

## Take home questions – Python Programming

- 1) As is the BLAST-Parser v3 script writes output to standard out. Modify the script by adding a nested 'with' loop to write the output to a file rather than standard out. Use 'sys.argv' to have the user provide the name of the output file.

The script uses a for loop to loop through the lines of the file. Replace the for loop with a while loop to accomplish the same goal. For this you will need the 'readline()' method that is associated with file objects.

- 2) The Fasta parser does not seem to take ambiguities in nucleotides sequences ('N') into account. Modify the script in a way that both nucleotide sequences with and without ambiguities are written to standard out. Note that multiple conditions can be strung together in an 'if' statement using 'and', 'or', or 'not'. Alternatively, 'elif' may provide a solution to the problem.

At this point, we are using the modulo operator ('%') to distinguish between Fasta header lines and sequences. Recall that string objects have a method associated with them called 'startswith()'. Rewrite the script using the 'startswith()' method to distinguish between the Fasta header and the sequence.