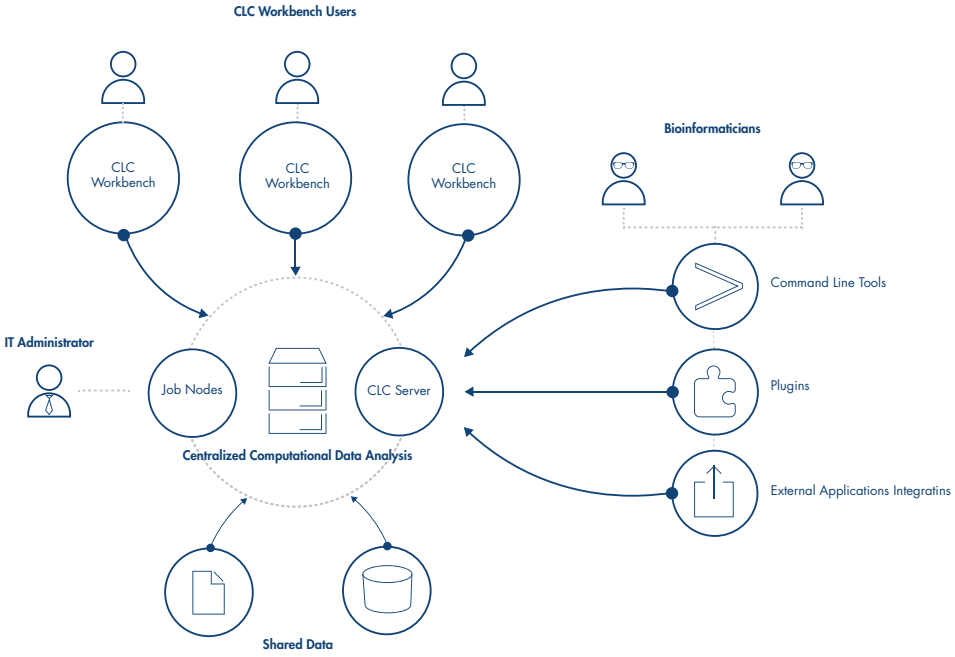
A QIAGEN Bioinformatics Solution

High Volume Sequencing

Our High Volume Sequencing Solutions are comprised of a number of CLC bio products that are used to perform the data analysis steps of next-generation sequencing (NGS) from high volume sequencers such as the Illumina HiSeq or HiSeq X Ten.

With the High Volume Sequencing Solution you get a solution that is:

- Cost Effective
- Scalable
- Easily integrates with IT
- User friendly
- Extensible
- Platform agnostic
- Secure
- Optimized for data sharing
- Workflow enabled



Sample to Insight

Challenges with high volume sequencing

The use of whole exome sequencing (WES) and whole genome sequencing (WGS) is accelerating at an unprecedented rate and the massive amounts of data generated as a result have created data analysis bottlenecks for many labs. The use of large desktop computers and ad-hoc scripts are no longer able to manage this volume of data, and the ability to scale testing is limited. Even labs that have the expertise to handle high volume sequencing still struggle with user-friendly delivery of the results and incur high costs.

Key needs of high volume sequencing users

- The ability to analyze samples at the same rate in which they are generated by high volume sequencers
- Management of the analysis workflow with centralized processing, standardized workflows, tracking, documentation, and result distribution to end users
- The ability to integrate the data analysis solutions with their existing IT infrastructure

High volume sequencing software solution are needed when:

- Running more than 10 whole exomes or 2 whole genomes per week
- The number of samples is too high or the samples sizes are too large to be analyzed in a desktop environment, or parallel sample processing is needed
- The number of end users is too large to ensure effective collaboration with shared data
- Using a mixture of NGS data from various sequencing platforms
- Data analysis is needed to occur on-premise, since the data sizes are too large to be moved around

Key benefits of the offering

Works with the same user-friendly, powerful visualization interface that the user is familiar with from the workbenches.

Provides scalable, fast, and efficient algorithms that are able to process up to HiseqX10 data output in real time.

Workflows automate repetitive work, enable reproducible results, create auditable documentation and lock-in best practice processes.

Ensures high quality through reproducible results, high specificity and sensitivity, quality controls, and ISO-certified development process (coming).

Works with all major sequencing platforms, any kind of NGS data or application, as well as any species.

Can be extended with plugins, open source tools, and own programs for specialized applications. Command-line interface and external application interface can be tailored to the customer's need by the customer itself, the custom solutions team, or in combination.

Ensures data security by keeping data under the customer's control, not somewhere in the cloud.

Supports centralized data sharing between multiple users.

Lower total cost of ownership due to savings in power to operate, hardware cost (for example, uses 35 nodes instead of 85 as per Illumina recommendations for X10 data processing) and lower maintenance effort.

Flexible business model supports perpetual license with optional maintenance after the first year, or annual subscription license. Modules can be added as needed, the user only pays for what he needs.

High Volume Seqeuncing Solutions meet the needs of a wide varity of end users across various industries and types of laboratories

- Academic/University/Nonprofit Research InstituteGovernment Agency
- Clinical Lab/Hospital CLIA Lab
- Genomic Services Provider
- Pharmaceutical/Biopharmaceutical Company
- Agricultire & Food Safety
- Academic Medical Center/Hospital
- Core Facilities
- Contract Research Organization
- Large Scale Genome projects (Population Scale Genomics)

Components of the solution

COMPONENT	USE
CLC Genomics Server, Master	Provides fundamental functionality of extensibility, job scheduling etc. Allows adding additional nodes for more compute power, server extensions to support various workbenches and modules
(Optional) CLC Genomics Server, Additional Grid/Job Node	Extends compute capacity to more processing nodes to scale up
(Optional) CLC [Genome Finishing / Biomedical Genomics] Server extension	Enables running Genome Finishing or Biomedical Genomics applications on the server. (Note: CLC Genomics Workbench is natively supported, and needs no extension)
CLC Custom Services for deployment	Expert support for deployment and configuring, troubleshooting, roll out, and training staff
CLC Custom Services for customization	Server deals are often larger deals of a consultative nature. Customers often have a need for custom development and are willing and able to pay for it
CLC Genomics Workbench and/or Biomedical Genomics Workbench and/or CLC Genome Finishing Module	Server deals usually require at least one workbench to act as the end user interface
(Optional) CLC Bioinformatics Database	Database Schemas that makes it possible to use a Relational DBMS (Oracle, MS SQL, PostgreSQL etc) as data storage instead of the file system. To support certain customer IT insfrastructures that contains Relational DBMS
(Standalone) CLC Assembly Cell	Standalone Command-Line tool for assembly or read mapping. Fast, efficient, memory efficient, and can be deployed on any existing server/cluster infrastructure. Mostly used by bioinformaticians. Is an independent tool from CLC Genomics Server and Workbench

For research use only. Not for use in diagnostic procedures.

To learn more from a sales or support solution specialist contact us by email or phone using the information below.

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