COMP 7295/8295 – Assignment 1

Due: 9/ 14/2017 (before class)

1. Write a Python function that generates random amino acid sequences. Recall that there are twenty amino acids, each of which is represented by a letter.
2. Write a Python function that implements a global alignment of two amino acid sequences. The algorithm is similar to the recursive edit distance. The difference is that in a global alignment, we want to find the maximum score between two sequences **x** and **y.** The scores of substituting an amino acid for another (including inserting/deleting an amino acid) is given by the BLOSUM matrix.

Turn in instruction:

- The name your solution file should be the same as your UID, plus a .py extension. For example, if your UID is jsmith (i.e. your email is jsmith@memphis.edu), then your solution file should be **jsmith.py**.

- In the file, put your full name, COMP 7295 or COMP 8295, and Assignment 1.

- Send your solution to the TA (Diem-Trang Pham, dpham2@memphis.edu) with the subject line "**COMP 7295 Assignment 1**".