# Installing BioLinux on Mac OS X or Windows

USitual Workshop on Spatial Genomic PataineR 16th to 20th November 2020









#### **Bio-Linux**

Bio-Linux is a free workstation platform that facilitates running hundreds of bioinformatics tools without the corresponding installation hassles.

These guidelines will help you installing Bio-Linux from the provided flash drive on your Mac or Windows computer.

### Requirements

- A computer with at least 20 GB available space on the hard drive. A minimum of 4 GB of RAM is needed.

- The installation can take 10-20 minutes excluding the download time.

#### **Create a virtual machine using VirtualBox**

To save time on installation, a Google drive is provided for the workshop. It contains the following files:

- 1. virtualbox-6.1\_6.1.16-140961\_Ubuntu\_trusty\_a md64.deb
- 2. VirtualBox-6.1.16-140961-OSX.dmghttps://drive.google.com/file/d/1
  MxjuzEagyNOaYrrq-yodK3xDO7U-Suf5/view?usp=sharing
- 3. VirtualBox-6.1.16-140961-Win.exe
  <a href="https://drive.google.com/file/d/1MxjuzEagyNOaYrrq-yodK3xDO7U-Suf5/view?usp=sharing">https://drive.google.com/file/d/1MxjuzEagyNOaYrrq-yodK3xDO7U-Suf5/view?usp=sharing</a>
  - 3. bio-linux-8-latest.ova

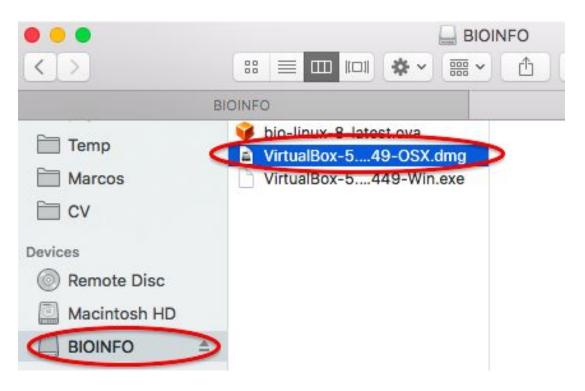
https://drive.google.com/file/d/1MxjuzEagyNOaYrrq-yodK3xDO7U-Suf5/view?usp=sharing Alternatively, you can download these files from <u>VirtualBox</u> and <u>Bio-Linux</u>, which may take several hours.

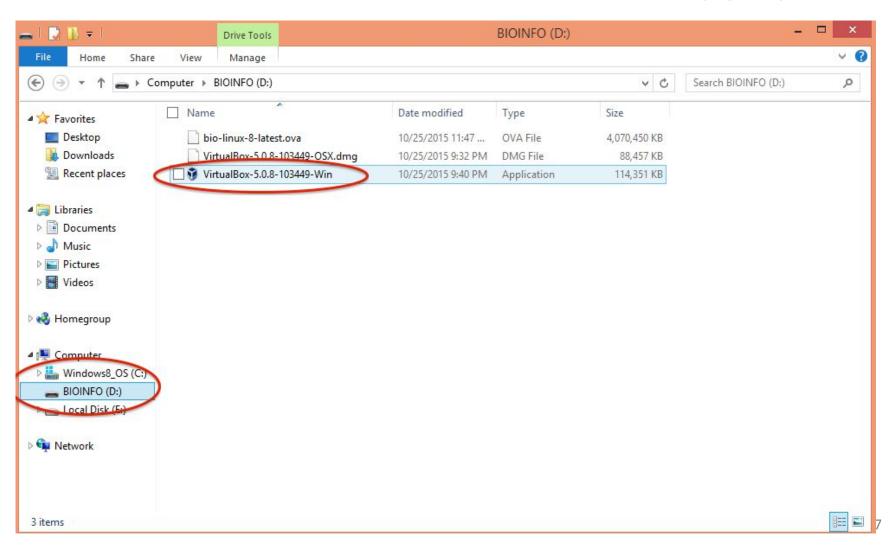
### Step 0: Close all your programs.

BioLinux needs extensive memory and CPU resources. Close all other programs unless you have a fast, high-performance computer.

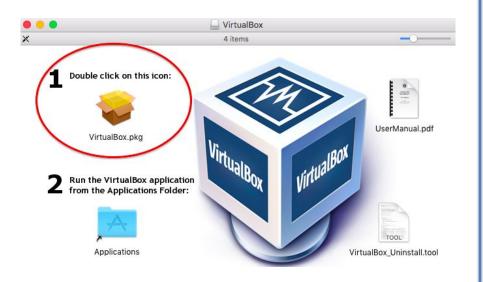
#### Mac OS X







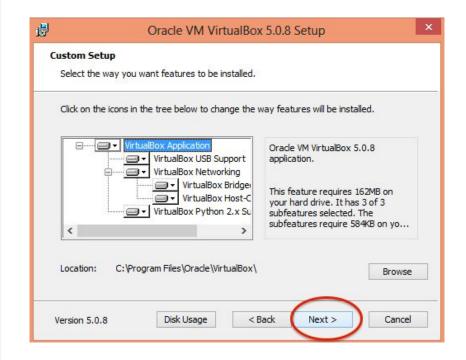
#### Mac OS X





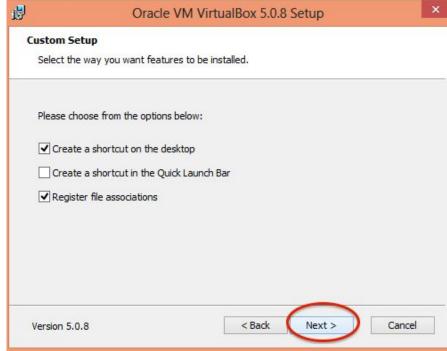
#### Mac OS X



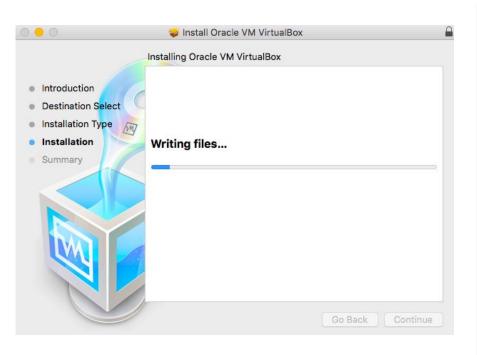


#### Mac OS X



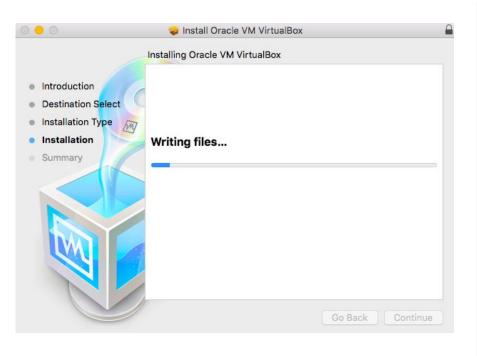


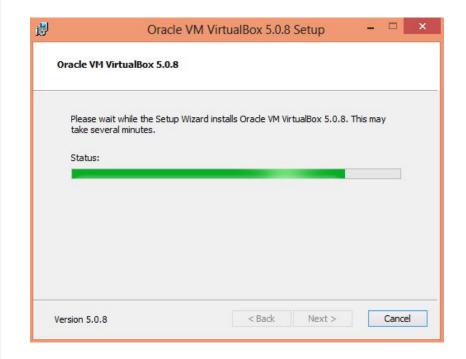
#### Mac OS X



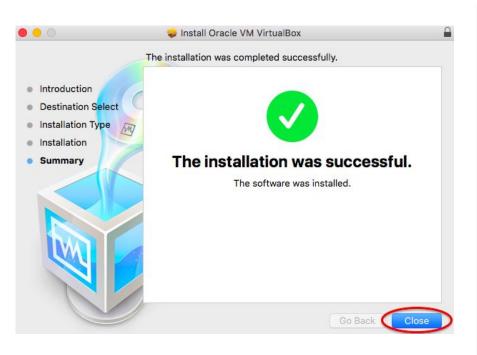


#### Mac OS X





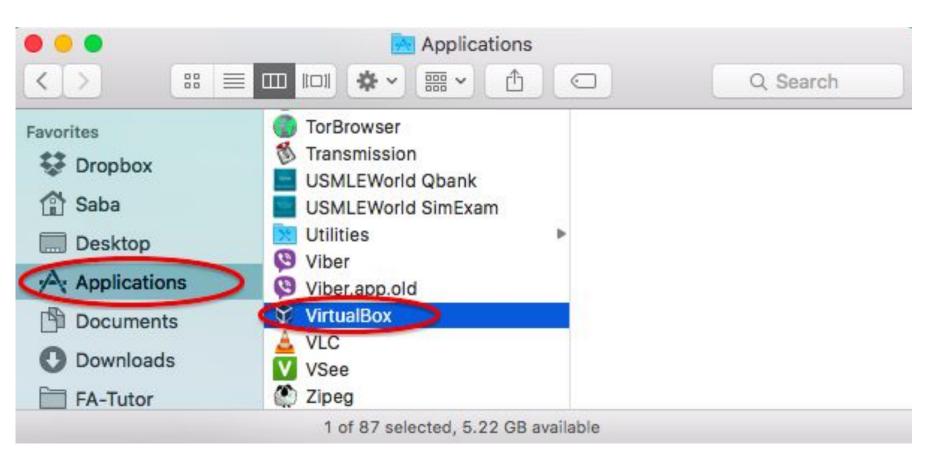
#### Mac OS X





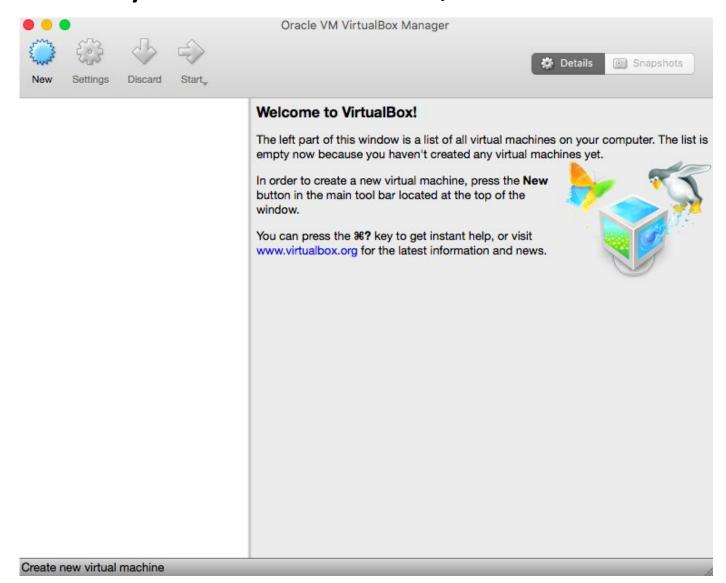
### **Step 2: Run VirtualBox**

#### Mac OS X



### **Step 2: Run VirtualBox**

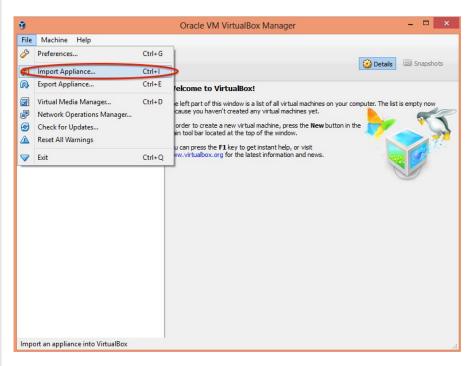
#### The first time you run VirtuaBox, it looks like this:



Mac OS X

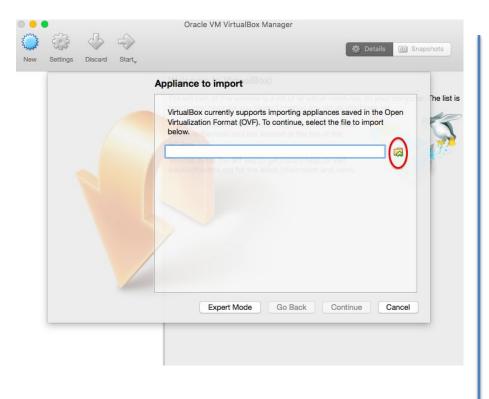
#### Windows

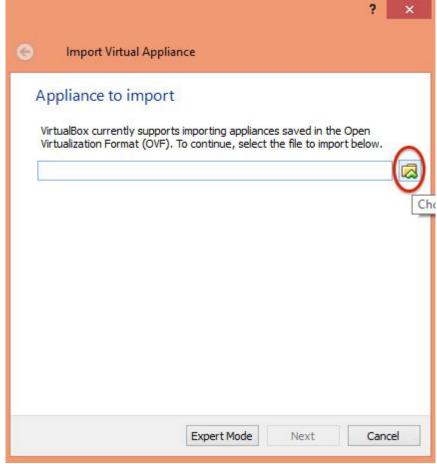




From the top menu, click on File>Import Appliance...

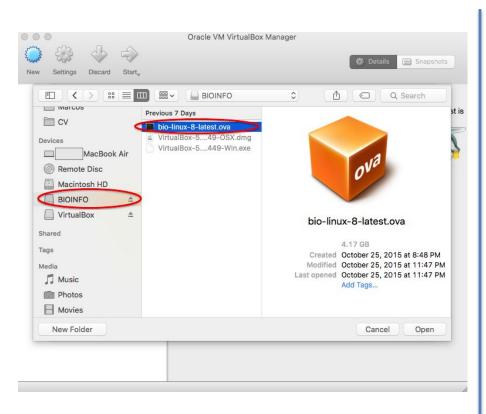
#### Mac OS X

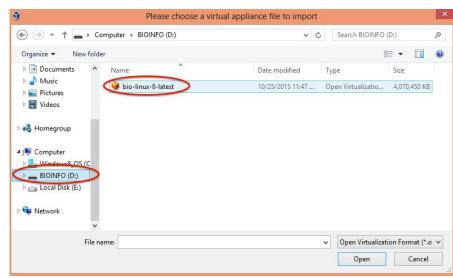




#### Mac OS X

#### Windows





Use the bio-linux-8-latest.ova file from the github account.

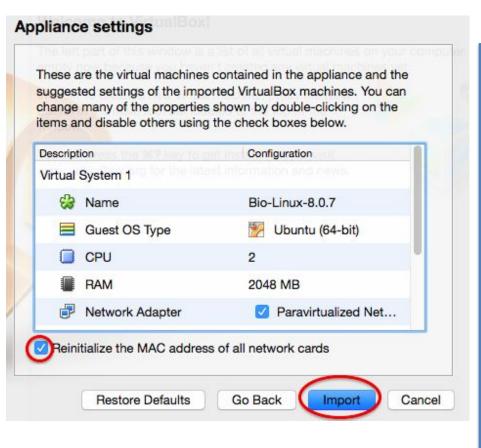
Mac OS X Windows

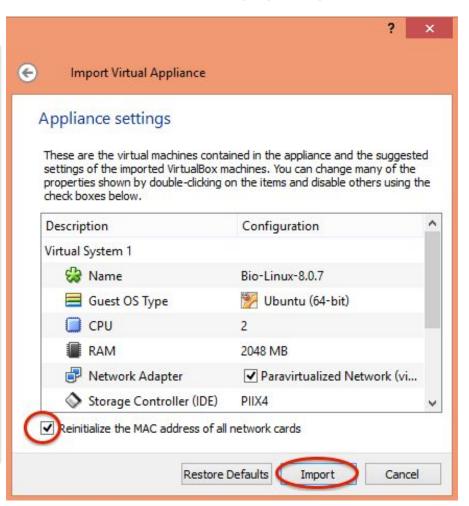
**Both Mac OS X and Windows** 

Make sure, in the next step, you will check

Reinitialize MAC address for all network cards.

#### Mac OS X





Mac OS X

**Windows** 



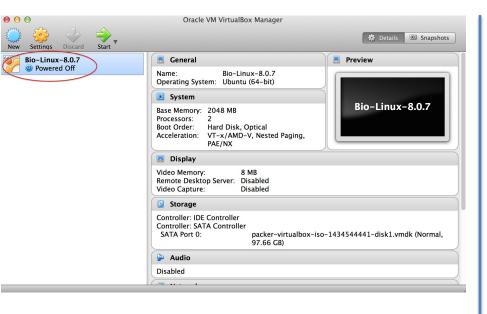


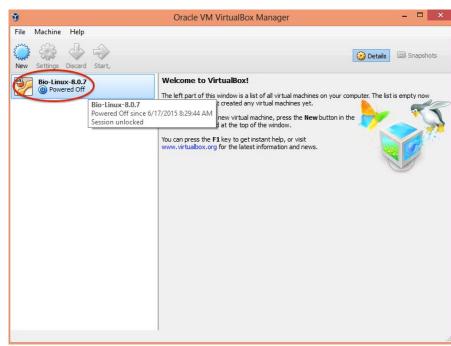
It can take 10-20 minutes ....

### **Step 4: Turn on BioLinux**

#### Mac OS X

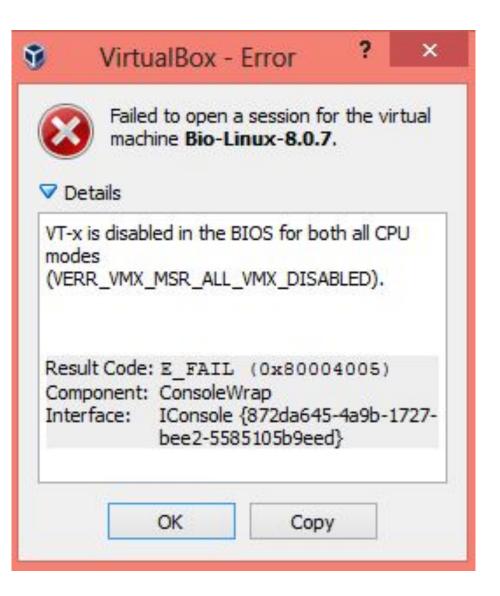
#### **Windows**





Double-click on Bio-Linux to turn it on.

### Step 4.5: Enable VT-x



#### Windows only

In Windows, you may get an error like this the first time you run Bio-Linux. To fix it, you need to enable Virtualization Technology (VT-x) by modifying BIOS, which is a little technical. Restart while pressing F2, F10, F12, or DEL.

## Step 4: Welcome to Linux world! Bio-Linux should appear after a black screen.



From this point on, there is not much difference between Mac OS X and Windows.

### Step 4: Welcome to Linux world!

Drag the bottom right corner of the screen to adjust it to your convenience.



### You are done!

- Bio-Linux is installed, and should work properly.

### Step 5: How To Install Packages on Ubuntu

Step 1: sudo apt-get update -y

Step 2: sudo apt-get install -y {package\_name}

Step 3: sudo apt-get install -y vcftools sudo apt-get install -y trimmomatic

### Step 5: How To Install Packages on Ubuntu - Trimmomatic

- Trimmomatic a flexible read trimming tool for Illumina NGS data.
- It is a Java-based tool:
- Step 1: which java
- Step 2: sudo apt-get install -y trimmomatic
- Step 3: which TrimmomaticPE
  - man TrimmomaticPE
- ☐ To use Trimmomatic, retrieve the ADAPTERS files (fasta format):
  - Step 4: cd /usr/local/bioinf

### Step 5: How To Install Packages on Ubuntu - Trimmomatic

Step 4: wget

http://www.usadellab.org/cms/uploads/supplementary/Trimmomatic/Trimmomatic-0.36.zip

#### Step 5: sudo unzip Trimmomatic-0.36.zip

Archive: Trimmomatic-0.36.zip creating: Trimmomatic-0.36/

inflating: Trimmomatic-0.36/LICENSE

inflating: Trimmomatic-0.36/trimmomatic-0.36.jar

creating: Trimmomatic-0.36/adapters/

. . . .

inflating: Trimmomatic-0.36/adapters/TruSeq3-SE.fa

#### Step 6: Run trimmomatic

TrimmomaticPE -phred33 sample1/sample1.raw.R1.fastq.gz sample1/sample1.raw.R2.fastq.gz sample1/sample1.raw.process.R1.fastq.gz sample1/sample1.raw.orphans.R1.fastq.gz sample1/sample1.raw.process.R2.fastq.gz sample1/sample1.raw.orphans.R2.fastq.gz ILLUMINACLIP:/usr/local/bioinf/Trimmomatic-0.36/adapters/NexteraPE-PE.fa:2:30:10:8:true LEADING:30 TRAILING:30 SLIDINGWINDOW:10:20 MINLEN:50

### Step 6: How To Install Packages on Ubuntu - RStudio

#### Step 1: Install R

#Ubuntu 14.04 ships with R but it's not the latest version.

sudo apt-get update sudo apt-get install r-base

#### Step 2: Install Rstudio

sudo apt-get install gdebi-core wget <a href="https://download1.rstudio.org/rstudio-1.0.44-amd64.deb">https://download1.rstudio.org/rstudio-1.0.44-amd64.deb</a> sudo gdebi

https://download1.rstudio.org/desktop/trusty/amd64/rstudio-1.2.5042-amd64.deb rm rstudio-1.2.5042-amd64.deb

#### Step 3: Launch Rstudio from the icons

#### **References:**

- These guidelines were based on a blog post by Dave Lunt. <a href="http://www.davelunt.net/evophylo/2011/07/bio-linux-in-a-virtualbox/">http://www.davelunt.net/evophylo/2011/07/bio-linux-in-a-virtualbox/</a>
- See the Bio-Linux website for documentation, training, and the list of supported software. <a href="http://environmentalomics.org/bio-linux/">http://environmentalomics.org/bio-linux/</a>
- I prepared these guidelines to facilitate the "Bioinformatics for biologists workshop" to be held on 20 Nov 2015, UTHSC – San Antonio.

http://oncinfo.org/Bioinformatics+for+biologist+workshop