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Installation instructions for phylogenetic analysis using a conda environment V.1

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1 *Works for me*   dx.doi.org/10.17504/protocols.io.bgd4js8w

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Version 1 ▾
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ABSTRACT

The purpose of this protocol is to define and provide instructions for creating a conda environment for phylogenetic analysis

Installing Miniconda

1   Open a terminal (Ctrl + Alt + T).

Create a directory called softwares to your HOME directory, switch to it and then download the 64-bit Python 3 Miniconda installer.
Install Miniconda quietly, accepting defaults.
After installation, remove the Miniconda installer from directory.
Set the Miniconda permanent PATH and update conda packages to the latest compatible version.

```
mkdir $HOME/softwares
cd $HOME/softwares
wget https://repo.continuum.io/miniconda/Miniconda3-latest-Linux-x86_64.sh
bash Miniconda3-latest-Linux-x86_64.sh -bfp $HOME/softwares/conda
rm Miniconda3-latest-Linux-x86_64.sh
export PATH="$HOME/softwares/conda/bin:/usr/local/share/rsi/idl/bin:$PATH"
echo 'export
PATH="$HOME/softwares/conda/bin:/usr/local/share/rsi/idl/bin:$PATH"' >>
$HOME/.bashrc
conda update -y -n base conda
```

Creating conda environment

2   Create a YML file to build a phylogenetic analysis environment called phy.

```
cat > phy.yml <<EOF
name: phy
channels:
  - bioconda
  - anaconda
dependencies:
  - bcftools
  - biopython
  - bwa
  - clustalo
  - fasttree
  - gbmunge
  - iqtree
  - mafft
  - modeltest-ng
  - phyml
  - samtools
EOF
```

3   Create the environment from the phy.yml file

```
conda env create -f phy.yml
```