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Exercise Sheet 11 for Combinatorial Algorithms, SS 13

Hand In: Until Monday, 15.07.2013, 12:00, box in the group's hallway or email to wild@cs.uni....

Problem 19 2 points

Prove Theorem 6.1 of [DFLS04], i.e., show that

$$\Pr[N \in n(1 \pm \varepsilon)] \rightarrow 1 \quad \text{as } n \rightarrow \infty,$$

where N is the random size of an object returned by $\mu C(x_n; n, \varepsilon)$.

Here, we briefly write $n(1 \pm \varepsilon)$ to mean the interval $(n(1 - \varepsilon), n(1 + \varepsilon)) \subset \mathbb{R}$.

Problem 20 2 + 1 + 2 points

Consider once again the class \mathcal{S} of RNA secondary structures, given by

$$S = \epsilon + \mathcal{Z}_* \times S + \mathcal{Z}_{(} \times S \times \mathcal{Z}_{)} \times S , \qquad (1)$$

and the Boltzmann sampler $\Gamma S(x)$ you built in Problem 18. In this exercise, we will tweak your sampler for efficiency.

- a) Check whether the Boltzmann model of RNA secondary structures fulfills the *Mean Value Condition* and the *Variance Condition* stated in equations (6.1) and (6.3) of [DFLS04]. What does Theorem 6.1 guarantee for your Boltzmann sampler?
- b) Determine the singular exponent $-\alpha$ for S(z) as defined in Section 6.2 of [DFLS04]. What does Theorem 6.3 of [DFLS04] guarantee about your Boltzmann sampler?
- c) Design a linear time approximate size Boltzmann sampler $\mu S(x; n, \varepsilon)$. Don't forget to prove your claims.

Extend your implementation from Problem 18 to incorporate this sampling algorithm. For simplicity, you may fix n=100 and compute all needed constants externally up front.

Use your sampler to draw 10 random RNA structures of size *exactly* 100. How many rejections did your sampler need until it found an object of correct size?

References

[DFLS04] Philippe Duchon, Philippe Flajolet, Guy Louchard, and Gilles Schaeffer. Boltzmann Samplers for the Random Generation of Combinatorial Structures. *Combinatorics, Probability and Computing*, 13(4-5):577–625, July 2004. doi:10.1017/S0963548304006315.