

Preparing for the course, general information.

In order to run the programs used in this course you will need to prepare your computer and gain a little knowledge about your computer. Most of the CBS (Center for Biological Sequence analysis) tools have no graphical interfaces but must be run on a Unix command-line. The tools have been collected in a customized operating system, *Biotools-xubuntu*, that all students will run on their computers.

IMPORTANT:

- NOTE! It is possible to use Note/Netbooks for the simulations in this course, but it is not recommended!
- NOTE! Your computer should have a minimum of 4 GB memory free
- NOTE! If xubuntu at any point asks you to update, do NOT update xubuntu.

Virtual computer setup.

For this course you will use a virtual computer that works almost like a normal computer. You will install a program that will allow you to run this virtual computer. You will import a setup for the computer, a so-called *virtual harddisk file*, that will hold all the tools you will need for a basic comparative genomics analysis.

Create a virtual computer on your local hard-drive.

- Download the program *virtualbox* from this link: <http://www.virtualbox.org/wiki/Downloads> (version: select the one that fits your computer).
- Install the program *VirtualBox* following the installation steps.
- Start the *VirtualBox*
- Click new (the blue icon on the left of the tool bar).
- Type *Biotools – xubuntu* in the VM name dialog box
- Select *linux* (Operating system) and *ubuntu* (Version) in the *Create New Virtual Machine* dialog.
- Leave the *Memory* form as default
- Select the *Biotools-ubuntu.vdi* file in the virtual hard disk settings
- Leave virtual disk creation wizard settings unchanged: file type = VDI
- Click create in the *Summary* dialog.