

Comparative Bacterial Genomics

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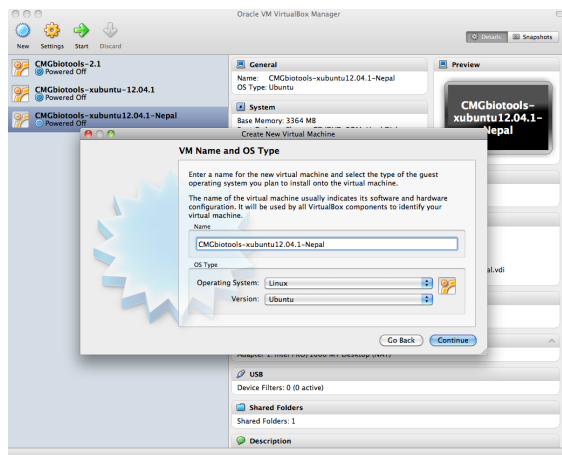
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1 Set up CMG-biotools

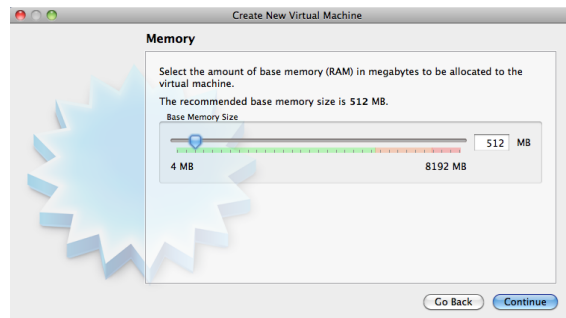
For this course you will use a virtual computer that works almost like a normal computer. Hopefully you have already installed the "Virtual Box" program that will allow you to run this virtual computer. You will import a setup for the computer, a so-called *virtual hard-disk file*, that will hold all the tools you will need for a basic comparative genomics analysis.

1.1 Install VirtualBox and start up CMG-biotools

- 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 **CMGbiotools-2.2** in the VM name dialog box (Figure 1(a)).
- Select **linux** (Operating system) and **ubuntu** (Version) in the **Create New Virtual Machine** dialog (Figure 1(a)).
- Leave the **Memory** form as default (Figure 1(b)).
- Select **Use existing hard disk** in the virtual hard disk settings (Figure 1(c))
- Select the **CMGbiotools-2.2.vdi** file in the virtual hard disk settings (Figure 1(c))
- Click **Create** in the **Summary** dialog (Figure 1(d)).
- Click the **Settings** icon for the computer. Under the **General** tab, select **Advanced**. In the menu **Shared Clipboard** select **Bidirectional** and click **OK** (Figure 1(e)).



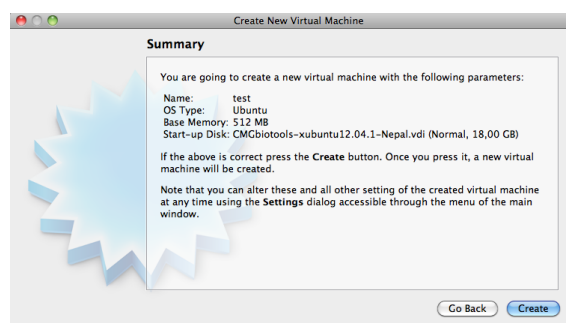
(a)



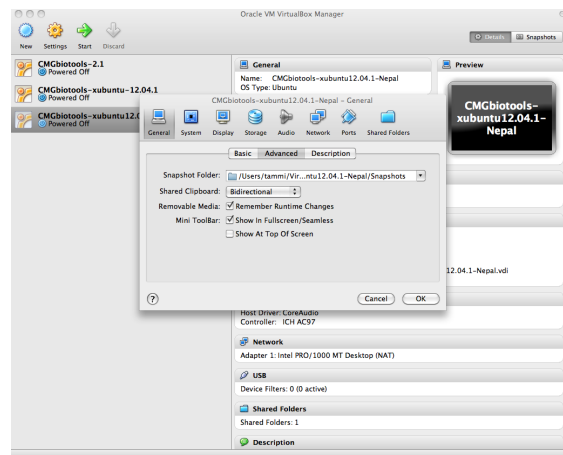
(b)



(c)



(d)



(e)

Figure 1: Create a virtual computer on your local hard-drive using *VirtualBox*.

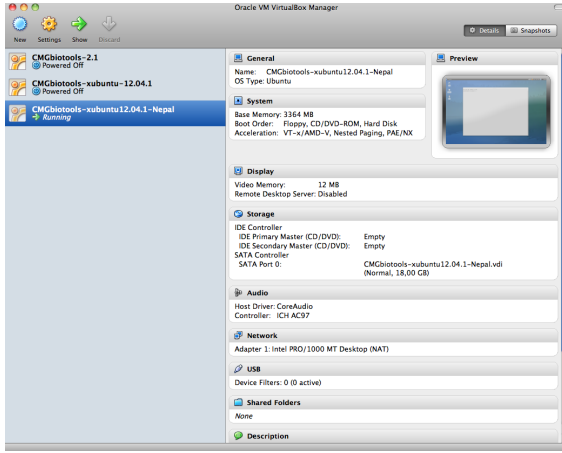
1.2 Set up a shared folder

The virtual computer runs as an independent computer on your hardware which means that it does not have access to the data which is on your local computer. It is possible to set up folders that the virtual computer can access, these are called **shared folders**. Keeping data in these folders, takes up less of the virtual computer space, making it possible to run a small virtual computer (4GB) while still having a large data set. Setting up a shared folder is a two step process. First, the folder is set up in the Virtualbox program.

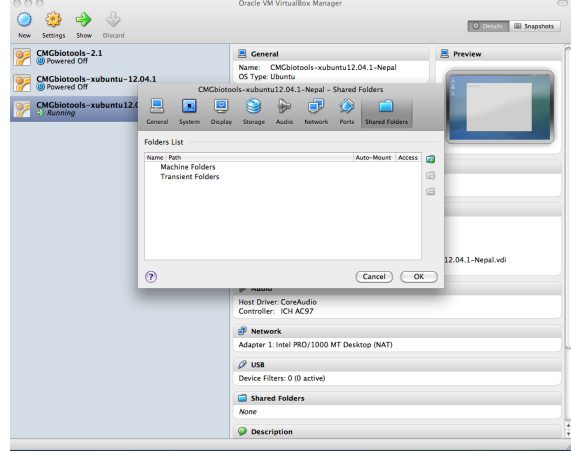
- In the Virtualbox window, click the **Settings** tab for the CMGbiotools computer (Figure 2(a)).
- In the new window, click the **Shared folders** (Figure 2(b)).
- Click the little folder icon with a green plus on it (Figure 2(b)).
- Select a folder on the local computer, create a dedicated folder for this and do not use the **Desktop** or **Documents**(Figure 2(c)).
- The **Folder Name** is automatically set to be the same as the folder you selected (Figure 2(c)). Manually set the name to **Vboxshare**
- Make the shared folder *Auto-mount* and **Make Permanent**, click OK (Figure 2(c)).
- The folder is now listed under the **Machine folders**, click OK (Figure 2(d)) and return to the Virtual computer by clicking the green arrow **Show**.

Next, the folder is set up in the virtual computer running the operating system **CMG-biotools**. Note, in the lower right corner of the virtual computer there is now a little blue folder icon. If no shared folder has been specified, this icon is grey.

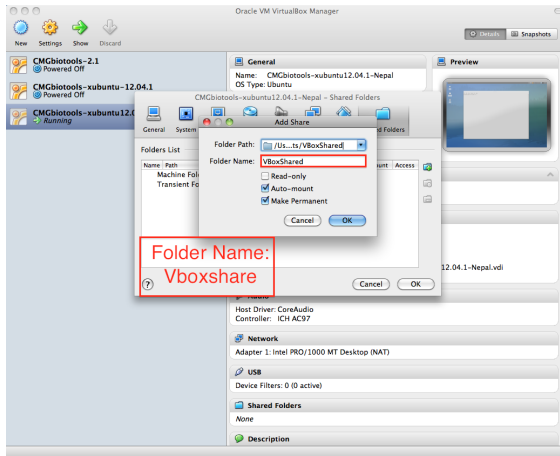
- Open the **Terminal Emulator** from the **Applications** menu (Figure 3(a)).
- In the terminal window, type the following command `sudo /etc/rc.local`
- Reboot the computer (Figure 3(b))



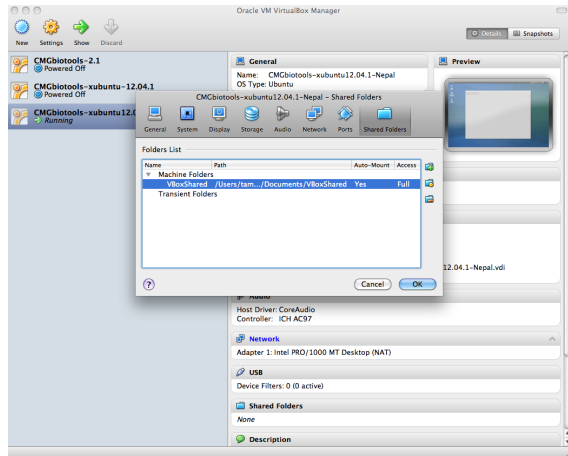
(a)



(b)

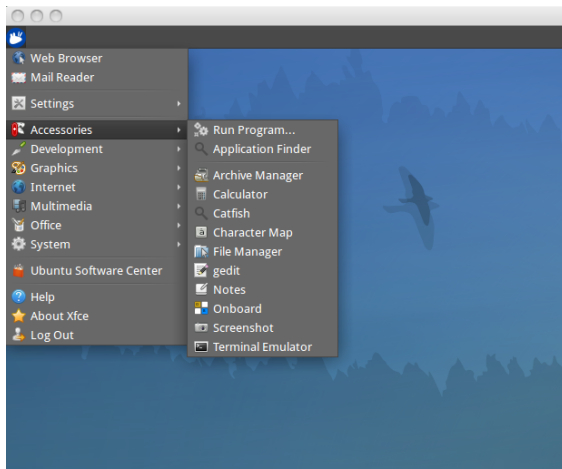


(c)

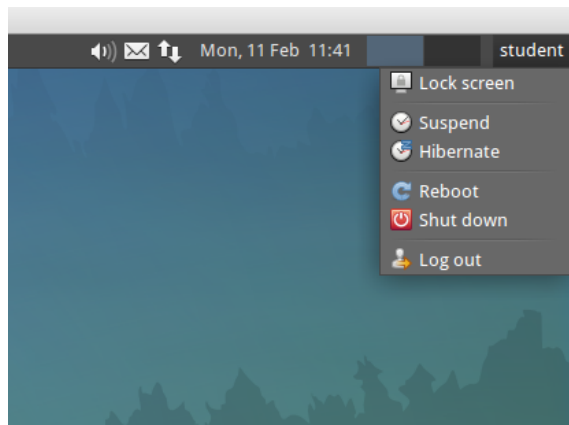


(d)

Figure 2: Setting up a shared folder between the local and virtual computer in *VirtualBox*.



(a)



(b)

Figure 3: Setting up a shared folder between the "host" and "guest" computer in *VirtualBox*.