Bioinformática 2019/2020

Exercise Aula 6 - Multiple Sequence Alignment

Student 1:	Number:
Student 2:	Number:

For the code exercises, submit a python file in moodle with the completed functions. The remaining answers submit as comments in the submitted .py file.

Task

- 1. Fill in the code in class MyAlign and MultipleAlignment with the code provided in the slides. Run the examples and indicate the results.
- 2. Write a method *ScoreColumn(self, charsCol)* to add to the *MultipleAlign* class that allows to calculate the score of each column in the alignment (charsCol is a list of characters from the column of the alignment that can be retrieved using the method column from the class MyAlign). The score is calculated using the Sum of Pairs (SP) approach, i.e. the score will be the sum of the scores of each pair of characters in the alignment. If two gaps are found in each pair then the score will be zero.
- 3. Using the existing methods, namely *ScoreColumn*, develop a new method called scoreSP(self, alignment) that returns the score of SP from a complete alignment.
- 4. For the 3 provided examples in *MultipleAlign* file indicate the sum of pais score (using *scoreSP*) for each alignment.