IQ-TREE is a bioinformatics software for phylogenetic/phylogenomic inference. It is available as a webserver and a standalone tool. In this article, we are going to install IQ-TREE on Ubuntu.

### Preparing system

Open a terminal by pressing Ctrl+Alt+T. Update and upgrade your system using the following commands:

$ sudo apt-get update

$ sudo apt-get upgrade

### Downloading IQ-TREE

Let’s change to a directory where you want to download the software. We are downloading in ‘Downloads‘.

$ cd Downloads/

To download the software either visit [this page](http://www.iqtree.org/#download) or paste the following commands. We are installing stable version 1.6.12 of IQ-TREE for 64-bit multicore Linux. You can also download for 32-bit.

$ wget https://github.com/Cibiv/IQ-TREE/releases/download/v1.6.12/iqtree-1.6.12-Linux.tar.gz

### Installing IQ-TREE

Now extract the downloaded file.

$ tar xvzf iqtree-1.6.12-Linux.tar.gz

A new directory will be created namely, ‘iqtree-1.6.12-Linux‘. Move inside this directory and then to the bin directory.

$ cd iqtree-1.6.12-Linux/bin/

Here you will find an executable file namely, iqtree. Move or copy this file to the /usr/bin/ directory so that you can execute it from anywhere you want.

$ sudo cp iqtree /usr/bin/

Now IQ-TREE can be easily run by typing $ iqtree in the terminal.

ModelFinder of IQ-TREE helps to identify the best fit model for data. It supports several substitution models for DNA, protein, codon, and binary alignment.

Follow the steps given below:

* Align your sequences using any alignment software or a webserver such as Clustalo, Muscle, and MAFFT.
* Save the alignment in Phylip, FASTA, MSF, NEXUS, or Clustal format.
* Now open a terminal by pressing Ctrl+Alt+T.
* Paste the following command:  
  $ iqtree -s aligned\_seqs.fasta -m <model\_name>  
  Here, -m refers to the model name such as TIM2+I+G, JC, TPM, WAG, and so on. You can select a model from [here](http://www.iqtree.org/doc/Substitution-Models).
* If you do not know an appropriate model for your data then use the following command to test all models:  
  $ iqtree -s aligned\_seqs.fasta -m MFP
* If you want to resemble jModelTest/ ProtTest, then use the following command:  
  $ iqtree -s aligned\_seqs.fasta -m TESTONLY
* You can also run the analysis on a tree as shown below:  
  $ iqtree -s input.phy -m <model\_name>
* To re-run the analysis, use the following command:  
  $ iqtree -s aligned\_seqs.fasta -m <model\_name> -redo