Installation tutorial

1. Installation
   The overall process is based on Python3
   Highly recommend to use a virtual environment for the study.

2. Create the virtual environment
   Before create the virth environment, make sure conda is installed.

   (1) If not, install miniconda (https://docs.conda.io/en/latest/miniconda.html) for conda.
   e.g. download Miniconda3-lastest-Linux-x86_64.sh, and use the following command to install Miniconda3
   $ sh Miniconda3-latest-Linux-x86_64.sh -b
   $ ~/miniconda3/bin/conda init
   (2) A virtual environment can be created and (de)activated as follows using conda
   # create the virth environment prot_study
   $ conda create -n prot_study python==3.8 (>=3.6 should work)
   # activate the virth environment prot_study
   $ conda activate prot_study
   # Install data analysis package
   $ conda install numpy pandas

3. Install bioinformatics tools
   (1) Create a folder
   $ mkdir protein_analysis

   (2) Install ASAquick for solvent accessibility study. Please refer
   http://mamiris.com/software.html
   # Download and upload to server
   $ ssh GENN+ASAquick2.tgz bullrocky@sc.rc.usf.edu:/home/b/bullrocky/protein_analysis
   # Install ASAquick in SC
   $ tar xvfz GENN+ASAquick2.tgz
   $ cd GENN+ASAquick2
   $ ./install
   $ export PATH=$PATH:$HOME/bin

   (3) Install mmseqs2 for searching and clustering the protein or nucleotide sequence sets for sequence conservation
   # install via conda
   conda install -c conda-forge -c bioconda mmseqs2
   or
   # static build with AVX2
   $ wget https://mmseqs.com/latest/mmseqs-linux-avx2.tar.gz
   $ tar xvfz mmseqs-linux-avx2.tar.gz
   $ export PATH=$(pwd)/mmseqs/bin/:$PATH