

Class 5: Data Viz with ggplot

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Intro to ggplot

There are many graphics systems in R (ways to make plots and figures). These include “base” R plots. Today we will focus mostly on the **ggplot2** package.

Q: Which plot types are typically NOT used to compare distributions of numeric variables? **Network graphs**

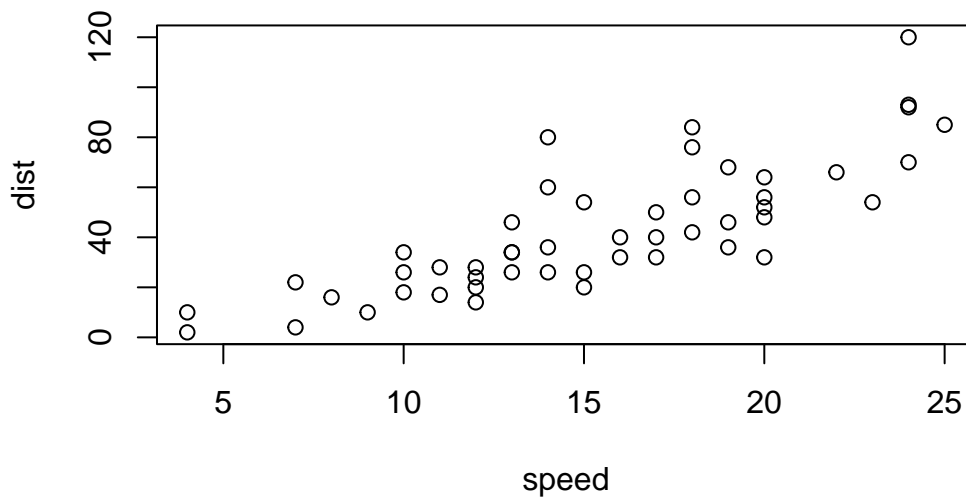
Q: Which statement about data visualization with ggplot2 is incorrect? **ggplot is the only way to create plots in R**

Let's start with a plot of a built-in dataset called **cars**.

```
head(cars)
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10

```
plot(cars)
```



Let's see how we can make this figure using **ggplot2**. For sake of clarity, I already have **ggplot2** installed, and thus have skipped the `install.package(ggplot2)` command. To install any package in R, I use the function `install_package()`.

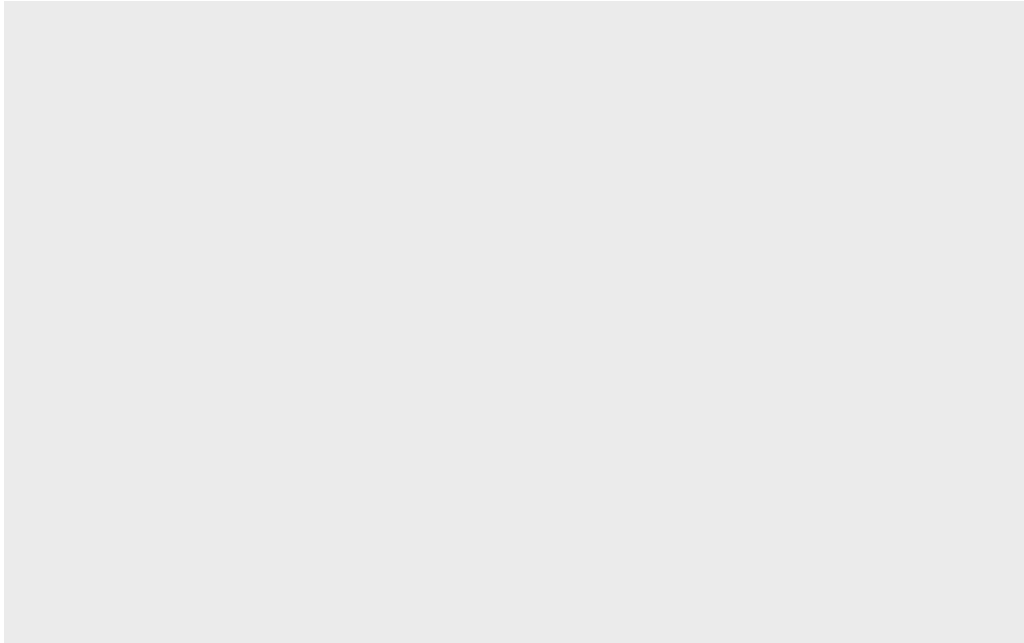
Note: do NOT install packages inside the Quarto document, it is better to do this directly in the console.

Before I can use any functions from add on packages, I must load the package using the “`library()`” function, in this case `library(ggplot2)`

```
library(ggplot2)
```

Warning: package 'ggplot2' was built under R version 4.3.3

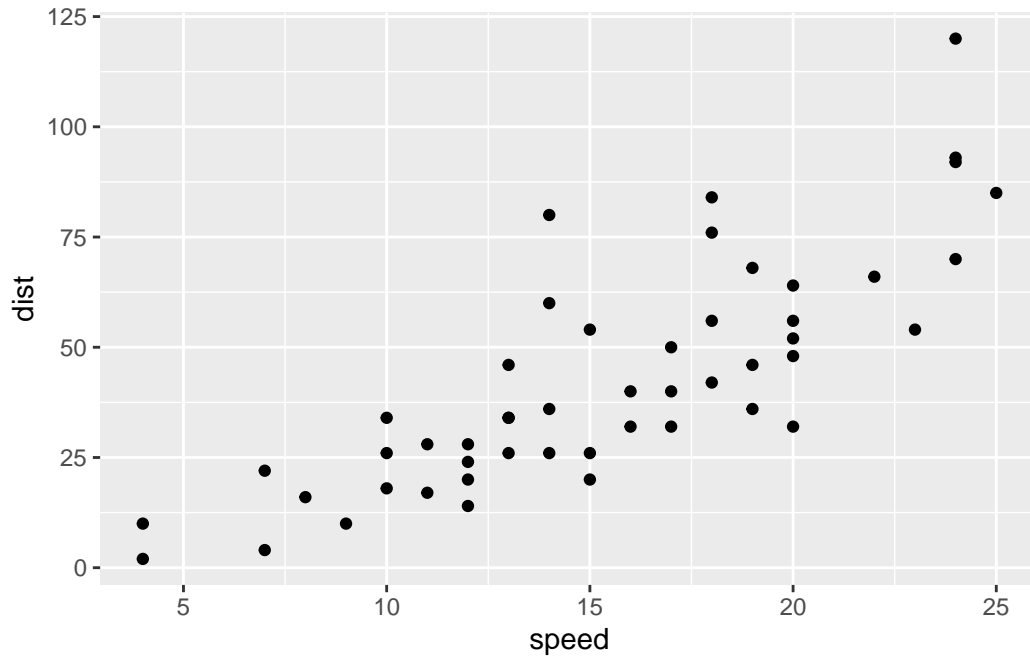
```
ggplot(cars)
```



All ggplot figures have at least 3 layers. These are:

- **Data** (input dataset to plot)
- **Aesthetics** (aes) (aesthetic mapping of data on plot)
- **Geometry** (geo) (point, line, bar, etc that I want to draw)

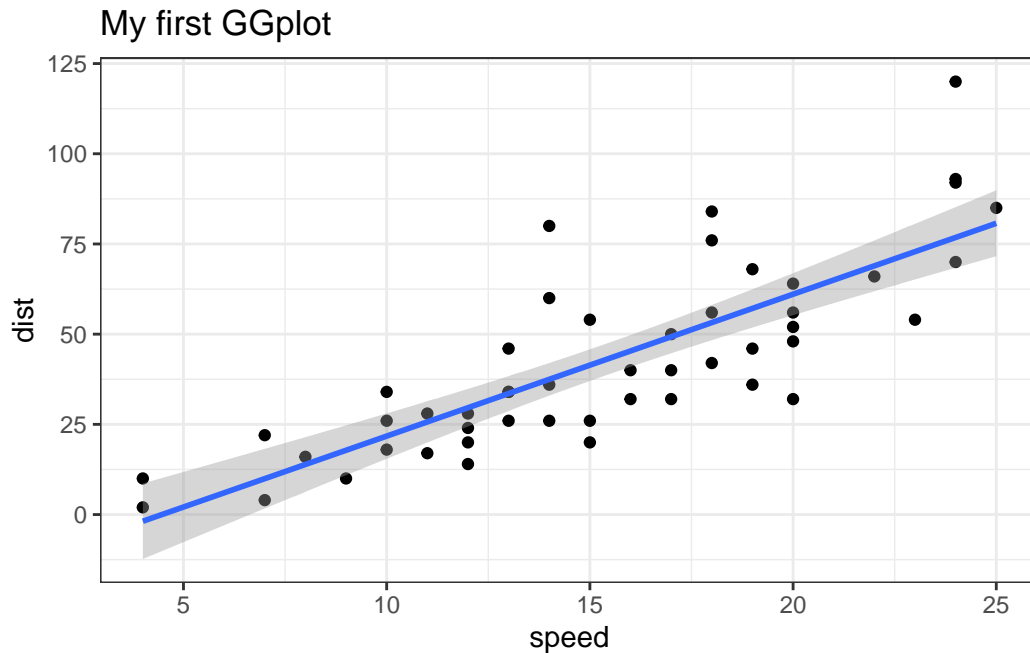
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```



Let's add a line to show the relationship between distance and speed

```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(method="lm") +  
  theme_bw() +  
  labs(title="My first GGplot")
```

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



Q: Which geometric layer should be used to create scatter plots in ggplot2?
geom_point()

Code to read the dataset:

```
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: Use the nrow() function to find out how many genes are in this dataset. What is your answer? **5196 rows**

```
nrow(genes)
```

```
[1] 5196
```

Q: Use the `colnames()` function and the `ncol()` function on the `genes` data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find? **4 columns**

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

Q: Use the `table()` function on the `State` column of this `data.frame` to find out how many 'up' regulated genes there are. What is your answer? **127 genes**

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

down	unchanging	up
72	4997	127

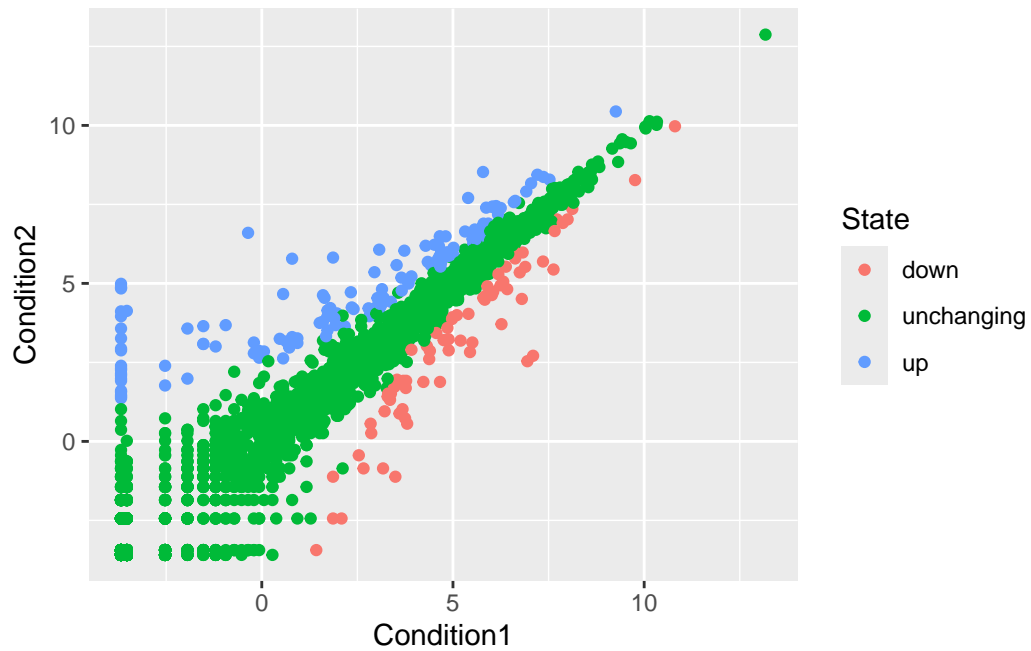
Q: Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset? **2.44 percent of genes**

```
round(table(genes$State)/nrow(genes), 4) * 100
```

down	unchanging	up
1.39	96.17	2.44

A first plot of this dataset:

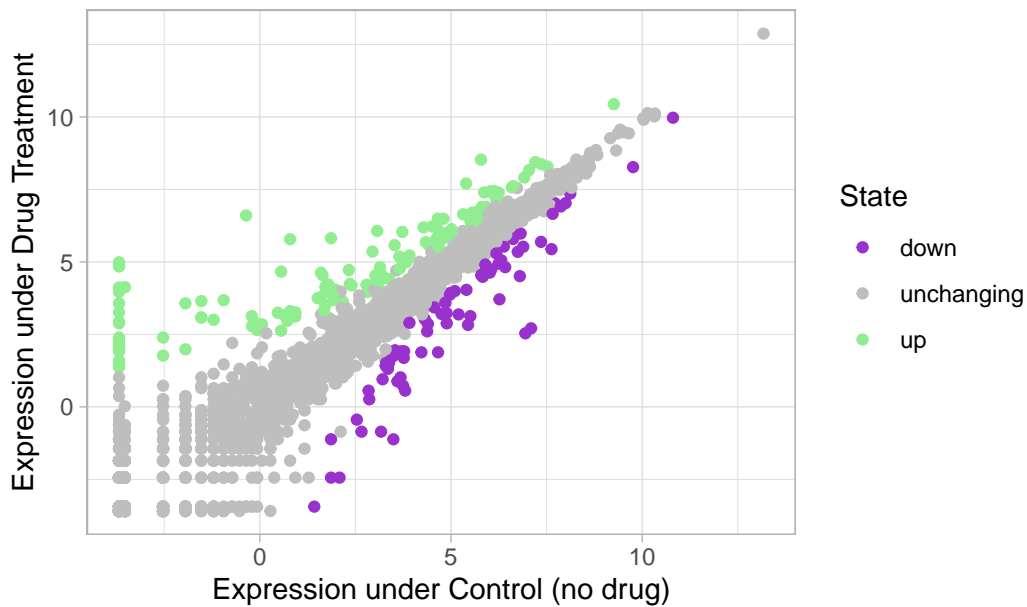
```
x <- ggplot(genes) +  
  aes(x=Condition1, y=Condition2, color=State) +  
  geom_point()  
x
```



Now let's fix the color scheme and add titles/labels:

```
x + scale_color_manual(values= c("darkorchid","gray","lightgreen")) +
labs(title="Gene Expression Changes with Drug Treatment",
      x="Expression under Control (no drug)",
      y="Expression under Drug Treatment") +
theme_light()
```

Gene Expression Changes with Drug Treatment



Let's explore more plots we can make using the ggplot2 package!

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"
gapminder <- read.delim(url)
library(dplyr)
```

Attaching package: 'dplyr'

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

filter, lag

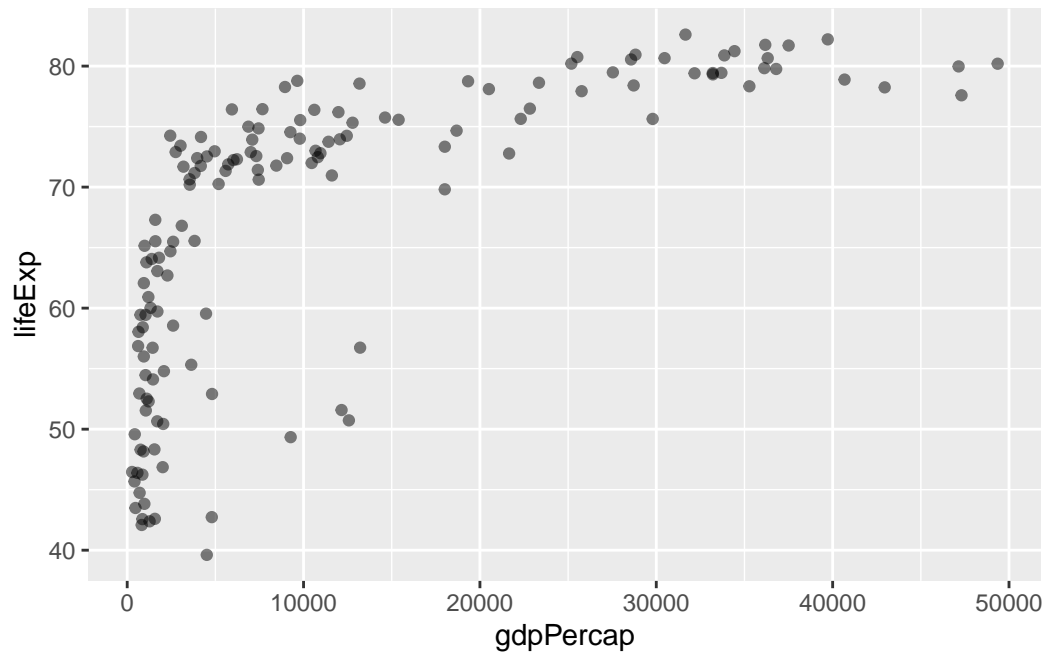
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

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

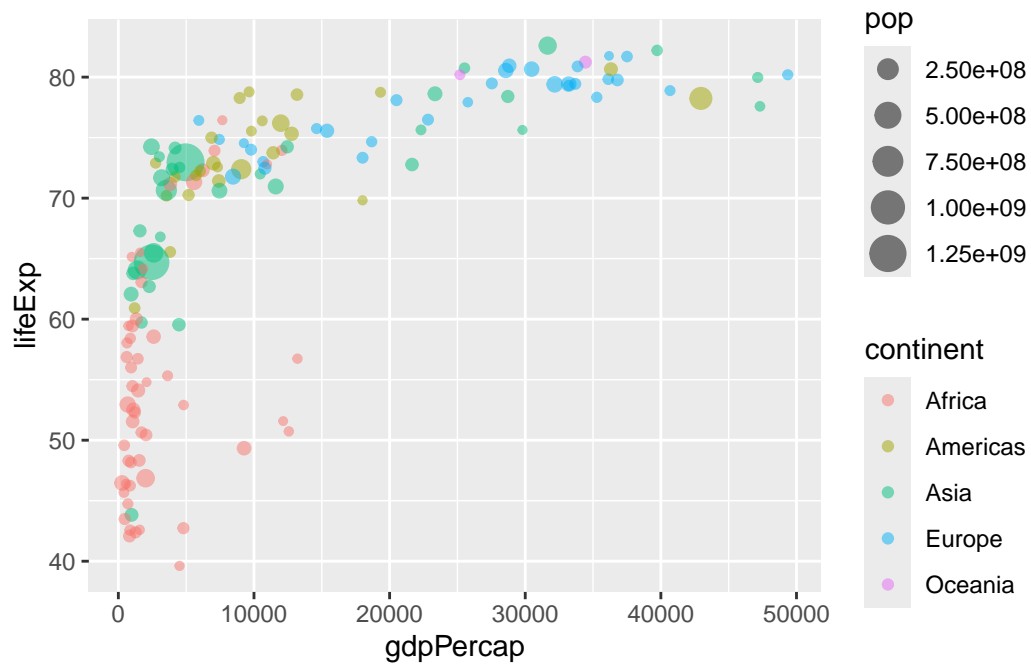
We have now filtered data from just 2007 in the gapminder dataset, I will now plot this:


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



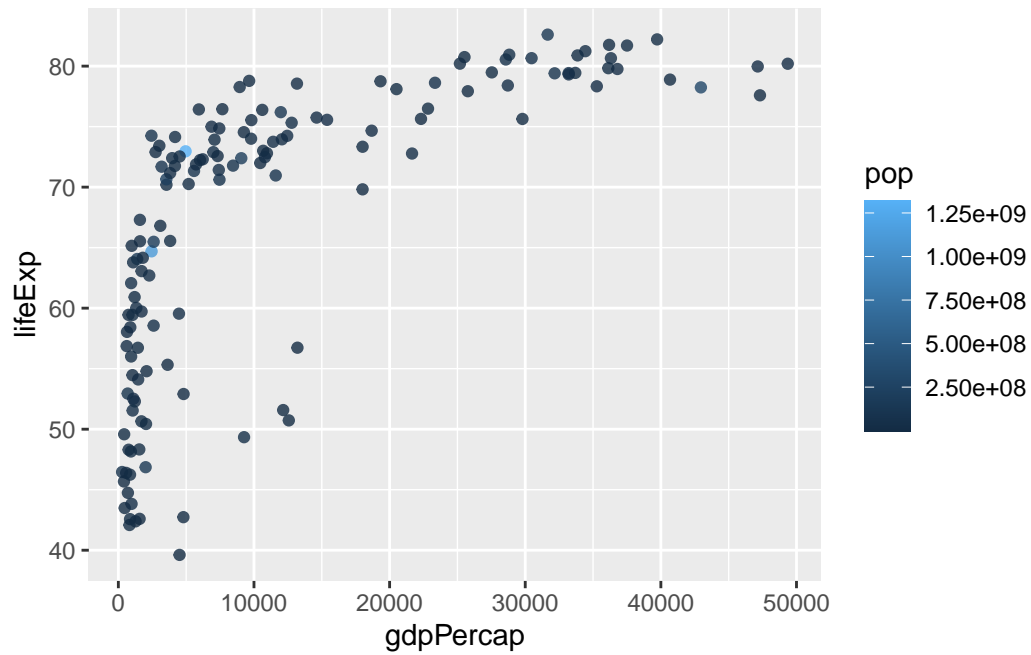
Let's add some additional aesthetics:

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



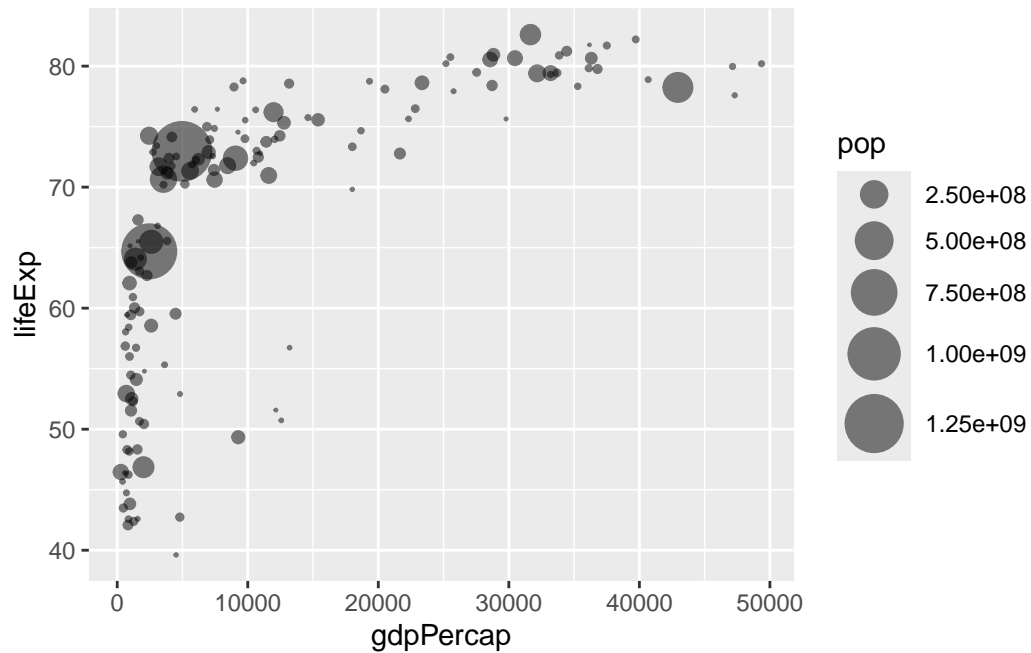
Let's look at the continuous variation upon this graph:

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



Let's look at population by size instead of color:

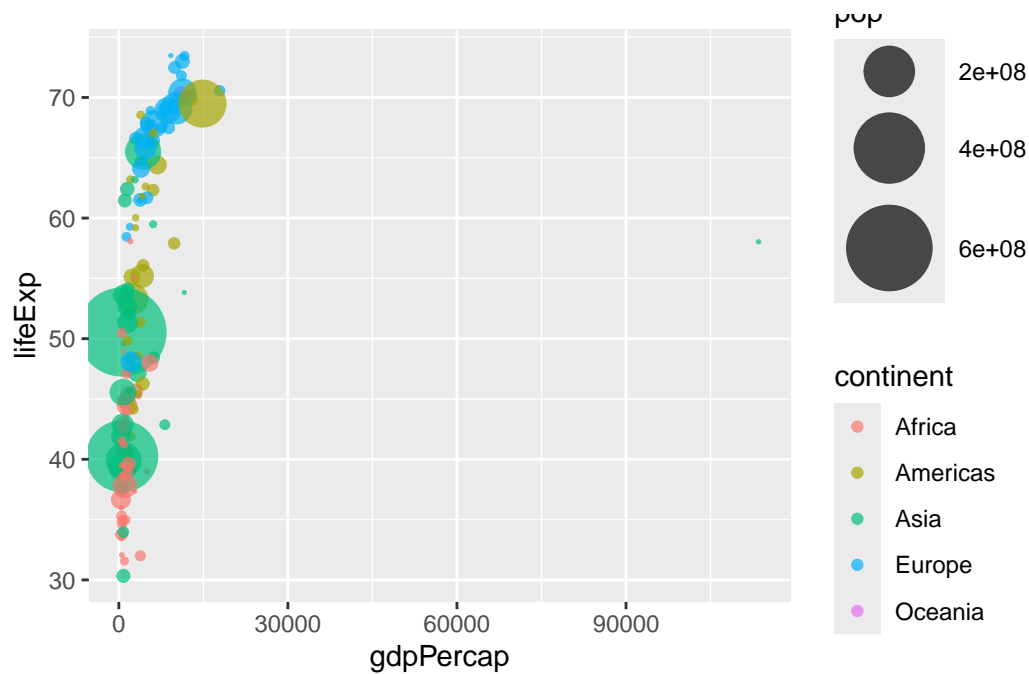
```
ggplot(gapminder_2007) +  
  aes(x=gdpPercap, y=lifeExp, size=pop)+  
  geom_point(alpha=0.5) +  
  scale_size_area(max_size = 10)
```



I will now do the same to data from 1957:

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

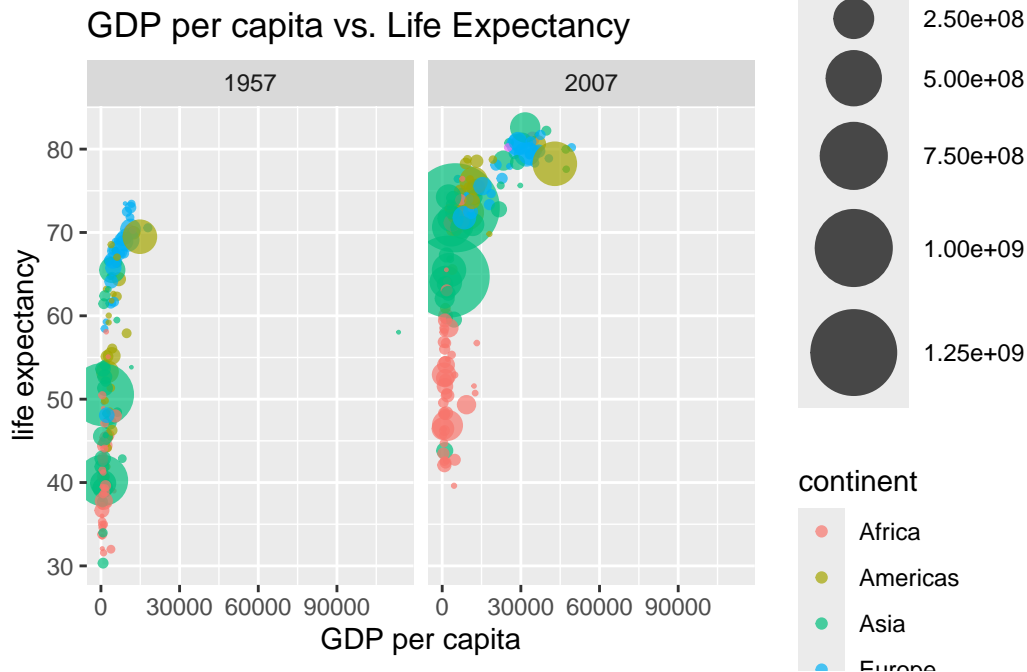
```
ggplot(gapminder_1957) +
  aes(x=gdpPerCap, y=lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.7)+
  scale_size_area(max_size=15)
```



I will now introduce both years:

```
gapminder_2years <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_2years) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.7)+
  scale_size_area(max_size=15)+
  facet_wrap(~year)+
  labs(title="GDP per capita vs. Life Expectancy",
       x="GDP per capita",
       y="life expectancy")
```



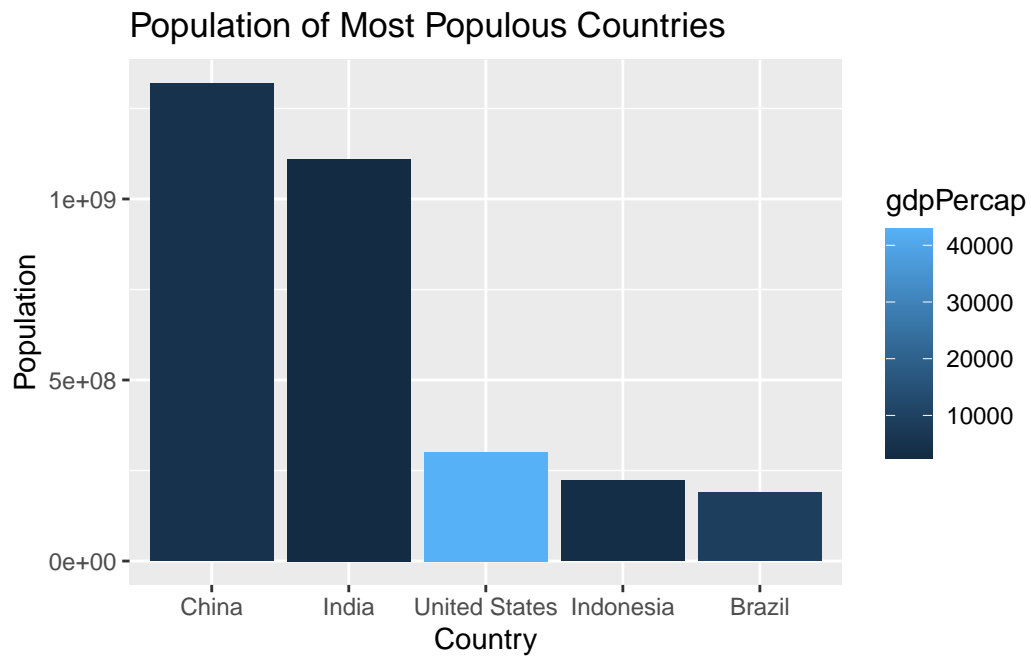
Let us now observe this data using boxplots:

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

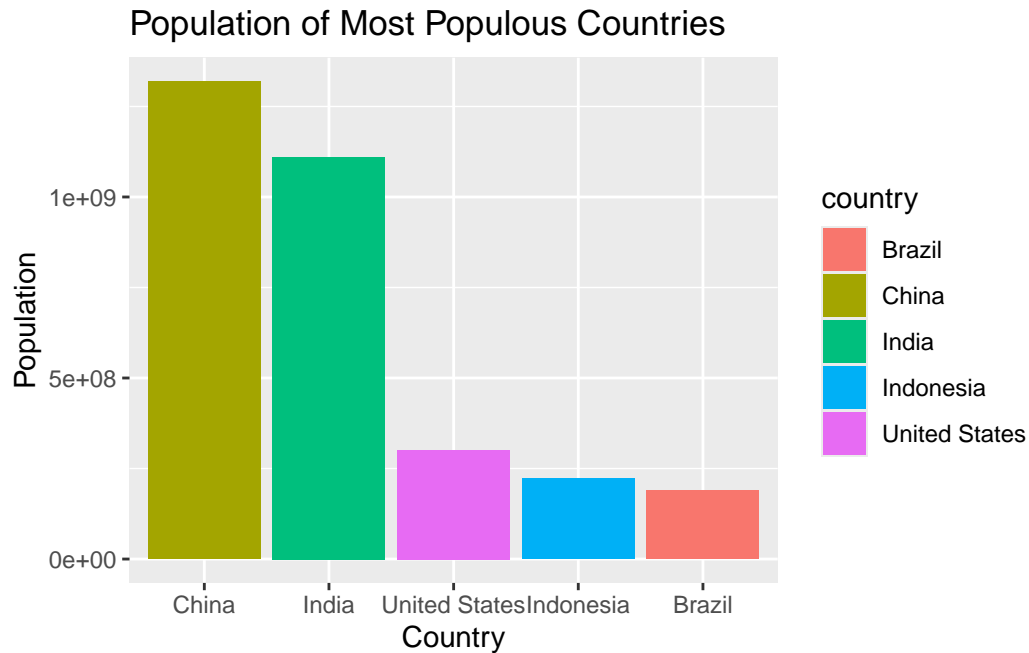
gapminder_top5
```

	country	continent	year	lifeExp	pop	gdpPercap
1	China	Asia	2007	72.961	1318683096	4959.115
2	India	Asia	2007	64.698	1110396331	2452.210
3	United States	Americas	2007	78.242	301139947	42951.653
4	Indonesia	Asia	2007	70.650	223547000	3540.652
5	Brazil	Americas	2007	72.390	190010647	9065.801

```
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=gdpPercap)+
  geom_col() +
  labs(title="Population of Most Populous Countries",
       x="Country",
       y="Population")
```



```
ggplot(gapminder_top5) +  
  aes(x=reorder(country, -pop), y=pop, fill=country)+  
  geom_col() +  
  labs(title="Population of Most Populous Countries",  
        x="Country",  
        y="Population")
```

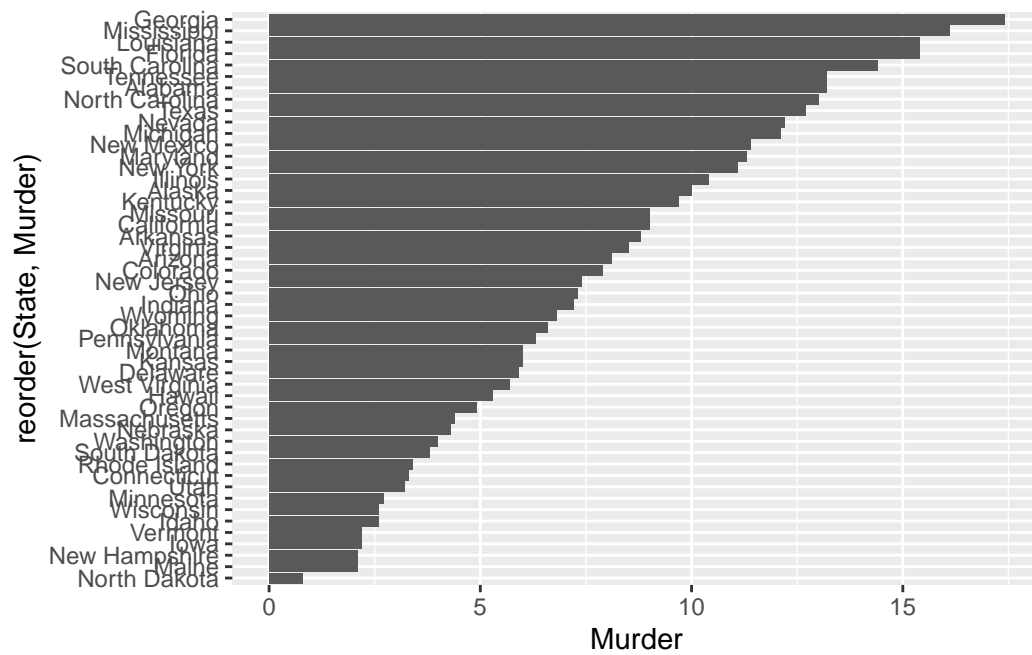


Flipping coordinates:

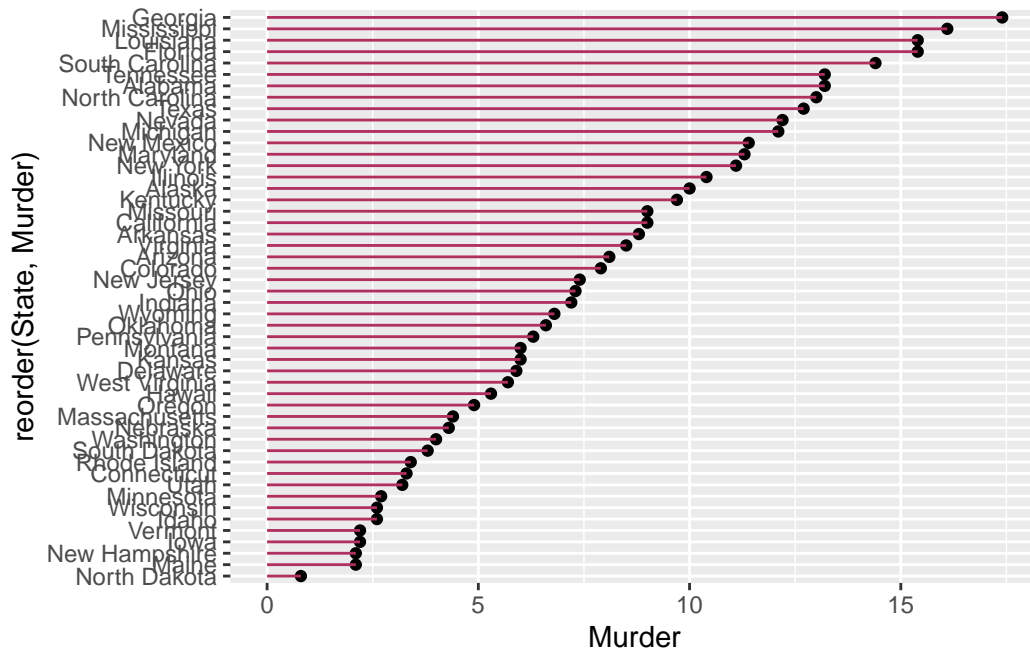
```
head(USArrests)
```

	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=State,xend=State,y=0,yend=Murder), color="maroon") +
  coord_flip()
```



Let's animate!

```
library(gifski)
```

Warning: package 'gifski' was built under R version 4.3.3

```
library(gganimate)
```

Warning: package 'gganimate' was built under R version 4.3.3

```
#ggplot(gapminder, aes(gdpPercap, lifeExp, size = pop, colour = country)) +
# geom_point(alpha = 0.7, show.legend = FALSE) +
# scale_colour_manual(values = country_colors) +
# scale_size(range = c(2, 12)) +
# scale_x_log10() +
# Facet by continent
#facet_wrap(~continent) +
# Here comes the gganimate specific bits
#labs(title = 'Year: {frame_time}', x = 'GDP per capita', y = 'life expectancy') +
# transition_time(year) +
# shadow_wake(wake_length = 0.1, alpha = FALSE)
```

Finally, let's make a multipanel figure:

```
library(patchwork)
```

Warning: package 'patchwork' was built under R version 4.3.3

```
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(dis, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

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

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

