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In this example we solve a forensic case where the soil microbiom on the suspect's boot can be attributed to a soil microbiom at the scene. Available as a PDF tutorial QIAGEN CLC Genomics Workbench, QIAGEN CLC Microbial Genomics Module Required plugin: CLC Microbial Genomics Module (commercial) From ScientificComputing CLC Genomics Server is a software solution for centralized bioanalytics analysis and data sharing generated from all High Throughput Sequencing platforms. It contains the same tool as clc Workbench, such as reading mapping to known references, assembly de novo, and variant calling. With one click inside the CLC CLC Workbench is possible to unload resource-demanding tasks to an HPC cluster, which is impossible to analyze in a desktop computer environment. Please find more information about CLC genomic workbench on the D-BIOL sharepoint page. CLC genomic server account requests use local accounts for authentication. If you wish to use this service, please contact cluster support to request your CLC account. Workbench version compatible with genomic server requirements to use CLC genomic servers To use CLC genomic server installations in Euler, certain requirements need to be met. First of all, you need to install the CLC genomic workbench client on your local computer. The client software is provided by IDEs. In addition, you need to install the CLC workbench client plugin, which is used for communication between CLC genomic workbench and CLC genomic servers. Start clc genomic workbench (on a Windows computer you need to start it as an administrator, that is, right-click the CLC genomics icon and select Run as administrator) Click the Plug-in Click on the Download Plug-in tab and select the CLC workbench client plugin and click Download and Install Download and install the plug-in As the last requirement you need to request a CLC genomic server account. To request an account, please contact cluster-support@id.ethz.ch To connect the CLC genomic workbench client to the CLC genomics server, the SSH tunnel is no longer required. CLC genomic servers in Euler run on virtual machines and clients can directly connect to these virtual machines. Connect the client to the CLC Genomic Workbench Client Open server (first only the local data is displayed in the menu in the top left) Open the File menu and click the CLC Server Login entry Enter the username, password of your CLC genomic server account Click on Advanced and enter clc01.hpc-ica.ethz.ch as the server host and 7777 as the server port. Then click the Login button After the login procedure, the location of the server data is displayed in the Navigation Area menu. When connected to a CLC genomics server, you will be able to see all server data locations (folders with blue dots next to them) but not their content. You will only be able to view and use the content of your own data location (unless you explicitly ask us to change permissions if you wish to share the data with other users). The login option in the File menu Enter user name, password, server host, and Connecting port to the server via the CLC genomic server web interface provides a web interface that allows users to connect to the server through their browser. It is possible to do more user-oriented things such as browsing data, uploading/downloading data, accessing/editing meta-data on data and querying data. Open the Enter web browser in the address field of your browser Enter your username and password The login screen of the web interface Browsing data in the Web interface Data management User data processed by the CLC genomic server installation in Euler first needs to be imported to the server. We therefore attach the location of the server data (one folder) to each CLC genomic server account created in Euler. Unless the user has some permanent space in Euler, the location of the server data is considered a scratch space that can be used for temporary data storage and will be cleaned regularly. Once the work is complete, the results should be copied back to the local machine or other storage location. Please note that there are no backups for this data set. In general, there are two different ways to import data to a server data location. On the one hand, data can be directly imported into the CLC genomic workbench client and then moved to the server data location with drag-and-drop within the client. For this, one must click on the file in the local CLC data location and move it to the location of the server data attached to each CLC genomic server account. The installation of NAS shares of the IT service storage group has been tested on Euler and should work. Submitting work from CLC genomic workbench clients For example to demonstrate how to send work from CLC genomic workbench clients to Euler clusters, we select BLAST search. For all the other tasks that can be accomplished with clc genomic workbench clients, it works the same way. There was one difference when comparing CLC's work on Euler with local runs using CLC genomic workbench clients. You should choose the grid option instead of workbench and then in the next step, you can select the queue. For CLC in Euler, we have several queues ranging from 1 to 24 cores. Please note that not all CLC genomic server applications can use multiple cores. Just select a queue with more than 1 core, if the app you want to use is listed here. Otherwise, please select 1 core queue. This list is based on the genomic server manual (: Basic Variant Detection BLAST Create Alignment Create Detailed Mapping Report Create Sequencing QC Report De Novo Assembly Extract and Count Fixed Ploidy Variant Detection K-mer Based Tree Construction Large Gap Read Mapper (current in beta, part of the Transcript Discovery plug-in) Locale Realignment Low Frequency Variant Detection Map Reads to Contigs Map Reads to Reference Maximum Likelihood Phylogeny Model Testing Probabilistic Variant Detection (legacy) Quality-based Variant Detection (legacy) RNA-Seq Analysis Trim Sequences When setting up blast searches, you can set the options in workbench how many threads should be used. set this to 12, when using core queue 12. Click on the data on the server location and the Job application submitted to the Job cluster has been completed, the data can be copied back Local BLAST Searches Euler provides a local BLAST database, which is currently static but in the future will be updated once a week from the NCBI reference. Local BLAST search is much faster than BLAST request, sent to NCBI. At the next stage of the project, users will also be able to provide their own database in addition to the BLAST one. Reference Genome Information about genome references available Tutorials Please find below the list of tutorials for CLC Genomics Workbench provided by Qiagen. You can find links to the data needed for tutorials inside PDF documents. Documentation about CLC Genomics Workbench CLC Bio provides a variety of documentation and tutorials to help users get started: getting started:

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