

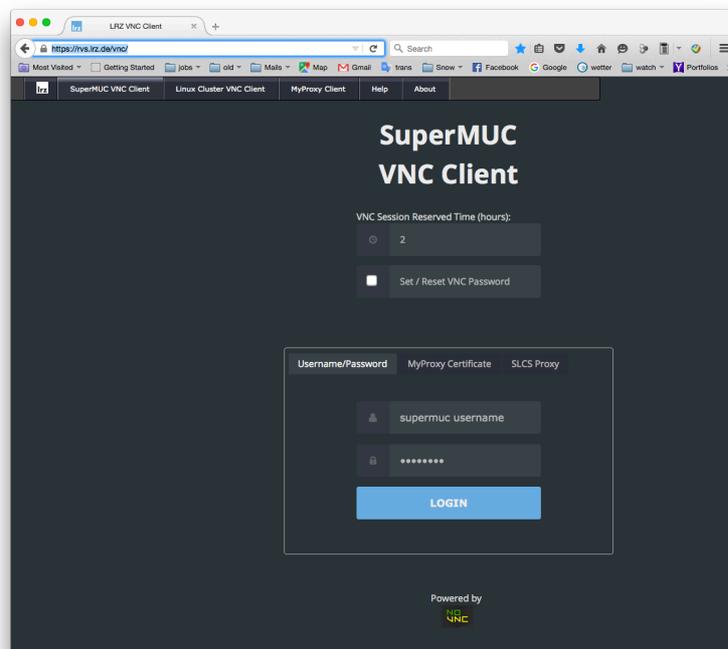
How to Use CLC at Leibniz Supercomputing Centre

Step-by-step Guide

The following is a step-by-step guide to launch CLC genomic workbench on LRZ infrastructure. The new module can be loaded by using module load CLC/10.1.1

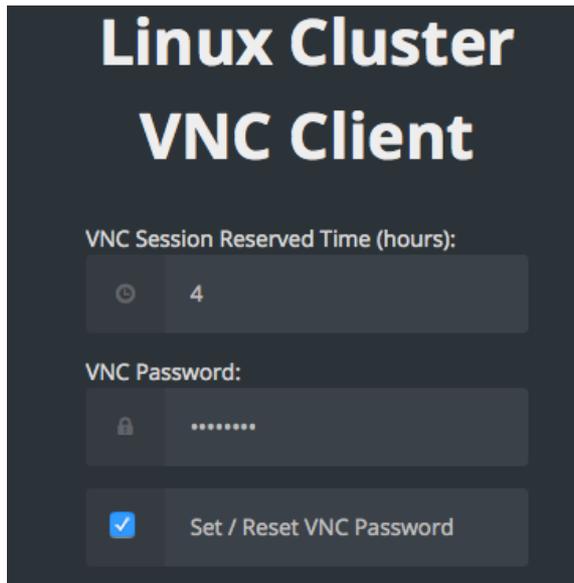
Please change the corresponding command in the screen shots below.

- 1) Go to <https://rvs.lrz.de/vnc/>

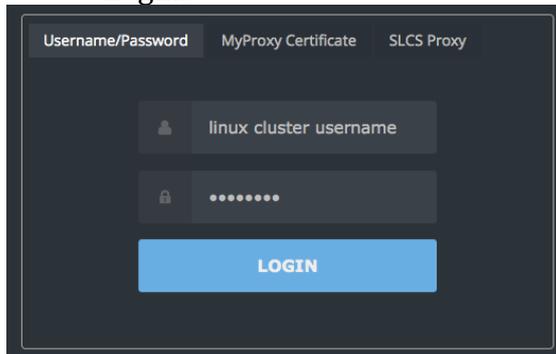


Linux Cluster VNC Client

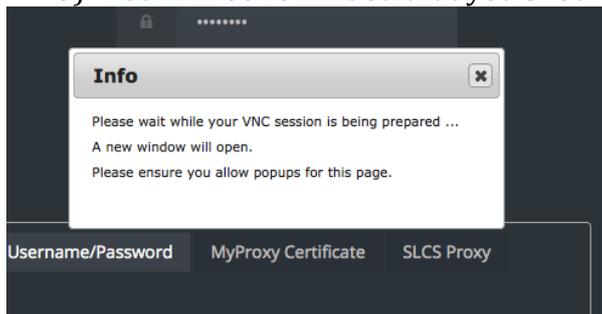
- 2) On the top panel, click on the button
- 3) Set your VNC session reserved time to 4 hours and set your VNC password, please note this VNC password is not your LRZ password. Once the VNC password has been set up, you can use it for upcoming VNC sessions as long as you want. For security reasons, you are encouraged to change your VNC password periodically. You may want to reserve less than 4 hours. The maximum running time for one session of CLC genomic workbench is 4 hours, if you reserve more than 4 hours VNC session, you won't be able to run CLC genomic workbench after you login.



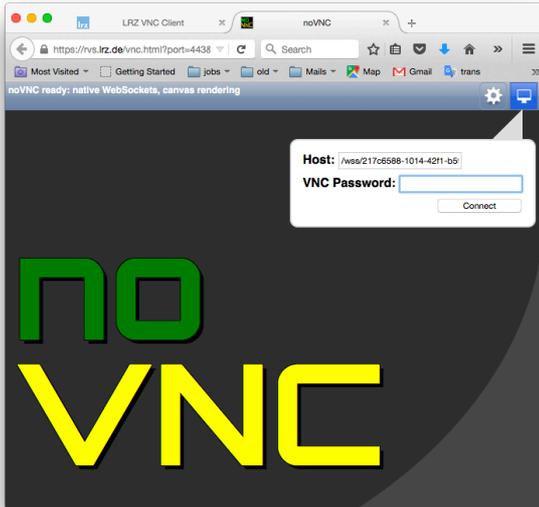
- 4) Enter your LRZ account and the corresponding password, then click on Login.



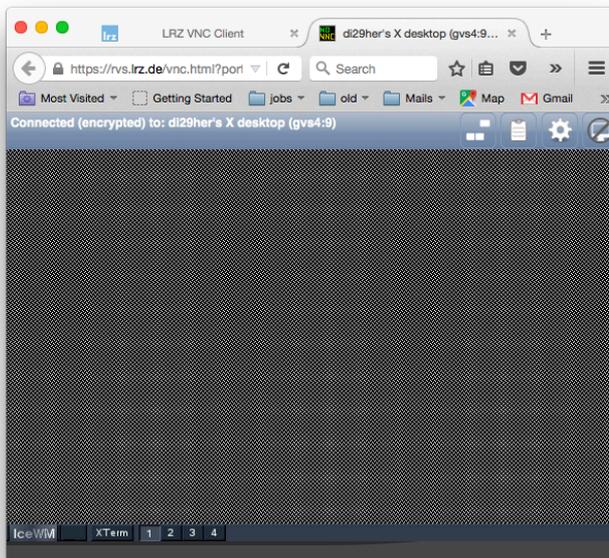
- 5) You will be reminded that you should allow popups for your browser.



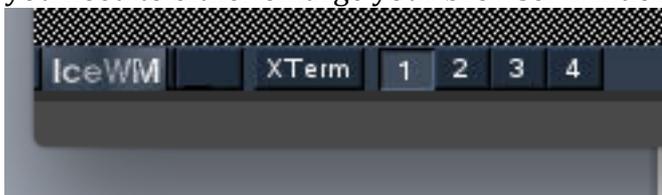
- 6) In some seconds a new window or a new tab will be open on your browser, depending on your browser configuration. “noVNC” is a browser based VNC client implemented using HTML5 Canvas and WebSockets. You probably notice that the name “noVNC” is as confusing as it could possibly be. You will be asked to enter your VNC password, which should be setup by you on Step 3.



7) After you enter your VNC password, your VNC session will start.



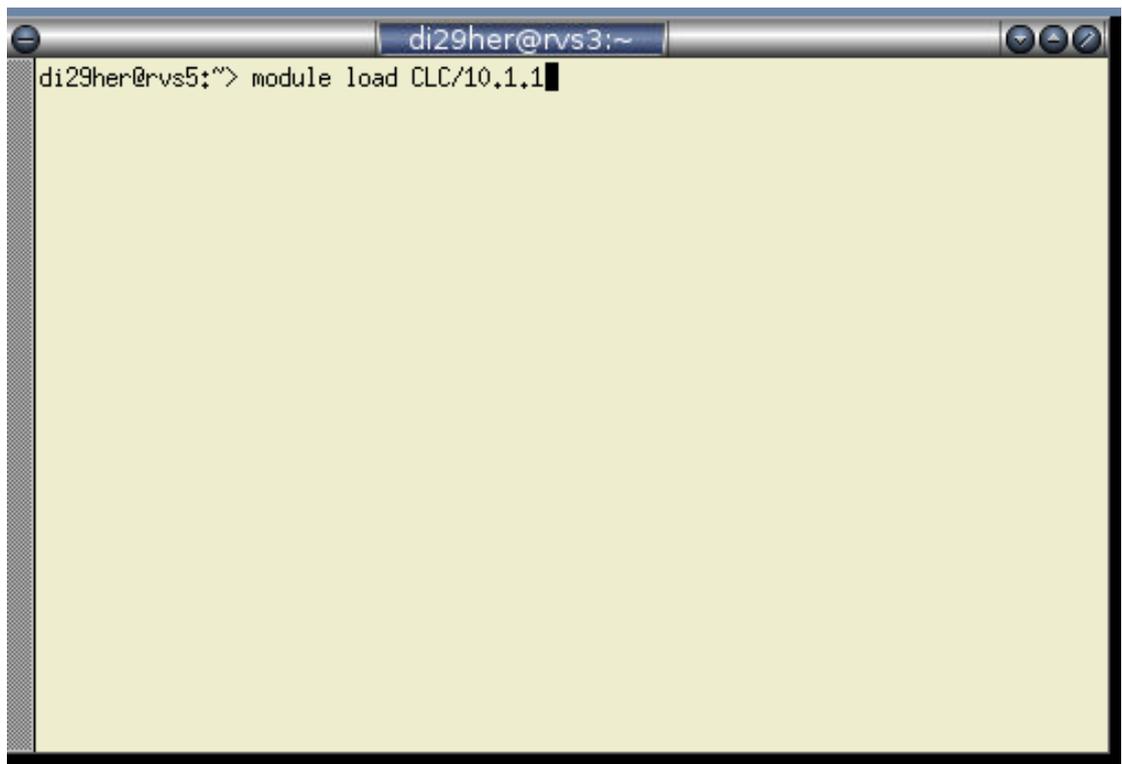
8) On the left lower corner, click on XTerm button. If you don't find this button, you need to either enlarge your browser window or scroll down.



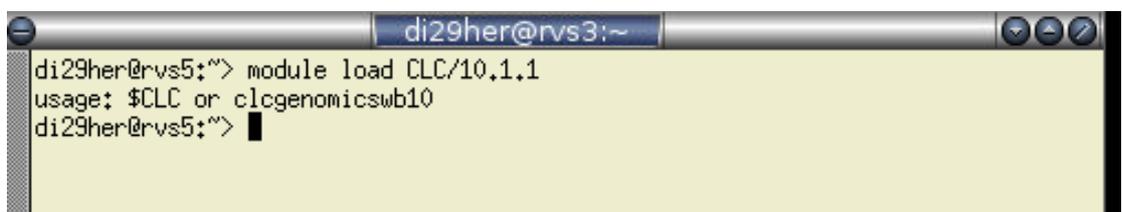
9) Now you have a terminal window at your disposal.



10) Type in command "module load CLC/10.1.1" (without double quote).



11) Now CLC genomic workbench has been made available, you can either type in \$CLC or clcgenomicswb10.

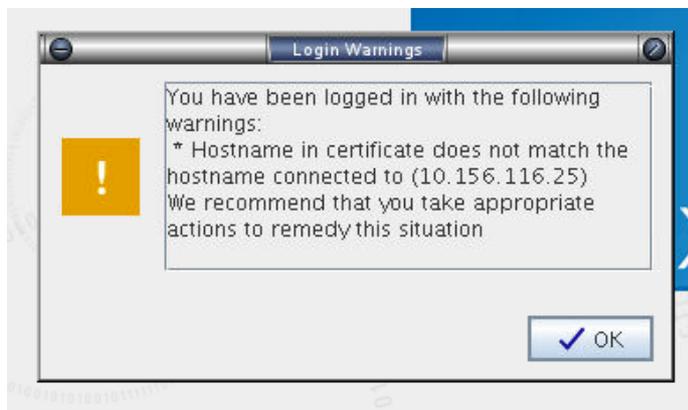


12) CLC genomic workbench starts to run, it will connect to the LRZ CLC genomic server. If it doesn't, you can always connect it to the server yourself.

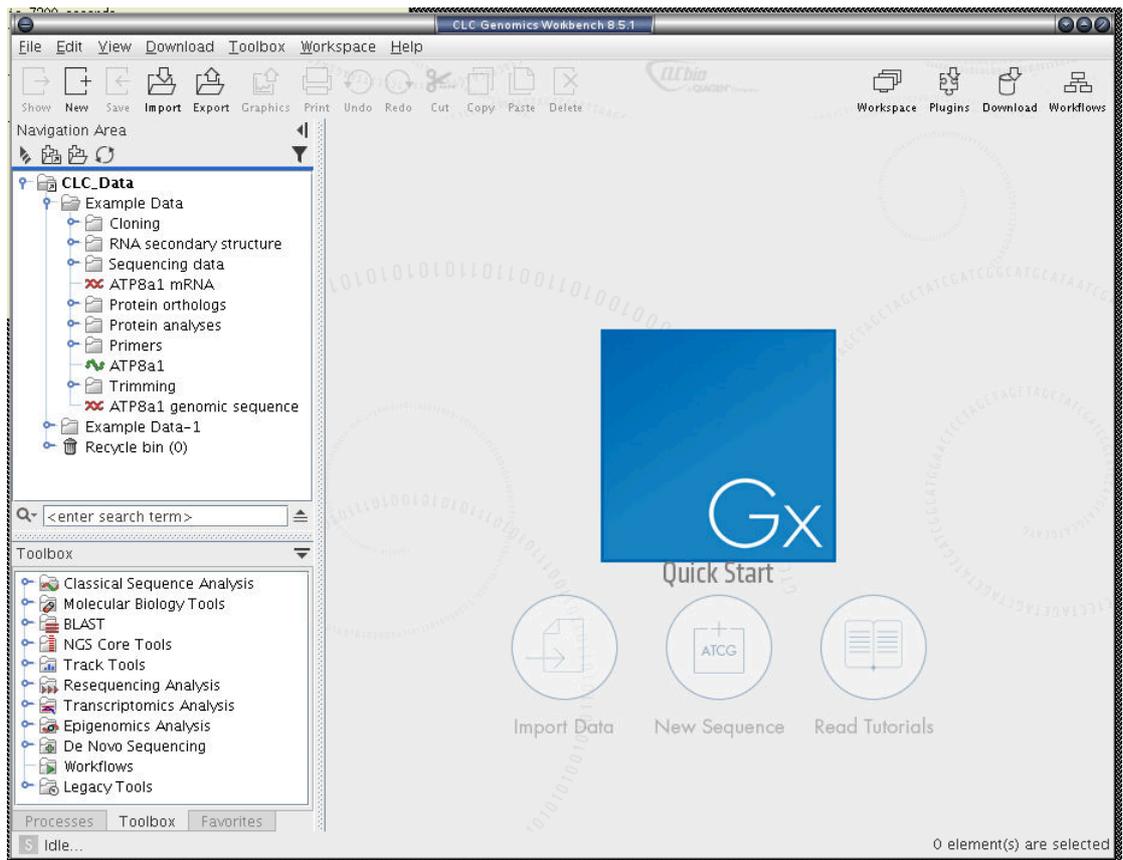


```
di29her@rvs5:~> module load CLC/10.1.1
usage: $CLC or clcgenomicswb10
di29her@rvs5:~> $CLC
Your current VNC session is 7200 seconds.
Logging to /home/hpc/pr28fa/di29her/.clcbio/workbench/log/clc-workbench.log
█
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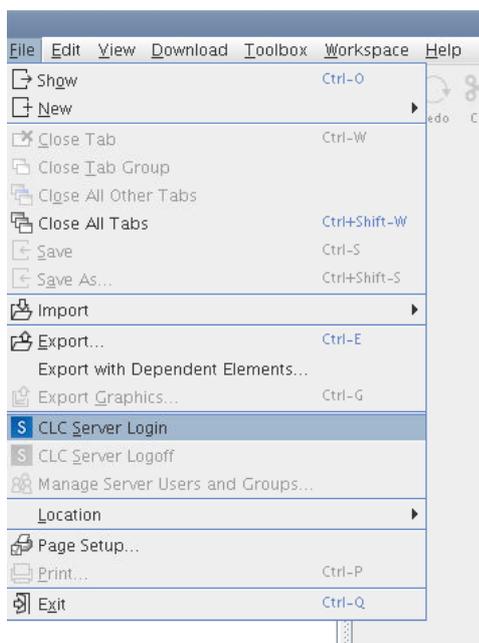
13) On the certificate we used to connect the CLC genomic server, we have used "clc-bio.srv.lrz.de" as the server name. If you connect to the server by using the ip address of the server, you may get a warning message as below. Just click on OK button to start to use CLC genomic workbench.



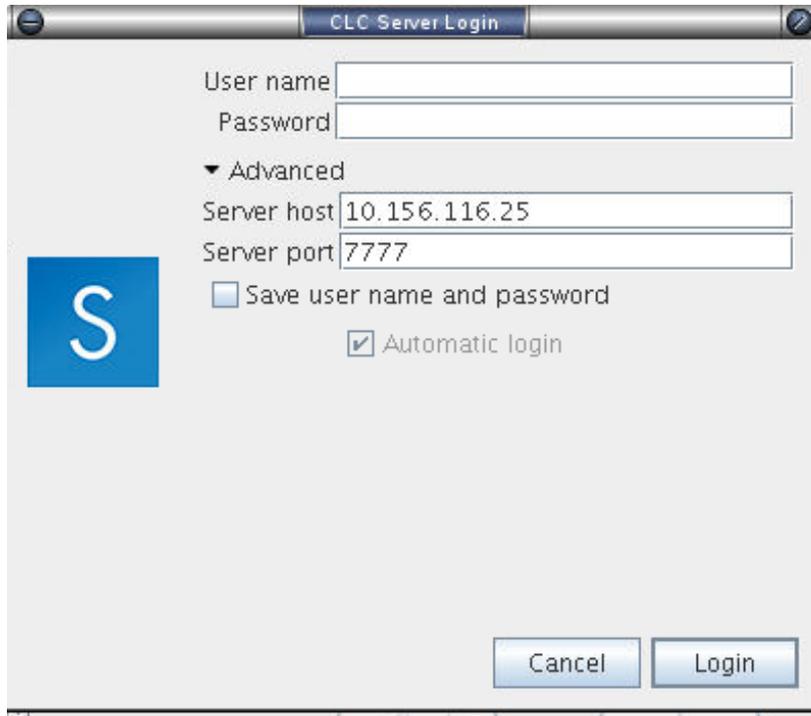
15) Now you can start to use CLC genomic workbench.



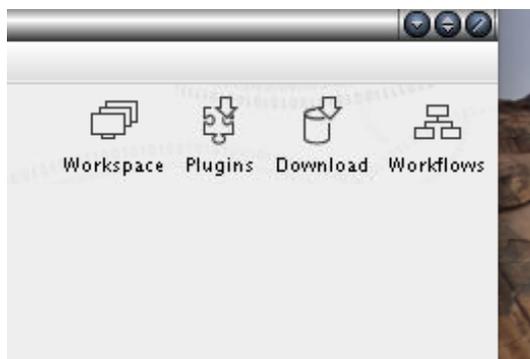
16) If you are not connected to the CLC genomic server, you can click on “File” on the left upper corner. You will get a pull down menu like below, please click on “CLC Server Login”.



17) A popup window will be shown on CLC genomic workbench. You can fill in your LRZ Linux cluster user name and password (Important, you have to have a valid LRZ Linux cluster user name, your normal TUM or LMU account does not work. Please confirm with your local system admin. <https://www.lrz.de/services/compute/antrag/>).



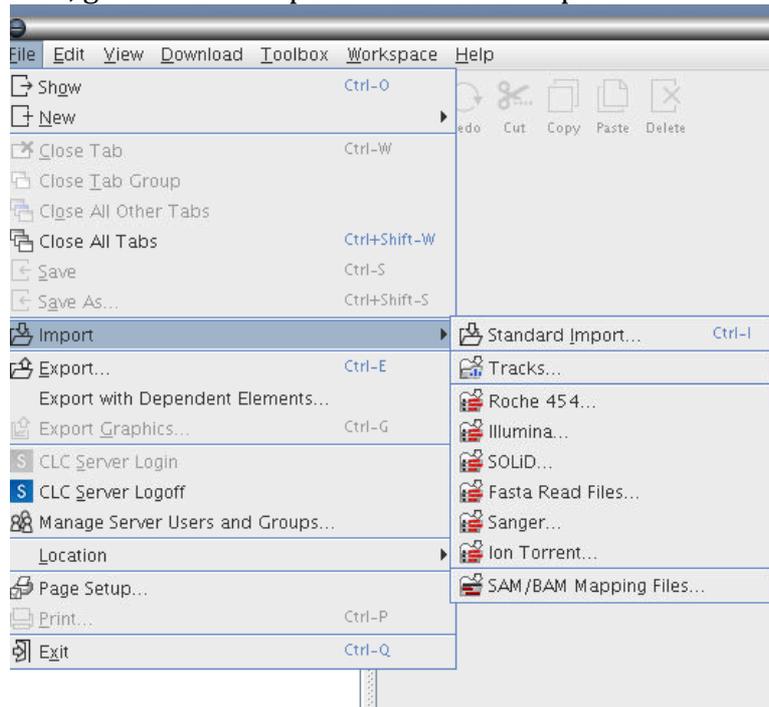
18) Tips. When CLC genomic workbench starts to run, it occupies the whole desktop. In order to resize the window, you can go to the right upper corner. There are three buttons, as show in the figure below. Click on the middle button and the whole desktop mode will be disabled. Now you can move the window by clicking and holding the top bar of the window and resize the window as you wish.



How to upload data to LRZ CLC genomic workbench

To access your data from CLC genomic workbench, you will have to first upload your data to your LRZ storage. LRZ storage can be accessed from the Linux

cluster (<http://tinyurl.com/gpc4qnr>). Please note there are different types of disk resources and file system layout (<http://tinyurl.com/nfprutg>). The basic directories you can use are your home directory (\$HOME, 100GByte, backup by LRZ) and project directory (\$WORK, 5TByte, self backup possible). If you have more data to analyze, you may be interested in a big data storage option (<http://tinyurl.com/jhcpt8n>). You are encouraged to transfer your data to LRZ by using Globus (<http://tinyurl.com/nrzgzn8>) or you can simply transfer by connecting to LRZ linux cluster by ssh (putty in Windows). Please consult your local system administrators if you are not familiar with Linux systems. Once you remotely transfer your data to LRZ, you can import them from CLC genomic workbench, go to File -> Import -> Standard Import.



You can browse the Linux file system to import your data either from \$HOME or \$WORK (/naslx/projects/your_project/your_account).

