class 5: Data visualization with ggplot

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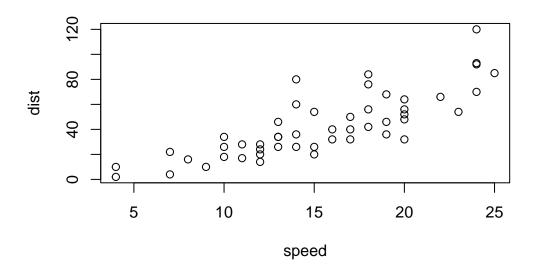
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Today we will have our first play with the **ggplot2** package - one of the most popular graphics packages on the planet.

There are many plotting systems in R. These include so called "base" plotting/graphics.

plot(cars)



Base plot is generally rather short code and somewhat dull plots - but it is always there for you and is fast for big datasets.

If i want to use **ggplot2** it takes some more work

```
# ggplot(cars)
```

I need to install the package first. To do this I can use the function 'install.packages("ggplot2")' Every time I want to use a package I need to load it up with a 'libarary()' call.

```
library(ggplot2)
```

Now finally I can use ggplot

```
ggplot(cars)
```

Every ggplot has at least 3 things:

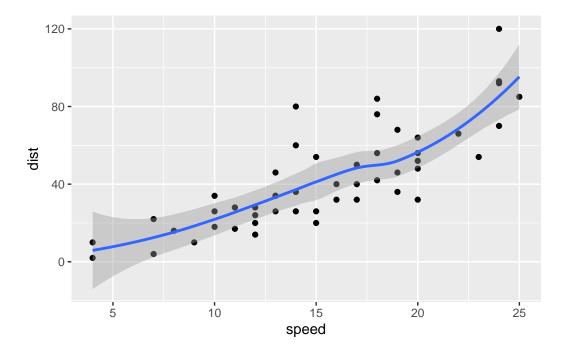
- data (the data.frame with the data you want to plot)
- aes (the asthetic mapping of the data to the plot)
- **geom** (how do you want the plot to look, points, lines, columns)

head(cars)

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

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

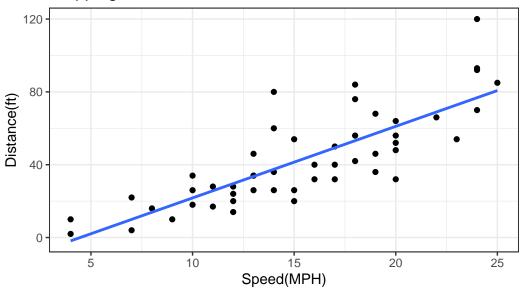
 $\ensuremath{\text{`geom_smooth()`}}\ using method = 'loess' and formula = 'y ~ x'$



I want a linear model and no standard error bounds shown on my plot.

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

Stopping Distnace of Old Cars



From the 'cars' dataset

A more complicated scatter plot

Here we make a plot of gene expression data:

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

```
Gene Condition1 Condition2
1
      A4GNT -3.6808610 -3.4401355 unchanging
2
       AAAS 4.5479580 4.3864126 unchanging
3
      AASDH 3.7190695 3.4787276 unchanging
       AATF
             5.0784720 5.0151916 unchanging
       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)
Γ1  4
  table(genes$State)
     down unchanging
                            up
       72
                4997
                           127
  genes$State == "up"
  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE TRUE FALSE
  [13] FALSE FALSE
  [25] FALSE FALSE
  [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
  [49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
  [61] FALSE FALSE
  [73] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
  [85] FALSE FALSE
  [97] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
[109] FALSE FALSE
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[589] FALSE FALSE
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[613] FALSE FALSE
```

```
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[1009] FALSE FALSE
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[1105] FALSE FALSE
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```

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```
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```
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[5137] FALSE FALSE
[5149] FALSE FALSE
[5161] FALSE FALSE
[5173] FALSE FALSE
[5185] FALSE FALSE
```

```
round( sum(genes$State == "up") / nrow(genes) * 100, 2)
```

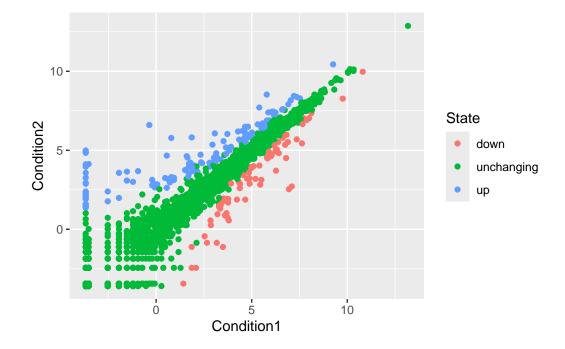
[1] 2.44

Another way to calculate percentage of total genes is up-regulated in this dataset?

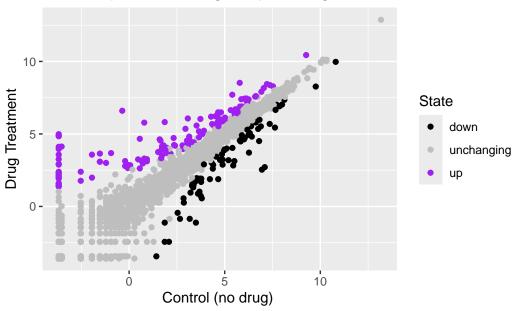
```
n.gene <- nrow(genes)
n.up <- sum(genes$State == "up")
up.present <- n.up/n.gene * 100
round (up.present, 2)</pre>
```

[1] 2.44

```
bp <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
bp</pre>
```







Exploring their gapmider dataset

Here we will load up the gaomider dataset to get practive with different as mappings.

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

How many rows and columns can be found in this dataframe?

```
row <- nrow(gapminder)
column <- ncol(gapminder)
row</pre>
```

[1] 1704

column

[1] 6

```
head(gapminder)
     country continent year lifeExp
                                        pop gdpPercap
1 Afghanistan
                  Asia 1952 28.801 8425333 779.4453
2 Afghanistan
                  Asia 1957 30.332 9240934 820.8530
3 Afghanistan
                  Asia 1962 31.997 10267083 853.1007
4 Afghanistan
                  Asia 1967
                            34.020 11537966 836.1971
5 Afghanistan
                  Asia 1972 36.088 13079460 739.9811
6 Afghanistan
                  Asia 1977 38.438 14880372 786.1134
Q. How many countries are there in this data set?
  table(gapminder$year)
1952 1957 1962 1967 1972 1977 1982 1987 1992 1997 2002 2007
 table(gapminder$continent)
 Africa Americas
                    Asia
                           Europe
                                   Oceania
    624
                     396
             300
                              360
                                        24
I could use the 'unique()' function...
  unique(gapminder$continent)
[1] "Asia"
              "Europe"
                         "Africa"
                                   "Americas" "Oceania"
  length (unique(gapminder$continent))
```

[1] 5

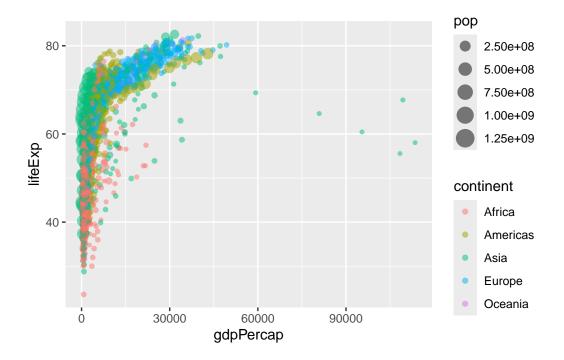
[1] 142

length (unique(gapminder\$country))

```
library(ggplot2)

ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.2)
```

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



library(dplyr)

Attaching package: 'dplyr'

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

filter, lag

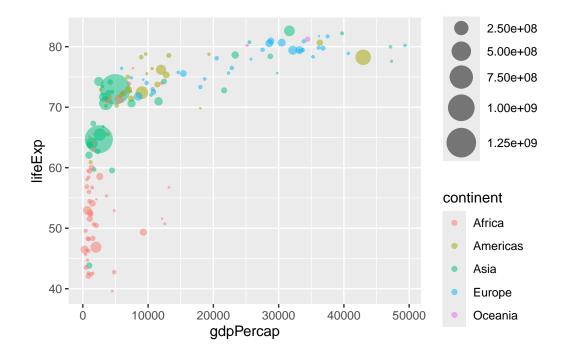
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

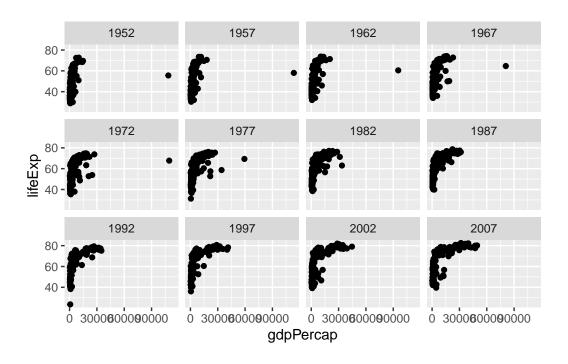
```
gapminder_2007 <- gapminder %>% filter(year==2007)
head(gapminder_2007)
```

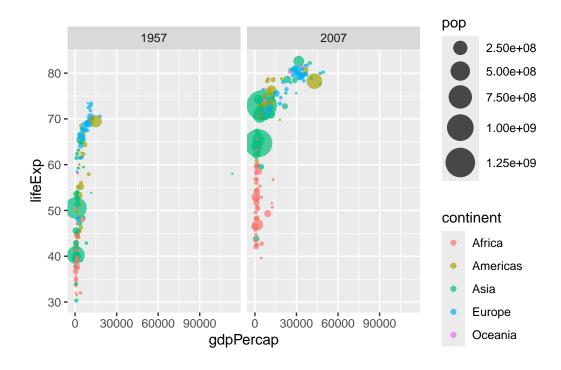
country continent year lifeExp pop gdpPercap
1 Afghanistan Asia 2007 43.828 31889923 974.5803
2 Albania Europe 2007 76.423 3600523 5937.0295

```
3 Algeria Africa 2007 72.301 33333216 6223.3675
4 Angola Africa 2007 42.731 12420476 4797.2313
5 Argentina Americas 2007 75.320 40301927 12779.3796
6 Australia Oceania 2007 81.235 20434176 34435.3674
```



```
ggplot(gapminder) +
  aes(x = gdpPercap, y = lifeExp) +
  geom_point() +
  facet_wrap(~year)
```





sessionInfo()

R version 4.3.3 (2024-02-29)

Platform: x86_64-apple-darwin20 (64-bit)

Running under: macOS Sonoma 14.0

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRblas.0.dylib LAPACK: /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRlapack.dylib;

locale:

[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/Los_Angeles

tzcode source: internal

attached base packages:

[1] stats graphics grDevices utils datasets methods base

other attached packages:

[1] dplyr_1.1.4 ggplot2_3.5.0

loaded via a namespace (and not attached):

[1]	vctrs_0.6.4	nlme_3.1-164	cli_3.6.1	knitr_1.45
[5]	rlang_1.1.2	xfun_0.41	generics_0.1.3	jsonlite_1.8.7
[9]	labeling_0.4.3	glue_1.6.2	colorspace_2.1-0	${\tt htmltools_0.5.7}$
[13]	scales_1.3.0	fansi_1.0.5	rmarkdown_2.25	grid_4.3.3
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[29]	digest_0.6.33	R6_2.5.1	tidyselect_1.2.0	utf8_1.2.4
[33]	splines_4.3.3	pillar_1.9.0	magrittr_2.0.3	Matrix_1.6-5
[37]	withr_2.5.2	tools_4.3.3	gtable_0.3.4	