



3rd Annual Training Course on Viral Bioinformatics and Genomics

Course dates: Monday 7th – Friday 11th of August 2017

Location: McCall Building, Garscube Campus, University of Glasgow, Glasgow, Scotland, UK

After the successful training courses in 2015 and 2016, the Viral Genomics & Bioinformatics team at the Centre for Virus Research (CVR) will be repeating the course this year. 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 surge of sequence data, with a focus on viral data sets and analyses. 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. Students will work on our high performance computing facilities at the CVR. The CVR has been designated an OIE Collaborating Centre for Viral Genomics and Bioinformatics at the 82nd OIE General Session.

The 2017 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.
- **The power of Unix:** 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. samtools, LoFreq, DiversiTools).
- **De-novo assembly:** overlap layout and de Bruijn graphs approaches for sequence assembly, quality assessment and merging contigs (e.g. ABySS, SPAdes, MIRA, IDBA-UD, QUAST, Mauve).
- **Metagenomic analyses:** sanitizing sequence datasets, assembling, annotating, visualizing (e.g. MetAMOS, Krona, DIAMOND, Kraken).
- **Genomics:** scaffolding, improving and finishing the assembly, gene annotation (e.g. ICORN, Artemis, RATT).
- **Phylogenetic analysis:** introduction to multiple sequence alignment and phylogenetic reconstruction (e.g. mafft, PhyML, FigTree).

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: (1) have some familiarity with HTS technologies; (2) have already or are planning to generate viral HTS data in their work; and (3) have an interest in computers and programming (some basic experience in a command-line environment is necessary)

Instructors

Richard Orton (Course Organiser), Quan Gu (Course Organiser), Andrew Davison, Ana Da Silva Filipe, Joseph Hughes, Maha Maabar, Sejal Modha, Sreenu Vattipally

Registration Fee

£500 for the 5-day course including lunches and tea/coffee breaks (**NB: participants are responsible for their own travel arrangements and accommodation**). To apply, fill in the application form before the 30th of April 2017: <http://goo.gl/TzSqxz>. For more information and for those unable to access this Google application form, please see <http://www.bioinformatics.cvr.ac.uk/>. You will be contacted within two weeks of the deadline if you have been shortlisted for the course this year.

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<http://www.bioinformatics.cvr.ac.uk/>

