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## 11th Exercise Sheet for Kombinatorische Algorithmen, WS 14/15

Hand In: Until Monday, 02.02.2015, 12:00,

deliver or email to Raphael (reitzig@cs.uni-kl.de).

## Problem 20

2 points

2 + 1 + 2 points

Prove Theorem 6.1 by Duchon et al. [1], that is 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 write  $n(1 \pm \varepsilon)$  for short and mean the interval  $[n(1 - \varepsilon), n(1 + \varepsilon)] \subset \mathbb{R}$ .

## Problem 21

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 19. 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 [1, equations (6.1) and (6.3)].

What guarantees does Theorem 6.1 of the same article provide for your sampler?

b) Determine the singular exponent  $-\alpha$  for S(z) as defined in Section 6.2 [1].

What guarantees does Theorem 6.3 of the same article provide for your sampler?

c) Design a linear time approximate size Boltzmann sampler  $\mu S(x; n, \varepsilon)$ ; remember to prove your claims.

Extend your implementation from Problem to incorporate this sampling algorithm. For simplicity, you may fix n = 100 and precompute all necessary constants externally.

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

 Philippe Duchon et al. "Boltzmann Samplers for the Random Generation of Combinatorial Structures." English. In: *Combinatorics, Probability and Computing* 13.4-5 (July 2004), pp. 577–625. ISSN: 1469-2163. DOI: 10.1017/S0963548304006315.