

Advanced Algorithms in Bioinformatics (P4)

Sequence and Structure Analysis

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Sommersemester 2011

8. Exercise sheet, 16. June 2011

Discussion: 22. June 2011

Exercise 1.

Nussinov SCFG

- Formulate the inside and outside algorithm for the Nussinov SCFG.
- Show how to use your inside and outside variables to calculate the probability that positions i and j are base-paired, summed over all structures.

Exercise 2.

Covariance models

```
Ara.ven. GGUCGC..GUCAACAGUGUUUGAU.CGAAC
Unc.ner. UUACCGCUUCAACAGUGCUUGAACGGCAA
Gal.gal. UUUAUC..AGUGACAGCGUUCACU.AUAAA
Del.leu. UCGUUC..GUCCUCAGUGCAGGGC.AACAG
SS_cons <<<<<...<<<<<.....>>>>>.>>>>>
```

- Build a covariance model for the alignment of RNAs. Visualize it as a tree, like presented in the lecture.
- Analyze the runtime and memory consumption of the CYK for CM database search.

Exercise 3.

Context free RNA grammars

Consider the hairpin loop CFG from the lecture:

- Write derivations for $s_1 = \text{CAGGAAACUG}$ and $s_2 = \text{GCUGCAAAGC}$.
- Consider the complete language generated by the CFG from the lecture. Write a regular grammar that generates exactly the same language. Does this seem like a good idea?

Exercise 4.

CNF

Convert the production rule $W \rightarrow aWbWWWc$ (a, b, c terminal symbols) into Chomsky normal form. If the probability of the original production is p , show the probabilities for the productions in normal form.