Nighres 2021 tutorial software set-up

This tutorial is based on a Linux virtual machine with the needed software installed as described below. You can perform the tutorial on a local installation on your computer, as long as all the related software is correctly installed there, but if you are not familiar with installing and compiling research software on your own, the virtual machine below is a safe option.
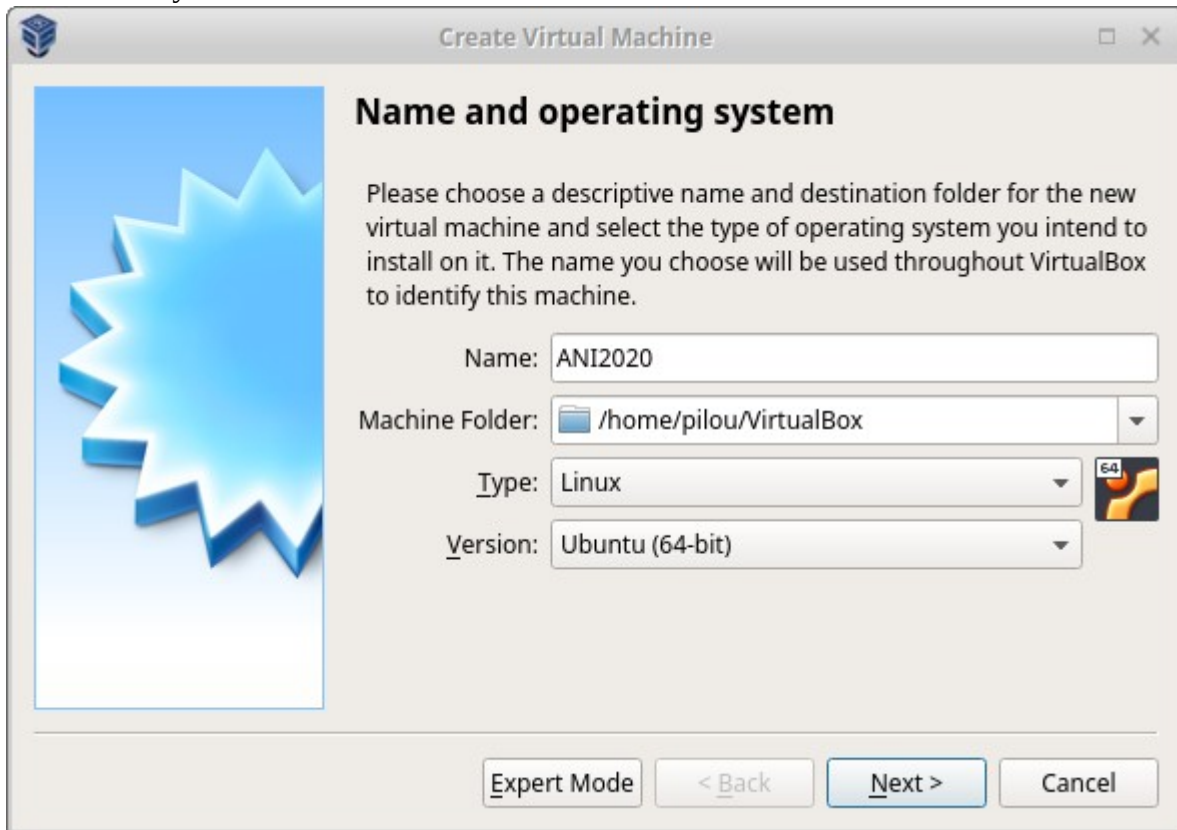
Step 1: building a linux virtual machine

First, download and install Oracle VM VirtualBox 6.1 for your OS.

Launch the program; in the VirtualBox Manager, select New
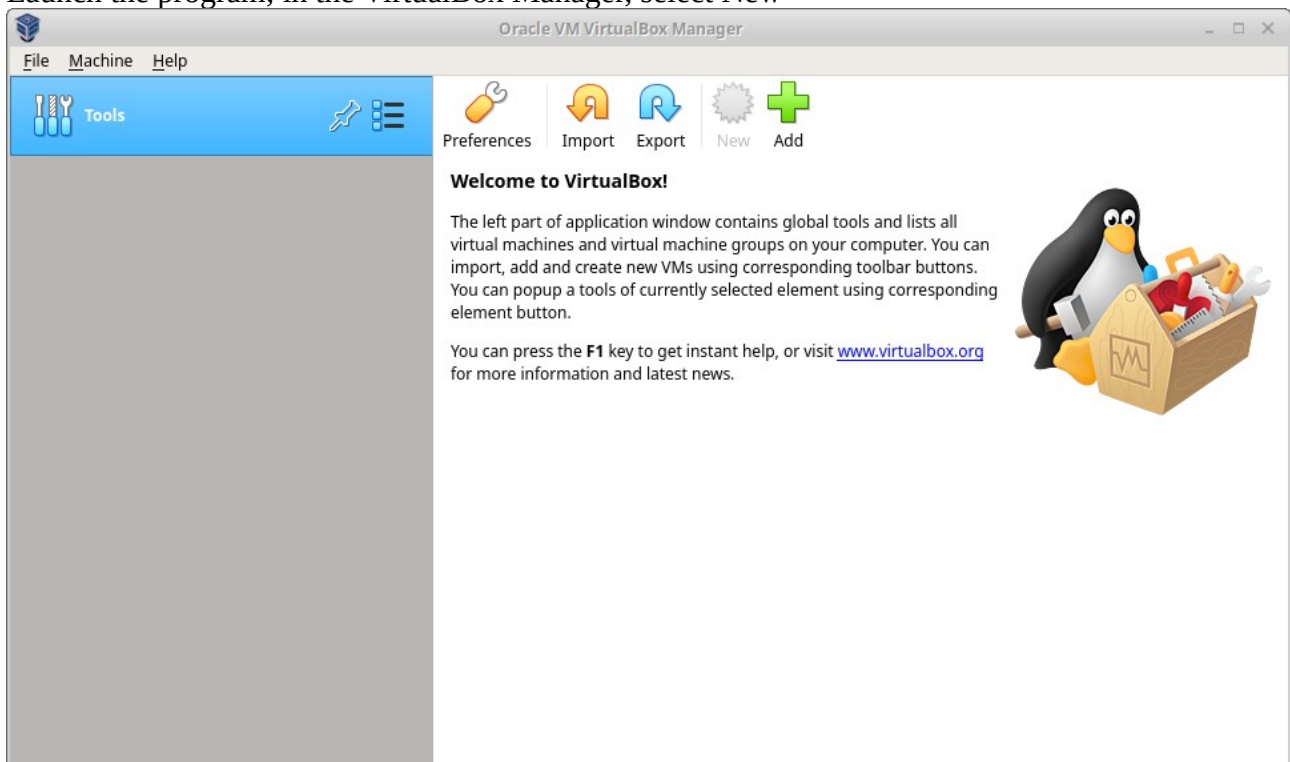
Choose the OS you need

Choose the RAM to allocate: I recommend 4096 MB (depends on computer)
Create a virtual disk (I recommend to reserve 40GB) with VDI settings, dynamically allocated.

Download (separately) the Xubuntu ISO image from website www.xubuntu.org.

Point to the .iso file on your disk as the starting point for your virtual machine.

The virtual machine will boot from the .iso, asking whether to try or install Xubuntu. Select install and go through the installation steps (for convenience, you can select to log in without password when prompted. You still have to give a password, which you will need for some installation procedures). You should end up with this:
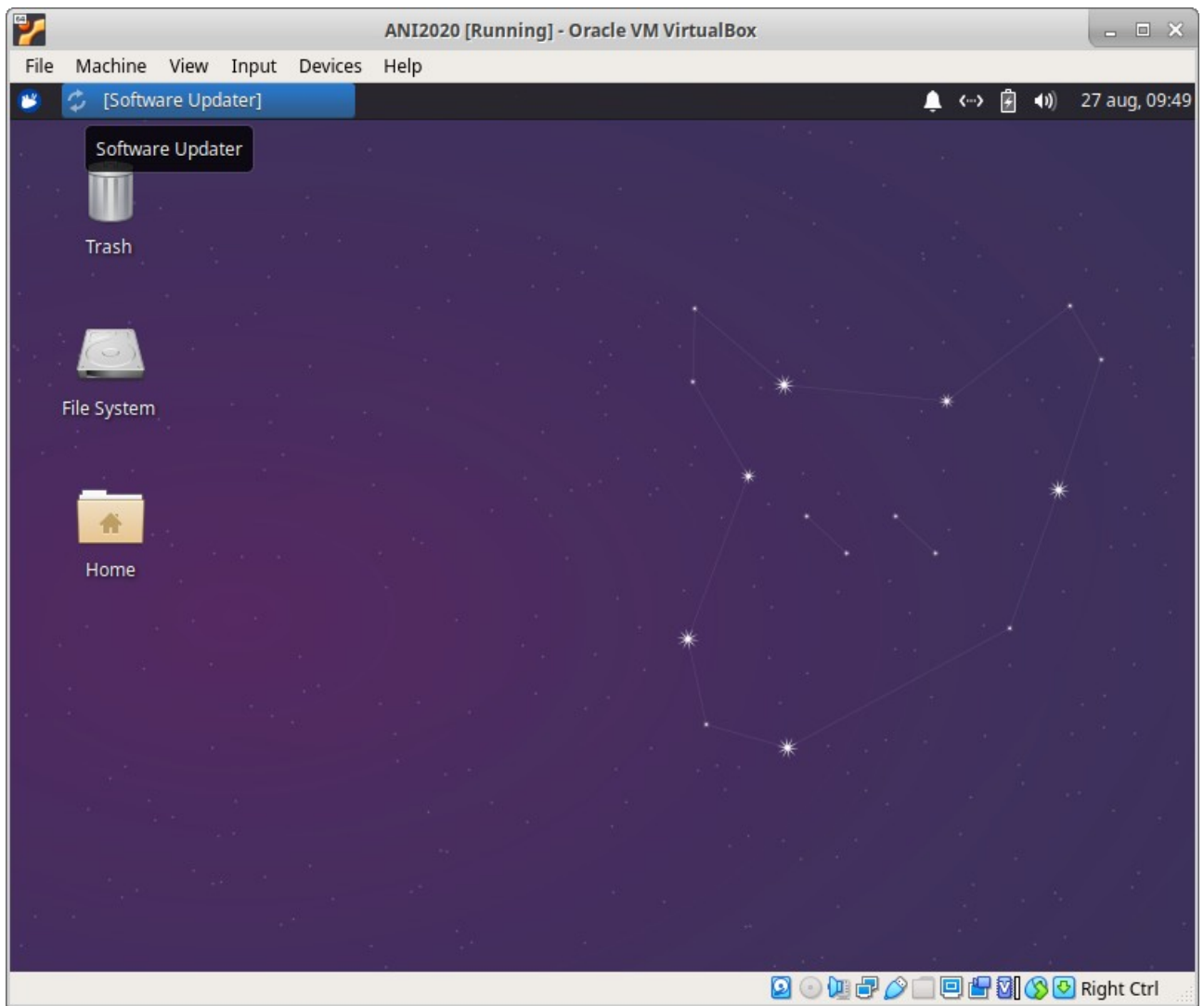
Congrats, you have a Xubuntu virtual machine!

Now we can start installing our new software...

Step 2: Installing various neuroimaging software packages

First, we'll make sure you have the basic tools needed to install and run programs:
python3, jupyter notebook, git, cmake, ...

Most installation steps in linux are done via the terminal. You can open it by typing 'term' in the mouse menu (top left) and clicking 'Terminal emulator'. You can also drag and drop the 'Terminal emulator' onto your desktop to create a shortcut (when asked, make executable).

In the terminal, run:
```
sudo apt-get install python3 python3-pip jupyter-notebook git cmake cmake-curses-gui
```

This will ask to install a bunch of software packages. When other packages are missing, the same approach will help you get the 'standard release' version easily. Some neuroimaging software is included in such 'standard' linux packages, but they are often outdated.

In case this line doesn't work (packages not found), open the 'Software & Updates' window, and check that you have 'Ubuntu Software' and 'Other Software' - 'Canonical partners' checked.

Next, let's start with installing standard and specialized python libraries we might need
```
python3 -m pip install numpy scipy pandas nibabel matplotlib scikit-learn nilearn
```

Now let's install the main packages we will use: Nighres, ANTs, and a few nice viewers

Nighres:

```
git clone https://github.com/nighres/nighres

sudo apt-get install openjdk-8-jdk
export JCC_JDK=/usr/lib/jvm/java-8-openjdk-amd64
python3 -m pip install jcc

cd nighres/
./build.sh
python3 -m pip install ./
```

Test:
```
cd ..
python3 -c 'import nighres'
```

Did you get any output? no? great, it means the toolbox loaded correctly!

For ANTs:

simplest instructions found so far (many options, with various problems):

```
Download installANTs.sh from https://github.com/cookpa/antsInstallExample
mkdir ANTs-Script
mv Downloads/installANTs.sh ANTs-Script/
cd ANTs-Script
bash installANTs.sh
```

should take some time (downloading and compiling all the code and associated libraries on your machine), and finish with this positive message:

```
-- Installing: /home/pilou/ANTs-Script/install/bin/antsJointLabelFusion.sh
-- Installing: /home/pilou/ANTs-Script/install/bin/antsMultivariateTemplateConstruction.sh
-- Installing: /home/pilou/ANTs-Script/install/bin/antsMultivariateTemplateConstruction2.sh
-- Installing: /home/pilou/ANTs-Script/install/bin/antsNetworkAnalysis.R
-- Installing: /home/pilou/ANTs-Script/install/bin/antsNeuroimagingBattery
-- Installing: /home/pilou/ANTs-Script/install/bin/antsRegistrationSyN.sh
-- Installing: /home/pilou/ANTs-Script/install/bin/antsRegistrationSyNQuick.sh
-- Installing: /home/pilou/ANTs-Script/install/bin/waitForPBSQJobs.pl
-- Installing: /home/pilou/ANTs-Script/install/bin/waitForSGEQJobs.pl
-- Installing: /home/pilou/ANTs-Script/install/bin/waitForXGridJobs.pl
-- Installing: /home/pilou/ANTs-Script/install/bin/waitForSlurmJobs.pl
Installation complete, running /home/pilou/ANTs-Script/install/bin/antsRegistration
ANTs Version: 2.3.4.dev188-g71778
Compiled: Aug 31 2020 20:35:20


Binaries and scripts are located in

  /home/pilou/ANTs-Script/install

Please see post installation instructions at

  https://github.com/ANTsX/ANTs/wiki/Compiling-ANTs-on-Linux-and-Mac-OS


(base) pilou@vb-ani:~/ANTs-Script$ ls /home/pilou//ANTs-Script/install
bin  lib
```

Then, you still need to make ANTs part of your standard software path. Open the bash configuration file:
```
mousepad ~/.bashrc
```

Then add these two lines:
```
export ANTSPATH=/home/{your username}/ANTs-Script/install/bin/
export PATH=${ANTSPATH}:$PATH
```

and save the file.
You have to refresh the terminal to things to work and test:
```
bash
which antsRegistration
```

should output the full path to the antsRegistration program, i.e. /home/{your username}/ANTs-Script/install/bin/antsRegistration

Viewers:

ITK-Snap:
```
sudo apt install itksnap
```

MIPAV:
go to https://mipav.cit.nih.gov/
follow installation instructions to download the installation file.
Run:
```
cd Downloads/
bash mipav_unix_10_0_0.sh
```
follow installation instructions, choosing the defaults