

BENG 202 / CSE 282 Homework 2

Due: Feb 8, 2012 by the start of class

Problem 1 (12 points)

Codons are tri-nucleotide codes in protein-coding RNA sequences instructing the ribosome to either start/end translation or to insert a specific amino acid at the corresponding position on the protein. A codon alignment between two RNA sequences u and v is defined as an alignment that (a) maximizes the number of matching amino acids regardless of the codon used to represent each amino acid, (b) resets the alignment score to zero if either u or v encode for a start codon, (c) requires a new start codon in the same sequence after every stop codon and (d) does not allow for frame-shifting indels (i.e., of length not divisible by 3). Alignment scores are defined as +1 for matching amino acids and -1 for each mismatch, insertion or deletion. Devise an algorithm that computes a highest-scoring local codon alignment between two RNA sequences u and v . Give pseudo code describing your algorithm, the running time of your algorithm, and a concise argument justifying the running time and correctness of the algorithm.

Problems from Jones&Pevzner

- Problem 7.5 (10 points)
- Problem 7.6 (10 points)
- Problem 8.6 (8 points)
- Problem 8.10 (15 points)