

# Workshop: Mendelian randomization analysis

Marielisa Graff, PhD. Research Associate Professor

## Command Line Cheat Sheet

### Directories

```
$ pwd
Displays the path to the current working directory
$ cd <directory>
Changes the current working directory to <directory>
$ cd ..
Navigate to parent directory
$ ls
List directory contents
$ ls -la
List detail directory content, including hidden files
$ ll
Shortcut - List detail directory content, including hidden files
```

### Output

```
$ cat <file>
Output the contents of <file>
$ head <file>
Output the first 10 lines of <file>
$ <cmd> > <file>
">": directs the output of <cmd> to <file>
$ clear
Clears the command line window
```

### Files

```
$ rm <file>
Deletes <file>
$ rm -r <directory>
Deletes <directory> and its contents
$ mv <file-old> <file-new>
Renames <file-old> to <file-new>
$ mv <file> <directory>
Moves <file> to <directory>
(Possibly overwriting an existing file)
$ cp <file> <directory>
Copy <file> to <directory>
(Possibly overwriting an existing file)
$ cp -r <directory1> <directory2>
Copy <directory1> and its contents to <directory2>
$ touch <file>
Creates a new <file> if it doesn't exist
```

### Search

```
$ find <directory> -name "<file>"
Find all files named "<file>" inside <directory>
$ grep "<text>" <file>
Output all occurrences of <text> inside <file>
$ grep -rl "<text>" <directory>
Search for all files containing <text> inside <directory>
```



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## R Cheat Sheet

**Tidyverse** is a powerful collection of R packages that are data tools for transforming and visualizing data.

The `%>%` pipe is an important part of the workflow; it is used to highlight a sequence of actions rather than the object on which the actions are performed.

It is used by first indicating the database to connect it to the function you want to apply.

```
> library(tidyverse)
> iris %>%
  head()
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

### Liberies

```
> install.packages(<package>)
```

Download and install packages from the CRAN repositories or from local files

```
> library(<package>)
```

Load the indicated `<package>` in the work area

### Utilidades

The assignment operator `"<-"` is used to assign values to variables

```
> x <- 10
> x
10
```

### Tidyverse

```
> filter()
```

Select a subgroup of data based on a logical condition

```
iris %>%
  filter(Species == "virginica")
```

```
> mutate()
```

Modify or create a variable

```
iris %>%
  mutate(Sepal.Length = Sepal.Length * 10)
```

```
> summarize()
```

Allows many observations to be converted into a single data point

Mainly used to obtain summary statistics from the database

```
iris %>%
  summarize(medianSL = median(Sepal.Length))
```

```
> read_csv()
```

Reads (imports) a ".csv" file

```
my_data <- read_csv("path_to_data/dat.csv")
```

```
> str_c()
```

Combines multiple character vectors into a single character vector

```
str_c("hello", "world", sep = " ")
```



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## MR Packages Cheat Sheet

Overview of the packages used in the workshop:

- **MendelianRandomization**  
Package developed to carry out various Mendelian randomisation analyses on genetic data in R.  
The package uses several methods to assess whether a risk factor (or exposure) has a causal effect on an outcome.
- **metafor**  
Provides functions for conducting meta-analyses in R.  
Includes functions for fitting fixed and random effects models. Allows the inclusion of moderator variables in the models.
- **TwoSampleMR**  
Two sample Mendelian randomisation (2SMR) is a method to estimate the causal effect of an exposure on an outcome using only summary statistics from genome wide association studies (GWAS).
- **MRPRESSO**  
Mendelian Randomization Pleiotropy RESidual Sum and Outlier is a method that allows for the evaluation of horizontal pleiotropy in multi-instrument Mendelian Randomization utilizing genome-wide summary association statistics.

