Technische Universität
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Exercise Sheet 6 zur Vorlesung Computational Biology (Part 2), WS 12/13

Hand In: *Until Monday, 21.01.2013, 10:00 am, email to* `wild@cs...` *or in lecture.*

Exercise 2013

2 + 4 Points

Let $s := s_1 s_2 \cdots s_n$ be an RNA sequence of length n, i. e. its primary structure is given. Assume that base pairs can be formed between Watson-Crick base pairs and $\mathsf{G}-\mathsf{U}$ wobble pairs. Moreover, hair pins must have a minimal length of one base.

a) Give a recurrence relation for the number of possible secondary structures for the given (fixed) primary structure s.

b) Now, consider a random sequence s were each base is chosen i. i. d. according to probabilities p_x for $x \in \{\mathsf{A}, \mathsf{C}, \mathsf{G}, \mathsf{U}\}$. In this model, the probability p for the event that bases s_i and s_j can form a pair is the same for all i and j.

   Determine precise *asymptotics* for the *expected* number of possible secondary structures for a random sequence of length n.

   If you cannot find a formula for general p, you may consider the special case $p = \frac{1}{4}$ for partial credit.

Happy New Year 2013!