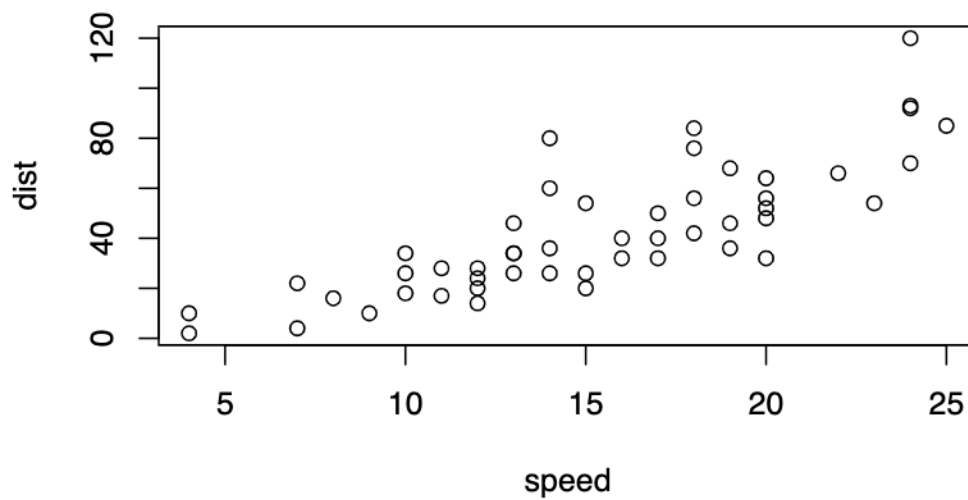


# Class 5: Visualization

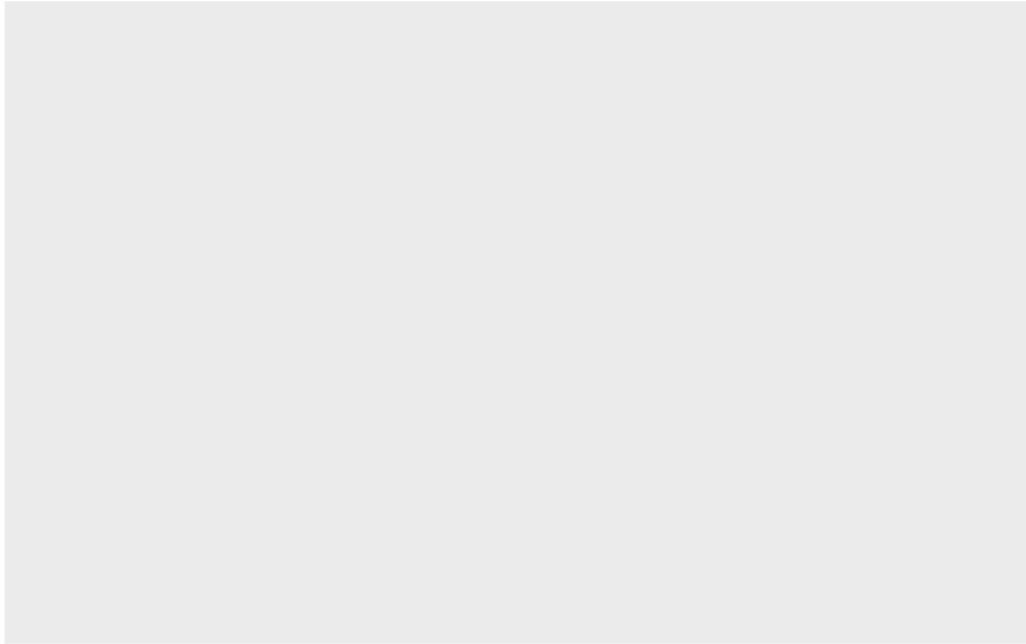
C.K

## Plotting in R

```
plot(cars)
```



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

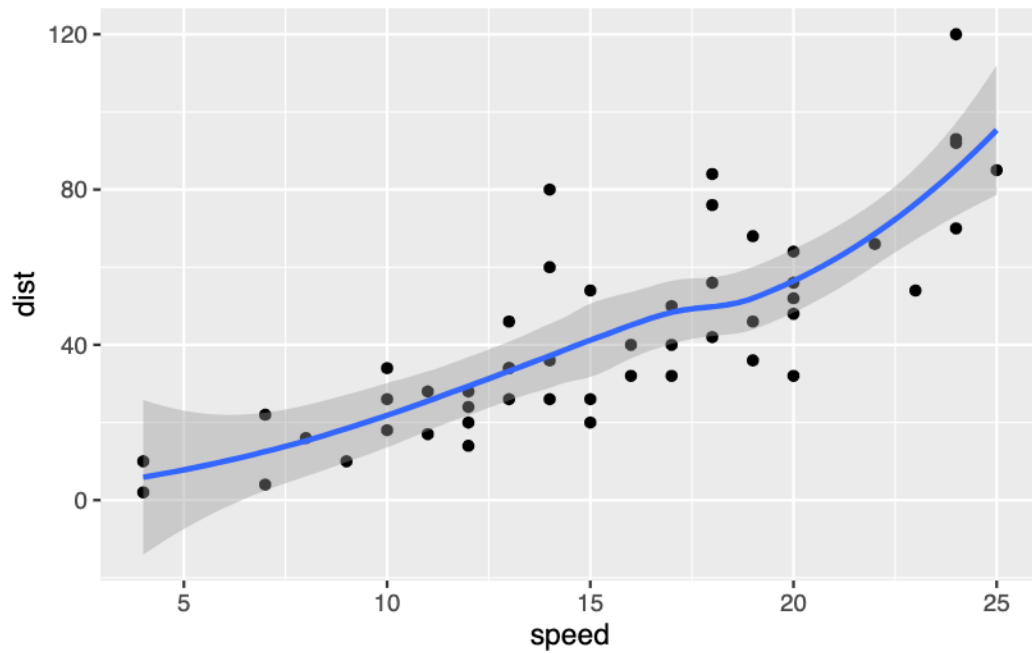


```
#install.packages("ggplot2")
```

```
#ggPlot ggplot(input data)+aesthetics() +geom_point() geom_smooth() put a line through  
it
```

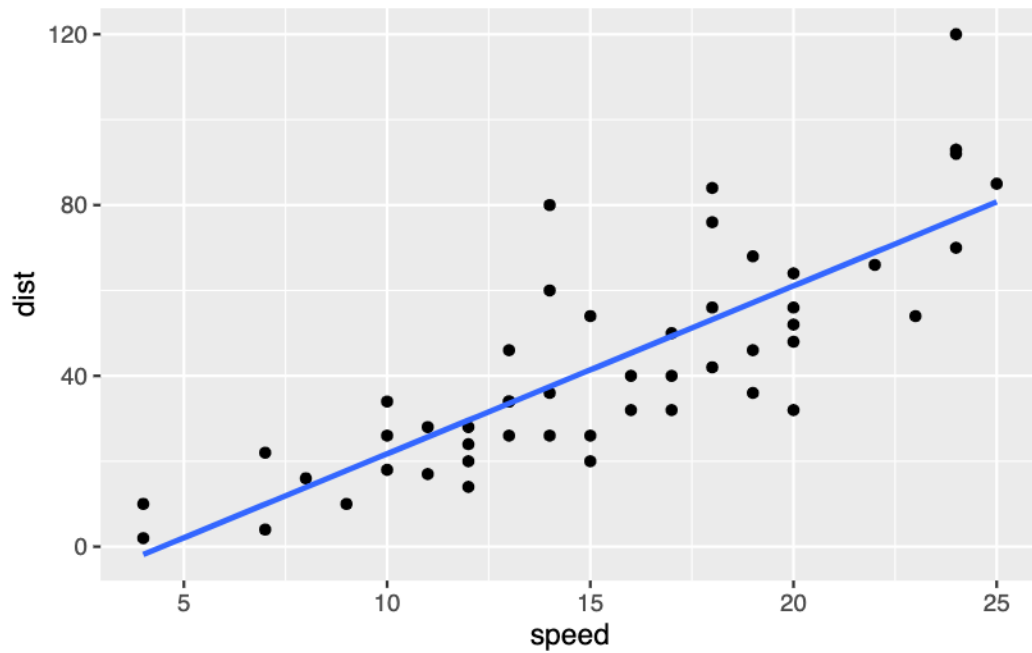
```
ggplot(data=cars)+aes(x=speed,y=dist)+geom_point()+geom_smooth()
```

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



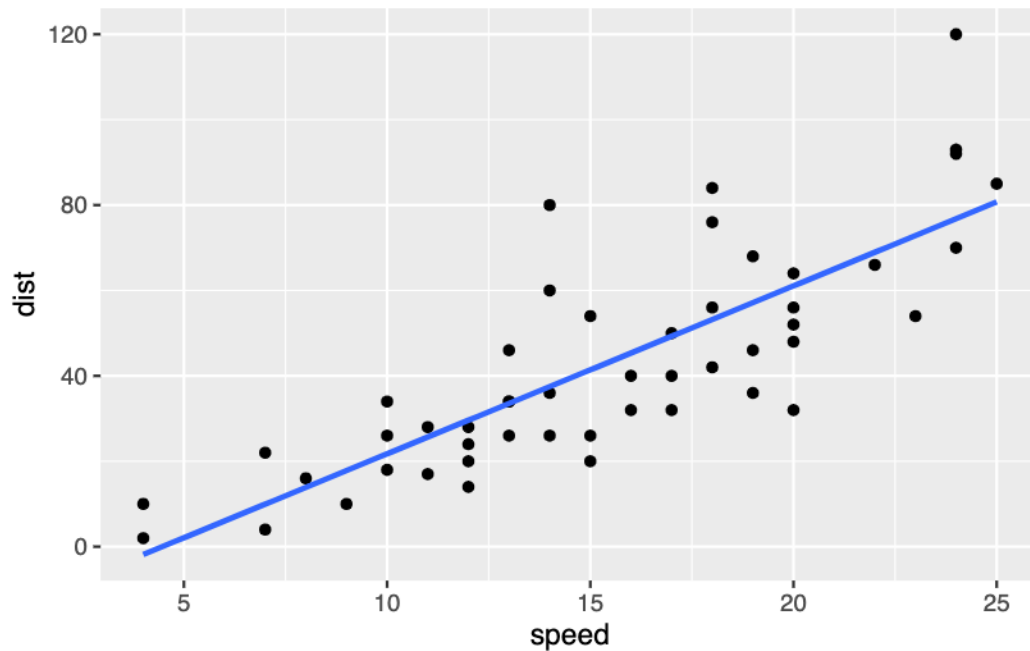
```
## different layers added on top of another
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE)
```

`geom\_smooth()` using formula = 'y ~ x'



```
#bb=ggplot(cars) +  
  #aes(x=speed, y=dist)+geom_point()  
bb=ggplot(cars,aes(x=speed, y=dist))+geom_point()  
# lm is the linear model  
bb+geom_smooth(method = "lm",se=FALSE)
```

`geom\_smooth()` using formula = 'y ~ x'



```
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"
```

```
ncol(genes)
```

```
[1] 4
```

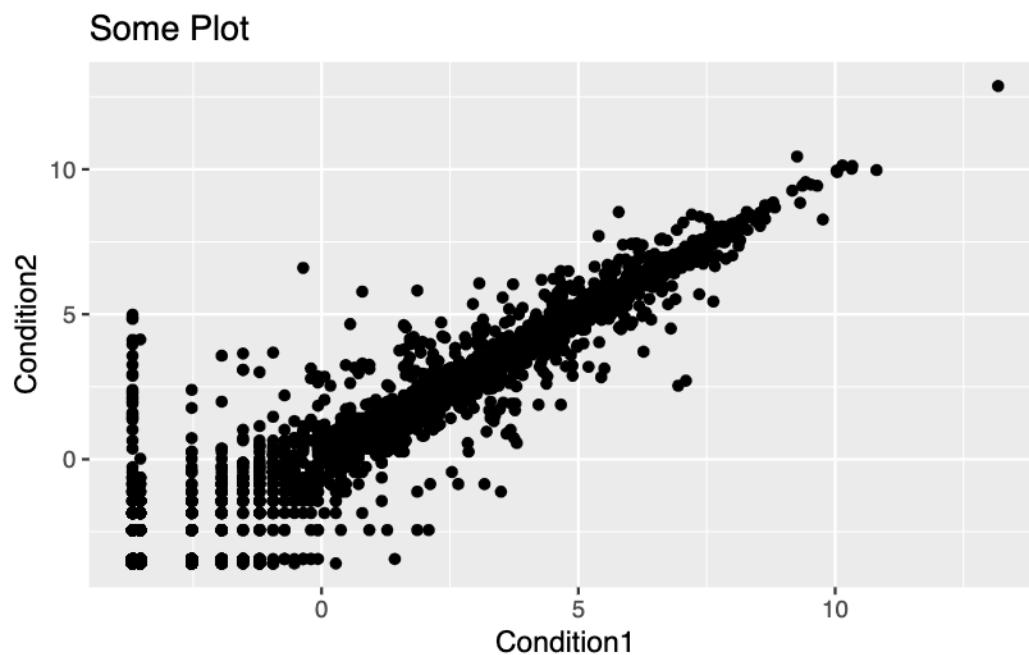
```
table(genes$State)
```

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

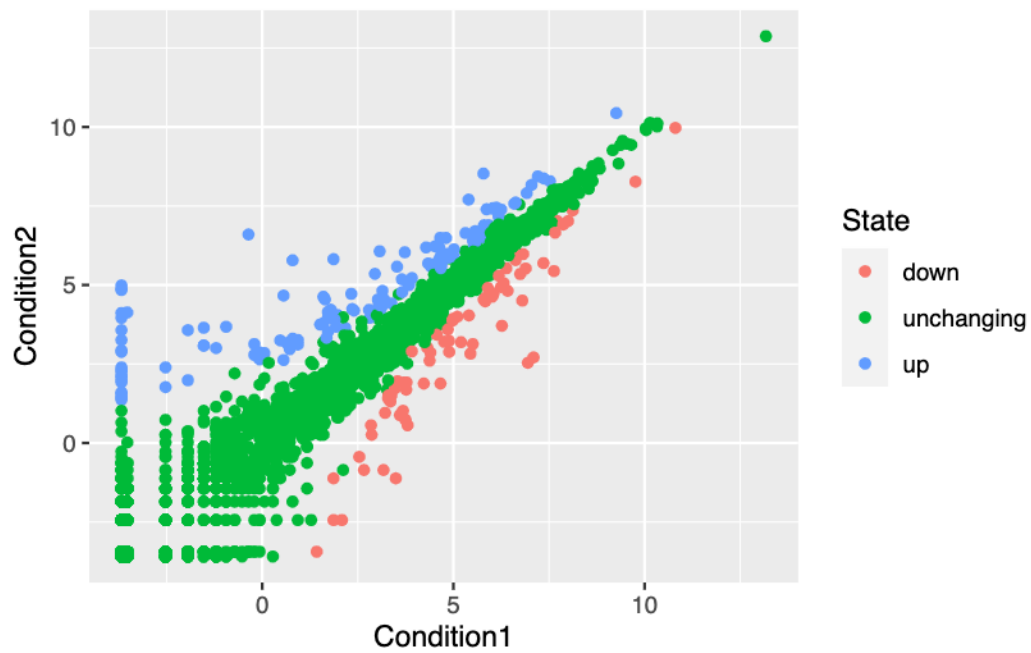
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

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

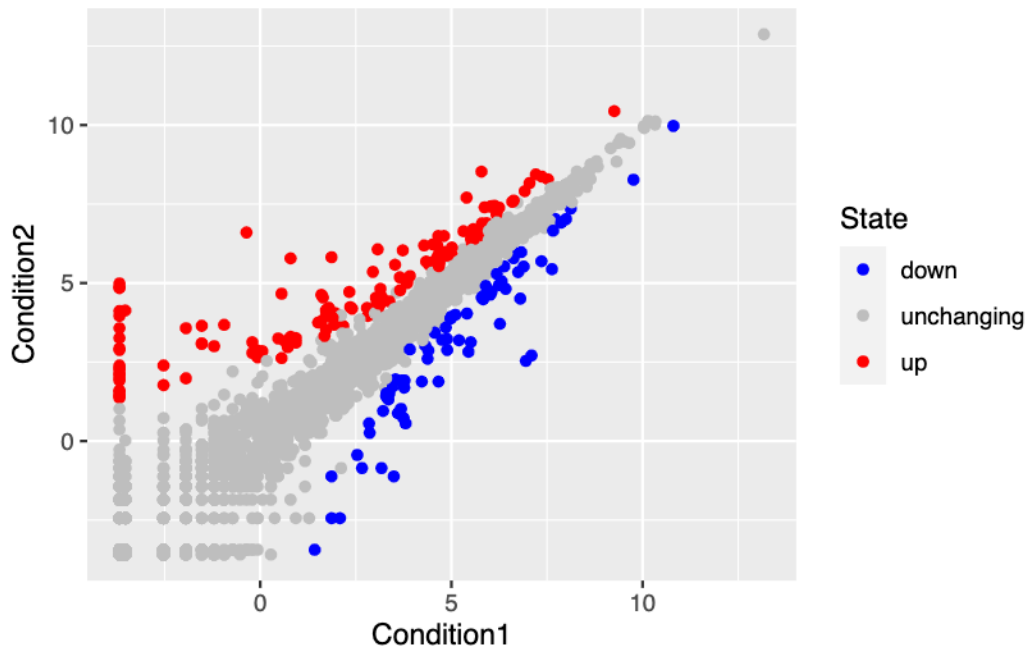
```
## check the aesthetic parameters to have different size, shape, colors for each individual  
ggplot(genes) +  
  aes(x=Condition1, y=Condition2) +  
  geom_point()+labs(title="Some Plot")
```



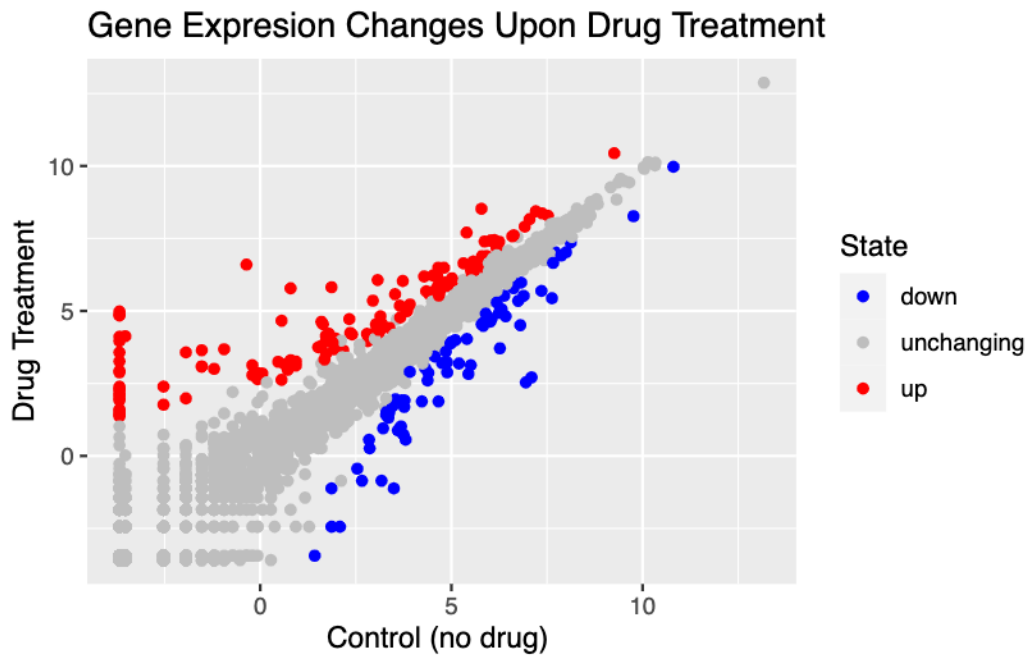
```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p
```



```
p + scale_colour_manual( values=c("blue","gray","red") )
```



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





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

gapminder <- read.delim(url)

library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

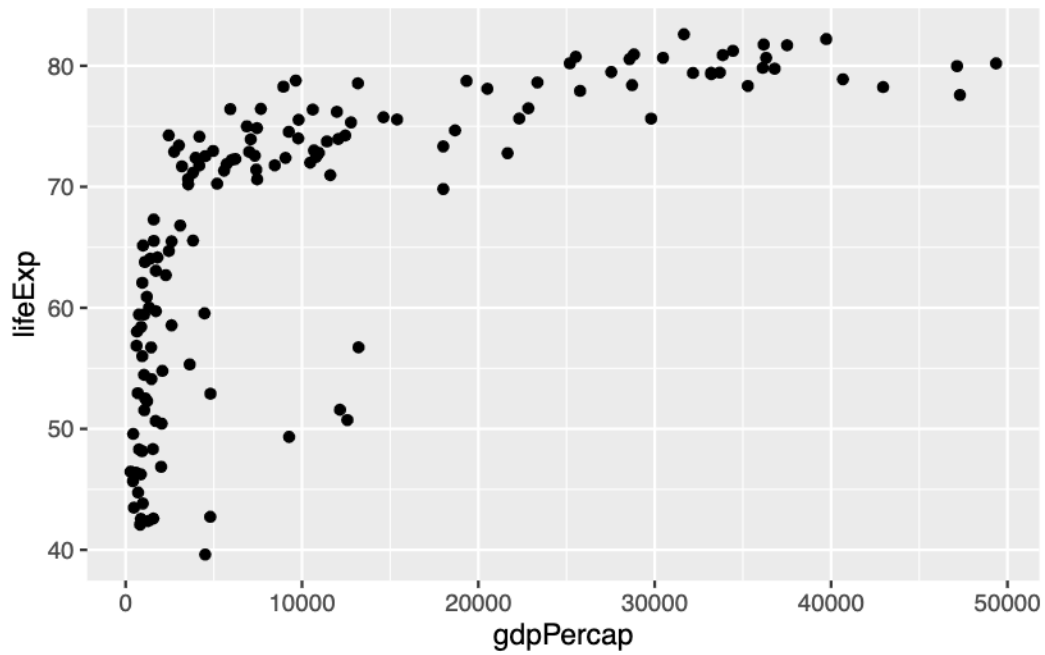
filter, lag

The following objects are masked from 'package:base':

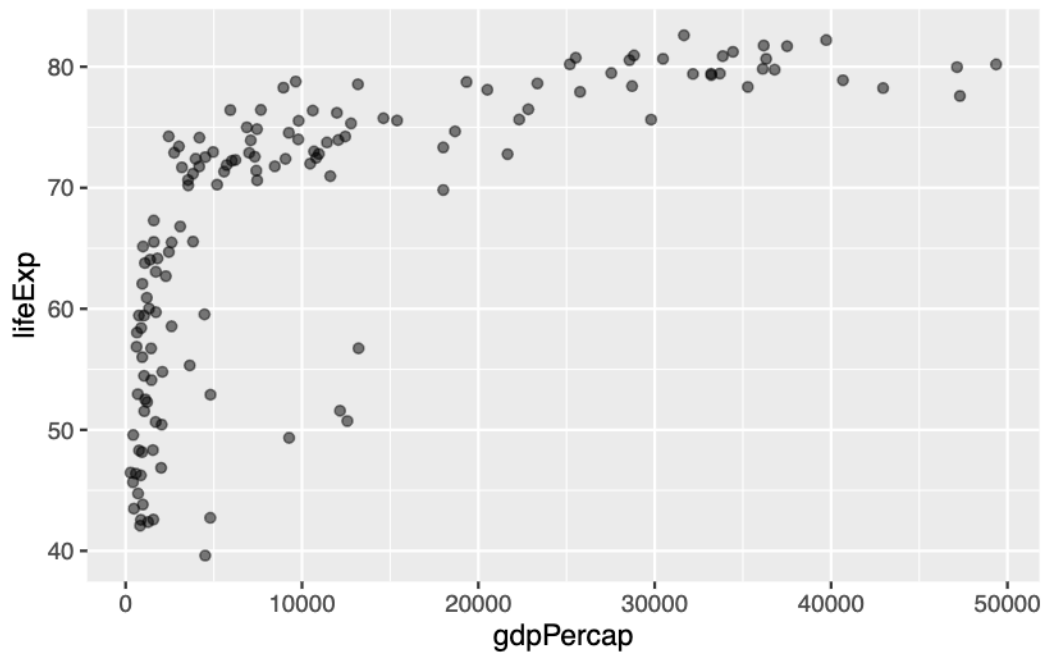
intersect, setdiff, setequal, union

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

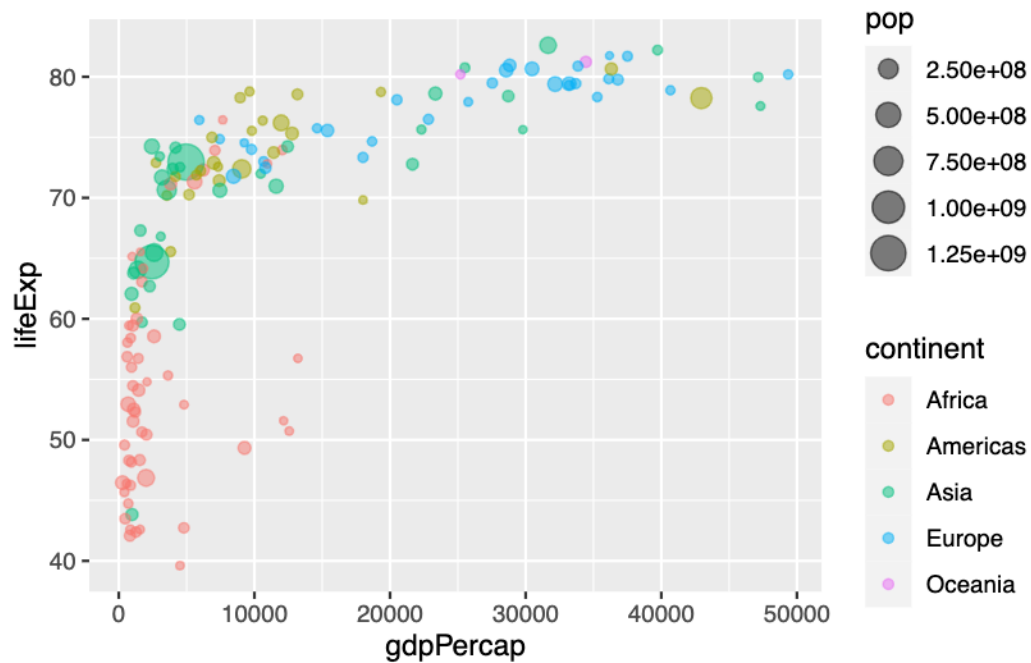
```
ggplot(gapminder_2007) +
  aes(x=gdpPerCap, y=lifeExp) +
  geom_point()
```



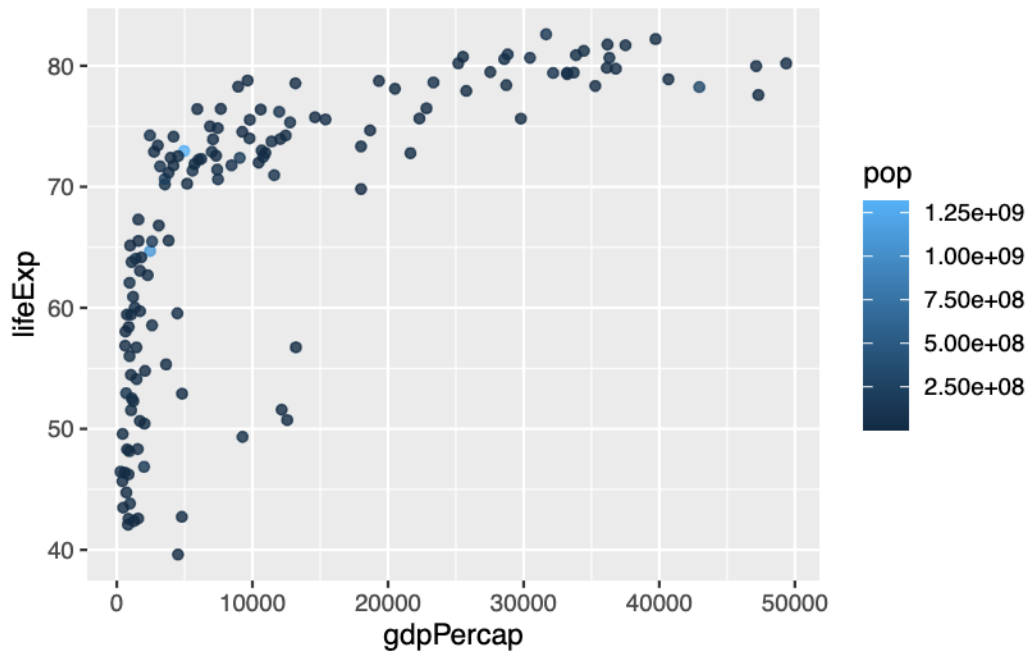
```
ggplot(gapminder_2007) +  
  aes(x=gdpPercap, y=lifeExp) +  
  geom_point(alpha=0.5)
```



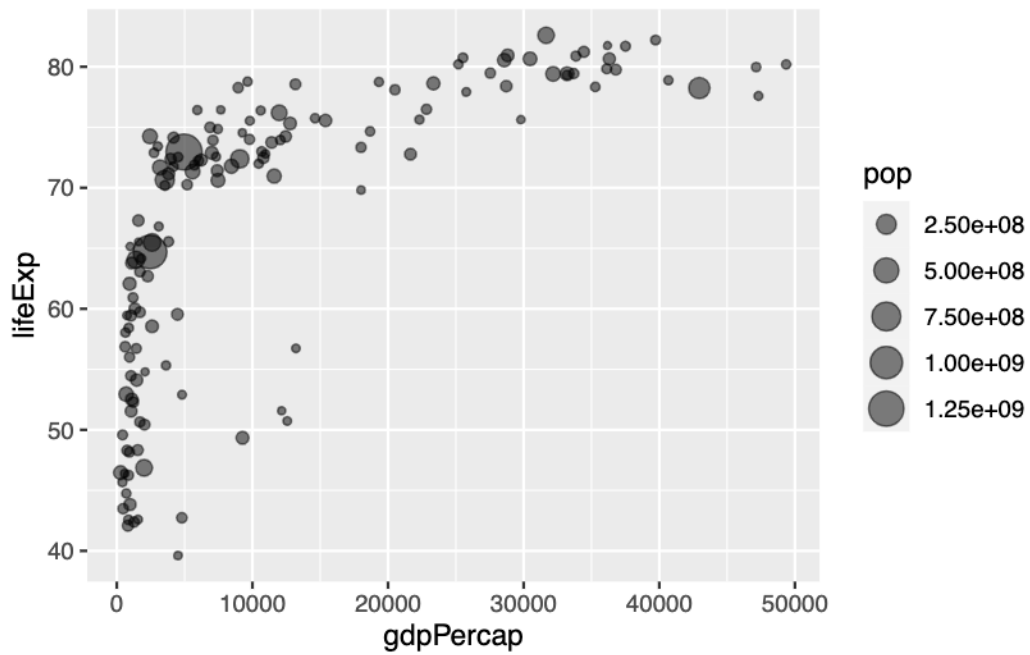
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



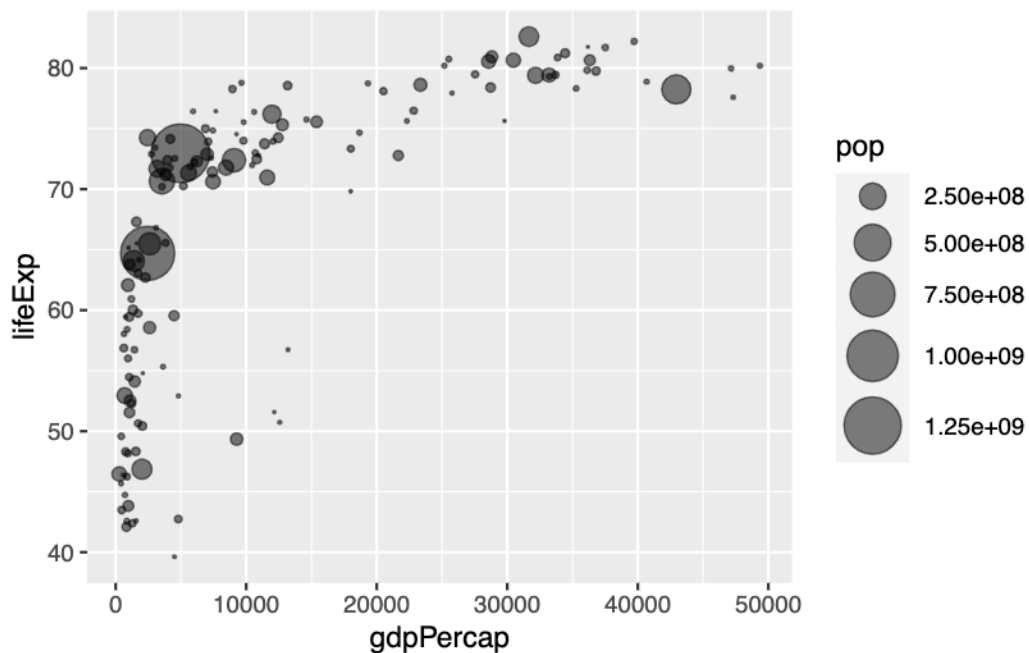
```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = pop) +
  geom_point(alpha=0.8)
```



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

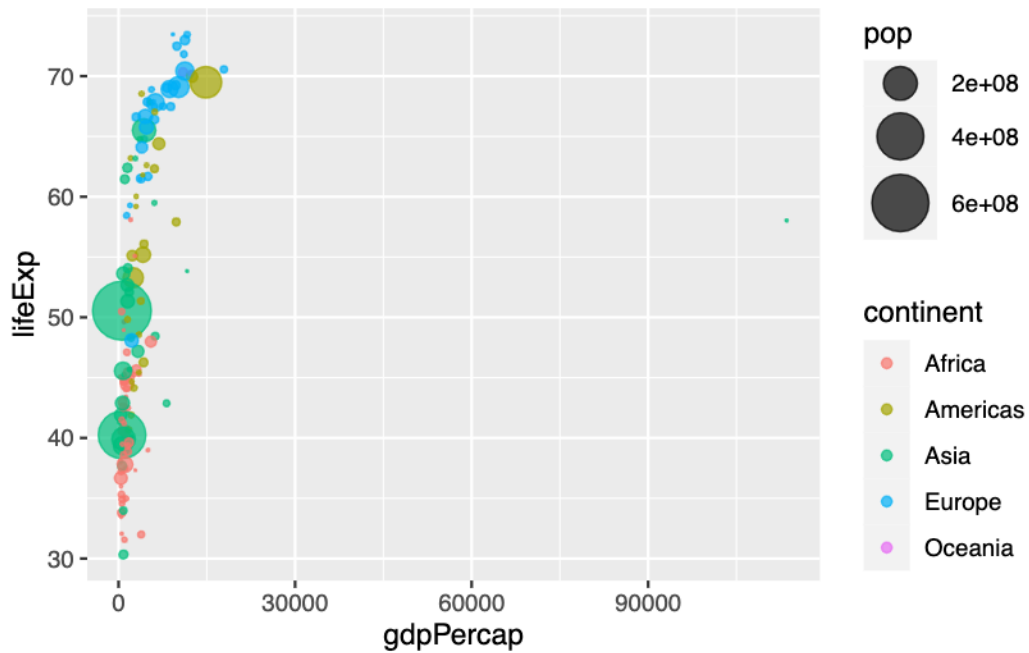


```
ggplot(gapminder_2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp,
                 size = pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```



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

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

