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Installation instructions for RNA-seq analysis using a conda environment V.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.

Command

```
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 rna-seq.

Command

```
cat > rna-seq.yml <<EOF
name: rna-seq
channels:
  - bioconda
dependencies:
  - bedtools
  - bioconductor-rdavidwebservice
  - bowtie2
  - bwa
  - cutadapt
  - fastqc
  - igv
  - multiqc
  - tophat
  - trimmomatic
  - samtools
  - star
  - subread
EOF
```

3 Create the environment from the phy.yml file

Command

```
conda env create -f rna-seq.yml
```