

CS 663: Algorithms in Structural Molecular Biology

Assignment #1

Due in class on 1/23/2013

Name:

Problem 1

For representing and storing molecular data, a number of complex data structures are used in computational biology. These data structures can range from simple lists and heaps to complex trees and graphs. In addition, the data structures can be linear or contain loops to model different aspects in molecular biology. It is therefore important and essential for softwares to be able to detect loops and cycles in these data structures.

Given a link list of nodes (with each node containing a data field and a pointer to the next node in the list), derive a linear time, constant space algorithm to detect whether or not the list is circular, i.e. if the last node of the list points back to any previous node. The length of the list is not known and no assumptions can be made about the number of nodes in the list. You will be given partial credit if your algorithm is correct but not linear time or constant space.