

Bioinformatics Programming – Final Assignment

- 1) Select a gene of your interest, and search its entry in GenBank.
- 2) Save the data in GenBank format (.gb)
- 3) Write a Python program that:
 - a. Loads the GenBank file from 2),
 - b. Runs a blastn search on it using the NCBIWWW module in Biopython.
 - c. Parses the results from the blast search and writes the 10 first aligned sequences to separate Fasta files.
- 4) Read chapter 17, sections 17.1 and 17.2. Use the techniques and Python code described there to generate primers for the 10 sequences obtained in the 3.c, using the program **primer3**.

Note 1: the assignment report should include print copies of the Python programs, the original sequence and obtained primers.

Note 2: Download the primer3 program for windows from the following page:
<http://fokker.wi.mit.edu/primer3/binary-distributions.html>