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.

**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.

**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.
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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.

**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
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Programme

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.

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.

Glasgow Polyomics

Glasgow Polyomics is a facility equipped for the collection, analysis and integration of genome, transcriptome, proteome and metabolome datasets.