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.

---

**Programme**

**Day 1:**
Wednesday 5th March 2014

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>9:30–10:30</td>
<td>An overview of CLC software</td>
</tr>
<tr>
<td>10:30–11:00</td>
<td>Phylogeny</td>
</tr>
<tr>
<td>11:00–11:30</td>
<td><strong>COFFEE BREAK</strong> (Wolfson Link Courtyard)</td>
</tr>
<tr>
<td>11:30–13:00</td>
<td><em>De novo assembly (basics)</em></td>
</tr>
<tr>
<td></td>
<td>• Importing sequence from various platforms (focusing on Illumina and</td>
</tr>
<tr>
<td></td>
<td>Ion Torrent)</td>
</tr>
<tr>
<td></td>
<td>• How to quality trim and remove adapters from the raw sequence data</td>
</tr>
<tr>
<td></td>
<td>• Assembly setting optimisation</td>
</tr>
<tr>
<td></td>
<td>• BLAST searching the contigs</td>
</tr>
<tr>
<td></td>
<td>• Annotation</td>
</tr>
<tr>
<td>13:00–14:00</td>
<td>LUNCH (Wolfson Link Courtyard)</td>
</tr>
</tbody>
</table>

**Day 2:**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>14:00–15:30</td>
<td><strong>Pipelines (basics)</strong></td>
</tr>
<tr>
<td></td>
<td>• Building analysis pipelines</td>
</tr>
<tr>
<td></td>
<td>• Sharing pipelines</td>
</tr>
<tr>
<td></td>
<td><strong>Resequencing and SNP protection (Continues after the break)</strong></td>
</tr>
<tr>
<td></td>
<td>• Importing sequence from various platforms (focusing on Illumina and</td>
</tr>
<tr>
<td></td>
<td>Ion Torrent)</td>
</tr>
<tr>
<td></td>
<td>• How to quality trim and remove adapters from the raw sequence data</td>
</tr>
<tr>
<td></td>
<td>• Dealing with repeat regions</td>
</tr>
<tr>
<td></td>
<td>• Handling multiple samples</td>
</tr>
<tr>
<td></td>
<td>• Whole-genome trio analysis</td>
</tr>
<tr>
<td>15:30–16:00</td>
<td><strong>COFFEE BREAK</strong> (Wolfson Link Courtyard)</td>
</tr>
<tr>
<td>16:00–17:00</td>
<td><strong>Resequencing and SNP detection (Continued)</strong></td>
</tr>
</tbody>
</table>

---

**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)
Priority will be given to users of Glasgow Polyomics.

**Further information**
Online at www.glasgow.ac.uk/polyomics/trainingcourses

Follow us on Twitter: @polyomics
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.

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

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.

Glasgow Polyomics

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

www.glasgow.ac.uk/polyomics
Follow us on Twitter: @polyomics