CSCI 1020 - Spring 2019 Handout: Exam 2 Information

Introduction to Computer Science: Bioinformatics

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Saint Louis University Friday, 29 March 2019

Exam 2 Information

- The second exam will be on Friday, 5 April 2019, from 11:00–11:50am.
- The exam is closed book, however you may prepare in advance <u>the back of this page</u> with whatever notes you wish to place on it, and you may use this page during the exam. When the exam is over, turn in this sheet with the rest of your exam.
- We envision questions of the following form:
 - For either the longest-common subsequence or sequence alignment with gap/mismatch penalties, and for either the Needleman-Wunsch or Smith-Waterman algorithms, you should be able to:
 - * Given original sequences X and Y of relatively small size, produce the matrix of intermediate calculations used in dynamic programming
 - * Given such a matrix of intermediate calculations, reconstruct an alignment that achieves the optimal result
 - Given a Python representation of a tree, such as

to be able to produce a rendering of the tree, akin to what might be produced by our tree drawing algorithms from lab07/lab08.

Given a rendering of a tree, produce its Python representation by our conventions, such as

$$(5, (3, ('A', (), ()), ('B', (), ())), ('C', (), ()))$$

Given a matrix of pairwise distance measures, to simulate the clustering algorithms on a small example, whether using single linkage, complete linkage, or UPGMA distances.