

Virtual Machine Description

This is the [VMWare](#) Virtual Machine (VM) for the following [UPM Master in Computational Biology](#) courses:

- Introduction to Computational Biology (Wilkinson & Wabnik) - Sept, 2020
- Bioinformatics Programming Challenges (Wilkinson) - Sept-Dec, 2020

Other courses will also use this VM for some or all of their lectures.

Description:

This is a **Ubuntu XFCE 64-bit** virtual machine. It includes **Python3, Ruby 2.5, Java 11** languages. The OS language is English by default. It is configured with a Spanish keyboard by default, with the option of a US English keyboard (click the flag icon, bottom right).

Installed are a wide range of bioinformatics tools (**blast, clustalw, fasta3, Brig**, and many others). The **Lighttpd** Web server is installed and running. **Docker** is installed and running. **Jupyter Labs** is installed. **Blazegraph** is available in a subfolder of your home folder. **Git** is installed.

ACCESS TO “R”: I have created a Docker image that provides access to R 4.0.0 and the libraries that are required for my lectures, and other lectures in the course. To start this interface, double click on the “start R” icon on the desktop. To stop it, double-click on the “stop R” icon. There is a folder (R-shared) in your home directory that is mounted inside of this docker image, providing a bridge between your host operating environment and the Docker container.

It requires (at a minimum) 4Gig of free memory to run the course assignments,

therefore, your laptop must have 8 Gig of RAM to run this machine, and do the course assignments.

If your laptop does not meet this requirement, you will likely not be able to complete the course.

Instructors will not spend additional time helping you solve problems related to lack of memory.

On the desktop is a friendly “start here” icon. Double-click that to download and open the introductory lecture.

You must be sure that the VM is working before you attend the (virtual) class on Sept 2 (for the introductory course) or Sept 30 (for the Bioinformatics Programming Challenges course)! If you have problems, email mark.wilkinson@upm.es to ask for help. The course is very busy, so I cannot take class time to troubleshoot installation problems.

Using the VM

Windows and Linux:

- 1) Download [VMWare Player](#)

- 2) Download the VM (the .zip file [in this folder](#)) and unzip it
- 3) Open VMWare Player and select the .vmx file
- 4) If you are asked, select the option “I moved it”

MacOS:

- 1) Download [VirtualBox for MacOS](#)
- 2) Download the VM (the .zip file [in this folder](#)) and unzip it
- 3) Follow instructions here: <https://techathlon.com/how-to-run-a-vmdk-file-in-oracle-virtualbox/>

Default Username: osboxes

Default Password: osboxes.org

Important Note:

It is important to let the VM fully shut down before you switch off or hibernate your host computer. Not doing so may leave it in a locked state that is non-recoverable. **All of your work will be lost!** So... at the end of every session, select the VM's “hibernate” or “shut down” option, and then watch the application icon until you see that the shut-down has completed (this can take as much as 1 minute!). *The fact that you cannot see the window on your screen does not mean that the VM has finished shutting down! Watch the icon until it shows that the process is complete.*