



Training course on Viral Bioinformatics and Genomics

Course dates: 10th-14th of August 2015

Location: Garscube Campus, University of Glasgow, Glasgow, UK

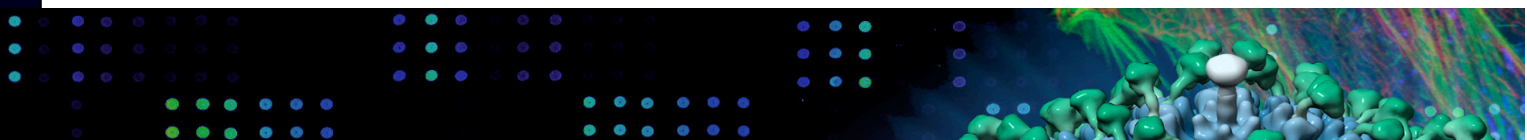
The need for effective and automated analyses of viral sequences has increased exponentially with the new high-throughput sequencing technologies. An understanding of the different bioinformatic approaches available for processing these data is an essential step in most virological studies.

We will be giving a 5-day course, which will consist of a series of lectures and practical exercises that directly address bioinformatic challenges posed by the current deluge of sequence data. We will enable participants to understand and deal with high-throughput sequence datasets and encourage the exchange of ideas among diagnosticians, virologists, bioinformaticians and evolutionary biologists.

The 2015 course will introduce the participants to the power of the UNIX command-line and bash scripts, as well as a suite of bioinformatics tools covering the following topics:

- **HTS sequencing technologies:** overview of the different HTS platforms and sample preparations.
- **Unix primer:** introduction to Bio-Linux and essential bash scripting.
- **Reference assembly:** aligning sequence reads to a known reference and visualizing the alignment; (e.g., bowtie2, BWA, Tanoti, Tablet, UGENE).
- **Variant calling:** consensus sequence generation, low frequency variant calling and error correction; (e.g., LoFreq, VPhaser).
- **De-novo assembly:** overlap layout and De Bruijn graphs approaches for sequence assembly; (e.g., Velvet, IDBA-UD).
- **Metagenomic analyses:** sanitizing sequence datasets, assembling, annotating, visualizing; (e.g., MetAMOS, Krona, MEGAN).
- **Genomics:** scaffolding, improving the assembly, finishing the assembly, gene annotation; (e.g., ICORN, Artemis).
- **Phylogenetic analysis:** introduction to multiple sequence alignment and phylogenetic reconstruction; (e.g., clustal, PhyML).

Students will work from their own laptop using a bootable Bio-Linux USB key or on a local desktop running Bio-Linux. They will also have the opportunity to use the high performance computing facilities at the CVR to analyse their own datasets under the guidance of the instructors.





CVR
Medical Research Council
University of Glasgow
Centre for Virus Research



University
of Glasgow

Oie
Collaborating Centre for
Viral Genomics and Bioinformatics

Instructors:

Joseph Hughes (Course Organiser)
Andrew Davison
Robert Gifford
Sejal Modha
Richard Orton
Sreenu Vattipally
Gavin Wilkie

Prerequisites:

To maintain a good ratio of tutors to participants, the enrolment will be limited to 15 students. Preference will be given to applicants who:

- have familiarity with HTS technologies
- have already generated HTS in their work
- have an interest in computers and programming (some experience in a command-line environment would be desirable)

Registration fee:

£250 for the 5-day course including lunches. To apply fill in the questionnaire before the 25nd of May [<http://goo.gl/forms/m8SxCMNXrH>]. You will be contacted if you are shortlisted for the course this year.

NB: Participants are responsible for their own travel arrangements and accommodation.

Our Address

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