**Script FastaFrameSetter.py**

1. Make sure you are running Python34
2. Open the command line in Windows (cmd.exe)
3. Navigate to the folder where you have placed the script and the file to be analyzed
4. Type python FastaFrameSetter.py –i inputfile –v
5. Press enter
6. The script will now ask you for a DNA sequence that will be used as a reference. Preferably paste a sequence that already is in reading frame +1. After pressing enter again, the sequence will be translated and the result will be displayed. After that you can choose whether to continue of whether you would like to try again in reading frame +2 or +3.
7. Now the script will process your inputfile and write the results in two new files: one file containing all sequences that have been placed in reading frame +1 and another file that contained all sequences that could not be placed in reading frame +1