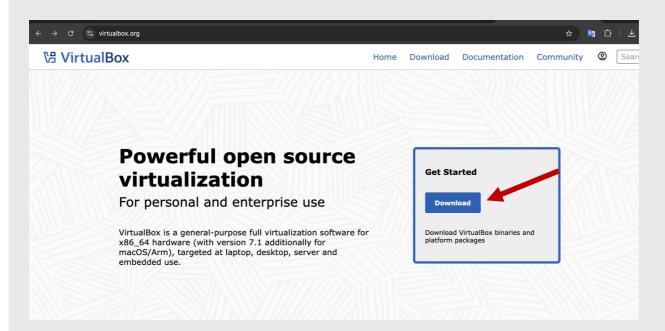


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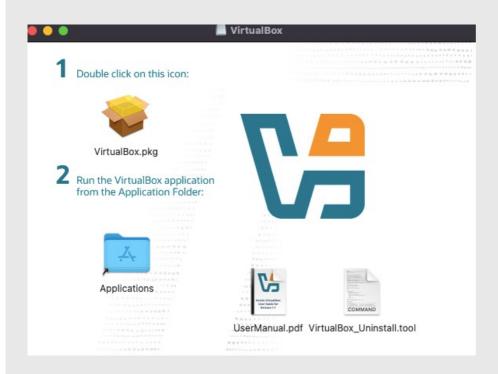
1.) Navigate to https://www.virtualbox.org/ and enter Download section

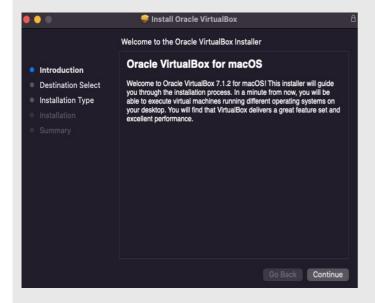


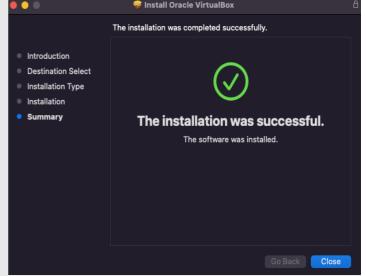
2.) Download the VM for your system, the extension pack, and the user guide.



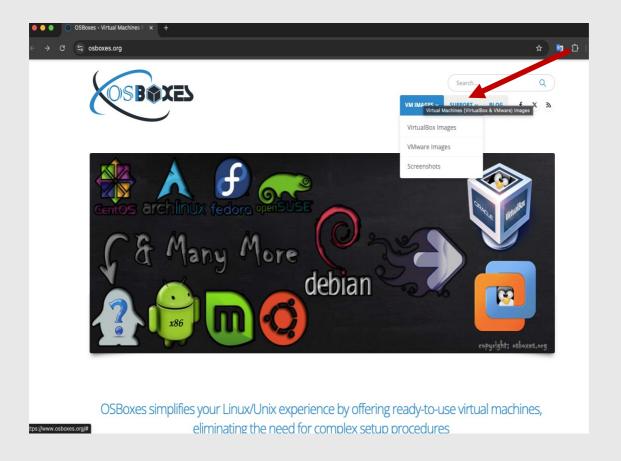
3.) Follow the installation instructions. Leave the default settings. These can be modified later. **Note:** It didn't work on my Mac with silicon chip (M2). Worked well on Intel Mac.



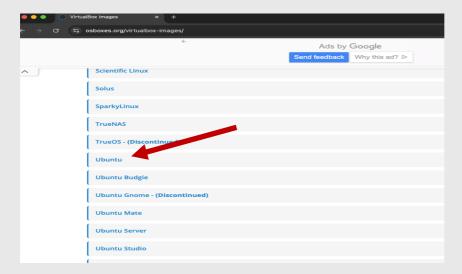




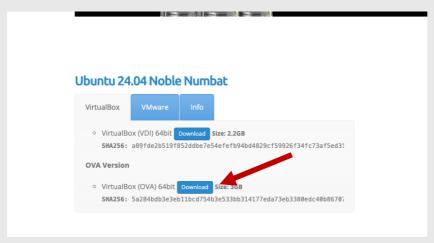
4.) Navigate to osboxes.org. Then VM images and enter VirtualBox Images



5.) Select Ubuntu



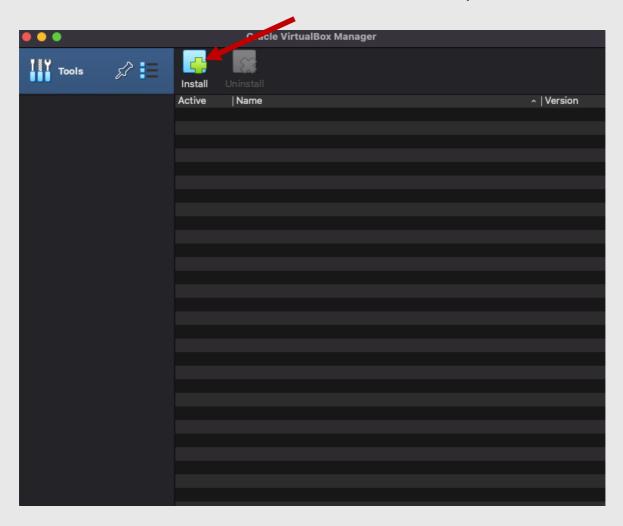
6.) Download the OVA Version



7.) Make a note of the password in the Info tab



8.) Open the VM and Install the expansion pack. Oracle_VirtualBox_Extension_Pack-7.1.2.vbox-extpack



9.) Double click on the Obuntu .ova file you downloaded. Follow the instructions. Also look the manual page 50.

1.15.2 Importing an Appliance in OVF Format

The following steps show how to import an appliance in OVF format.

1. Double-click the OVF or OVA file.

Oracle VirtualBox creates file type associations automatically for any OVF and OVA files on your host OS.

The **Appliance Settings** page of the **Import Virtual Appliance** wizard is shown. This page shows the VMs described in the OVF or OVA file and enables you to change the VM settings.

By default, membership of VM groups is preserved on import for VMs that were initially exported from Oracle VirtualBox. You can change this behavior by using the **Primary Group** setting for the VM.

The following global settings apply to all of the VMs that you import:

 Base Folder: Specifies the directory on the host in which to store the imported VMs.

If an appliance has multiple VMs, you can specify a different directory for each VM by editing the **Base Folder** setting for the VM.

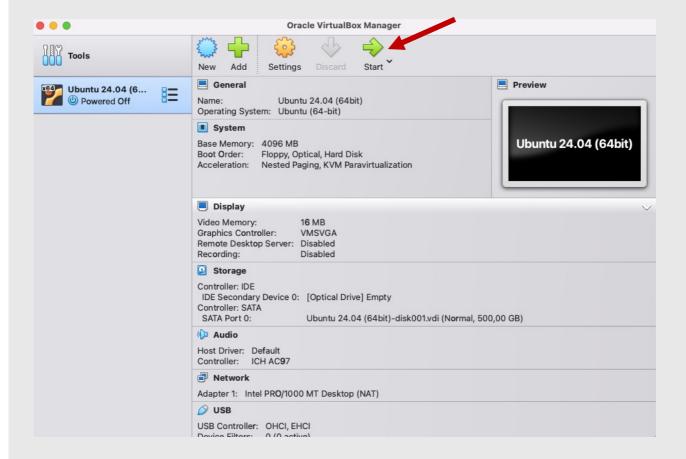
- MAC Address Policy: Reinitializes the MAC addresses of network cards in your VMs prior to import, by default. You can override the default behavior and preserve the MAC addresses on import.
- Import Hard Drives as VDI: Imports hard drives in the VDI format rather than in the default VMDK format.
- 3. Click Finish to import the appliance.

Oracle VirtualBox copies the disk images and creates local VMs with the settings described on the **Appliance Settings** page. The imported VMs are shown in the list of VMs in VirtualBox Manager.

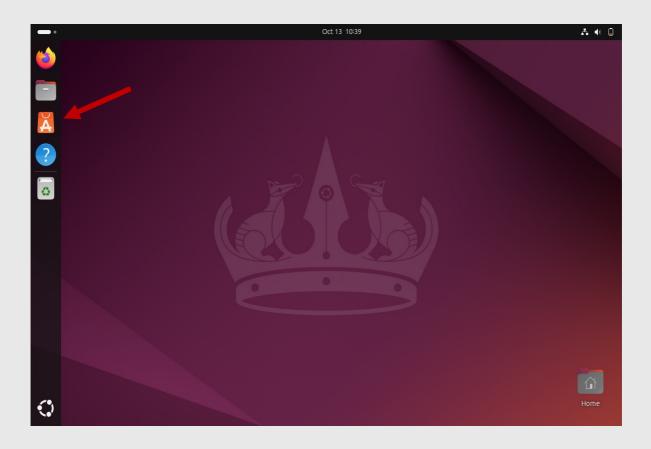
Because disk images are large, the VMDK images that are included with virtual appliances are shipped in a compressed format that cannot be used directly by VMs. So, the images are first unpacked and copied, which might take several minutes.

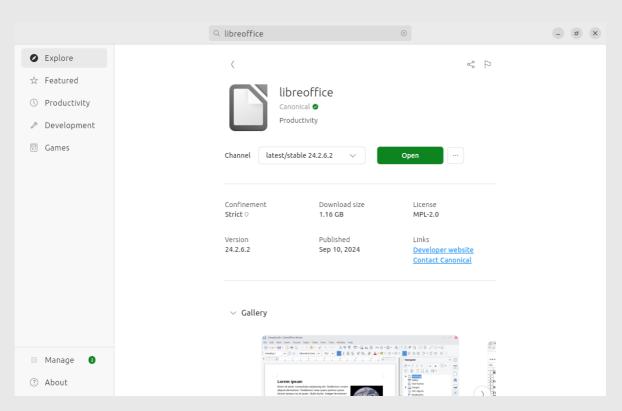
You can use the VBoxManage import command to import an appliance. See 8.29 VBoxManage import on page 310.

10.) Start the Vm and enter the password



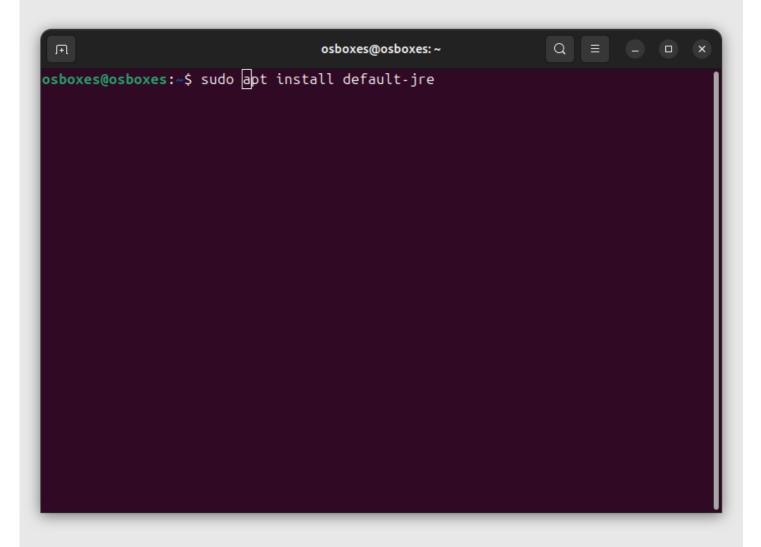
11.) Install LibreOffice from the App Center in Obuntu





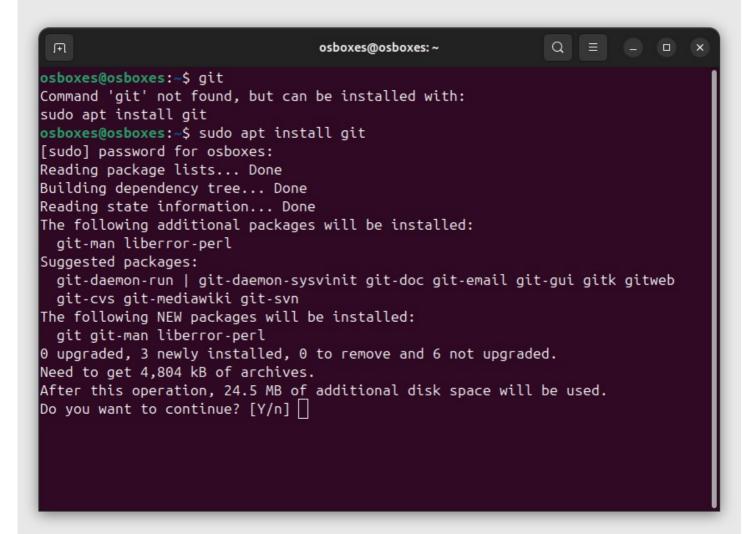
Install Java

\$ sudo apt install default-jre



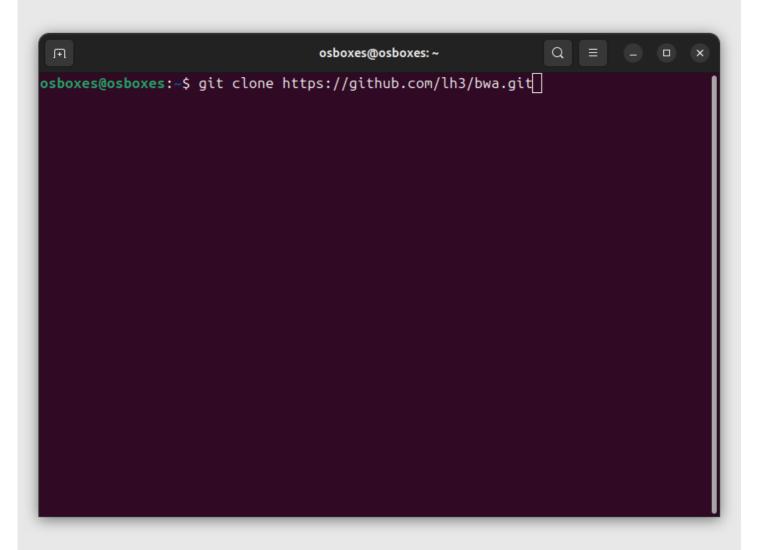
Install Git

\$ sudo apt install git



Use git to clone the bwa repository

\$ git clone https://github.com/lh3/bwa.git



Download samtools, bcftools, htslib

https://www.htslib.org/download/



Current releases

SAMtools and BCFtools are distributed as individual packages. The code uses HTSlib internally, but these source packages contain their own copies of htslib so they can be built independently.

HTSlib is also distributed as a separate package which can be intalled if you are writing our own programs cannot the HTSlib API. HTSlib also provides the bgzip, htsfile, and tabix utilities, so you may also want to build and install the bib to get these utilities of see the addition instructions in INSTALL to install them from a samtools or boftools source package.

See also release notes for **samtools**, **bcftools**, and **htslib**.

New releases are announced on the samtools mailing lists and by @htslib on Twitter. Previous releases are available from the samtools GitHub organisation (see samtools, bcftools, or htslib releases) or from the samtools Sourceforge project.

Building and installing

Building each desired package from source is very simple:

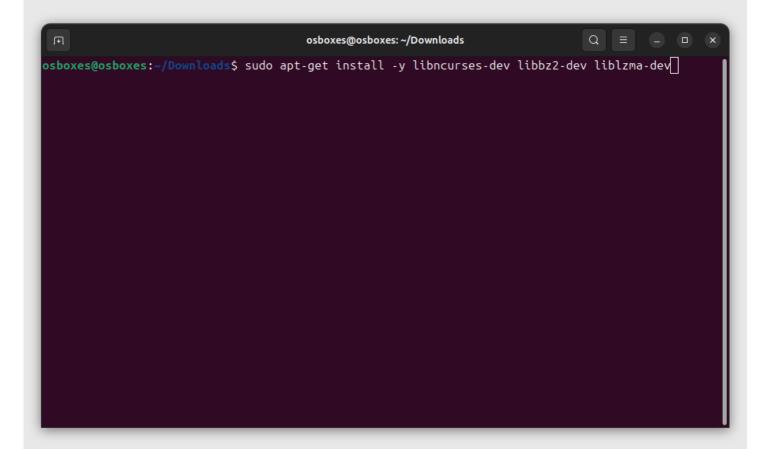
```
cd samtools=1.x  # and similarly for bcftools and htslib
./configure =-prefix=/where/to/install
make
make install
```

See INSTALL in each of the source directories for further details.

The executable programs will be installed to a bin subdirectory under your specified prefix, so you may wish to add this directory to your \$PATH:



Navigate to the Download folder and install these libraries first \$ sudo apt-get install –y libraries-dev libbz2-dev liblzma-deb



Untar the tar.bz2 samtools, bcftools and htslib bundles

\$ tar –vxjf htslib-1.21.tar.bz2

Install samtools, bcftools, and htslib. Follow the commands below in order.

- \$ cd samtoos 1.x
- \$./configure --prefix=/path/ # we will decide in class. Default /usr/bin
- \$ make
- \$ make install

Building and installing

Building each desired package from source is very simple:

```
cd samtools-1.x  # and similarly for bcftools and htslib
./configure --prefix=/where/to/install
make
make install
```

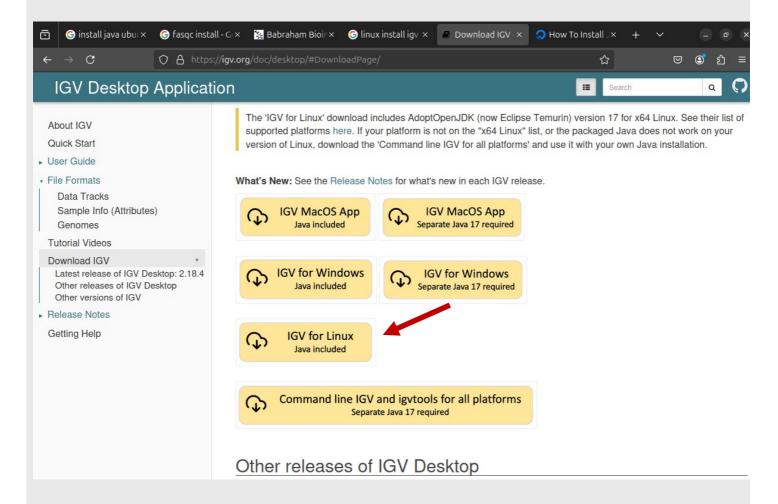
See INSTALL in each of the source directories for further details.

The executable programs will be installed to a bin subdirectory under your specified prefix, so you may wish to add this directory to your \$PATH:

```
export PATH=/where/to/install/bin:$PATH  # for sh or bash users

setenv PATH /where/to/install/bin:$PATH  # for csh users
```

Download IGV genome viewer



To lunch IGV

