CENTRE FOR GENOME ENABLED BIOLOGY AND MEDICINE
University of Aberdeen

Genome Assembly and Annotation
Using Galaxy and the Command Line

Date: 9 am – 5 pm GMT, Thursday 2ⁿᵈ December 2021

Location: Comp F86, Edward Wright Building, University of Aberdeen, Old Aberdeen Campus.

Format: Instructor led computer-based tutorial with support demonstrators.

Instructors: CGEBM Bioinformaticians (Dr Antonio Ribeiro, Ellen Smith and Dr Louie van de Lagemaat)

Description: Taking next generation sequencing data and transforming this into an assembled genome with annotated genes allows for further insight into the functionality of a species, allows for comparisons with other organisms, and provides a reference genome for other sequencing applications. This workshop will demonstrate a number of software choices and show the process from start to finish using both Galaxy and the command line. It is aimed at researchers who are (or will be) carrying out *de novo* assembly on organisms that do not have a reference genome. For information on resequencing a species that has a reference please attend the Alignment, Visualisation and Variant Calling Workshop later in the academic year.

Topics:

- Genome Assembly
- Identification of Contamination
- Gene Calling
- Gene Annotation

Who should attend: This workshop is aimed at researchers, staff and PhD students, interested in genome assembly and annotation. The aim of the workshop is to demonstrate software choices for genome assembly and some of the approaches available for annotation.

Pre-requisites: Introduction to the University of Aberdeen HPC Cluster and Basic Unix Skills workshop or alternative experience with the command line and HPC.

An account on the teaching HPC, Macleod, is needed. We are providing teaching accounts for all participants to use for the duration of the workshop. If you would like to use the research HPC, Maxwell, after the workshop you will need to obtain an account. For more details see http://www.abdn.ac.uk/staffnet/working-here/hpc.php. Macleod and Maxwell have the same file structure, operating system and scheduler. What you learn on the course is applicable to both University of Aberdeen HPC clusters.

Optional: Quality Control of Next Generation Sequencing Reads workshop. QC and filtering of reads will not be covered in the workshop and attendance at the QC workshop is recommended.

Closing Date for registrations: 25/11/2021

Closing Date for cancellations: Cancellations received by 25/11/2021 will receive a full refund minus a £40 admin fee. Full course fees will be charged for cancellations after this date.

Cost: For University of Aberdeen staff and PhD students the workshop is £180. Payments must be made before registration. Please enter your order details on the registration form. Details on how to raise an internal order for the course fees are provided on the registration form. Separate course fees apply for external or commercial delegates. Please contact us for further details before registering.

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Registrations: To register for this course, please complete the registration form at https://forms.office.com/r/AUu70inAaR or scan the QR code

Further Information: Please contact Elaina Collie-Duguid (e.collie-duguid@abdn.ac.uk)