

Algorithms in Structural Bioinformatics

Assignment 2 (I.Emiris)

announced 26/3/13. Deadline: Tue. 5/3/13

RNA Secondary structure

Find all optimal secondary structures of RNA sequence *CACGGUUAG* by Zuker's energy minimization, using initialization

$$j + 3 > i \Rightarrow V(i, j) = W(i, j) = \infty,$$

hairpin energy $h(i, j) = j - i + 5$, and stem function $s(i, j) = -3, 0$ and 3 , respectively, for Watson-Crick pairs, *GU* pairs, and all other pairs. You may ignore multiloops and bulges.

Show all backtrack paths leading to the minimum score and, for each, draw the secondary structure of the RNA sequence. How many matched pairs are there? How many unmatched nucleotides?

You may consult (updated) slide 1.dynprog.pdf, where the i, j range over columns and rows respectively. It is easier if you develop an implementation, e.g. in Matlab or Maple; if so, upload your code.