

From Scratch:

1. Install conda on Linux:
 - 1.1. Go to <https://www.anaconda.com/download> and download the sh file
 - 1.2. \$ `bash <conda-installer-name>-latest-Linux-x86_64.sh`
2. Create a **Python 3.6.3** environment using conda:
 - 2.1. \$ `conda create -n env_name python=3.6.3`
 - 2.2. \$ `conda activate env_name`
3. Install scikit-learn and bio
 - 3.1. \$ `pip install scikit-learn==0.22`
 - 3.2. \$ `pip install bio`
4. Run IncSVM inside the created environment:
\$ `python IncSVM.py -c <inputfile>.fasta --model <model>_model.sav -o <outputfile>.csv`

For running the script:

\$ `sudo apt-get update`

1. Install dos2unix:
\$ `sudo apt-get install dos2unix`
2. Convert to UNIX format using dos2unix
\$ `dos2unix <scriptfile>.sh`
3. Add execution permissions:
\$ `chmod +x <scriptfile>.sh`
4. Run the bash script:
\$ `./<scriptfile>.sh`

Note:

1. For running the script, all the steps, in our context, have to be run in the Python 3.6.3 environment created above.
2. DO NOT use sudo mode for running the script. It will execute outside the environment and will not be able to find the installed modules (like bio).

For Systems at the Bioinformatics Lab:

1. Navigate to the folder containing the IncSVM package, and open the terminal:
\$ `conda activate Incenv`
\$ `python IncSVM.py -c test.fasta --model dt_model.sav -o dt_output.csv` //for example
2. For Linear SVM, switch from scikit-learn V0.22 to V0.19.1:
\$ `pip uninstall scikit-learn` //press Y if prompted
\$ `pip install scikit-learn==0.19.1`
\$ `python IncSVM.py -c test.fasta --model lsvm_model.sav -o lsvm_output.csv`

3. To run the script (ensuring scikit-learn V0.22 is installed), just do:
\$ **./lncmachine.sh** //and provide input file name, here "test.fasta"

For any queries, write to f20200611@pilani.bits-pilani.ac.in