

CLC Genomics Workbench Training

Two-day training course

A two-day course in which participants will receive practical training in processing and analysing genomic and transcriptomic datasets.

Topics include: read alignment, variant analysis, RNA-seq analysis, ChIP-Seq analysis, and *de novo* assembly.

Participants can choose to attend one or more of three course modules. The programme also includes a problem session in Day 2.

Date

14–15 November 2013

Time

Day 1: 9:00AM–5:00PM

Day 2: 10:30AM–5:00PM

Course fee

Participation is free of charge

Lunch & refreshments are provided

Target group

Research students and staff who wish to develop their ability to analyse their next-generation sequencing datasets using the CLC Genomics Workbench.

Venue

Jura teaching lab, Level 4 Annexe, University Library

Speakers

Representatives from CLC Bio: Holger Karas, Patrick Dekker, Miles Collier

Registration and enquiries

Contact Tanita Casci

(Tanita.Casci@glasgow.ac.uk)

Priority will be given to users of Glasgow Polyomics.

When booking, participants should indicate the module they prefer:

- Module 1 (Day 1, morning and afternoon sessions)
- Module 2 (Day 2, morning session only)
- Module 3, Problem session (Day 2, afternoon session only)

Further information

Online at www.glasgow.ac.uk/polyomics/trainingcourses

Follow us on Twitter: @polyomics

Programme

MODULE 1

Day 1: Thursday 14th November 2013

9:00–10:00

An overview of CLC software

10:00–11:00

Alignment against reference genomes

- Importing sequence from various platforms (focusing on Illumina and Ion Torrent).
- How to quality trim and remove adapters from the raw sequence data.
- Dealing with repeat regions.

11:00–11:30

COFFEE BREAK (room 416)

11:30–13:00

Variant analysis

- Importing sequence from various platforms (focusing on Illumina and Ion Torrent).
- How to quality trim and remove adapters from the raw sequence data.
- Handling multiple samples.
- Whole-genome trio analysis
- *De novo* assembled samples.

13:00–14:00

LUNCH (room 416)

14:00–15:30

RNA-Seq analysis

- Importing sequence from various platforms (focusing on Illumina and Ion Torrent).
- How to quality trim and remove adapters from the raw sequence data.
- Raw data processing.
- Novel exons and splice site discovery.
- Differential expression analysis.

15:30–16:00

COFFEE BREAK (room 416)

16:00–17:00

ChIP-Seq analysis

- Importing sequence from various platforms (focusing on Illumina and Ion Torrent).
- How to quality trim and remove adapters from the raw sequence data.
- Peak finding and annotation.
- Sample comparison.

END OF MODULE 1



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MODULE 2

Day 2: Friday 15th November 2013

10:30–11:30

De novo assembly

- Importing sequence from various platforms (focusing on Illumina and Ion Torrent).
- How to quality trim and remove adapters from the raw sequence data.
- Assembly setting optimisation.
- BLAST searching the contigs.
- Annotation.

11:30–12:00

COFFEE BREAK (room 416)

12:00–13:30

Pipelines

- Building analysis pipelines.
- Sharing pipelines.

END OF MODULE 2

MODULE 3

13:30–14:30

LUNCH (room 416)

14:30–17:00

User-led problem session

Participants will be able to discuss the problems they are having with the analysis of NGS data in a 15-minute session with CLC Bio training staff.

Those wishing to take advantage of this session should email Tanita (Tanita.Casci@glasgow.ac.uk) by the 8th of November with a brief description of their problem.

Participants will be given an appointment schedule. Users should bring their own laptop for this problem session so that they can work on their dataset directly.

END OF MODULE 3

