



## Certificate of Achievement

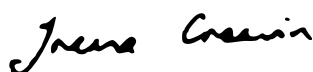
# Juan Carlos García

has completed the following course:

### BIOINFORMATICS FOR BIOLOGISTS: AN INTRODUCTION TO LINUX, BASH SCRIPTING, AND R WELLCOME CONNECTING SCIENCE

This course covered main characteristics of Linux applied to biology, the structure and navigation of the Linux file system, Linux commands to manipulate and interrogate data files, running simple shell scripts in order to automate processing of data and use of R for data analysis and visualisation.

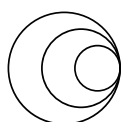
3 weeks, 5 hours per week



**Dr Treasa Creavin**  
Scientific Programme Manager  
Wellcome Connecting Science



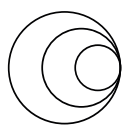
**Martin Aslett**  
IT Manager  
Wellcome Connecting Science



**wellcome  
connecting  
science**

The person named on this certificate has completed the activities in the attached transcript. For more information about Certificates of Achievement and the effort required to become eligible, visit [futurelearn.com/proof-of-learning/certificate-of-achievement](https://futurelearn.com/proof-of-learning/certificate-of-achievement).

This certificate represents proof of learning. It is not a formal qualification, degree, or part of a degree.



## Juan Carlos García

has completed the following course:

### **BIOINFORMATICS FOR BIOLOGISTS: AN INTRODUCTION TO LINUX, BASH SCRIPTING, AND R WELLCOME CONNECTING SCIENCE**

**80%**  
OVERALL  
SCORE

This course covered: main characteristics of Linux and its use in biology, the structure of the Linux file system and use of Linux commands to navigate it, Linux commands to manipulate and interrogate biological data files, writing and executing simple shell scripts in order to automate processing of data and preparation of biological data files for exporting into other environments such as R for analysis and visualisation.

#### **STUDY REQUIREMENT**

3 weeks, 5 hours per week

#### **LEARNING OUTCOMES**

- Identify main characteristics of Linux and its use in biology
- Describe the structure of a Linux file system
- Use Linux commands to navigate the file system
- Perform Linux commands to manipulate and interrogate biological data files
- Prepare biological data files under Linux for exporting into other environments such as R
- Write and execute simple shell scripts in order to automate processing of data

#### **SYLLABUS**

- What is Linux? Why Linux for biologists?
- The Linux file system and navigating around it via the command line
- Manipulation and searching of data files using the command line to access useful biological data
- The basics of writing Bash scripts and its use for process automation

- Guidelines and recommendations for best practice preparation of data files under Linux for exporting to other environments (use of R for further analysis and visualisation)
- Exercising on biological data using different case scenarios