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Certificate of Achievement

Kanmani mathiyazhagan

has completed the following course:

BIOINFORMATICS FOR BIOLOGISTS: ANALYSING AND INTERPRETING GENOMICS DATASETS
WELLCOME CONNECTING SCIENCE

The course covered NGS sequencing, file formats used, Linux commands for sequence quality control, mapping, and variant calling. Same tasks were performed using Nextflow, applied to viralrecon pipeline with data visualization of variants obtained from genomic data as part of the downstream analysis.

3 weeks, 6 hours per week

Dr Treasa Creavin
Head of Scientific Meetings and Digital Learning
Wellcome Connecting Science

Dr Fatma Guerfali
Researcher
Institut Pasteur de Tunis

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.

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

TRANSCRIPT

wellcome connecting science

Kanmani mathiyazhagan

has completed the following course:

BIOINFORMATICS FOR BIOLOGISTS: ANALYSING AND INTERPRETING GENOMICS DATASETS

WELLCOME CONNECTING SCIENCE

80% OVERALL SCORE

The course covered Next Generation Sequencing and its significance in genomics, the installation of widely-used bioinformatics tools, the use of different file formats, and Linux commands for sequence quality control, mapping, and variant calling. The analysis was also performed using the workflow management system Nextflow, and applied to viralrecon, an existing bioinformatics pipeline. Downstream analysis included RStudio data visualization of variants obtained from genomic data sample.

STUDY REQUIREMENT

3 weeks, 6 hours per week

LEARNING OUTCOMES

- Use software managers to install and run reproducible bioinformatics tools
- Handle and analyse sequence datasets through hands-on exercises
- Analyse quality control metrics for sequencing data
- Modify existing workflows to suit specific task requirements and optimise analysis processes
- Interrogate and interpret the results obtained from running bioinformatics pipelines
- Perform downstream analyses of pipeline outputs using R, enabling data visualisation and further exploration

SYLLABUS

- Brief introduction to sequencing technologies and an overview of current sequencing outputs
- Sequence quality control to ensure data accuracy and reliability
- Bioinformatics workflows utilising tools such as Nextflow using nf-core pipelines
- Mapping sequencing data to a reference genome for alignment and variant calling
- Working with pipeline outputs in R to perform downstream analysis and visualisation.