# Algorithms for Biological Sequence Analysis (Midterm \#2) 

Instructor: Kun-Mao Chao

TA: Yi-Ching Chen
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Problem $1 \mathbf{( 3 0 \% ) :}$ : In this problem, you are given a number sequence $A=\langle 8,3,5,7,9,6,8,5,9,6\rangle$.
(a) ( $\mathbf{1 0 \%} \mathbf{)}$ : Draw a left-skew decomposition for every prefix of A.
(b) (8\%): Use this example sequence to explain why the left-skew decomposition can be used to find the maximum-average segment ending at each index of A.
(c) (7\%): Use this example sequence to explain why the left-skew decompositions for all prefixes can be done in linear time.
(a) $\mathbf{5 \%}$ ): Draw a right-skew decomposition for every suffix of A.

Problem 2 (15\%): Given a number sequence $A=\left\langle a_{1}, a_{2}, \ldots, a_{n}\right\rangle$, design a linear-time algorithm for finding the nearest smaller element for every element of the sequence.

Problem 3 (10\%): Give an algorithm that solves the RMQ (Range Minima Query) problem in $O(n \log n)$-preprocessing time and $O(1)$-query time, where $n$ is the length of the number sequence. (Hint: For each index, compute the minima of the segments starting from it which are of lengths $1,2,2^{2}, 2^{3}, \ldots$ )

Problem 4 ( $\mathbf{1 5 \%}$ ): Let $X$ be an algorithm for solving the RMSQ (Range Maximum-Sum Segment Query) problem in $O(g(n))$-preprocessing time and $O(1)$-query time, where $n$ is the length of the number sequence. Show that $X$ can be used to solve the RMQ (Range Minima Query) problem for a number sequence of length $n$ in $O(g(n)+n)$ preprocessing time and $O(1)$-query time.

Problem 5 (30\%): The goal of the International HapMap Project is to develop a haplotype map of the human genome, the HapMap, which will describe the common patterns of human DNA sequence variation. (http://www.hapmap.org/abouthapmap.html)
(a) $\mathbf{( 1 0 \% ) : ~ D e f i n e ~ t h e ~ h a p l o t y p e ~ i n f e r e n c e ~ p r o b l e m ? ~}$
(b) (5\%): Give an Integer Quadratic Programming formulation for haplotype inference.
(d) (5\%): What are tag SNPs?
(e) (5\%): Use an example to show how to reduce the tag SNP problem to the minimum test set problem introduced in class.
(e) (5\%): Use an example to describe the idea of LD bins.

