

Viral Bioinformatics and Genomics Courses

In collaboration with [Makerere University](#), Kampala, Uganda, we are pleased to announce the 2019 overseas course in Viral Bioinformatics and Genomics.

Viral animal and human diseases including zoonotic infections are a major production and public health burden across the world. This has a negative impact on livelihoods especially in low and middle-income countries in Asia, Africa and Latin America where diagnosis and surveillance of viral diseases are challenging. In Africa, Ebola, haemorrhagic fevers, Rift Valley Fever, HIV, Malaria, Cholera, African swine fever, Foot-and-mouth disease, and rabies are some of the viral diseases that cause hundreds of thousands of deaths each year. Apart from health risks, emerging viral infections and outbreaks also pose an economic burden globally.

Advances in research technologies are enabling access to improved detection, surveillance and management of viral diseases. In the recent years, next generation sequencing (NGS) technologies have played an important role in the identification and classification of viruses, the detection of drug resistance mutations and the treatment and surveillance of viral diseases. Early identification of a virus and rapid analysis of its genome will aid towards better treatment and help in controlling the disease spread. Despite the advances in NGS data generation, the main challenge is the computational and data manipulation approaches for proper interpretation. This is still a big problem, particularly in Africa.

The course will provide participants with a working knowledge of viral genome sequence analysis and interpretation of genomics data generated from large-scale sequencing. Participants will have an opportunity to establish links and networks and develop future collaborative projects. Topics will include the use of the command line to perform analysis of viral NGS data, quality control of genomics data, reference and de-novo assemblies, pathogen detection from metagenomics data, annotation transfer from a reference genome and building phylogenetic trees.

Target audience
The course is free to attend and open to applicants based in Africa engaged in relevant research/clinical activities. The programme is aimed at researchers at various levels including Senior Research Assistants, PhD students, Postdoctoral Researchers, Laboratory Scientists and Clinical Scientists/Healthcare Professionals.

Deadlines (at 23:59 UTC): Application and bursary deadline 07 March 2019

Source link: <https://coursesandconferences.wellcomegenomecampus.org/our-events/viral-...>