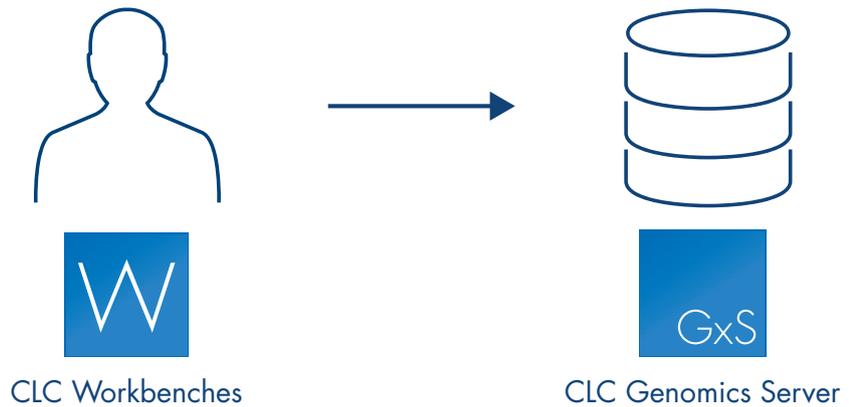


CLC Genomics Server

CLC Genomics Server is a software solution for deployment on your central compute cluster or compute server for centralized bioinformatics analysis and sharing of data generated from all High-Throughput Sequencing platforms.



CLC Genomics Server comes with the same bioinformatics data analysis tools that are known from our successful CLC Genomics Workbench, such as mapping of reads to a known reference, de novo assembly, and variant calling. From a single click within CLC Genomics Workbench it is possible to utilize your central compute clusters or servers to schedule analysis of amounts of data that are not possible to analyse in a desktop computer environment.

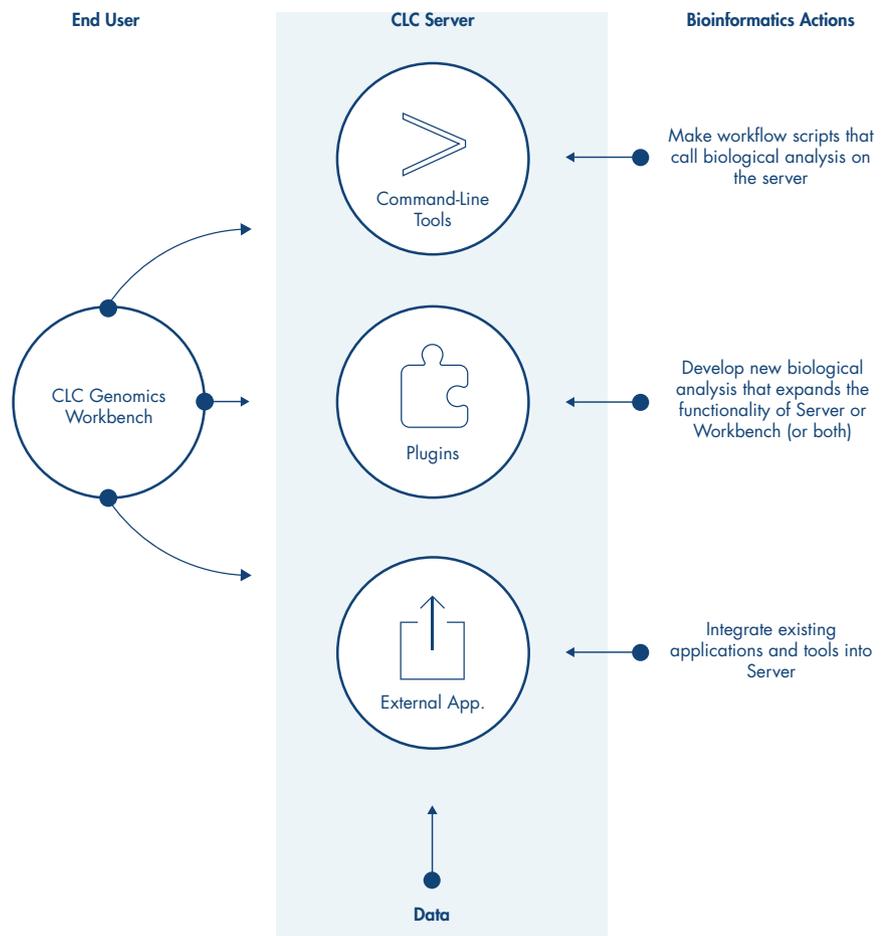
Customizable

Bioinformaticians will appreciate the Command-Line Tools, built-in support for external applications, and our API/SDK, so they can integrate and deploy either functionality provided by CLC Genomics Server or functionality provided

by an external application or in-house developed pipeline.

Command-Line Tools

The CLC Server Command-Line Tools enables comprehensive access to functionality, data,



and even pre-made workflows directly from a script without any need for a graphical-user interface (GUI).

External Applications Integration

The built-in support for external applications makes it possible to integrate any command-line software, such as popular open source tools, all the way to CLC Genomics Workbench without a single line of programming.

API and SDK

The Application Programming Interface (API) and Software Development Kit (SDK) allow developers to utilize a flexible plugin system that makes it possible to tightly integrate their own algorithms directly into the software and make them conveniently available in CLC Genomics Workbench.

The purpose of these advanced capabilities is to make the software ready for both current and future custom needs, and it has proven to be very valuable for both bioinformaticians as well as biologists.

More information can be found at:
www.clcdeveloperconnection.com

Professional Help and Services

The QIAGEN Informatics Custom Solutions team is dedicated to helping your organization achieve maximal value from its data. We are able to provide a comprehensive suite of consulting, development, training, and professional services that match bioinformatics and integration requirements regardless of com-

plexity. We have built this organization to help your organization achieve its scientific, IT, and business goals, because we realize the special needs that every customer has.

Scalability through compute cluster management

With the built-in Job Node Support or by using the most popular external grid scheduling systems, it is possible to enable an array of server compute nodes to do the data analysis. This ensures a fit into the organization with both an existing shared compute cluster or a setup of dedicated compute nodes for CLC Genomics Server.

External grid integration

Besides the internal scheduling system (Job Node Support), CLC Genomics Server can use an external grid scheduling system via a DRMAA interface. The systems we currently support are:

- Oracle Grid Engine
- PBS Pro by Altair
- IBM Platform LSF

Support of all major file formats

All major bioinformatics file formats such as fastq, fasta, BAM, VCF, and BED are supported on both input and output side."

Shared data

Centrally stored data can be shared among all users with a use of standard access privilege rules.

Data Management

CLC Genomics Server enables sharing of data towards all end-users with CLC Genomics Workbench through mounting of the data folders from the central data storage system attached to the compute cluster or server. With a group based access privilege system on folder level, it is possible to define which user groups should have access to reading and writing of specific data folders. Users and groups can be managed either with a built-in directory system or through a connection to well known LDAP based directory systems.

It is also possible to share data through a central relational database management system like Oracle, MySQL, or PostgreSQL with CLC Bioinformatics Database.

System requirements

CLC Genomics Server is available for Windows, Mac OS X, and Linux (Red Hat 5 or later, SUSE 10.2 or later, Fedora 6 or later). For detailed system requirements, please refer to clcbio.com/support/system-requirements.

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