



ACEFA EPIDEMIC MODELLING & ANALYTICS SHORT COURSE

INTRODUCTION TO R: PRACTICAL

Background information

In this practical, we will be introducing the programming language R, using the interface R Studio. We will then use R to implement the SIR models explored in Practical 1.

To prepare for the practical, please install the R programming language and R Studio.

To install R, follow the instructions at:

<https://cran.r-project.org/bin/windows/base/>

To install R Studio, follow the instructions at:

<https://posit.co/download/rstudio-desktop/>

Once these are installed, please open R Studio. If you have not used R before, you might like to explore the interface and try it out – there are many online guides to using R and R Studio. We will also have a section in this practical on using R, but any prior experience will be helpful.

To be ready for the course, please open R Studio and go to the console, usually on the bottom left:

```
R - R 4.5.0 - ~/R/ACEFA_course/
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.

> |
```

To install the required packages, type in each of the following lines (hit Enter after each line):

```
install.packages("tidyverse")
```

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

```
install.packages("patchwork")
```

```
install.packages("EpiNow2")
```

```
install.packages("deSolve")
```

Optional practical sections

For those looking for an R refresher, you can work through the following practical sections:

part0_R_basics.R

part1_R_plotting.R

In the R basics section, you can work through an introduction to using R in R Studio. You will look at basic operations and assignments, functions, working with dataframes, and reading in data.

In the R plotting script, you can work through how to create some plots using a package called ggplot2.



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The practical

In this R tutorial, we will replicate the deterministic and stochastic SIR models that we explored in the first practical. This will allow us to examine how the implementation of SIR models translates from a spreadsheet format into R code, and we will see how a number of parts of model implementation and analysis become easier in R.

To start open the file

part2_SIR_models.R

Deterministic model

1. To start with, we are going to implement the deterministic version of the SIR model. However, instead of formulating the model as a series of difference equations (in discrete time), we are going to implement the model as a set of differential equations, in continuous time, using an ordinary differential equation solver package called “deSolve”.

Start by stepping through the code and familiarising yourself with the model framework, until you reach the part where you plot the model outputs.

2. Can you calculate the final attack rate?
3. Can you calculate the timing of the epidemic peak?
4. Can you calculate the basic reproduction number, and the effective reproduction number over time? Create a plot of R_{eff} over time.
5. Increase R_0 by setting $\beta = 0.8$, and rerun the model. Does the model output change as expected?

Stochastic model

6. Now we are going to implement the stochastic version of the SIR model, in the same fashion as was implemented in Excel. Change the beta back to the original value of 0.4. Step through the stochastic implementation of the model and plot the model output.
7. What happens if you change the total population size? Try running the model with $N = 100$, or $N = 10,000$. It can be helpful to compare the deterministic and stochastic outputs by plotting on the same figure panel.



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Visualisations

8. Test out the code to plot both the deterministic and stochastic model outputs on the same graph.
9. It can be useful to visualise a number of stochastic simulations on the same graph – experiment with different numbers of runs.
10. What other visualisations can you create using these model outputs?

Prevalence and incidence

11. In the last practical, we noted that we have focussed on modelling prevalence $I(t)$ and discussed how we might instead model infection incidence. See if you can work out how you might calculate incidence for the deterministic model.