
Bioinformática 2019/2020

Exercise 5 – Searching for Similar Sequences in Databases

Student 1:

Number:

Student 2:

Number:

Submit a python file in Moodle with the completed functions. Write the remaining answers as comments in the code file.

Task 1 – Review and write the code

1. Revise the code from the slides and complete the methods for the `MyBlast.py` class.
2. In the function `hit_best_score` explain what is the criteria to untie extended hits with equal best score? Explain what is the rational for this criteria.
3. Describe the meaning for each of the parameters in the function `best_alignment`?
4. Write a test function for the query sequences in `query1.fasta` and `query2.fasta` that finds the most similar sequence in `seqBlast.txt` (use as identifier the number of the sequence in the file). Print the respective score of the best alignment.