CS 573: Graduate Algorithms, Fall 2008
Homework 2

Due at 11:59:59pm, Wednesday, October 1, 2008

- For this and all future homeworks, groups of up to three students may submit a single, common solution. Please neatly print (or typeset) the full name, NetID, and alias (if any) of every group member on the first page of your submission.
- We will use the following point breakdown to grade dynamic programming algorithms: 60% for a correct recurrence (including base cases), 20% for correct running time analysis of the memoized recurrence, 10% for correctly transforming the memoized recursion into an iterative algorithm.
- A greedy algorithm *must* be accompanied by a proof of correctness in order to receive *any* credit.

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1. (a) Let $X[1..m]$ and $Y[1..n]$ be two arbitrary arrays of numbers. A ***common supersequence*** of X and Y is another sequence that contains both X and Y as subsequences. Describe and analyze an efficient algorithm to compute the function $scs(X, Y)$, which gives the length of the *shortest* common supersequence of X and Y.

   (b) Call a sequence $X[1..n]$ of numbers ***oscillating*** if $X[i] < X[i+1]$ for all even i, and $X[i] > X[i+1]$ for all odd i. Describe and analyze an efficient algorithm to compute the function $los(X)$, which gives the length of the longest oscillating subsequence of an arbitrary array X of integers.

   (c) Call a sequence $X[1..n]$ of numbers ***accelerating*** if $2 \cdot X[i] < X[i-1] + X[i+1]$ for all i. Describe and analyze an efficient algorithm to compute the function $lxs(X)$, which gives the length of the longest accelerating subsequence of an arbitrary array X of integers.

2. A *palindrome* is a string that reads the same forwards and backwards, like `x`, `pop`, `noon`, `redivider`, or `amanaplanacatahamayakayamahatacanalpanama`. Any string can be broken into sequence of palindromes. For example, the string `bubbaseesabanana` ('Bubba sees a banana.') can be broken into palindromes in several different ways; for example:

   `bub + baseesab + anana`
   `b + u + bb + a + sees + aba + nan + a`
   `b + u + bb + a + sees + a + b + anana`
   `b + u + b + b + a + s + e + e + s + a + b + a + n + a + n + a`

   Describe and analyze an efficient algorithm to find the smallest number of palindromes that make up a given input string. For example, given the input string `bubbaseesabanana`, your algorithm would return the integer 3.

3. Describe and analyze an algorithm to solve the traveling salesman problem in $O(2^n \operatorname{poly}(n))$ time. Given an undirected n-vertex graph G with weighted edges, your algorithm should return the weight of the lightest Hamiltonian cycle in G, or ∞ if G has no Hamiltonian cycles. *[Hint: The obvious recursive algorithm takes $O(n!)$ time.]*

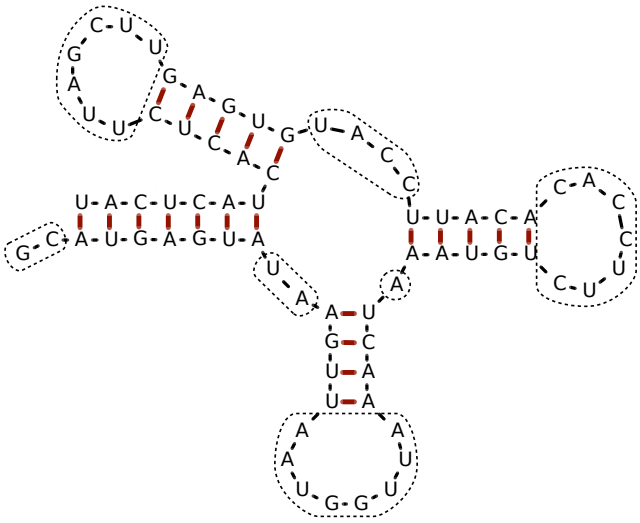
4. Ribonucleic acid (RNA) molecules are long chains of millions of nucleotides or *bases* of four different types: adenine (A), cytosine (C), guanine (G), and uracil (U). The *sequence* of an RNA molecule is a string $b[1..n]$, where each character $b[i] \in \{A, C, G, U\}$ corresponds to a base. In addition to the chemical bonds between adjacent bases in the sequence, hydrogen bonds can form between certain pairs of bases. The set of bonded base pairs is called the *secondary structure* of the RNA molecule.

   We say that two base pairs (i, j) and (i', j') with $i < j$ and $i' < j'$ ***overlap*** if $i < i' < j < j'$ or $i' < i < j' < j$. In practice, most base pairs are non-overlapping. Overlapping base pairs create so-called *pseudoknots* in the secondary structure, which are essential for some RNA functions, but are more difficult to predict.

   Suppose we want to predict the best possible secondary structure for a given RNA sequence. We will adopt a drastically simplified model of secondary structure:

   - Each base can be paired with at most one other base.
   - Only A-U pairs and C-G pairs can bond.
   - Pairs of the form $(i, i+1)$ and $(i, i+2)$ cannot bond.
   - Overlapping base pairs cannot bond.

   The last restriction allows us to visualize RNA secondary structure as a sort of fat tree.



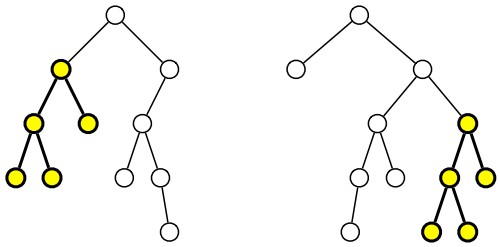
Example RNA secondary structure with 21 base pairs, indicated by heavy red lines.
Gaps are indicated by dotted curves. This structure has score $2^2 + 2^2 + 8^2 + 1^2 + 7^2 + 4^2 + 7^2 = 187$

   (a) Describe and analyze an algorithm that computes the maximum possible *number* of base pairs in a secondary structure for a given RNA sequence.

   (b) A *gap* in a secondary structure is a maximal substring of unpaired bases. Large gaps lead to chemical instabilities, so secondary structures with smaller gaps are more likely. To account for this preference, let's define the *score* of a secondary structure to be the sum of the *squares* of the gap lengths.[1] Describe and analyze an algorithm that computes the minimum possible score of a secondary structure for a given RNA sequence.

[1] This score function has absolutely no connection to reality; I just made it up. Real RNA structure prediction requires much more complicated scoring functions.

5. A *subtree* of a (rooted, ordered) binary tree T consists of a node and all its descendants. Design and analyze an efficient algorithm to compute the ***largest common subtree*** of two given binary trees T_1 and T_2; this is the largest subtree of T_1 that is isomorphic to a subtree in T_2. The contents of the nodes are irrelevant; we are only interested in matching the underlying combinatorial structure.



Two binary trees, with their largest common subtree emphasized

*6. ***[Extra credit]*** Let $D[1..n]$ be an array of digits, each an integer between 0 and 9. A ***digital subsequence*** of D is an sequence of positive integers composed in the usual way from disjoint substrings of D. For example, $3, 4, 5, 6, 23, 38, 62, 64, 83, 279$ is an increasing digital subsequence of the first several digits of π:

$$\boxed{3}, 1, \boxed{4}, 1, \boxed{5}, 9, \boxed{6}, \boxed{2,3}, 4, \boxed{3,8}, 4, \boxed{6,2}, \boxed{6,4}, 3, 3, \boxed{8,3}, \boxed{2,7,9}$$

The *length* of a digital subsequence is the number of integers it contains, *not* the number of digits; the previous example has length 10.

Describe and analyze an efficient algorithm to compute the longest increasing digital subsequence of D. *[Hint: Be careful about your computational assumptions. How long does it take to compare two k-digit numbers?]*