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title: "Class 5: Data Viz with ggplot"
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```

R has lots of ways to make figures and graphs
****"Base" R**** – the `plot()` function

```

```{r}
plot(cars)
```

```

A very popular package is ****ggplot2****
 Before I can use any package, i need to install it; `install.packages("ggplot2")`
 command/function.

Then to use the package I need to load it as `library(ggplot2)`

```

```{r}
library(ggplot2)
ggplot(cars) + aes(x = speed, y = dist) + geom_point()
```

```

For "simple" plots like this one base R code will be much better than ggplot code

Let's fit a model and show it on my plot.

```

```{r}
ggplot(cars) +
 aes(x = speed, y = dist) +
 geom_point() +
 geom_smooth()
```

```

```

```{r}
ggplot(cars) +
 aes(x = speed, y = dist) +
 geom_point() +
 labs(title = "Speed and Stopping Distances of Cars",
 x = "Speed (MPH)",
 y = "Stopping Distance (ft)",
 subtitle = "Correlation between stopping distance and speed of cars",
 caption = "Dataset: 'cars'") +
 geom_smooth(method = "lm", se = FALSE)
theme_bw()
```

```

Every ggplot has at least 3 layers

- ****data**** (data.frame – the numbers or stuff you want to plot)
- ****aes**** (aesthetics (mapping of your data columns to your plot, position, size, line type, line width, color, shape))
- ****geom**** (`geom_point()`, `geom_line()`, `geom_col()`)

```

```{r}
head(mtcars)

#Make me a ggplot of the `mtcars` data set using `mpg` vs `disp` and set the size of
the points to the `hp` and set the color to `am`

ggplot(mtcars) +
 aes(x = mpg, y = disp, size = hp, col = am) +
 geom_point() +
 facet_wrap(~am)
```

```{r}
ggplot(mtcars) +
 aes(x = mpg, y = disp, size = hp, col = am) +
 geom_point(col = "blue")
```

```{r}
library(ggrepel)

ggplot(mtcars) +
 aes(x = mpg, y = disp, size = hp, col = am, label = rownames(mtcars)) +
 geom_point()+
 geom_text_repel()
```

```{r}
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```{r}
nrow(genes)
```

```{r}
colnames(genes)
ncol(genes)
```

```{r}
table(genes$State)
```

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

```{r}
ggplot(genes) +
 aes(x = Condition1, y = Condition2) +
 geom_point()
```

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

```

```

 labs(title = "Gene Expression Changes Upon Drug Treatment",
 x = "Control (no drug)",
 y = "Drug Treatment")
...

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

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

```{r}
library(dplyr)

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

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

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

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

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

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

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

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

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

```

```

` ``
` ``{r}
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)
` ``

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

gapminder_top5
` ``

` ``{r}
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop))
` ``

` ``{r}
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill = continent))
` ``

` ``{r}
ggplot(gapminder_top5) +
  geom_col(aes(x = country, y = pop, fill = lifeExp))
` ``

` ``{r}
ggplot(gapminder_top5) +
  aes(x=country, y=pop, fill=gdpPercap) +
  geom_col()
` ``

` ``{r}
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=gdpPercap) +
  geom_col()
` ``

` ``{r}
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=country) +
  geom_col(col="gray30") +
  guides(fill="none")
` ``

` ``{r}
head(USArrests)
` ``

` ``{r}
USArrests$State <- rownames(USArrests)

```

```

ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_col() +
  coord_flip()
``

```{r}
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()
``

```{r}

```