

# 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.

The programme includes a problem session in Day 2.

### Date

5–6 March 2014

### Time

Day 1: 9:30AM–5:00PM

Day 2: 9:30AM–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

West Medical Building, Computer Cluster,  
Room 515

### Speakers

Representatives from CLC Bio: Holger Karas,  
Patrick Dekker, Sarah Nema

### Registration and enquiries

Contact Tanita Casci

([Tanita.Casci@glasgow.ac.uk](mailto:Tanita.Casci@glasgow.ac.uk))

Priority will be given to users of Glasgow  
Polyomics.

### Further information

Online at [www.glasgow.ac.uk/polyomics/  
trainingcourses](http://www.glasgow.ac.uk/polyomics/trainingcourses)

Follow us on Twitter: @polyomics

## Programme

### Day 1: Wednesday 5th March 2014

#### 9:30–10:30

An overview of CLC software

#### 10:30–11:00

**Phylogeny**

#### 11:00–11:30

COFFEE BREAK (Wolfson Link Courtyard)

#### 11:30–13:00

**De novo assembly (basics)**

- 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

#### 13:00–14:00

LUNCH (Wolfson Link Courtyard)

#### 14:00–15:30

**Pipelines (basics)**

- Building analysis pipelines
- Sharing pipelines

**Resequencing and SNP protection  
(Continues after the break)**

- 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
- Handling multiple samples
- Whole-genome trio analysis

#### 15:30–16:00

COFFEE BREAK (Wolfson Link Courtyard)

#### 16:00–17:00

**Resequencing and SNP detection  
(Continued)**



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## Programme

### Day 2: Thursday 6th March 2014

9:30–11:00

#### 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

#### 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

#### Small RNA

11:00–11:30

COFFEE BREAK (Wolfson Link Courtyard)

11:30–13:30

**De novo assembly (advanced)**

**Pipelines (advanced)**

13:30–14:30

LUNCH (Wolfson Link Courtyard)

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.

Users should bring their own laptop for this problem session so that they can work on their dataset directly.

