

Starting your virtual workspace

Objective:

You will learn how to connect to your virtual workspace, where you find input files and where to save your work, how to transfer files between the remote desktop and your own computer, and how to connect from the remote desktop to the ETH High Performance Cluster (HPC) “Euler”.

Introduction:

In the course “Introduction to Bioinformatics”, lectures are accompanied by practical exercises that introduce the use of common bioinformatic methods and basic programming. You will perform these exercises on your own computer by means of connecting via a “remote desktop” application to a virtual workspace that is connected to a shared server system. Using a remote desktop system for the course allows us to pre-install software and make large datasets available to all students without having to copy them many times. The remote desktop will run a Microsoft Windows operating system and you will have 20 GB personal storage space. Please always carefully follow instructions that specify a certain storage or workspace other than your home folder, as otherwise you might run quickly out of storage space.

Connecting to the remote desktop works from anywhere inside the ETH. For connections from outside ETH you need an ETH VPN connection (e.g., Cisco AnyConnect).

How to connect:

1) Change password

Go to <https://passwort.ethz.ch>, log in with the provided username/password and change the password to a password that you can remember.

2a) If you work on a Microsoft Windows operating system:

- Download the Remote Desktop Configuration File (RDP) file from the moodle course page: <https://moodle-app2.let.ethz.ch/course/view.php?id=4693#section-0>
- Open the RDP file
- Enter your “biolcourse” username and the [changed] password

2b) If you work on a Mac running OS X 10.11 (El Capitan) or higher:

- Go to the “App Store” and download the “Microsoft Remote Desktop” app (v10.x.x)
- Open the app, add a “remote resource” and enter <https://biolcourse.ethz.ch/RDWeb/feed/webfeed.aspx>
- Add user account and enter your “biolcourse” username and the [changed] password

2c) If you work on a Mac running OS X 10.10 (Yosemite) or lower you have two options:

- Change from your own computer to one of the Microsoft Windows computers in the course room and follow the instructions in 2a (this option is recommended!)
- Connect to the remote desktop using a current internet browser. Just go to: <https://biolcourse.ethz.ch/RDWeb/webclient/index.html> and login using your “biolcourse” username and the [changed] password

How to work on your virtual workspace:

During the course you will have the opportunity to use different softwares and programming languages to explore the fields of genomics, metagenomics, network bioinformatics, and imaging. You will receive detailed instructions on each of the exercises individually, but some common concepts are needed throughout the course:

Where to find input files:

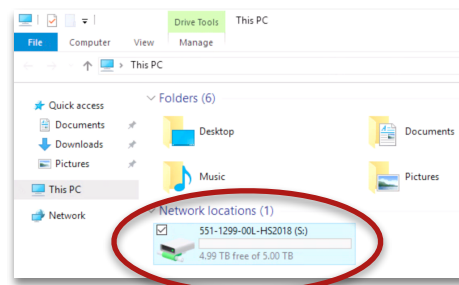
All input files can be found in a shared folder on the ETH “Network Attached Storage (NAS)” server.

The NAS folder can be accessed from multiple locations:

- From the remote desktop: the NAS is automatically mounted after you login. Open the “Windows Explorer” to see files and folders.
- From within the HPC cluster “Euler”: navigate to `/nfs/nas22/nas/fs2201/biol_isg_course_1/551-1299-00L-HS2018`

```
cd /nfs/nas22/nas/fs2201/biol_isg_course_1/551-1299-00L-HS2018
```

- From your Mac: open the “Finder”, click on “Go”, “Connect to server”, enter `smb://nas22/biol_isg_course_1/551-1299-00L-HS2018`, click “Connect”, enter your “biolcourse” username and the (changed) password



Where to save your work:

Your own storage space will be in the same folder as the input files (see above). Once you navigated to the biolcourse folder, create a new folder with **your ETH username**. This will be the place where you save your work. Only you will have writing access to this folder.

How to transfer files to your own computer:

If you want to save plots or scripts that you’ve created on the “NAS” to your own computer, you can simply copy them manually. This doesn’t work if you use the remote desktop in the internet browser. Please connect via the “Finder” to the NAS (see above) to copy files.

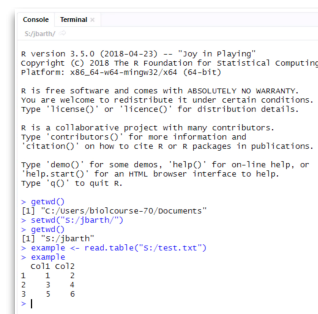
Where and how to work in “R”:

- Open “RStudio”.
- In the console, change from the remote Desktop location to YOUR folder on the NAS by executing:

```
setwd("S:/YOUR_ETH_USERNAME/")
```

- Load the example text file by executing:

```
example <- read.table("S:/test.txt")
```



How to connect to “Euler”:

- Open “PuTTY”
- Enter “euler.ethz.ch” as host name, make sure the port is “22”, leave anything else unchanged, press “open”
- In the terminal window, enter your “biolcourse” username and the (changed) password

