**Learn to experiment with R to make analyses and figures more reproducible**

**Overview**

An increase in the complexity and scale of biological data means biologists are increasingly required to develop the data skills needed to design reproducible workflows for the simulation, collection, organisation, processing, analysis and presentation of data. Developing such data skills requires at least some coding, also known as scripting. This makes your work (everything you do with your raw data) explicitly described, totally transparent and completely reproducible. However, learning to code can be a daunting prospect for many biologists. That's where an Introduction to reproducible analyses in R comes in.

R is a free and open source language especially well-suited to data analysis and visualisation and has a relatively inclusive and newbie-friendly community. R caters to users who do not see themselves as programmers, but then allows them to slide gradually into programming.

**Who is this course for?**

Introduction to reproducible analyses in R is aimed at researchers at all stages of their careers interested in experimenting with R to make their analyses and figures more reproducible.

**Prerequisites**

No previous coding experience will be assumed. Participants will work on their own laptops. It would be ideal have installed R and RStudio already. This is straightforward but there will be a chance to get help with it during registration.

**Learning outcomes**

After this workshop the successful learner will be able to:

1. Find their way around the RStudio windows
2. Create and plot data using the base package and ggplot
3. Explain the rationale for scripting analysis
4. Use the help pages
5. Know how to make additional packages available in an R session
6. Reproducibly Import data in a variety of formats
7. Understand what is meant by the working directory, absolute and relative paths and be able to apply these concepts to data import
8. Summarise data in a single group or in multiple groups
9. Recognise tidy data format and carry out some typical data tidying tasks
10. Develop highly organised analyses including well-commented scripts that can be understood by future you and others
11. Use markdown to produce reproducible analyses, figures and reports

**Course tutor**

**Emma Rand** is a teaching and scholarship lecturer in the department of biology, the University of York. She specialises in experimental design and reproducible data science from pre-processing and exploration to statistical analysis and visualisation. She is an invited [**tutor at useR!2019**](http://www.user2019.fr/tutorials/), the International R User Conference supported by the The R Foundation and a co-tutor of "Practical Python: Resources for analysing biological data with Python" at the Biochemical Society's[**Life Sciences 2019: Post-translational modifications and cell signalling**](https://www.eventsforce.net/biochemsoc/frontend/reg/thome.csp?pageID=16990&eventID=41&traceRedir=2) meeting in March. She is twice the winner of the University of York Student Union's headline [**Excellence Award**](https://www.yusu.org/opportunities/recognition/excellence), Teacher of Year.

Her philosophy is that:

* anyone can code
* coding can be fun
* R/Python doesn't really matter, is coding at all that is important
* some reproducibility is better than none
* the perfect is the enemy of the good

**Certification and Continuing Professional Development (CPD)**

A certificate of attendance will be provided after the event.  
We evaluate all of our training events, to make sure that we maintain a high quality of training.  
  
This event has been approved by the Royal Society of Biology for purposes of [**CPD**](https://www.rsb.org.uk/careers-and-cpd/cpd) and can be counted as **X CPD points**.