

Bioinformatics approaches for Next Generation Sequencing [NGS] Analysis Course

Eligibility

African research scientists from any country in sub-Saharan Africa who hold a Master's or PhD degree, or who are currently enrolled for a Master's or PhD degree.

Course requirements: basic familiarity with using computers, some programming experience in any language (for example with R, Matlab or SPSS), and a basic familiarity with genetics and genomics techniques. The course will then build on these to introduce participants to more advanced programming and analysis techniques.

The course is very intensive and a strong motivation and drive is required. Students will be selected on the basis of their academic record and written statements concerning their need for NGS bioinformatics training, how they expect to benefit from participating in the course, and how they expect to apply the new skills to their own research. There will be no attendance fee, but the students will be selected based on merit. There are a total of 24 spaces available for the course.

A small number of scholarships available for international students. The students will be selected based on merit, and the selected students will receive economy round-trip airfare from a major international airport in their country to Nairobi. Full Board accommodation will be provided for international students, and meals to local students.

For more details about the course, please visit the organizers website;
<http://41.57.109.242/zoonotic/Sites/bioinfo/index.html>

Aims and Scope of the Workshop

To introduce a range of bioinformatics analysis techniques for dealing with Next Generation Sequencing (NGS) data, including an introduction to programming and analysis best practices. The course will start with an introduction to programming, mainly focusing on the R statistical programming language. It will then build on this foundation to introduce tools for data visualisation and analysis. It will introduce software development concepts such as databases and version control. It will then cover NGS analysis topics including de novo genome and transcriptome assembly, ChIP-seq and RNA-seq, rare variant calling and population genetics. There will be a focus on using freely available data and open source technologies, and encouraging open reproducible research.

Workshop Description

The workshop will be run over the course of six days. The morning lectures will cover the theory of experimental design, different sequencing datasets and how to deal with them, and a range of applications of NGS technology including RNA-seq, methylome analysis, GWAS and rare variant calling. The afternoon programming practicals will focus on building up the students' skills in using R and Unix to undertake bioinformatics analysis, including data processing and visualisation, as well as programming best practices such as testing and version control. The

students will also work in small groups with each of the instructors to undertake a specialised project and get hands on analysis time, and the course will also include a scientific communication component. Throughout the course there will be a strong emphasis on the usage of open source technologies and an active “Do it yourself” spirit will be encouraged.