

#####

RefBifSelector Pipeline

#####

This pipeline compare an input list of nt fasta genomes Vs. a pre-build database RefBi-IS nt fasta genomes.

To run this pipeline is required an updated python version and other modules;

List of required packages:

Manual installation in root pathway:

```
sudo apt install ncbi-blast+
```

```
sudo apt-get update
```

```
sudo apt-get install python 3.9.7
```

```
sudo pip install PySimpleGUI
```

```
sudo apt-get install python3-tk
```

```
pip install biopython
```

```
pip install biopython --upgrade
```

Alternatively, there is a pre-compiled conda installation:

```
conda activate
```

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

```
conda activate RefBifSelector
```

Then, launch the graphical software:

```
chmod 755 Software
```

```
python3 RefBifSelectort.py
```

1) Press "Browse" button ;

2) Select the folder containing the nucleotide fasta files of genomes you want compare to RefBif-IS models ;

3) Then, in the List-Box must be appear the list of all the fasta files names ;

4) Press the "Submit" button to execute the program ;

5) Results will be then placed inside "Results" directory, with "Summary_Results.txt" file as the main output.