CLC Genomics Workbench

www.clcbio.com/genomics

Features & Benefits

Associate Professor at the Department of Life Sciences at Aalborg University, Denmark, Dr. Kåre Lehmann Nielsen, states,

'As one of the leading bio-informatics companies in the world, CLC bio has a very high level of understanding and experience in working with cutting edge technology and advanced algorithm design. With their multifaceted workbench structure, they provide a stabile and user-friendly platform for Next Generation Sequencing.'

Facing the analysis challenges of Next Generation Sequencing

With Next Generation Sequencing machines, *High Throughput Sequencing* has become accessible to a very large group of researchers. However, data analysis represents a serious bottleneck in NGS pipelines of most R&D departments, which in turn dramatically reduces the Return of Investment (ROI) of current NGS investments.

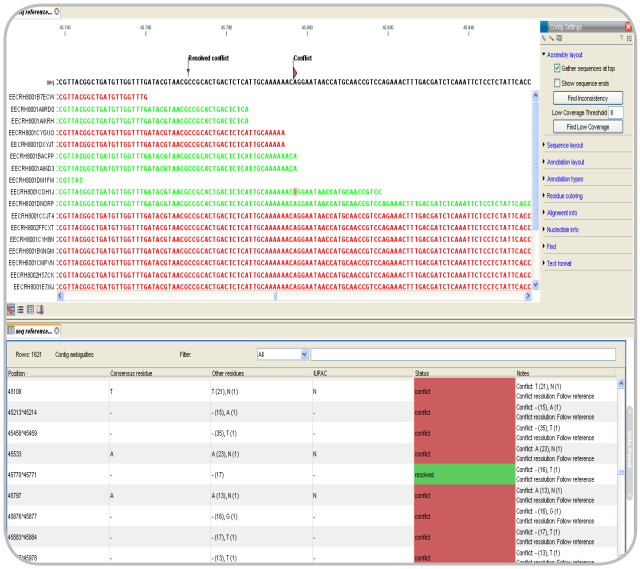
CLC Genomics Workbench solves this problem and will enable everyone to rapidly analyze and visualize the huge amounts of data generated by NGS machines. The user-friendly and intuitive interface essentially takes *High Throughput Analysis* from hardcore bioinformatics programmers doing command-line scripts, to ordinary researchers and scientists. Furthermore, the versatile nature of CLC Genomics Workbench allows it to blend seamlessly into existing sequencing analysis workflows, easing implementation and maximizing ROI.

Features

CLC Genomics Workbench is our solution to analyze and visualize the massive amounts of data coming from *Next Generation Sequencing* (NGS) machines. This workbench represents by far the most ambitious software package completely dedicated to NGS and related analyses.

CLC Genomics Workbench includes *High Performance Computing*, accelerated assembly of *Next Generation Sequencing* data and support for a number of downstream analyses and work tasks, such as:

- Reference assembly of Sanger, 454, Solexa, SOLiD, and Helicos sequencing data
- Assembly of genomes of any size (only limited by RAM available)
- De novo assembly of genomes
- SNP detection using advanced statistical models
- Support for multiplexing with DNA barcoding
- Detection of large-scale genomic events
- Incorporation of paired-end data
- Several statics for easy overview
- Scrolling and view of all reads on large contigs
- Primer design
- Molecular cloning
- BLAST
- HMMER
- Alignments
- Phylogenetic trees
- Advanced RNA structure prediction and editing
- Integrated 3D molecule analysis
- Secondary protein structure predictions



Assembly view, zoomed to 100%, together with a conflict table view. A row in the table has been selected, and the associated conflict position is automatically highlighted in the assembly view.

CLC Genomics Workbench is the first comprehensive analysis package which can analyze and visualize data from all major NGS platforms, such as *SOLiD* from Applied Biosystems, *454 GS flx* from Roche Applied Science, and *Solexa* from Illumina - and soon Helicos' *HeliScope* as well as others will be included. Collaboration with the instrument vendors is a natural part of CLC bio's development process.

Version 1.0 for Windows, Mac OS X, and Linux

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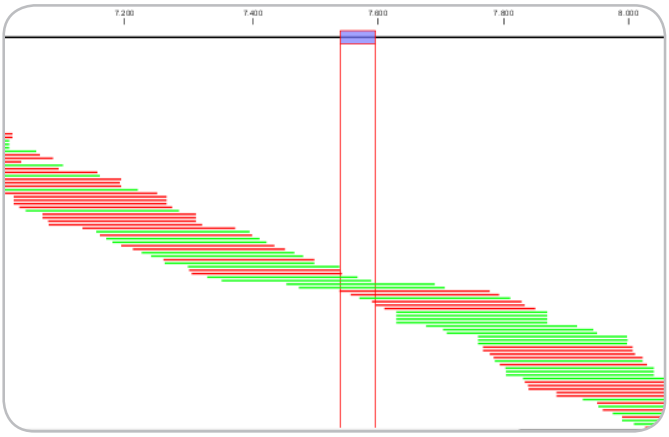


Assembly view, zoomed out, together with a sequence view showing details of the contig sequence. A region of low coverage has been found in the assembly view, and the corresponding region of the contig sequence is automatically highlighted in the sequence view.

Very fast sequence assembly

CLC bio's world renowned scientists have designed completely new and innovative algorithms to power the features of CLC Genomics Workbench. These highly advanced and cutting edge algorithms incorporate SIMD processor accelerating technology to yield a significant speed-up of the assembly process.

A few benchmarks	Minutes
454: Reference assembly and visualization of 439,000 reads to e.Coli (5 mega bases) on a 1,500 USD 2GB dual core, 2.13 GHz, 32 bit laptop computer	2
Solexa: Reference assembly and visualization of 2 x 2.7 = 5.4 million paired end reads (1 lane) to e.Coli (5 mega bases) on a 1,500 USD 8GB dual core, 2.5 GHz, 64 bit desktop computer	7

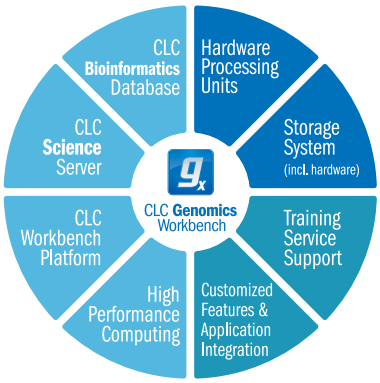
Database Integration

CLC Genomics Workbench is fully integrated with CLC Bioinformatics Database, supporting Oracle, MySQL, PostgreSQL, H2, and Microsoft SQL Server.
This enables all users to share and search data in a flexible, secure, and very user-friendly environment.

Customized Workbench

A new and fast evolving technology, Next Generation Sequencing constantly provides researchers with new scientific opportunities and new ways of analyzing the huge amounts of data.
The problem is not lack of ideas or lack of data. The problem is lack of efficient software for carrying out the analyses or for removing manual bottlenecks in the workflow.

CLC bio eliminates these challenges by designing and developing customized add-on modules for CLC Genomics Workbench, based on specific customer requests.
This is a quick and cost effective way of improving both the speed and the quality of your research.



Data Analysis

CLC bio carries out analysis of Next Generation Sequecing data for customers who wish to get the maximum knowledge out of their experiments in the shortest possible time without starting their own bioinformatics department.

This is a very effective way of keeping your fixed costs down.

CLC Genomics Workbench is cross-platform, enabling scientists and researches alike to share and collaborate on data across different operating systems and physical locations.

System requirements

- Mac OS X 10.4 or later (including Intel-based Macs)
- Windows 2000, Windows XP, or Windows Vista
- Linux: Redhat or SuSE
- 32 bit version and 64 bit versions of operating system/computer on all platforms
- 2 GB RAM required
- 2 to 8 GB required for large assemblies
- 1024 x 768 display recommended

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