

Installing MODELLER on Linux/Ubuntu

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MODELLER is a software package which is used to predict protein three-dimensional structures [1,2]. MODELLER can be used for other tasks such as modeling of loops in proteins, multiple alignments of structures, comparison of protein structures, and many others. In this article, I will explain how to install MODELLER on Linux/Ubuntu.

1. Download

Let's update and upgrade the system first.

Open the terminal (Ctrl+T) and type the following commands:

```
$ sudo apt-get update
```

```
$ sudo apt-get upgrade
```

Now start downloading the software in a directory, say, *Downloads*, by typing the following command:

```
$ sudo wget https://salilab.org/modeller/9.22/modeller-9.22.tar.gz
```

2. Install

Extract the tar package:

```
$ tar xvzf modeller-9.22.tar.gz
```

It will create a new directory in *Downloads*, named *modeller-9.22*. cd to that directory and start installing.

```
$ cd modeller-9.22
```

```
$ ./install
```

It will prompt some questions, answer them, and then you are finally done!

You can run MODELLER either by:

1. using python (assuming python 2.3 – 3.7 is already installed on your system)

```
$ python modeller_script.py
```

2. using mod9.22 scripts

```
$ mod9.22 modeller_script.py
```

That's all for the installation of MODELLER.

If you have any query, please email at info@bioinformaticsreview.com.

References

1. Webb, B., & Sali, A. (2014). Comparative protein structure modeling using MODELLER. *Current protocols in bioinformatics*, 47(1), 5-6.
2. Martí-Renom, M. A., Stuart, A. C., Fiser, A., Sánchez, R., Melo, F., & Šali, A. (2000). Comparative protein structure modeling of genes and genomes. *Annual review of biophysics and biomolecular structure*, 29(1), 291-325.

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