Getting Started With R

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Installing `R` and RStudio

Tip

You are NOT expected to become an expert in R programming or required to be one for doing this course.
Feel free to post your queries regarding R and RStudio on the class discussion forum on Stream.

R https://www.r-project.org/ is an open-source (i.e., free) software package. This software is available for essentially all computing platforms (e.g. Windows, Linux, Unix, Mac) is maintained and developed by an energetic community of users including many of the world's foremost statisticians.

R is also a programming language but you may not be required to do a lot of programming for your course work. R includes functions which enables us to perform a full range of statistical analyses.

For installing R software, please visit https://cran.stat.auckland.ac.nz/ and follow the instructions.

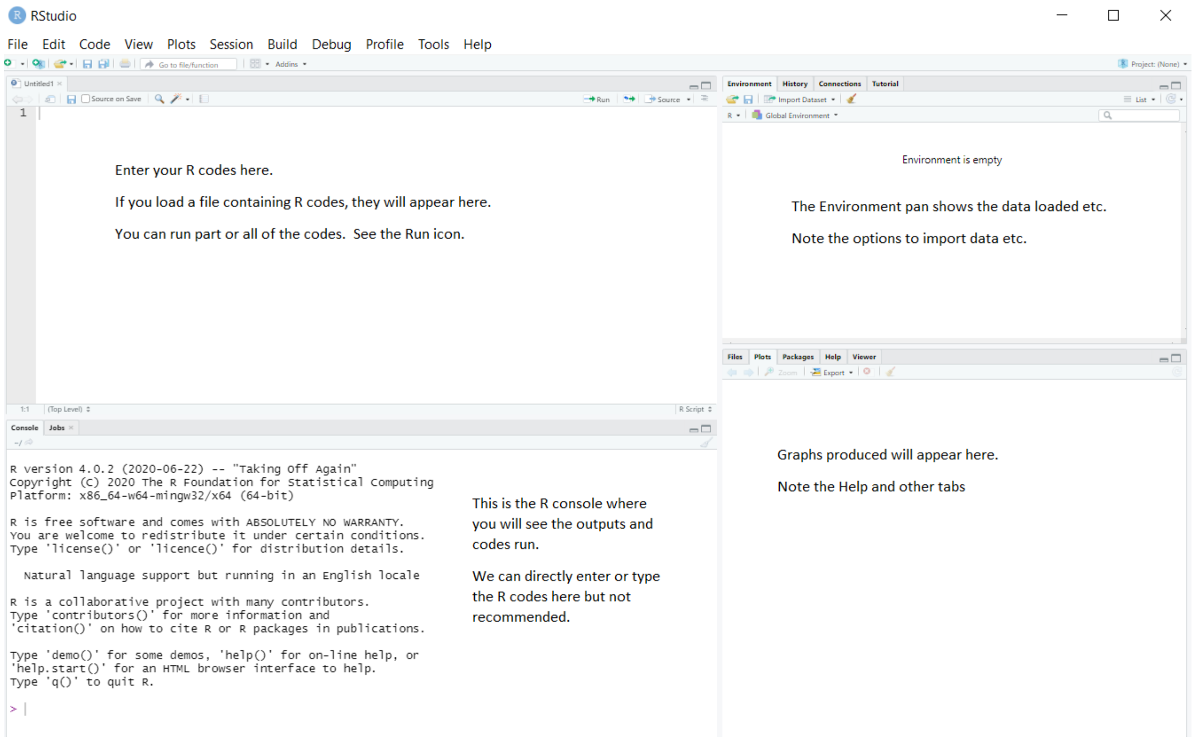
Note that the R software will be sitting in the background in RStudio and you will not be using it directly for this course.

RStudio https://www.rstudio.com/products/rstudio/ is an integrated development environment (IDE) for R. It includes a console, syntax-highlighting editor (as well as to quickly jump to R function definitions) that supports direct R code execution. It also contains tools for plotting, history, debugging, workspace and project management. RStudio has many other features such as authoring HTML, PDF, Word Documents, and slide shows. In order to download RStudio (Desktop edition, open source), go to

https://www.rstudio.com/products/rstudio/download/

Download the installation file and run it. **Note that RStudio must be installed after installing R.**

R/RStudio can also be used using the cloud platform at https://rstudio.cloud/ after creating a *free* account but occasionally some of the packages covered in this course may fail to work in the cloud platform.


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Untitled1
Source on Save
Run
Source
Environment History Connections Tutorial
Import Dataset
Global Environment
List
Environment is empty
Console Jobs
Files Plots Packages Help Viewer
Export
R Script

Enter your R codes here.

If you load a file containing R codes, they will appear here.

You can run part or all of the codes. See the Run icon.

The Environment pan shows the data loaded etc.

Note the options to import data etc.

```
R version 4.0.2 (2020-06-22) -- "Taking Off Again"
Copyright (C) 2020 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

This is the R console where you will see the outputs and codes run.

We can directly enter or type the R codes here but not recommended.

Graphs produced will appear here.

Note the Help and other tabs

Figure 1: An RStudio window

If you open RStudio, you will see something similar to the screen shot shown in Figure 1:

RStudio has many options, such as uploading files to a server, creating documents etc. You will be using only a few of the options. You will *not* be using the menus such as *Build*, *Debug*, *Profile* at all in this course.

You can either type or copy and paste the R codes appearing in this section on to the R Script window and run them.

Some `R` basics

- `R` is case sensitive, so `data` is not the same as `DATA`
- `<-` (read as "gets") is the assignment operator. That is, you use `<-` to assign some content to a variable. The operator `=` has a slightly different meaning but it can be used in the same way as `<-`. In R Studio, press `ALT` and minus key when you are in the R script mode (File » New File » R Script).
- Comments are denoted by the # symbol. Anything after a `#` symbol is ignored by `R` .
- R coding can be hard to write from scratch. So do not hesitate to adopt R codes written by others. Search the internet for R code to do what you want to do. The usual `copy and paste` trick works!

Working directory

In RStudio, set the working directory under the *Session* menu. It is a good idea to start your analysis as a new project in the File menu so that the entire work and data files can be saved and re-opened easily later on.

R/RStudio as a calculator

In RStudio, use the File » New File » R Script menu to type or copy and paste the commands and execute them

Type `1+1` to see `2` on the console (or `->Run` the code in RStudio).

```
1+1
```

```
[1] 2
```

Type `a=1;b=2;a/b` to see `0.5`.

```
a=1;b=2;a/b
```

```
[1] 0.5
```

Note that semicolon separates various commands. It is optional to use them as long as you type the commands one by one as follows:

```
a=1
b=2
a/b
```

```
[1] 0.5
```

There are many built-in functions. Try the following.

`27^3` `sqrt(10)` `round(sqrt(10),2)` `abs(-4)` `log(10)` `exp(10)` `rnorm(100)` `mean(rnorm(100))` `sd(rnorm(100))`

You may wonder what was the base used for `log(10)`. A help on this can be obtained by placing a question mark (?) before log as `?log` or by

help(log)

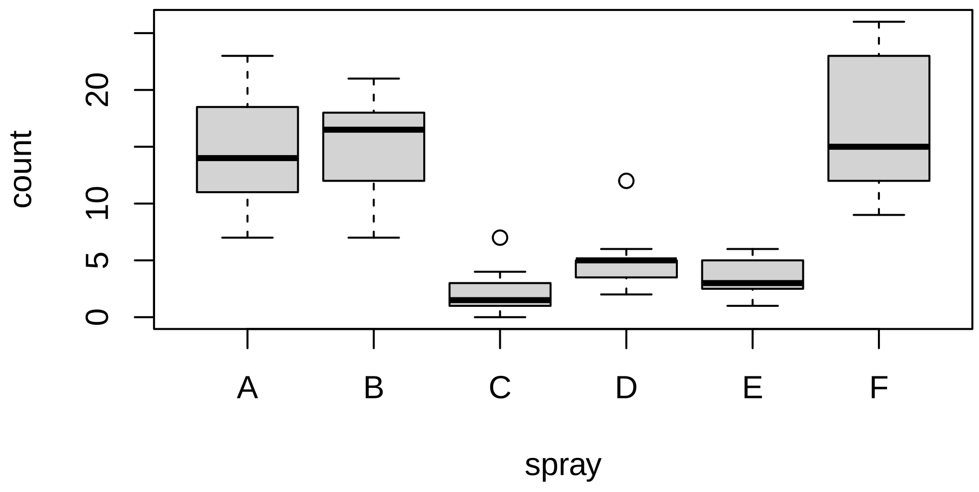
There are a few exceptions. The command `?if` wont work but `?"if"` will. In other words, `?"log"` or `help("log")` are safer ways of getting help on "built-in" functions.

In RStudio, use the R Editor (menu *File > New Script*) to type the commands and submit them (shortcut: *CNTRL+R*).

Default examples

The command `example()` will produce the available HELP examples, and will work for most functions. For example, try `example(boxplot)`. You will see many boxplot examples such as the following:

```
boxplot(count ~ spray, data = InsectSprays, col = "lightgray")
```



There are also demos available, explore using the command `demo()`. The basic R system produces somewhat old style graphs.

So we will be largely using the newer plotting system **ggplot** which is part of the `tidyverse` suite of packages; see https://www.tidyverse.org/.

Let's load that package now:

```
library(tidyverse)
```

A huge number of other dedicated packages are available to improve the power of R. Many R packages are hosted at a repository called CRAN (*C*omprehensive *R* *A*rchive *N*etwork). The package install option within RStudio can download and install these optional packages under the menu `Packages >> Install`. You can also do this using the command `install.packages`. For example

```
install.packages(c("tidyverse", "car"), dependencies = TRUE)
```

This command installs two packages `tidyverse` and `car` in one go.

Contributed R packages are grouped in various headings at https://cran.r-project.org/web/views/. They can be installed in bulk using the `ctv` package command `install.views()`.

You might have to install quite a few packages as you work through this course.

Quarto

I encourage you to get into the habit of using Quarto `*.qmd` files rather than raw `*.R` files. If you've heard of Rmarkdown, Quarto is the successor to Rmarkdown. So, if you're just starting to use R, then you should begin with Quarto rather than Rmarkdown, because most/all new development will be going into Quarto.

Quarto files contain text and code, and can be 'knitted' to produce a nicely formatted document, usually in HTML or PDF format, containing sections, text, code, plots, and output. Quarto can also be used to make websites; in fact, the website for this course was made using Quarto.

Here's some information to get you started: https://quarto.org/docs/get-started/hello/rstudio.html.

And some other useful tips: https://r4ds.hadley.nz/quarto.

R Projects and GitHub

Instead of putting your R code into an ordinary directory on your computer, I encourage you to use Rstudio Projects. A Project is a self-contained directory of code and data, pertaining to a particular project. You might create a single project for your work during this course, with a folder for workshops and another folder for assignments.

Here's a primer on R projects: https://r4ds.hadley.nz/workflow-scripts#projects

An advantage of Projects is that they work nicely with GitHub, a cloud code-repository service. If you plan to do any programming during your career, you'll probably need to learn how to use GitHub. It can be a little tricky to use at first. You don't have to use it for this course, but feel free to have a go at it if you're interested.

If you're using R projects and GitHub, this online book is a great place to start: Happy Git and GitHub for the useR.

Loading/Importing Data

Most data sets we shall consider in this course are in a tabular form. This means that each variable is a column, each row is an observation, columns are separated by white space (or comma), and each column or row may have a name.

If the data file is stored locally, you should put the data into the same directory as your Quarto or R markdown script. That way, you can (usually) load it easily without having to type the full pathway (e.g., `mydata.csv` rather than `C:/Users/anhsmith/Work/Project1/data/mydata.csv`). Better yet, Projects make this much easier.

You can also load data from the web using a URL. For example,

```r
read_csv("https://www.massey.ac.nz/~anhsmith/data/rangitikei.csv")
```

```
Rows: 33 Columns: 10
-- Column specification --------------------------------------------------------
Delimiter: ","
dbl (10): id, loc, time, w.e, cl, wind, temp, river, people, vehicle

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# A tibble: 33 x 10
      id   loc  time   w.e    cl  wind  temp river people vehicle
   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>   <dbl>
 1     1     1     2     1     1     2     2     1     37      15
 2     2     1     1     1     1     2     1     2     23       6
 3     3     1     2     1     1     2     2     3     87      31
 4     4     2     2     1     1     2     1     1     86      27
 5     5     2     1     1     1     2     2     2     19       2
 6     6     2     2     1     2     1     3     3    136      23
 7     7     1     2     2     2     2     2     3     14       8
 8     8     1     2     1     2     2     2     3     67      26
 9     9     1     1     2     1     3     1     2      4       3
10    10     2     2     1     2     2     2     3    127      45
# i 23 more rows
```

We'd usually want to store the data as an object though, like so:

```
rangitikei <- read_csv("https://www.massey.ac.nz/~anhsmith/data/rangitikei.csv")
```

```
Rows: 33 Columns: 10
-- Column specification --------------------------------------------------------
Delimiter: ","
dbl (10): id, loc, time, w.e, cl, wind, temp, river, people, vehicle

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Now the data are available in R as an object.

```
glimpse(rangitikei)
```

```
Rows: 33
Columns: 10
$ id      <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,~
$ loc     <dbl> 1, 1, 1, 2, 2, 2, 1, 1, 1, 2, 2, 2, 2, 1, 1, 1, 2, 2, 2, 1, 1,~
$ time    <dbl> 2, 1, 2, 2, 1, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 1, 2,~
$ w.e     <dbl> 1, 1, 1, 1, 1, 1, 2, 1, 2, 1, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 2,~
$ cl      <dbl> 1, 1, 1, 1, 1, 2, 2, 2, 1, 2, 1, 2, 1, 1, 1, 2, 2, 2, 1, 2, 2,~
$ wind    <dbl> 2, 2, 2, 2, 2, 1, 2, 2, 3, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 3, 2,~
$ temp    <dbl> 2, 1, 2, 1, 2, 3, 2, 2, 1, 2, 2, 3, 1, 2, 2, 2, 3, 2, 2, 2, 2,~
$ river   <dbl> 1, 2, 3, 1, 2, 3, 3, 3, 2, 3, 1, 3, 1, 3, 1, 1, 2, 1, 2, 2, 3,~
$ people  <dbl> 37, 23, 87, 86, 19, 136, 14, 67, 4, 127, 43, 190, 50, 47, 32, ~
$ vehicle <dbl> 15, 6, 31, 27, 2, 23, 8, 26, 3, 45, 7, 53, 22, 18, 10, 3, 11, ~
```

If the data are stored as a `*.csv` or "comma separated values" file, then you can use the `read.csv()` or `read_csv()` function to load the file. If it's a text file with columns separated by spaces or tabs, you can use `read.table()` or `read_table()` function. The ones with underscores (`read_csv()` and `read_table()`) are in the `readr` package, so you'll need to load it first (though `readr` is part of `tidyverse`, so if you load `tidyverse` you're all set).

You can also load Microsoft Excel files using functions `read_excel()`, available in the `readxl` package.

As an exercise, try importing the Telomeres data file (in Excel format) available at

https://rs.figshare.com/ndownloader/files/22850096

Note that Excel files usually contain blanks for missing or unreported data or allocate many rows for variable description, which can cause issues while importing them.

Native R data, stored as `*.RData` or `*.rds` files, can be loaded using the `load()` or `readRDS()` functions, respectively.

SQLite is a public-domain, light-weight database engine (https://sqlite.org/about.html). The R package `RSQLite` will import *.sqlite files. Databases are usually large in size, and hence R packages such as `dbplyr` can be used package to query a database.

Graphing with ggplot2

The R library ggplot2 is very powerful for plotting but you may find the syntax little strange. There are plenty of examples at the ggplot2 online help website. The ggplot2 package is loaded as part of the tidyverse set of packages.

Advantages of ggplot2 are the following:

- employs the "grammar of graphics" of [1]
- plotting involves a high level of abstraction
- very flexible and complete graphics system
- theme system for getting attractive plots
- Fast growing and actively developed

Some disadvantages of ggplot2 are the following:

- 3-dimensional graphics (opt for rgl package instead)
- Graph-theory type graphs (nodes/edges layout; opt for igraph and other packages)
- Interactive graphics (opt for plotly, ggvis and other packages)

Grammar of Graphics

The main idea behind the grammar of graphics of [1] is to mimic the manual graphing approach and define building blocks and combine them to create a graphical display. The building blocks of a graph are:

- data
- aesthetic mapping
- geometric object
- transformation or re-expression of data
- scales
- coordinate system
- position adjustments
- faceting

If have not installed ggplot2 or tidyverse, install it with the following commands.

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

We can now load the `ggplot2` library with the commands:

```
library(ggplot2)
```

In order to work with `ggplot2`, we must have a `data frame` or a `tibble` containing our data. We need to specify the `aesthetics` or how the columns of our data frame can be translated into positions, colours, sizes, and shapes of graphical elements.

The geometric objects and aesthetics of the ggplot2 system are explained below:

Aesthetic Mapping (`aes`)

In ggplot land *aesthetic* means visualisation features or aesthetics. These are

- position (i.e., on the x and y axes)
- color ("outside" color)
- fill ("inside" color)
- shape (of points)
- linetype
- size

Aesthetic mappings are set with the `aes()` function.

Geometric Objects (`geom`)

Geometric objects or `geoms` are the actual marking or inking on a plot such as:

- points (`geom_point`, for scatter plots, dot plots, etc)
- lines (`geom_line`, for time series, trend lines, etc)
- boxplot (`geom_boxplot`, for boxplots)

A plot must have at least one `geom` *but there is no upper limit.* In order to add a `geom` to a plot, the `+` operator is employed. A list of available geometric objects can be obtained by typing `geom_<tab>` in Rstudio. The following command can also be used which will open a Help window.

```
help.search("geom_", package = "ggplot2")
```

Consider the study guide dataset `rangitikei.txt` (Recreational Use of the Rangitikei river). The first 10 rows of this dataset are shown below:

```
   id loc time w.e cl wind temp river people vehicle
1   1   1    2   1  1    2    2     1     37      15
2   2   1    1   1  1    2    1     2     23       6
3   3   1    2   1  1    2    2     3     87      31
4   4   2    2   1  1    2    1     1     86      27
5   5   2    1   1  1    2    2     2     19       2
6   6   2    2   1  2    1    3     3    136      23
7   7   1    2   2  2    2    2     3     14       8
8   8   1    2   1  2    2    2     3     67      26
9   9   1    1   2  1    3    1     2      4       3
10 10   2    2   1  2    2    2     3    127      45
```

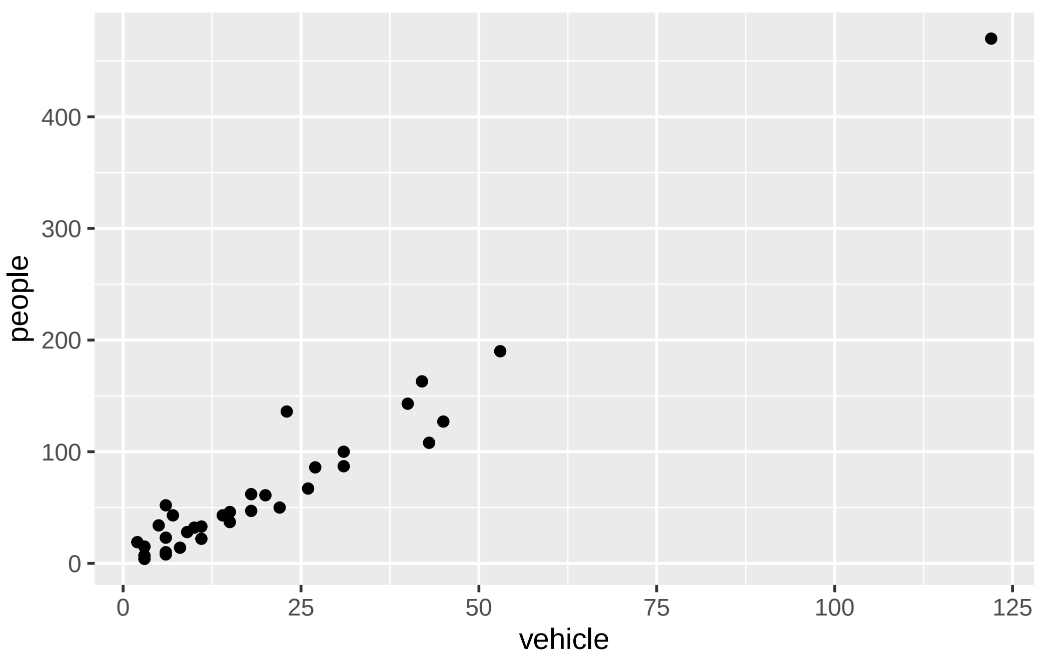
The description of the variables is given below:

`loc` - two locations were surveyed, coded 1, 2
`time` - time of day, 1 for morning, 2 for afternoon
`w.e` - coded 1 for weekend, 2 for weekday
`cl`- cloud cover, 1 for >50%, 2 for <50%
`wind`- coded 1 through 4 for increasing wind speed
`temp` - temperature, 1, 2 or 3 increasing temp
`river`- murkiness of river in 3 increasing categories
`people` - number of people at that location and time
`vehicle`- number of vehicles at that location at that time

This dataset is downloaded from the web using the following commands.

```r
my.data <- read.csv(
  "https://www.massey.ac.nz/~anhsmith/data/rangitikei.csv",
  header=TRUE
  )
```

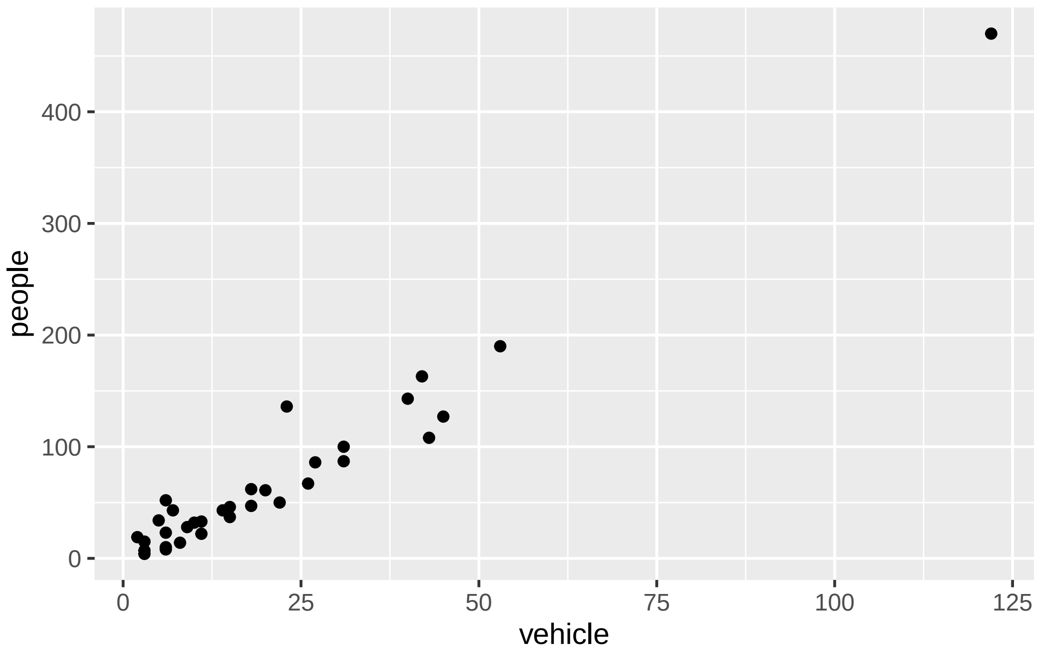
```r
ggplot(data = my.data,
       mapping = aes(x = vehicle, y = people)
       ) +
  geom_point()
```



The `aes` part defines the "aesthetics", which is how columns of the dataframe map to graphical attributes such as x and y position, colour, size, etc. An aesthetic can be either numeric or categorical and an appropriate scale will be used. After this, we add layers of graphics. `geom_point` layer is employed to map x and y and we need not specify all the options for `geom_point`.

The `aes()` can be specified within the `ggplot` function or as its own separate function. I prefer this format.

```
ggplot(my.data) +
  aes(x = vehicle, y = people) +
  geom_point()
```



We can add a title using *labs()* or *ggtitle()* functions. Try-

```
ggplot(my.data) +
  aes(x = vehicle, y = people) +
  geom_point() +
  ggtitle("No. of people vs No. of vehicles")
```

or

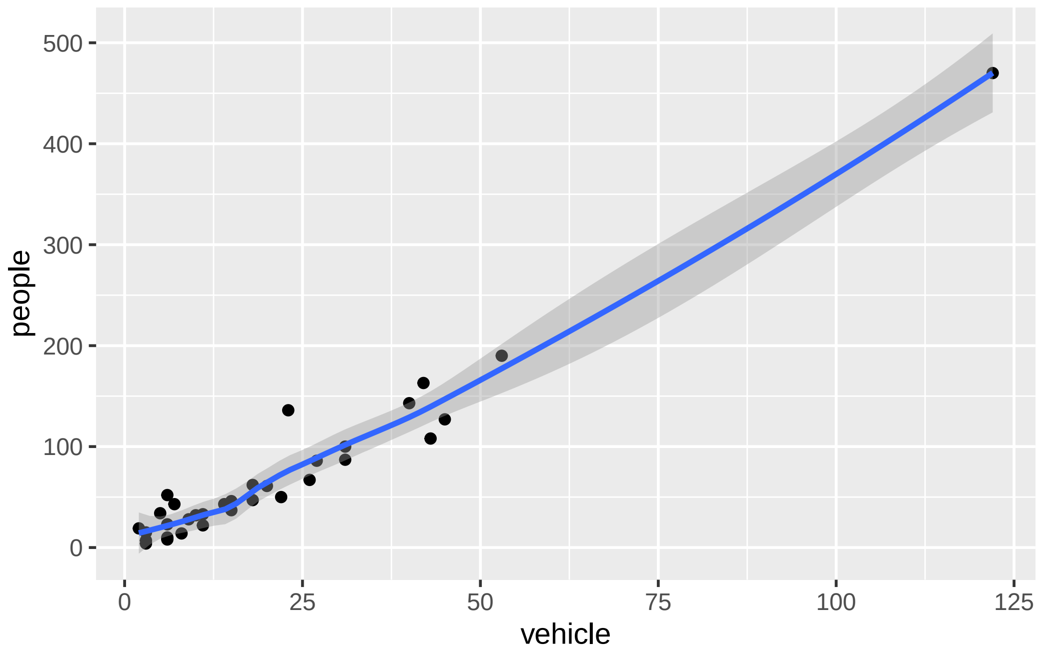
```
ggplot(my.data)+
  aes(x = vehicle, y = people) +
  geom_point() +
  labs(title = "No. of people vs No. of vehicles")
```

Note that *labs()* allows captions and subtitles.

`geom_smooth` is additionally used to show trends.

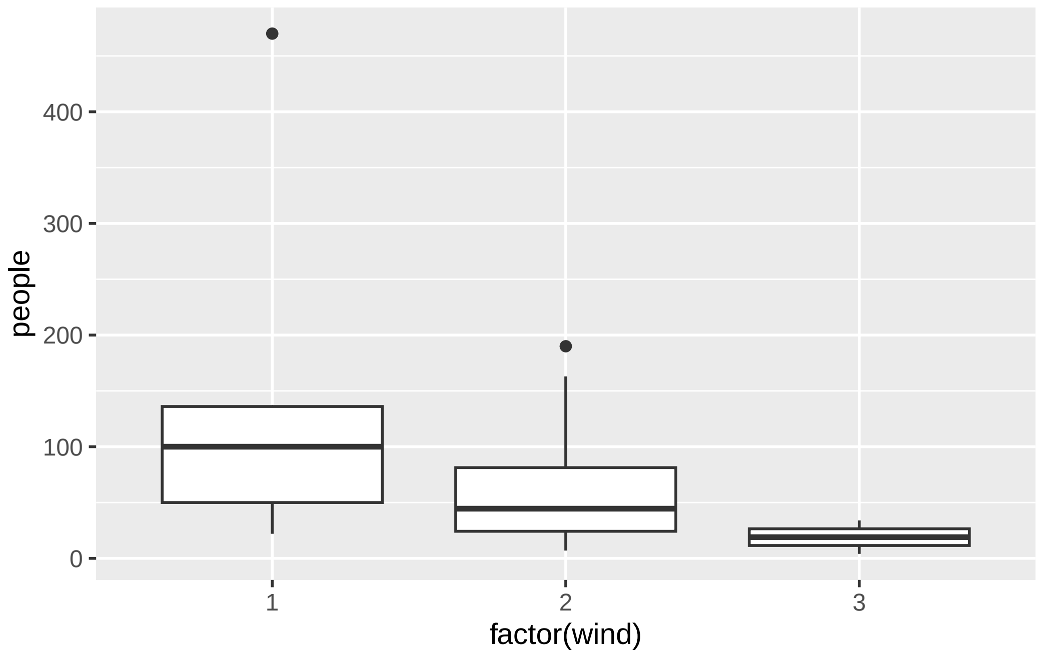
```
ggplot(my.data) +
  aes(x = vehicle, y = people) +
  geom_point() +
  geom_smooth()
```

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



Similar to `geom_smooth`, a variety of `geoms` are available.

```
ggplot(my.data) +
  aes(x = factor(wind), y = people) +
  geom_boxplot()
```

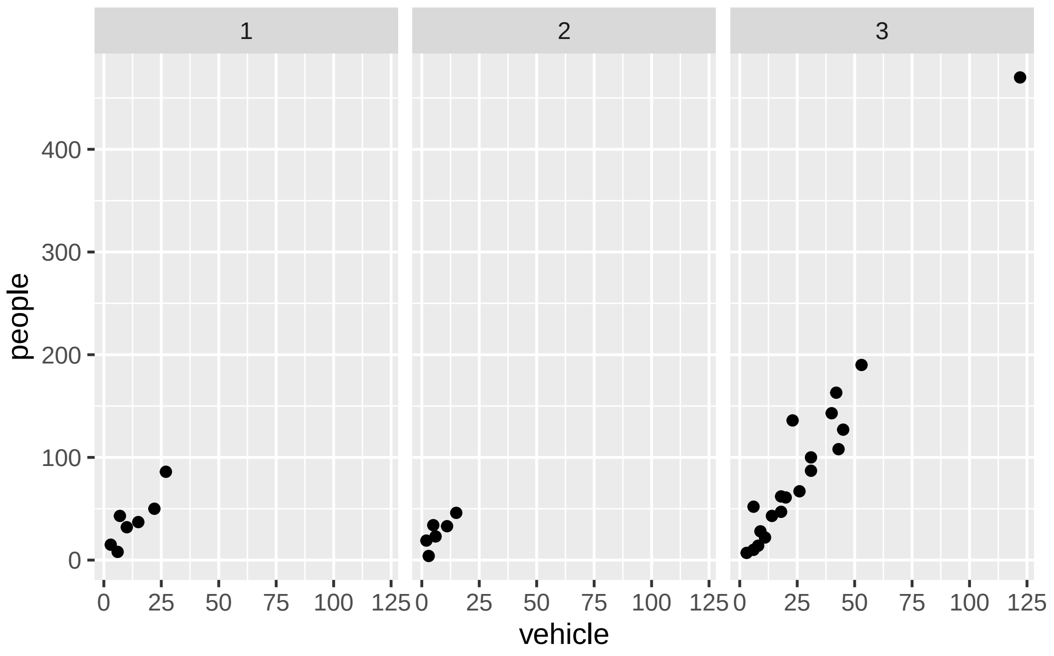


Each `geom` accepts a particular set of mappings;for example `geom_text()` accepts a `labels` mapping. Try-

```
ggplot(my.data) +
  aes(x = vehicle, y = people) +
  geom_point() +
  geom_text(aes(label = w.e),
            size = 5)
```

The faceting option allows a collection of small plots with the same scales. Try-

```
ggplot(my.data) +
  aes(x=vehicle, y=people) +
  geom_point() +
  facet_wrap(~ river)
```



Faceting is the `ggplot2` option to create separate graphs for subsets of data. `ggplot2` offers two functions for creating small multiples:

1. `facet_wrap()`: define subsets as the levels of a single grouping variable
2. `facet_grid()`: define subsets as the crossing of two grouping variables

The following arguments are common to most scales in `ggplot2`:

- **name:** the first argument gives the axis or legend title
- **limits:** the minimum and maximum of the scale
- **breaks:** the points along the scale where labels should appear
- **labels:** the labels that appear at each break

Specific scale functions may have additional arguments. Some of the available Scales are:

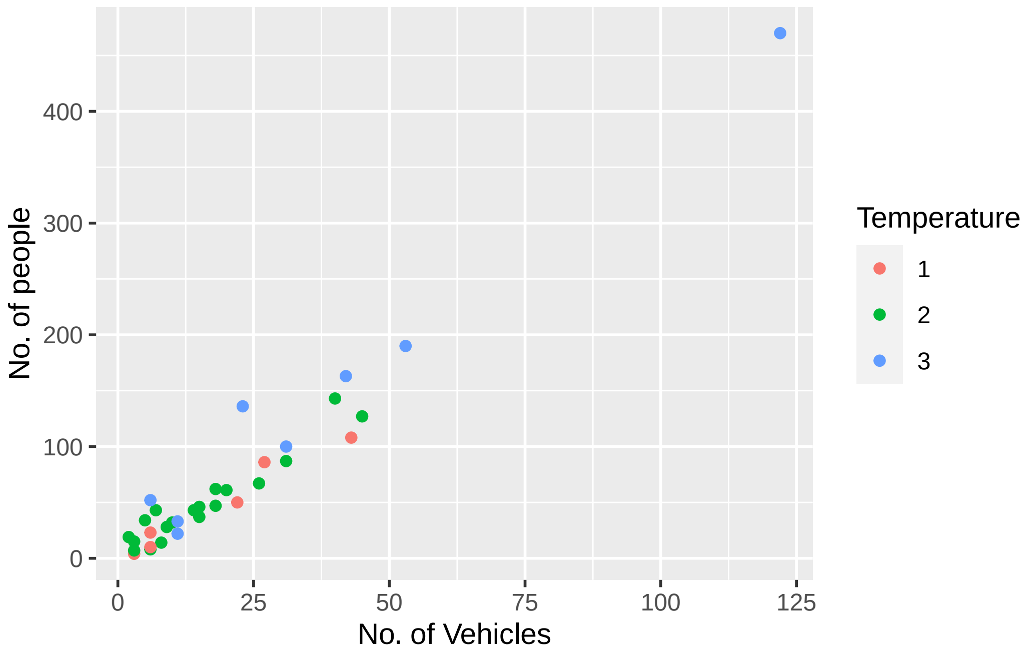
Scale	**Examples**
`scale_color_`	`scale_color_discrete`
`scale_fill_`	`scale_fill_continuous`
`scale_size_`	`scale_size_manual`
	`scale_size_discrete`
`scale_shape_`	`scale_shape_discrete`
	`scale_shape_manual`

Scale	Examples
`scale_linetype_`	`scale_linetype_discrete`
`scale_x_`	`scale_x_continuous`
	`scale_x_log`
	`scale_x_date`
`scale_y_`	`scale_y_reverse`
	`scale_y_discrete`
	`scale_y_datetime`

In RStudio, we can type `scale_` followed by TAB to get the whole list of available scales.

Try-

```
ggplot(my.data) +
  aes(x = vehicle, y = people, color = factor(temp)) +
  geom_point() +
  scale_x_continuous(name = "No. of Vehicles") +
  scale_y_continuous(name = "No. of people") +
  scale_color_discrete(name = "Temperature")
```



The other coding option is shown below:

```
ggplot(my.data) +
  aes(x = vehicle, y = people, color = factor(temp)) +
  geom_point() +
  xlab("No. of Vehicles") +
  ylab("No. of people") +
  labs(colour="Temperature")
```

Note that a desired graph can be obtained in more than one way.

The `ggplot2` theme system handles plot elements (not data based) such as

- Axis labels
- Plot background
- Facet label background
- Legend appearance

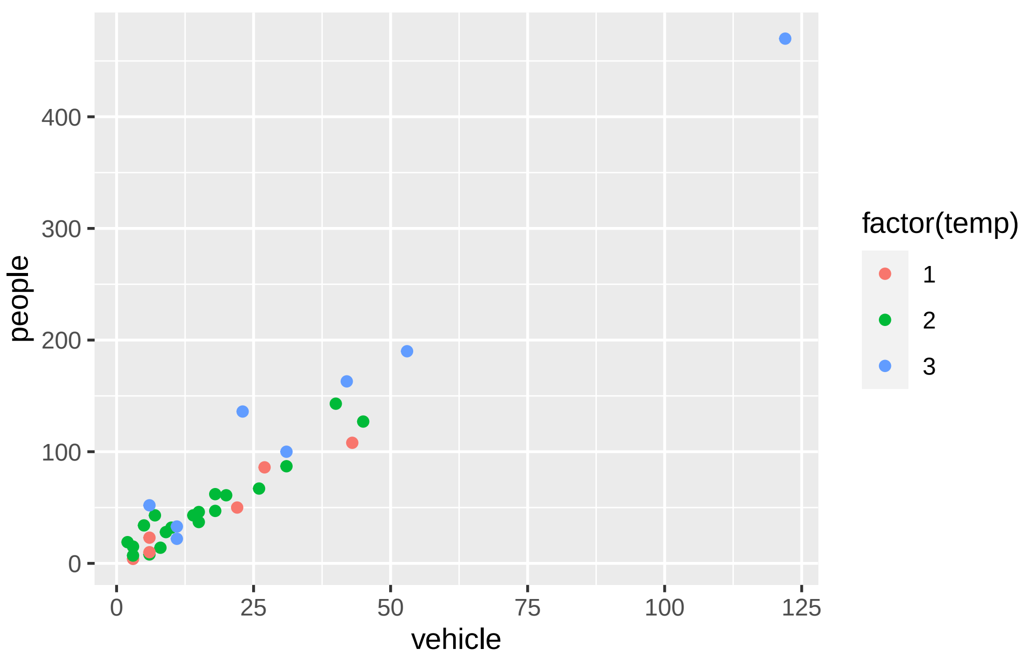
Built-in themes include:

- `theme_gray()` (default)
- `theme_bw()`
- `theme_minimal()`
- `theme_classic()`

```
p1 <- ggplot(my.data) +
  aes(x = vehicle, y = people, color = factor(temp)) +
  geom_point()
```

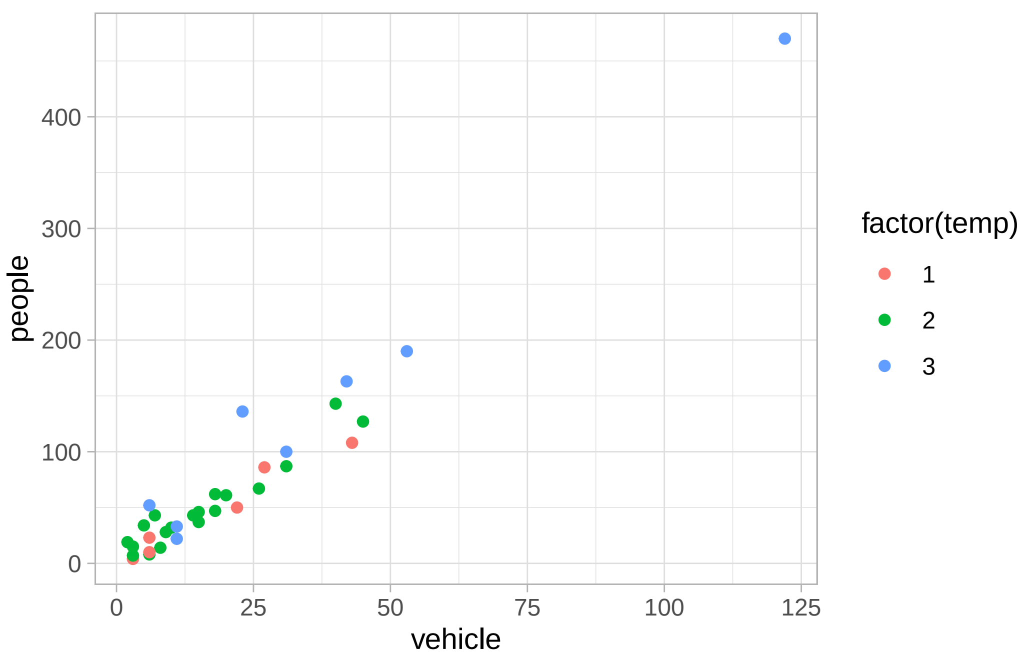
Note that the graph is assigned an object name `p1` and nothing will be printed unless we then print the object `p1`.

```
p1 <- ggplot(my.data) +
  aes(x = vehicle, y = people, color = factor(temp)) +
  geom_point()

p1
```

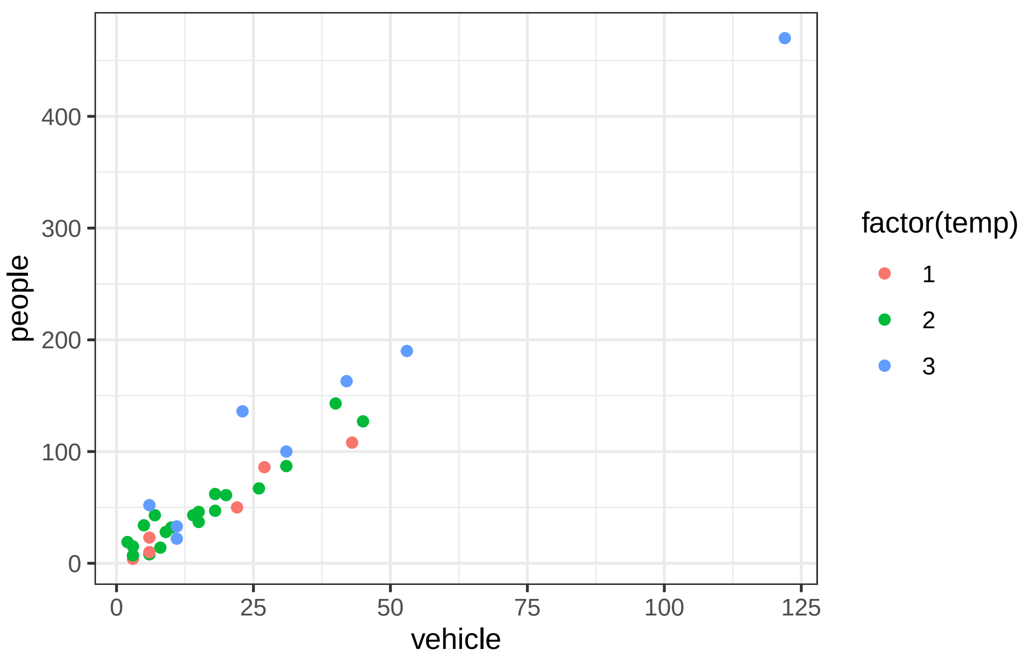


Try-

```
p1 + theme_light()
```

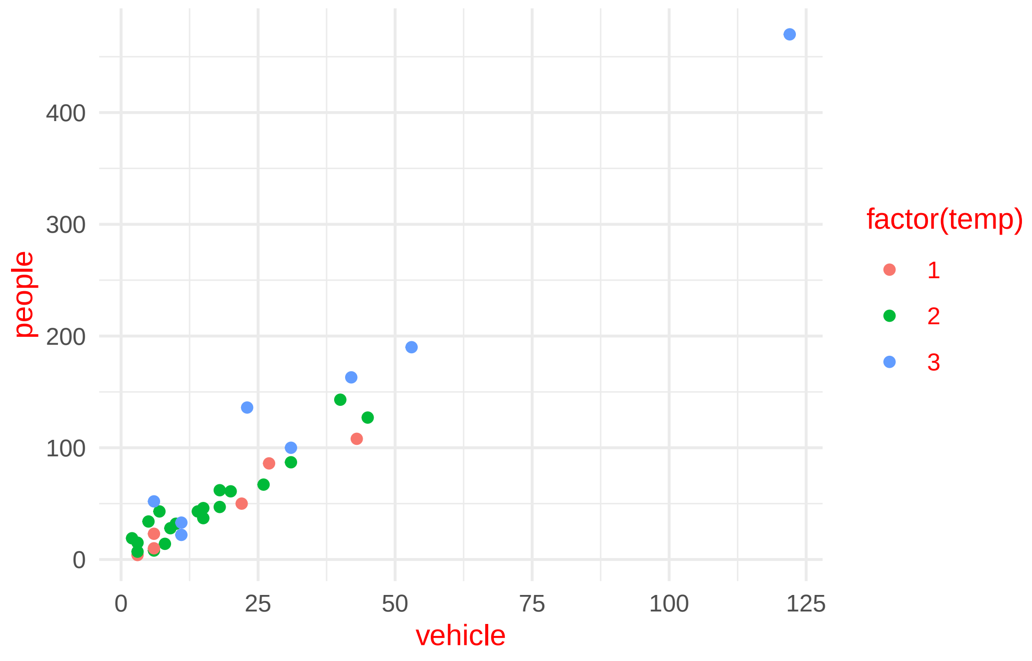

people
400
300
200
100
0
0
25
50
75
100
125
vehicle
factor(temp)
1
2
3

```r
p1 + theme_bw()
```


people
400
300
200
100
0
0
25
50
75
100
125
vehicle
factor(temp)
1
2
3

Specific theme elements can be overridden using `theme()`. For example:

```
p1 + theme_minimal() +
  theme(text = element_text(color = "red"))
```



All theme options can be seen with `?theme`.

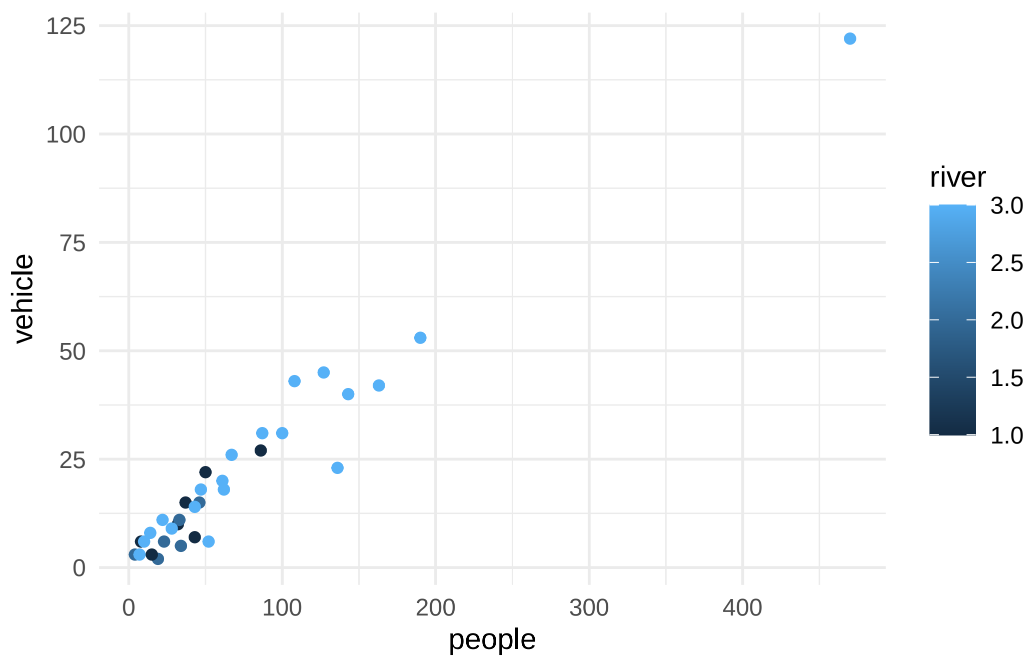
To specify a theme for a whole document, use

```
theme_set(theme_minimal())
```

Minimal graphing can be done using the `qplot` option that will produce a few standard formatted graphs quickly.

```
qplot(people, vehicle, data = my.data, colour = river)
```

```
Warning: `qplot()` was deprecated in ggplot2 3.4.0.
```



Try-

`qplot(people, data = my.data)`

`qplot(people, fill=factor(river), data=my.data)`

`qplot(people, data = my.data, geom = "dotplot")`

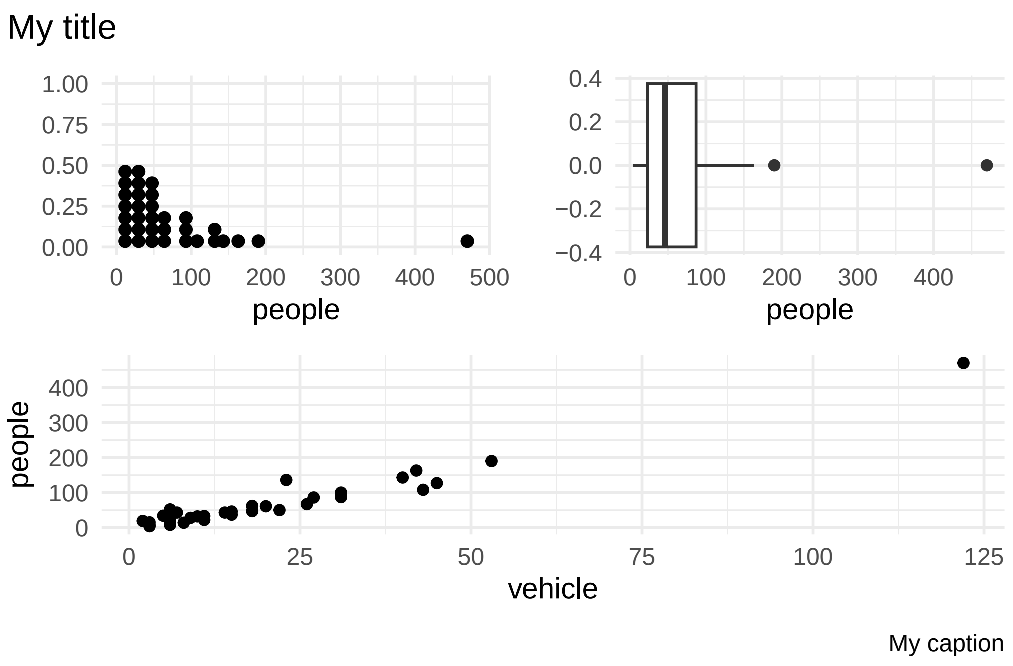
`qplot(factor(river), people, data = my.data, geom = "boxplot")`

A cheat sheet for `ggplot2` is available at https://www.rstudio.com/resources/cheatsheets/ (optional to download). There are many other packages which incorporate `ggplot2` based graphs or dependent on it.

The library *patchwork* allows complex composition arbitrary plots, which are not produced using the faceting option. Try

```
library(patchwork)

p1 <- qplot(people, data = my.data, geom = "dotplot")
p2 <- qplot(people, data = my.data, geom = "boxplot")
p3 <- ggplot(my.data, aes(x = vehicle, y = people)) + geom_point()

(p1 + p2) / p3 +
  plot_annotation("My title", caption = "My caption")
```

```
Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.
```



`ggplot` builder

A nice `R` package, known as `esquisse` is available to build few simple `ggplot` graphics interactively. This may help in the early stages of learning to use `ggplot` graphing.

If this package is not installed, install it first & then try.

```
library(esquisse)
options("esquisse.display.mode" = "browser")
esquisse::esquisser(data = iris)
```

You can also load the desired dataset within `R` studio and select the dataset.

The other option is to load a dataset from the course data web folder and then launch `esquisse`. Try-

```
url1 <- "https://www.massey.ac.nz/~anhsmith/data/rangitikei.RData"
download.file(url = url1, destfile = "rangitikei.RData")
load("rangitikei.RData")
esquisse::esquisser(data = rangitikei, viewer = "browser")
```

You can also download the associated R codes or save the graph within the `esquisse` web app.

`tidyverse` and related packages

In the recent years, `tidyverse` suite of packages, which includes `ggplot2` has become the popular tool for data handling and plotting. In this section, a brief intro to the data management packages such as `dplyr` is given.

For detailed coverage of the `tidyverse` system, go to https://www.tidyverse.org/.

`dplyr`

The following six functions of `dplyr` are very useful for data wrangling :

- For selecting columns, use `select()`
- For subsetting data, use `filter()`
- For re-ordering (e.g. ascending/descending), use `arrange()`
- For augmenting new calculated columns, use `mutate()`
- For computing summary measures, use `summarise()`
- For group-wise computations (e.g. summary measures), use `group_by()`

There are many other functions such as `transmute()` which will add newly calculated columns to the existing data frame but drop all unused columns. The `across()` function extends `group_by()` and `summarise()` functions for multiple column and function summaries. For example, you like to report rounded data in a table, which calls for an operation across both rows and columns.

Piping

Tip

The piping operation is a fundamental aspect of computer programming. The semantics of pipes is taking the output from the left-hand side and passing it as input to the right-hand side.

The R package magrittr introduced the pipe operator %>% and can be pronounced as "then". In RStudio windows/Linux versions, press Ctrl+Shift+M to insert the pipe operator. On a Mac, use Cmd+Shift+M.

R also has its own pipe, |>, which is an alternative to %>%. I tend to use |>. If you want to change the pipe inserted automatically with Ctrl+Shift+M, find on the menu **Tools > Global Options**, then click on **Code** and check the box that says "**Use Native Pipe Operator**".

We often pipe the dplyr functions, and the advantage is that we show the flow of data manipulation and subsequent graphing. This approach also helps to save memory, and dataframes are not unnecessarily created, a necessity for a big data framework.

Try the following examples after loading the rangitikei dataset.

select()

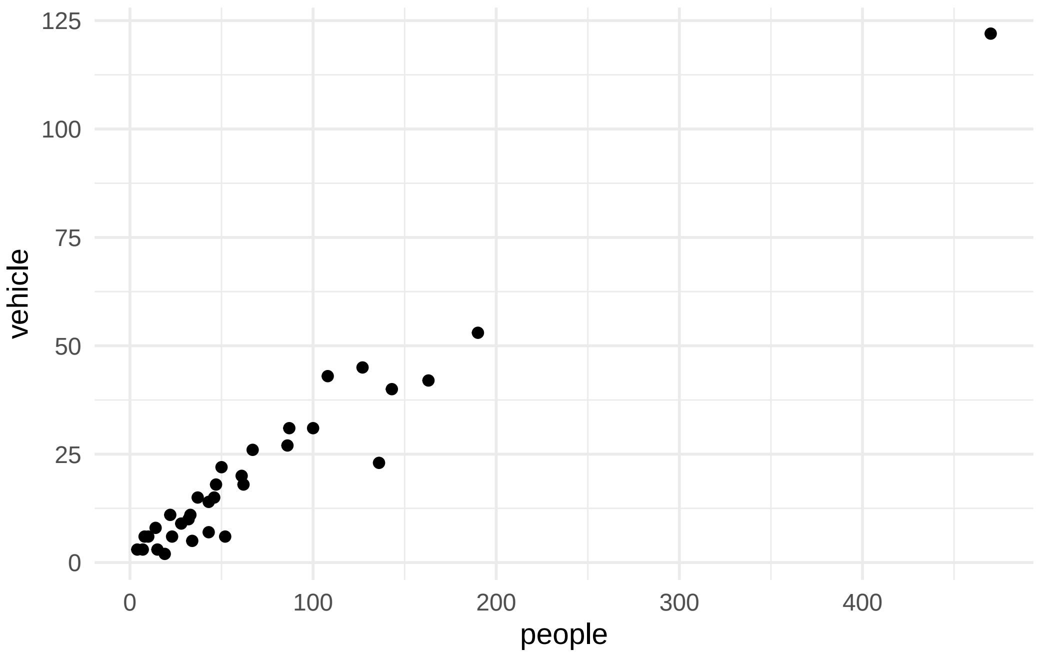
```
my.data <- read.csv("https://www.massey.ac.nz/~anhsmith/data/rangitikei.csv", header=TRUE)

names(my.data)
```

```
 [1] "id"      "loc"     "time"    "w.e"     "cl"      "wind"    "temp"
 [8] "river"   "people"  "vehicle"
```

```
library(tidyverse)

new.data <- my.data |>
  select(people, vehicle)

names(new.data)
```

```
[1] "people"  "vehicle"
```

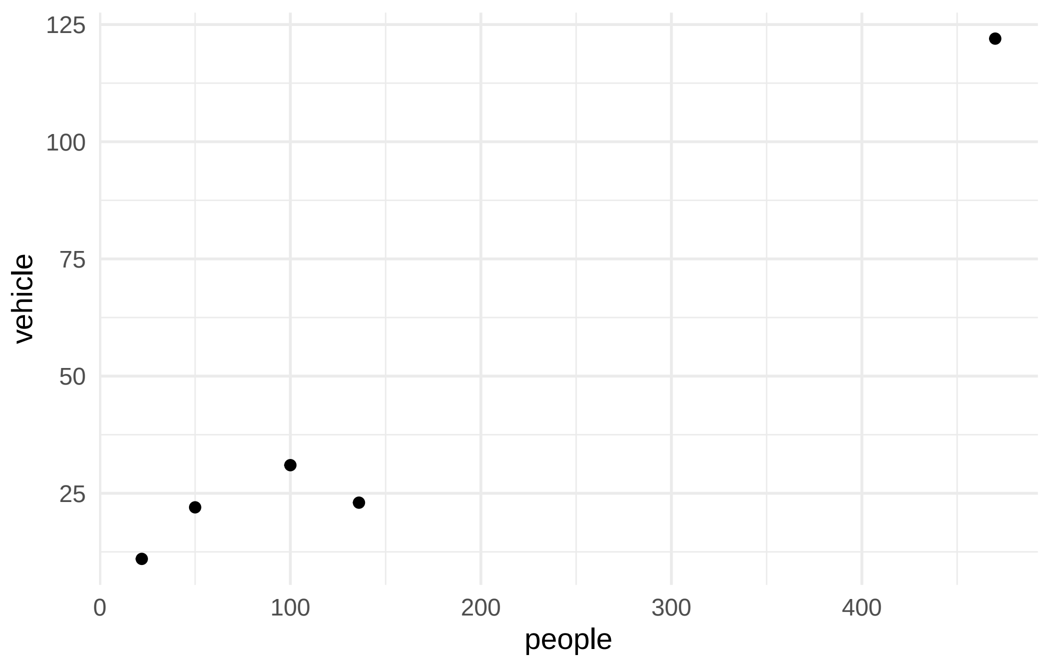
```
my.data |>
  select(people, vehicle) |>
  ggplot() +
  aes(x=people, y=vehicle) +
  geom_point()
```



We select two columns and create a scatter plot with the above commands.

`filter()`

```
my.data |>
  filter(wind==1) |>
  select(people, vehicle) |>
  ggplot() +
  aes(x=people, y=vehicle) +
  geom_point()
```



The above commands filter the data for the low wind days and plots vehicle against people.

`arrange()`

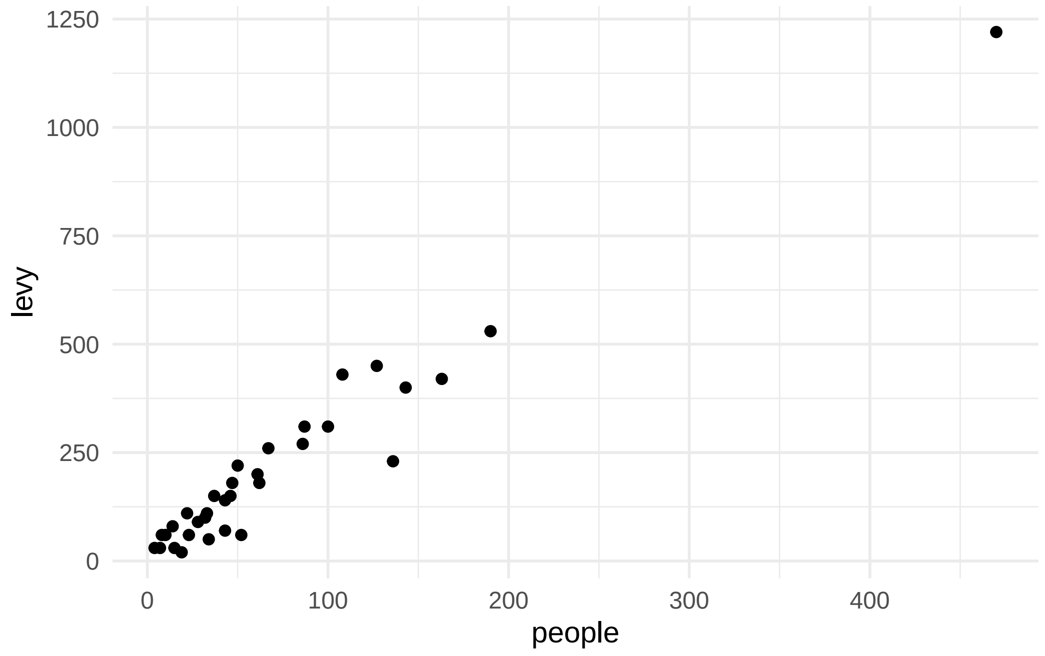
```
my.data |>
  filter(wind==1) |>
  arrange(w.e) |>
  select(w.e, people, vehicle)
```

```
  w.e people vehicle
1   1    136      23
2   1     50      22
3   1    100      31
4   1    470     122
5   2     22      11
```

`mutate()`

Assume that a $10 levy is collected for each vehicle. We can create this new `levy` column as follows.

```
my.data |>
  mutate(levy = vehicle*10) |>
  select(people, levy) |>
  ggplot() +
  aes(x = people, y=levy) +
  geom_point()
```



Note that the pipe operation was used to create a scatter plot using the newly created column.

`summarise()`

```
my.data |>
  summarise(total = n(),
            avg = mean(people)
            )
```

```
  total      avg
1    33 71.72727
```

We obtain the selected summary measures namely the total and the mean number of people. Try-

```r
my.data |>
  filter(wind == 1) |>
  summarise(total = n(),
            avg = mean(people)
            )
```

```
  total   avg
1     5 155.6
```

`group_by()`

We obtain the wind group-wise summaries below:

```r
my.data |>
  group_by(wind) |>
  summarise(total=n(),
            avg=mean(people))
```

```
# A tibble: 3 x 3
   wind total   avg
  <int> <int> <dbl>
1     1     5 156.
2     2    26  59.7
3     3     2  19
```

There are many more commands such as the `transmute` function which conserves the only the needed columns. Try

```r
my.data |>
  group_by(wind, w.e) |>
  transmute(total=n(),
            avg=mean(people))
```

```
# A tibble: 33 x 4
# Groups:   wind, w.e [6]
    wind   w.e total   avg
   <int> <int> <int> <dbl>
 1     2     1    18  72.1
 2     2     1    18  72.1
 3     2     1    18  72.1
 4     2     1    18  72.1
 5     2     1    18  72.1
 6     1     1     4 189  
 7     2     2     8  31.8
 8     2     1    18  72.1
 9     3     2     1   4  
10     2     1    18  72.1
# i 23 more rows
```

A simple frequency table is found using `count()`. Try-

```
my.data |>
  group_by(wind, w.e) |>
  count(temp)
```

```
# A tibble: 10 x 4
# Groups:   wind, w.e [6]
    wind   w.e  temp     n
   <int> <int> <int> <int>
 1     1     1     1     1
 2     1     1     3     3
 3     1     2     3     1
 4     2     1     1     4
 5     2     1     2    12
 6     2     1     3     2
 7     2     2     2     6
 8     2     2     3     2
 9     3     1     2     1
10     3     2     1     1
```

```
my.data |>
  group_by(wind, w.e) |>
  count(temp, river)
```

```
# A tibble: 16 x 5
# Groups:   wind, w.e [6]
    wind   w.e  temp river     n
   <int> <int> <int> <int> <int>
 1     1     1     1     1     1
 2     1     1     3     3     3
 3     1     2     3     3     1
 4     2     1     1     1     1
 5     2     1     1     2     1
 6     2     1     1     3     2
 7     2     1     2     1     3
 8     2     1     2     2     2
 9     2     1     2     3     7
10     2     1     3     3     2
11     2     2     2     1     2
12     2     2     2     3     4
13     2     2     3     2     1
14     2     2     3     3     1
15     3     1     2     2     1
16     3     2     1     2     1
```

The `count()` is useful to check the balanced nature of the data when many subgroups are involved.

`tidyr`

By the phrase `tidy data`, it is meant the preferred way of arranging data that is easy to analyse. The principles of tidy data are:

- Each variable forms a column.
- Each observation forms a row.
- Each type of observational unit forms a table.

The hospital admissions dataset is untidy because it does allocate many columns for a variable.

```
my.data <- read.table(
  "https://www.massey.ac.nz/~anhsmith/data/hospital.txt",
  header=TRUE, sep=",")

head(my.data)
```

```
  YEAR PERI NORTH1 NORTH2 NORTH3 SOUTH1 SOUTH2 SOUTH3
1 1980    1      0      4     27      4     16     27
2 1980    2      6     11     31      8     18     21
3 1980    3      6      4     25     20     16     24
4 1980    4      1     10     31     22     17     20
```

```
5 1980     5       4      16      22      21      30      31
6 1980     6       3       8      28      31      20      30
```

The main response variable namely the number of admissions is allocated different columns depending on the North and South locations. This format is also called `wide format` which can be made into a tidy `long format`. Try-

```
library(tidyr)

my.data |>
  gather(NORTH1, NORTH2, NORTH3,
         SOUTH1, SOUTH2, SOUTH3)
```

The command `spread()` does the opposite to `gather()`. The `tidyr` package many other functions such as `unite()`, `separate()` etc to deal with columns. A better approach would be to use the `dplyr` function `pivot_longer()`. Try-

```
my.data |>
  pivot_longer(cols = NORTH1:SOUTH3,
               names_to = "location",
               values_to = "Admissions")
```

The command `pivot_wider()` does the opposite to `pivot_longer()`

The `dplyr` package also has functions to deal with two-tables which can be joined either conditionally or unconditionally using commands such as `full_join()`. For a detailed notes and examples, you may visit https://dplyr.tidyverse.org/articles/two-table.html but we will be using such functions very occasionally in this course.

The `reshape2` and `data.table` packages also have functions to do the same task.

A typical data analysis session in R/RStudio

A data analysis session in R/RStudio involves loading the data, graphing, and modelling. You finally save your outputs or produce a Report.

When you begin your analysis in RStudio, start it as a new project in the File menu. You can save all your work in one go when you quit the RStudio software. You can always load your project later on to continue the analysis.

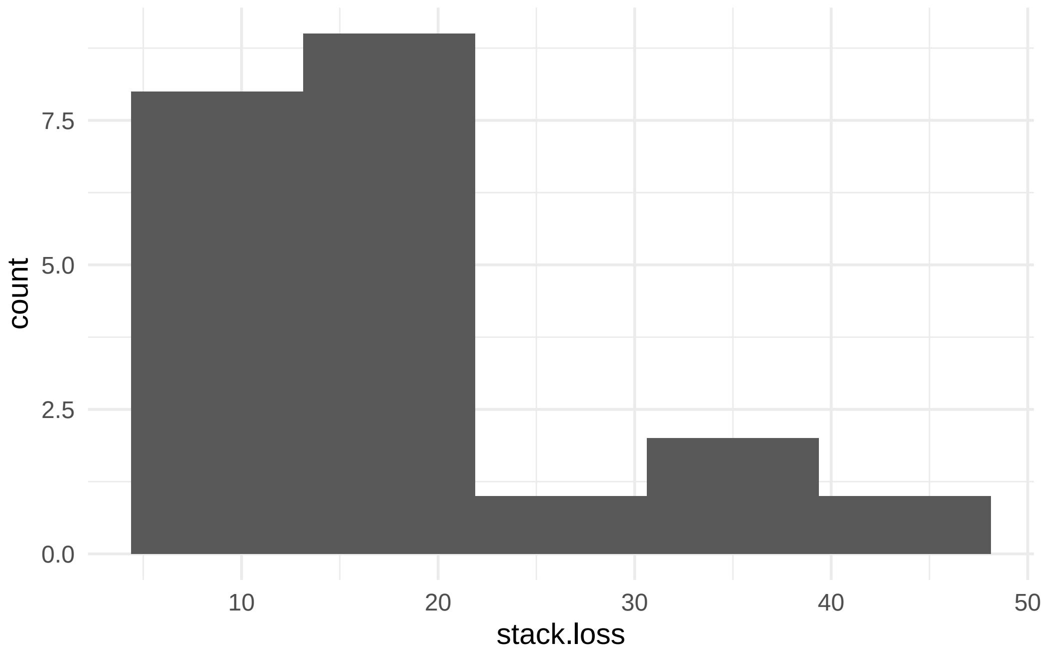
For the sack of simplicity, let us use an R default dataset called `stackloss` giving the operational data of a plant for the oxidation of ammonia to nitric acid.

```
data("stackloss")
head(stackloss, 5)
```

```
  Air.Flow Water.Temp Acid.Conc. stack.loss
1       80         27         89         42
2       80         27         88         37
3       75         25         90         37
4       62         24         87         28
5       62         22         87         18
```

The distribution of the response variable `stack.loss` is explored using a histogram below:

```
stackloss |>
  ggplot() +
  aes(stack.loss) +
  geom_histogram(bins = 5)
```



Histograms are not good displays for small datasets. In order to see the size or length of `stack.loss` data, we select the stack.loss variable and then summarise the size using the *n()* option.

```
stackloss |>
  select(stack.loss) |>
  summarise(n())
```

```
  n()
1  21
```

The following commands will also work.

```
length(stackloss$stack.loss)
```

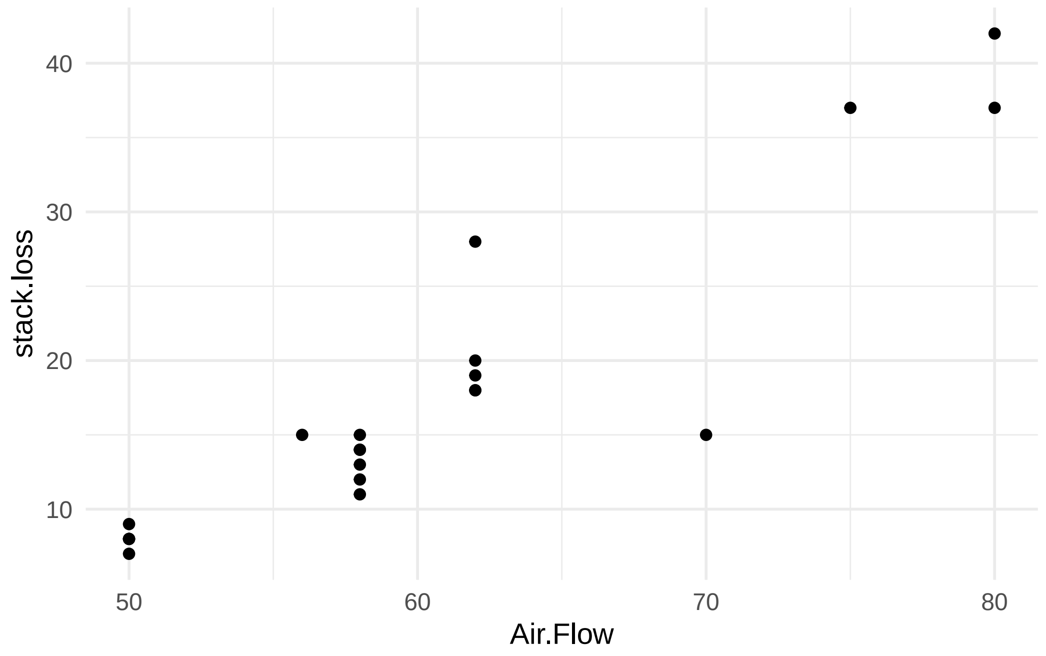
```
[1] 21
```

```
stackloss |> pull(stack.loss) |> length()
```

```
[1] 21
```

We may also explore how well `stack.loss` is related `Air.Flow` to using a scatter plot. For this, we type the command `plot`

```
stackloss |>
  ggplot() +
  aes(y=stack.loss, x=Air.Flow) +
  geom_point()
```



The relationship is roughly linear. So we may fit a straight line model using the `lm` command.

```
st.line.model <- lm(stack.loss~Air.Flow, data=stackloss)
```

We can query this model asking for its summary using the `summary()` function.

```
summary(st.line.model)
```

```
Call:
lm(formula = stack.loss ~ Air.Flow, data = stackloss)

Residuals:
     Min       1Q   Median       3Q      Max
```

```
-12.2896  -1.1272  -0.0459   1.1166   8.8728

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -44.13202    6.10586  -7.228 7.31e-07 ***
Air.Flow      1.02031    0.09995  10.208 3.77e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.098 on 19 degrees of freedom
Multiple R-squared:  0.8458,    Adjusted R-squared:  0.8377
F-statistic: 104.2 on 1 and 19 DF,  p-value: 3.774e-09
```

`R` default model summary is bit too long. We may just glance the overall quality measures of the fitted model as follows:

```r
library(tidyverse)
library(broom)
library(kableExtra)
```

```

Attaching package: 'kableExtra'

The following object is masked from 'package:dplyr':

    group_rows
```

```r
out1 <- st.line.model |>
  glance() |>
  mutate(across(where(is.numeric),
                ~round(., 2))
         )

out1 |> t() |> kable() |>
  kable_classic(full_width = F)
```

For processing using Rmarkdown, we may use the codes which will give a tidy tabular output in the word-processed output.

```r
library(tidyverse)
library(broom)
```

r.squared	0.85
adj.r.squared	0.84
sigma	4.10
statistic	104.20
p.value	0.00
df	1.00
logLik	-58.37
AIC	122.74
BIC	125.87
deviance	319.12
df.residual	19.00
nobs	21.00

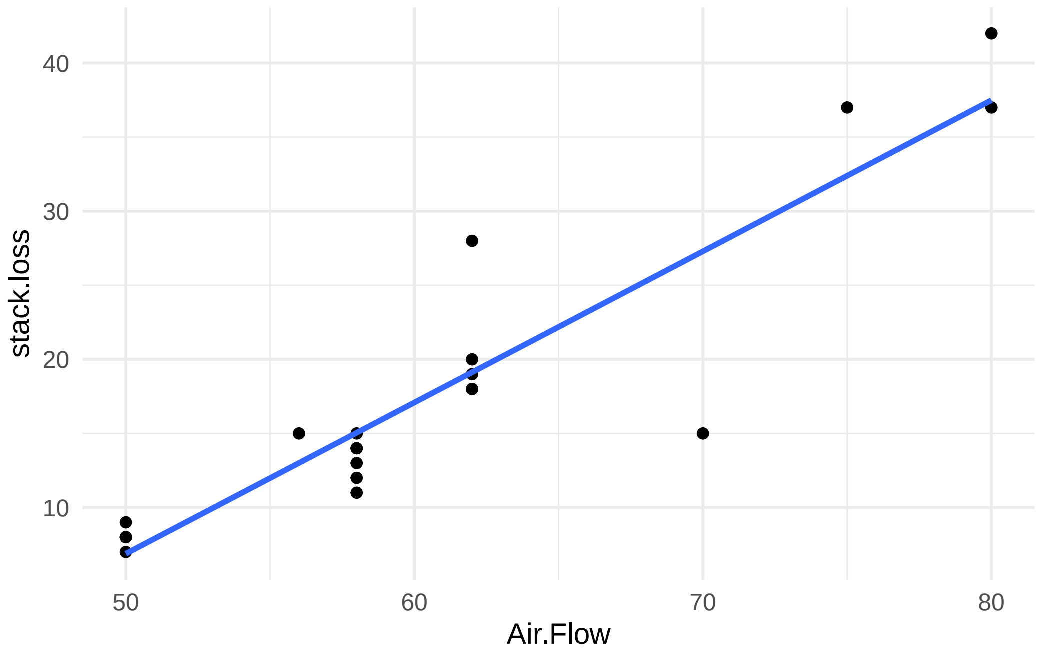
term	estimate	std.error	statistic	p.value
(Intercept)	-44.13	6.11	-7.23	0
Air.Flow	1.02	0.10	10.21	0

```r
library(kableExtra)

out1 <- st.line.model |>
  tidy() |>
  mutate(across(where(is.numeric), ~round(., 2)))

kable(out1) |>
  kable_classic(full_width = F)
```

The fitted model is shown below:

```r
ggplot(stackloss) +
  aes(y=stack.loss, x=Air.Flow) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE)
```

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



The fitted model can also be displayed on the scatter plot using the old style `plot` and `abline` commands.

```
plot(stack.loss ~ Air.Flow, data=stackloss)
st.line.model <- lm(stack.loss~Air.Flow, data=stackloss)
abline(st.line.model)
```

Data Quality Checks

It is a good idea to check the quality of secondary data sourced from elsewhere. For example, there could be missing values in the dataset. Consider the Telomeres data downloaded from http://www.massey.ac.nz/~anhsmith/data/rsos192136_si_001.xlsx

```
url <- "http://www.massey.ac.nz/~anhsmith/data/rsos192136_si_001.xlsx"
destfile <- "rsos192136_si_001.xlsx"

download.file(url, destfile)
```

```
library(readxl)
rsos192136_si_001 <- read_excel("rsos192136_si_001.xlsx")
```

The missingness of data can be quickly explored using many R packages. The downloaded Telomeres dataset contain many missing values.

```r
library(VIM)
```

```
Loading required package: colorspace
```

```
Loading required package: grid
```

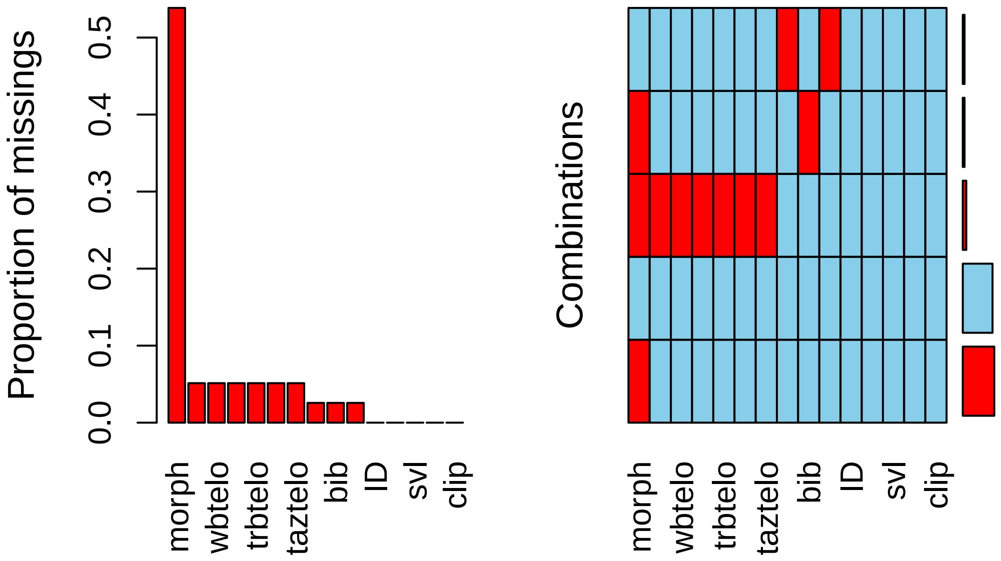
```
VIM is ready to use.
```

```
Suggestions and bug-reports can be submitted at: https://github.com/statistikat/VIM/issues
```

```

Attaching package: 'VIM'
```

```
The following object is masked from 'package:datasets':

    sleep
```

```r
res <- rsos192136_si_001 |>
  aggr(sortVar=TRUE) |>
  summary() |>
  pluck("combinations")
```



or

```r
library(naniar)
gg_miss_var(rsos192136_si_001)
```

The term *Missing completely at random* (MCAR) is often used to mean there is there is no pattern to the missing data themselves or alternatively the missingness is not related to any other variable or data in the dataset. In other words, the probability of missingness is the same for all units. So no bias is caused by the missing data, and we can discard cases with missing data when we fit models.

In practice, we often find missing data do have a relationship with other variables in the dataset but the actual missing values are random. This situation of data conditionally missing at random is called *Missing at random (MAR)* data. For a particular survey question, the response rate may differ depending on the respondent's gender. In this situation, the actual missingness may be random but still related to the gender variable.

Missing not at random (MNAR) is the pattern when missingness is related to other variables in the dataset, as well as the values of the missing data are not random. In other words, there is a predictable pattern in the missingness. So we cannot avoid the bias when missing cases are omitted.

There are also situations such as censoring where we just record a single value without actually measuring the variable of interest.

Imputation of data can be made except for the case of MCAR type. A number of R packages are available for data imputation; see https://cran.r-project.org/web/views/MissingData.html or https://stefvanbuuren.name/fimd/. We may occasionally cover data imputation issue in an assignment question.

There are also R packages to perform automatic investigation for data cleaning. Try-

```r
library(dataMaid)

makeDataReport(rsos192136_si_001, output="html", replace=TRUE)

# or
library(DataExplorer)

create_report(rsos192136_si_001)
```

Rule based validation is enabled in the R package *validate*. The R package *janitor* has a function get_dupes() to find duplicate entries in the dataset. *Cleaner* package will allow to clean the variables so that the columns are consistent in terms of the factor, date, numerical variable types. You will be largely using data that are already cleaned for your assignments but be aware that you have to perform data cleaning and perform necessary quality checks before analysis.

Further Help

There are a number of online sources (tutorials, discussion groups etc) for getting help with R. These links are available at your class Stream. You may also use the advanced search facility of Goggle at https://www.google.com/advanced_search; more specifically at https://stackoverflow.com.

- For further online tutorials
  - https://r4ds.had.co.nz/
  - https://www.datacamp.org
- For further graphing example
  - https://www.r-graph-gallery.com/all-graphs
- Getting help:
  - RStudio cheat sheets: https://www.rstudio.com/resources/cheatsheets
  - RStudio resources https://resources.rstudio.com
  - Recommended R packages by topic: https://cran.r-project.org/web/views/
  - StackOverflow: https://stackoverflow.com/questions/tagged/r

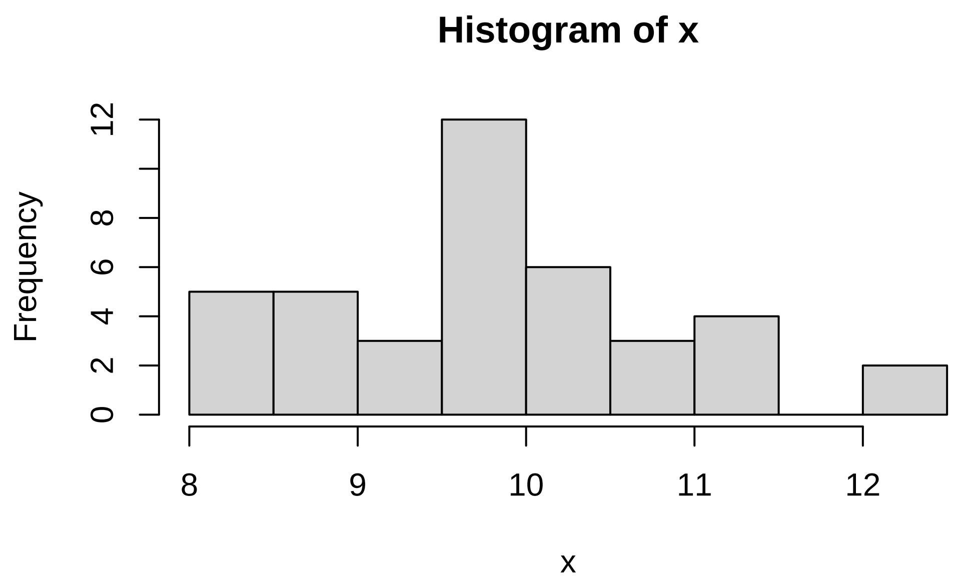
R default (base) Graphing

For a simple bar chart, try

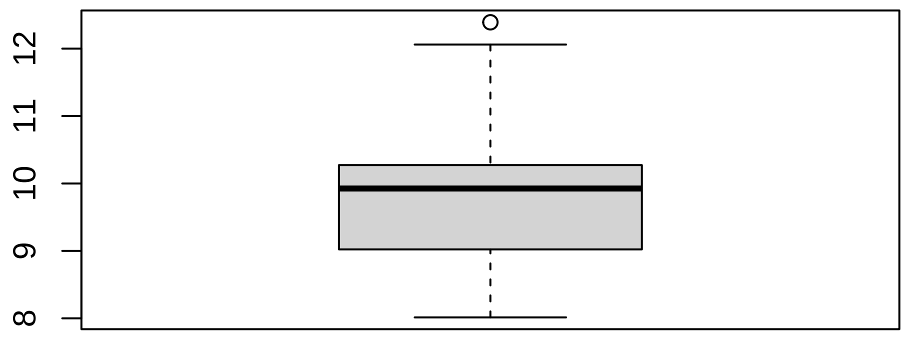
```
freq <- c(1, 2, 3, 4, 5)
names <- c("A","B","C","D","E")
barplot(freq, names.arg=names)
```

Let us generate random data from the normal distribution *N(10,1)* distribution and form a batch of data for illustrating graphing in R. Try the following commands one by one.

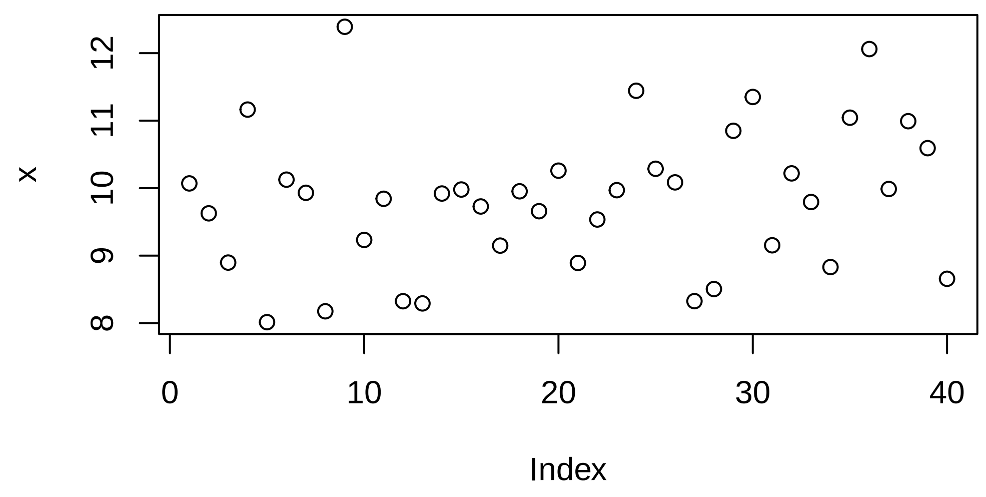
```
x  <-  rnorm(40, 10,1)

hist(x)
```



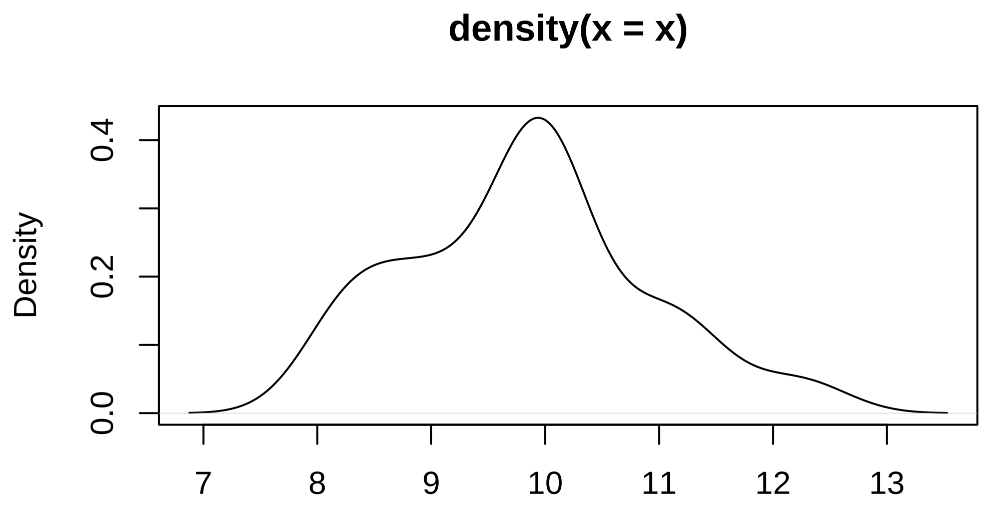
```r
boxplot(x)
```



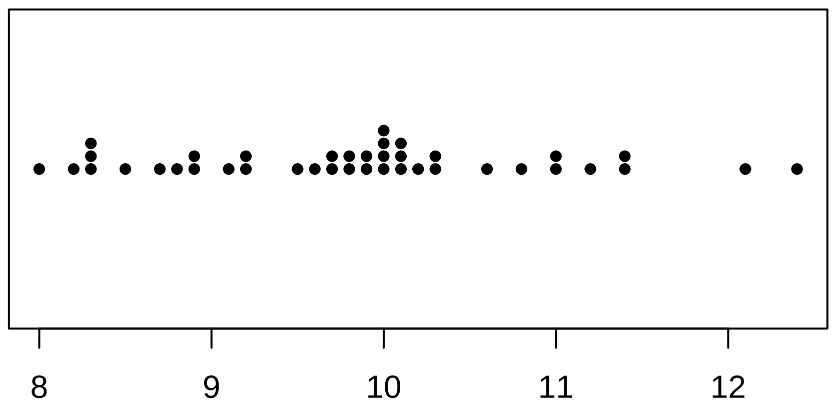
```r
plot(x)
```



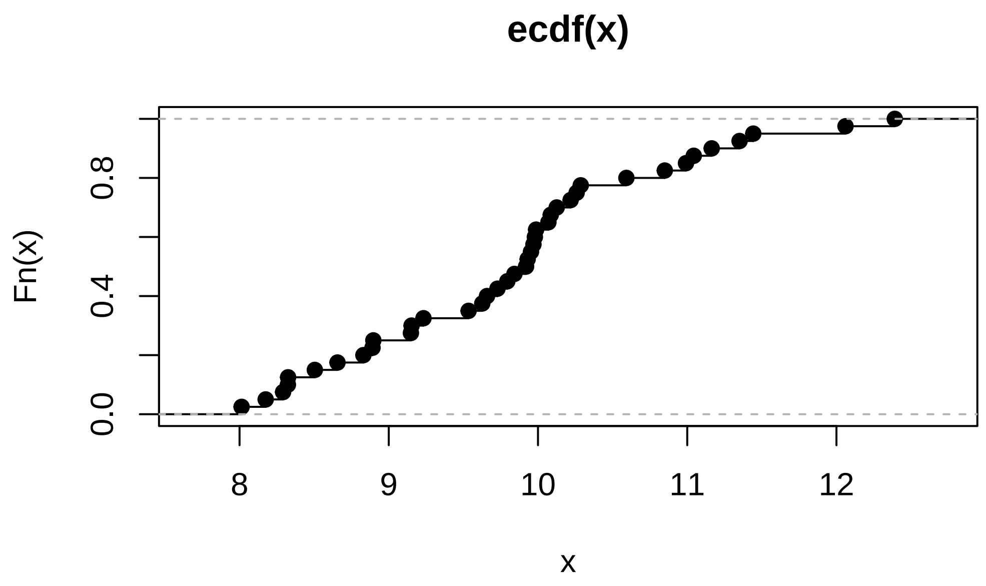
```
plot(density(x), xlab="")
```



```
stripchart(round(x,1), method = "stack", pch=20)
```

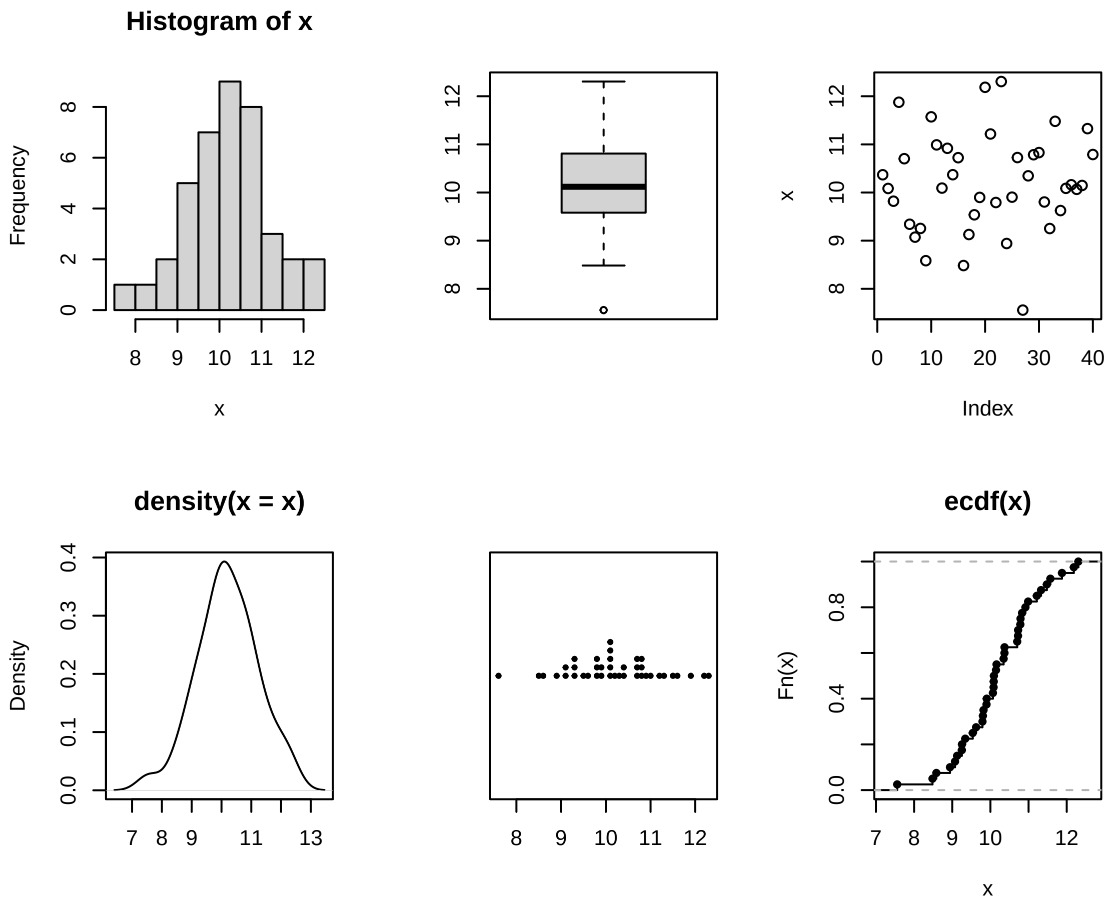


```
plot(ecdf(x), verticals=TRUE)
```



We can form a matrix of order 3X2 or (or 2X3) and display all the above six graphs in a panel. This is done using the option `par()`, which controls the graphics *par*ameters.

```
x  <- rnorm(40, 10,1)

par(mfrow = c(2, 3))

hist(x)

boxplot(x)

plot(x)

plot(density(x), xlab='')

stripchart(round(x,1), method = "stack", pch=20)

plot(ecdf(x), verticals=TRUE)
```



Although we shall not cover them here, many plotting options can be set using `par()` function; including size of margins, font types, the colour of axis labels etc. See `help("par")`. The option `par(new=T)` will be useful for an overlaid graph (instead of splitting a graph). Try the following:

```
x  <- rnorm(40, 10,1)

plot(x, type = "o", pch = 1, ylab = "",
     ylim = c(6.5, 13.5), lty = 1)

par(new=T)

y  <-  rnorm(40, 10,1)
```

```r
plot(y, type = "o", pch = 2,
     ylab = "Two Batches of Random Normal Data",
     ylim = c(6.5, 13.5), lty = 2)
```

Note that `pch` specifies for the plotting character and `lty` specifies the line type. You can add a legend by the following command line:

```
legend("topright", c("Batch I", "Batch II"), pch=1:2, lty=1:2)
```

For scatter and other related plots, the command is `plot()`. Try

```r
x  <-  rnorm(40, 10,1)
y  <- rnorm(40, 10,1)
plot(y~x)  # or plot(x,y)
```

Add a title by the command

```
title("This is my title")
```

Add a reference line for the mean at the x-axis by the command

```
abline(v=10)
```

and again with `abline(h=10)` for the y-axis. A 45 degree (Y=X) line can be added by the command

```
abline(0,1) #slope, b=1, y-intercept a=1
```

You may also specify two points on the graph, and ask them to be connected using the command

```
lines(c(8, 12), c(8, 12), lty=2, col=4, lwd=2)
```

Note that the `line()` has extra arguments to control the line type, line width, and colour.

The command `rug(x)` draws will draw small vertical lines on the x-axis (the command actually suits better for one dimensional graphs such as a boxplot). Try

```
rug(x)
```

```
rug(y, side=2)  #side =2 specifies y-axis
```

Graphs can be saved in various file formats, such as PDF (.pdf), JPEG (.jpeg or .jpg), or postscript (.ps), by enclosing the plotting function in the appropriate commands. For example, to save a simple figure as a PDF file, we use the `pdf()` function.

```
x  <-  1:10
```

```
y  <-  x^2
```

```
pdf(file = "Fig.pdf")
```

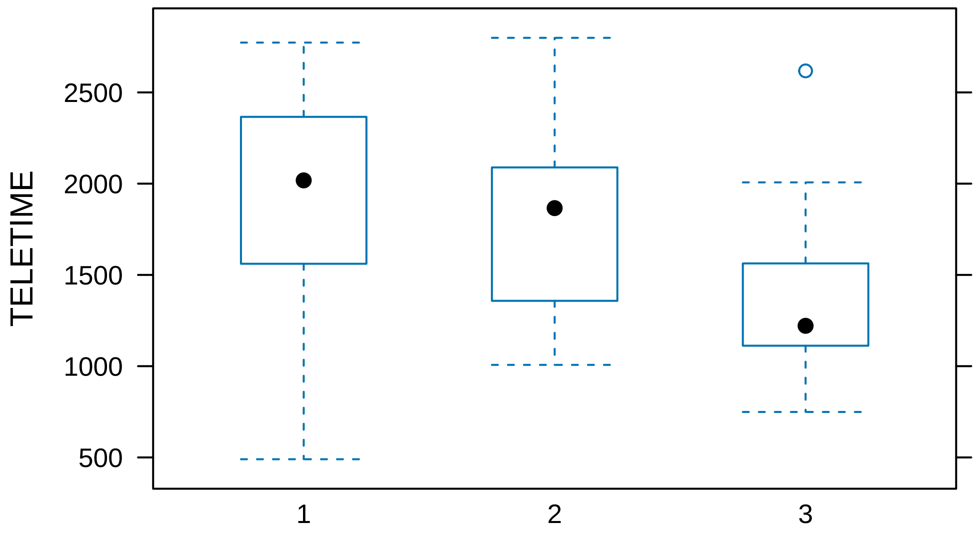
```
plot(x, y)
```

```
dev.off()
```

The `command dev.off()` closes the file. You may use the copy and paste facility for processing graphs or use the RStudio option to save graphs.

The`lattice` package contains extra graphing facilities but such graphs can be produced using `ggplot2` package. Try-

```
my.data <-read.csv(
  "https://www.massey.ac.nz/~anhsmith/data/tv.csv",
  header=TRUE)

library(lattice)

bwplot(TELETIME ~ factor(SCHOOL),
       data = my.data)
```



It requires a bit of coding to combine base, lattice and ggplot graphs. Try the following codes which combines three density plots of the same data produced in different styles.

```r
library("grid")
library("ggplotify")

x= rnorm(30)

p1 <- as.grob(~plot(density(x)))
p1 <- as.ggplot(p1)

p2 <- as.grob(densityplot(x))
p2 <- as.ggplot(p2)

library(ggplot2)

p3 <- data.frame(x=x) |>
  ggplot() +
  aes(x) +
  geom_density()

library(patchwork)

p1/(p2+p3)
```

Tip

It is optional to work through the activities that follow to gain an appreciation of how R works. Do not try to remember how to do everything right now. For your assignment work, we will be given the R codes to load data, graphing and modelling. These codes will give you a head-start. Note that we often often learn R by doing and sometime making mistakes.

R Objects, Model Syntax etc.

In R, we work with objects. There are different classes of objects including: `character`, `integer`, `numeric`, `vector`, `matrix`, `array`, `data.frame`, `list`, `lm` (linear model). An object may belong to several classes at once.

Suppose that your data consists of 4 numbers say 1 to 4. We can combine these numbers using the `c()` function namely `c(1,2,3,4)` and then assign it to `x`, an object.

```
x <- c(1,2,3,4)
```

Alternatively, we can use the `scan()` function to enter the data manually one by one. In practice we load/import data and these details are explained in the next section.

Evidently `x` is a vector and also belongs to other classes of objects. This can be queried as follows:

```
is(x)
```

The main class it belongs to is queried as

```
class(x)
```

Our data are actually integers and arranged in a pattern. So we can define `x` as follows:

```
x <- 1:4
```

The colon (:) operator created the desired pattern. Alternative expressions include

```
x <- seq(1, 4, by=1)
```

Try `is(x)` and `class(x)` and check whether our data are recognised as integer class.

We can do many mathematical manipulations on `x`. Try

```
mean(x)
min(x)
max(x)
```

```r
sum(x)
sd(x)
var(x)
sort(x, T)
trunc(x/2)
```

Vector elements are accessed by square brackets, []. Try

```r
x[2]+x[4]
x[2:3]
x[c(1,3)]
x[-2]
```

Assume that our data are actually categorical codes. Then the correct way of defining the character data is to use single quotes as

```r
x <- c('a', 'b', 'c', 'd')
```

Now try Try is(x) and class(x). For large patterned categorical data, placing quotes is laborious. So we can change the class as follows:

```r
x <- as.character(1:4)
```

Assume that you have two batches of data. The first one is

```r
x <- 1:4
```

and the second one is

```r
y <- c('a', 'b', 'c', 'd')
```

These two batches can be combined into a matrix as follows:

```r
m <- cbind(x,y)
```

Here the matrix m is formed by binding the columns (vectors). The other option is to bind as rows

```r
m <- rbind(x,y)
```

Evidently vectors must be of the same length for these commands to work. We can also form a matrix by splitting a vector. Try

```r
x <- 1:6
m <- matrix(x, byrow = TRUE, ncol = 3)
m <- matrix(x, byrow = TRUE, ncol = 2)
```

and just type `m` to see the generated matrix on the R console.

```r
m
```

To access the first of row of the matrix `m`, we use `m[1,]`; to access the first column of `m`, we use `m[,1]`.

A `data frame` is an R object that contains vectors; the vectors are stored vertically in a matrix like structure, and can be referred to by the name of the column. The main advantage of a data frame is that the variables in a data frame do not all need to be the same type; e.g. some variables can be of class numeric, and some variables can be of class character. We can create a data frame object using the `data.frame()` function. This data frame contains two small vectors, the first of which is named `ID`, and the second `NAME`. Try

```r
x <- 1:4
y <- c('a', 'b', 'c', 'd')
my.data <-data.frame(ID=x, NAME=y)
my.data
```

We can access the original vector of interest in the following way:

```r
my.data$NAME
```

or with `tidyverse`

```r
my.data |> pull(NAME)
```

There are times when it is useful to convert a data frame into a matrix; we can do this with the `as.matrix()` function.

```r
m <- as.matrix(my.data)
```

Type `class(m)` and see the changes.

Two data frames can also be merged into a single data frame using the `merge` command.

The internal structure of an R object can be viewed using the diagnostic function `str()`.

Simple Manipulations

There is always more than one-way of manipulating the data, producing summaries and tables from raw data.

One of the simplest manipulations on a batch of data we may do is to change the data type say numeric to character. For example, the television viewing time data in the text file `tv.csv` is read into a dataframe by the command line

```
my.data <- read.csv(
  "https://www.massey.ac.nz/~anhsmith/data/tv.csv",
  header =TRUE
  )
```

We can improve the `read.csv` command to recognise the data type while reading the table as follows, using the `read_csv` command from the `readr` package:

```
my.data <- read_csv(
  "https://www.massey.ac.nz/~anhsmith/data/tv.csv",
  col_types = "nfcc"
  )
```

The argument `col_types = "nfcc"` stands for {`numeric`, `factor`, `character`, `character`}, to match the order of the columns.

```
my.data
```

```
# A tibble: 46 x 4
   TELETIME SEX   SCHOOL STANDARD
      <dbl> <fct> <chr>  <chr>
 1     1482 1     1      4
 2     2018 1     1      4
 3     1849 1     1      4
 4      857 1     1      4
 5     2027 2     1      4
 6     2368 2     1      4
 7     1783 2     1      4
 8     1769 2     1      4
 9     2534 1     1      3
10     2366 1     1      3
# i 36 more rows
```

We often do a summary of a numerical variable for a given categorical variable. For example, we like to see obtain the summary statistics of TV viewing times for various schools. The commands

```
attach(my.data)
by(TELETIME, SCHOOL, summary)
```

We employed the `by()` command above and instead, we may also use `tapply()` `aggregate()` functions:

`tapply(TELETIME, SCHOOL, summary)`

`aggregate(TELETIME, list(SCHOOL), summary)`

A tabulated summary of categorical data is obtained using the `table()` command.

```
my.data <- read.csv(
  "https://www.massey.ac.nz/~anhsmith/data/rangitikei.csv",
  header=TRUE
  )

wind <- my.data |> pull(wind)
river <- my.data |> pull(river)

table(wind, river)
```

It is sometimes convenient to work with matrices for some R functions such as `apply()`. For example, the number of admissions data in `hospital.txt` data can be formed as a matrix. Note that this is possible because we have the same number of observations for each hospital location.

```
data <- read.table(
  "https://www.massey.ac.nz/~anhsmith/data/hospital.txt",
  header=TRUE,
  sep=",")

M <- data |>
  select(NORTH1, NORTH2, NORTH3,
         SOUTH1, SOUTH2, SOUTH3) |>
  sqrt()

means <- apply(M, 1, mean)
sds <- apply(M, 1, sd)

plot(means, sds)
```

R default options for Hypothesis tests and modelling

The stats default package in R has a number of functions for performing hypothesis tests. However you will only use the following for this course:

ks.test - Kolmogorov-Smirnov Tests

shapiro.test - Shapiro-Wilk Normality Test

t.test - Student's t-Test (one & two samples, paired t-test etc)

pairwise.t.test - Pairwise t tests (for multiple comparison)

oneway.test - Test for Equal Means in a One-Way Layout

TukeyHSD - To Compute Tukey's Honest Significant Differences

var.test - F Test to Compare Two Variances

bartlett.test - Bartlett Test of Homogeneity of Variances

fisher.test - Fisher's Exact Test for Count Data

chisq.test - Pearson's Chi-squared Test for Count Data

cor.test - Test for Association/Correlation Between Paired Samples

The car package is needed for the following:

durbinWatsonTest Durbin-Watson Test for autocorrelated Errors

leveneTest Levene's Test

We will largely use the R function lm in this course. The syntax for specifying a model under lm command (and various other model related commands) is explained below:

The structure of the model is that the response variable is modelled as a function of the response variables. The symbol ~ (tilde) is used to say "a function of". The simple regression of y on x is therefore specified as

```
lm(y ~ x)
```

The same applies to a one-way ANOVA in which x is a categorical factor. For example, consider tv.txt dataset and the one-way ANOVA model of TELETIME for SCHOOL is specified as follows:

```r
mydata <- read.csv(
  "https://www.massey.ac.nz/~anhsmith/data/tv.csv",
  header=TRUE
  )

mymodel <- lm(TELETIME ~ factor(SCHOOL),
              data = mydata) # replace lm by aov and try
```

```r
summary(mymodel)
```

The function `summary()` gives the summary of the model (F statistics, residual SD etc). The model summary output can be stored into a text file using the function `sink()` or copy and paste in the windows version. Graphs associated with a model can be obtained using the command

`plot(mymodel)`

In the above context, we may also use the specific test command which will give the same result but this test can also be performed without assuming equal variances.

```r
oneway.test(TELETIME ~ SCHOOL,
            var.equal = TRUE,
            data = mydata)
```

For the `lm` command, note the following:

`+` indicates inclusion (not addition) of an explanatory variable in the model

`-` indicates deletion (not subtraction) of an explanatory variable from the model

`*` indicates the inclusion of the explanatory variables and their interaction (not multiplication) between explanatory variables

`:` (colon) means only interaction between explanatory variables

`/` indicates the nesting (not division) of explanatory variables

`|` indicates the conditioning (for example `y ~ x|z` means that y is a function of x for given z).

For our course, you will not use the last two types. Some model examples are given below:

`lm(y ~ x + z)` #regression of y on x and z (flat surface fit)

`lm(y ~ x*z)` #includes the interaction term ie `lm(y ~ x + z + x:z)`

`lm(y ~ x + I(x^2)` # fits a quadratic model or use `poly(x,2)`

`lm(log(y) ~ sqrt(x) + log(z))` #all variables are transformed

As a further example, consider a study guide dataset. The following commands fit a simple regression model and then plot the fitted line on a scatter plot. Note that commands can be shortened but deliberately shown this way.

```r
mydata <- read.csv(
  "https://www.massey.ac.nz/~anhsmith/data/horsehearts.csv",
  header=TRUE
  )

x <- mydata$EXTDIA
y <- mydata$WEIGHT

simplereg <- lm(y ~ x)
```

Note that our model object `simplereg` can be queried in many ways. The command `summary()` gives the following output.

```
summary(simplereg)
# or
# library(broom)
# tidy(simplereg)
# glance(simplereg)
```

The command `names(simplereg)` will gives the names of many individual components of the object `simplereg` we created. For example, a plot of the residuals against the fitted values can be obtained as

```
plot(residuals(simplereg) ~ fitted.values(simplereg))
```

Bibliography

[1] L. Wilkinson. *The Grammar of Graphics*. Berlin, Heidelberg: Springer-Verlag, 2005. ISBN: 0387245448.