

# Algorithms in Bioinformatics I, WS2006/7

## Assignment sheet # 8

Christian Rausch

December 4, 2006

To solve the following problems, please download:

<http://www-ab.informatik.uni-tuebingen.de/teaching/ws06/albi1/assign/java/java08.zip>

and modify the file `Nussinov.java`. Please use the methods supplied in `NussinovBase.java`. Please run the program `RunNussinov.java`.

### 1 Implementation of the fill stage of the Nussinov algorithm (3 points)

Please implement the fill stage of the Nussinov algorithm.

### 2 Implementation of the traceback stage of the Nussinov algorithm (4 points)

Please implement the traceback stage of the Nussinov algorithm, writing all base pairings to a string that then can be retrieved later using the *getSecondaryStructure* method.

### 3 Comparison of secondary structure predictions (3 points)

#### 3.1 Get familiar with the Vienna RNA Package (0.5 points)

Browse the web page of the Vienna RNA Package <http://www.tbi.univie.ac.at/RNA/>, download (source and Windows binaries available), install and try the program `RNAfold` (by I.L. Hofacker, W. Fontana, S. Bonhoeffer and P.F. Stadler). `RNAfold` is an implementation of a further development of Zuker's algorithm for RNA secondary structure prediction. Run the program on all input files present in the download file and report the result. Try also `RNAplot` which accepts a RNA secondary structure in bracket notation and produces a plot. [Note that `RNAfold` can also be used online at: <http://bioweb.pasteur.fr/seqanal/interfaces/rnafold.html>.]

#### 3.2 Bracket notation output by your program (2 points)

Modify your program so that it outputs the structure in bracket notation understandable for `RNAplot`.

#### 3.3 Compare your Nussinov implementation with `RNAfold` (0.5 points)

Run your program and `RNAfold` on all input files present in the download file. Draw each of the secondary structure predictions with the help of `RNAplot`. Compare the structure pairs and decide which algorithm returns the better prediction. Why? Optional exploration:

You may compare the predictions with the results of the original Zuker algorithm (the implementation is called `mfold`) and even with `mfold`'s successor `UNAFold` following this link: <http://www.bioinfo.rpi.edu/applications/mfold/>.

**Due by 10am, Monday, 11 Dec 2006**