**COMPUTEROME 2.0 USERS WORKSHOP EXERCISES**

In this exercise, you will log in to and move around the Computerome 2.0 Sandbox to get a feel for your environment. First, please check that you have completed all the steps in the list below:

* You have access to a SSH client, e.g. a terminal.

For MobaXterm users makes sure you have configured so you can use the two-factor authentication system. Please see: <https://www.computerome.dk/display/C2W/Getting+Started+-+new+users> or <https://www.computerome.dk/display/C2W/Video+Tutorials>

* You have installed and set up the **Entrust App** on your phone. Please see: <https://www.computerome.dk/display/C2W/Two-factor+authentication>
* ***IF*** you would like to try to log in using the virtual environment (optional), you should have the **ThinLinc Client** installed: <https://www.computerome.dk/display/C2W/Virtual+Desktop>

Importantly, you should have received an email from the Computerome team with your username.

**Exercise 1 – Getting started**

1. Log in to the Computerome 2.0 Sandbox: ssh username@ssh.computerome.dk

When you log in the first time you will be asked to change your password. You will need your **Entrust app** at hand to get the token (code) you need for the authentication step (you may be able to just press confirm in the app instead).

***IF*** you are using the virtual environment, open ThinLinc and make sure that the server is set to desktop.computerome.dk. Enter your username and password.

Open a terminal window from the toolbar at the top of the window (you can use F8 to minimize the window if you would like). Continue to point 2 below.

1. When you have logged in, use pwd to print your working directory. You should be here: /home/people/username.

Now, check your <project\_name> by typing id. Move to your project folder /home/projects/project\_name

1. Great success ;-) You are now in your project folder, have a look around. Move to your folder in the subdirectory people and make a file called: <your name>Qscript.

**Exercise 2 - Hands-on Session: Using Modules**

1. Login to Computerome 2.0
2. Start iqsub for **2h, 2 CPU, 0 GPU, 20G** of memory

*iqsub*

1. Load the tools module:

module load tools

1. Bcl2fastq is a tool for genomics, converting bcl2 files into fastq files. Load bcl2fastq/2.19.1 and check the help for this software:

*module avail bcl2*

*module load bcl2fastq/2.19.1*

*bcl2fastq --help*

1. Samtools is another tool used for exploring genomics data:
   1. Is samtools available on C2?
   2. Can you load a version?
   3. Explore the help?
2. Some more explorations:
   1. Can you start R?
   2. Can you get the help information on R?
   3. Can you start python (HINT: python is handled by anaconda packages)?
   4. What python packages are available (HINT: conda list)?