

# Algoritmos para Bioinformática / Bioinformática

## 2021/2022

### *Aula 9 – Multiple Sequence Alignment*

#### **Task 1 – Complete the code**

1. In the class *MyAlign* complete the function *Consensus*.
2. Test all the examples in each of the classes, except the *MultipleAlignment* class.

#### **Task 2 – Complete class *MultipleAlignment***

3. Write a method *ScoreColumn(self, charsCol)* to add to the *MultipleAlignment* 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.
4. Using the existing methods, namely *ScoreColumn*, develop a new method called *scoreSP(self, alignment)* that returns the score of SP from a complete alignment.
5. For the three provided sequence examples (s1, s2, s3) in *MultipleAlignment* file indicate the sum of pairs score (using *scoreSP*) for each alignment.