

Nussinov: Problem Definition

Definition (Problem of RNA **non-crossing** Secondary Structure Prediction by Base Pair Maximization)

IN: RNA sequence S

OUT: a **non-crossing** RNA structure P of S that maximizes $|P|$ (= number of base pairs in P).

Remarks:

- We defined two variants of the problem. One with the additional requirement that structures are **non-crossing** and one without. Without this restriction the problem is NP-hard (at least for interesting scoring schemes) — with the restriction there will be an efficient algorithm for solving the problem.
- Maximizing base pairs will help to understand the more realistic case of minimizing energy.
- RNA structure prediction is often called *RNA folding* also we do not model the folding process but only predict the result.

Nussinov Algorithm — Matrix definition

Let S be an RNA sequence of length n .

The Nussinov Algorithm solves the problem of RNA non-crossing secondary structure prediction by base pair maximization with input S .

Definition (Nussinov Matrix)

The *Nussinov matrix* $N = (N_{ij})_{\substack{1 \leq i \leq n \\ i-1 \leq j \leq n}}$ of S is defined by

$$N_{ij} := \max \{ |P| \mid P \text{ is non-crossing RNA } ij\text{-substructure of } S \}$$

where we use:

Definition (RNA Substructure)

An RNA structure P of S is called *ij-substructure* of S iff $P \subseteq \{i, \dots, j\}^2$.

Nussinov algorithm: determines the maximal number of bonds that a structure P for a sequence S can have

Definition (Nussinov matrix)

Let S be an RNA sequence.

The Nussinov matrix $(N_{i,j})_{\substack{1 \leq i \leq |S| \\ i-1 \leq j \leq |S| \wedge j > 1}}$ is defined by

$$N_{i,j} = \max \left\{ |P| \mid \begin{array}{l} P \text{ is a nested structure} \\ \text{of the subsequence } S_i \dots S_j \end{array} \right\}$$

Nussinov Algorithm — Recursive computation of $N_{i,j}$

Init: (for $1 \leq i \leq n$)

$$N_{ii} = 0 \text{ and } N_{i,i-1} = 0$$

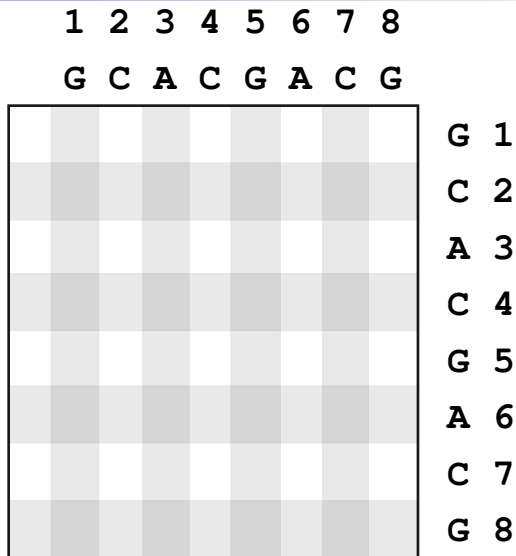
Recursion: (for $1 \leq i < j \leq n$)

$$N_{ij} = \max \left\{ \begin{array}{l} N_{ij-1} \\ \max_{\substack{S_k, S_j \text{ complementary} \\ i \leq k < j}} N_{ik-1} + N_{k+1j-1} + 1 \end{array} \right.$$

Remarks:

- case 2 of recursion covers base pair (i, j) for $k = i$; then: N_{ik-1} (initialized with 0!) is max. number of base pairs in empty sequence.
- $S_{1,n}$ is the maximal $|P|$ of any P of S .
- Recursion furnishes a DP-Algorithm for computing the Nussinov matrix (including $S_{1,n}$) in $O(n^3)$ time and $O(n^2)$ space.
- How to restrict loop length?
- What happens without restriction non-crossing?

Nussinov Algorithm — Example



Note: example with minimal loop length 0.

Nussinov Algorithm — Example

	1	2	3	4	5	6	7	8	
	G	C	A	C	G	A	C	G	
0	0								G 1
	0	0							C 2
		0	0						A 3
			0	0					C 4
				0	0				G 5
					0	0			A 6
						0	0		C 7
							0	0	G 8

Note: example with minimal loop length 0.

Nussinov Algorithm — Example

	1	2	3	4	5	6	7	8	
	G	C	A	C	G	A	C	G	
0	0	1	1	1	2	2	2	3	G 1
	0	0	0	0	1	1	1	2	C 2
		0	0	0	1	1	1	2	A 3
			0	0	1	1	1	2	C 4
				0	0	0	1	1	G 5
					0	0	0	1	A 6
						0	0	1	C 7
							0	0	G 8

Note: example with minimal loop length 0.

Nussinov Algorithm — Traceback

Determine one nc RNA structure P with maximal $|P|$.

pre: Nussinov matrix N of S :

	1	2	3	4	5	6	7	8	
	G	C	A	C	G	A	C	G	
0	0	1	1	1	2	2	2	3	G 1
	0	0	0	0	1	1	1	2	C 2
		0	0	0	1	1	1	2	A 3
			0	0	1	1	1	2	C 4
				0	0	0	1	1	G 5
					0	0	0	1	A 6
						0	0	1	C 7
							0	0	G 8

Idea:

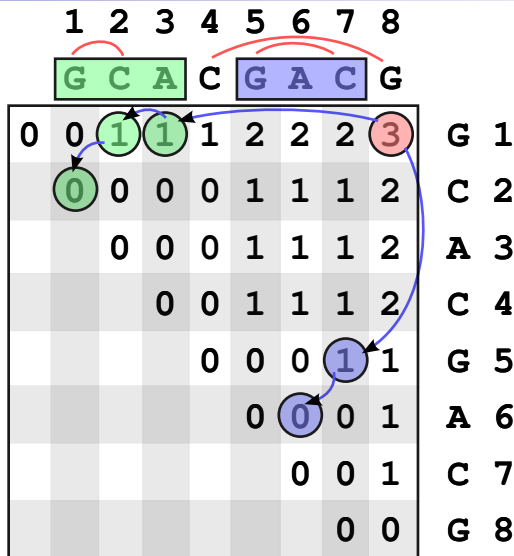
- start with entry at upper right corner N_{1n}
- determine recursion case (and the entries in N) that yield maximum for this entry
- trace back the entries where we recursed to

Nussinov Algorithm — Traceback Example

	1	2	3	4	5	6	7	8	
	G	C	A	C	G	A	C	G	
0	0	1	1	1	2	2	2	3	G 1
	0	0	0	0	1	1	1	2	C 2
		0	0	0	1	1	1	2	A 3
			0	0	1	1	1	2	C 4
				0	0	0	1	1	G 5
					0	0	0	1	A 6
						0	0	1	C 7
							0	0	G 8

Recall: example with minimal loop length 0 and without G-U pairing.

Nussinov Algorithm — Traceback Example



Recall: example with minimal loop length 0 and without G-U pairing.

Nussinov Algorithm — Traceback Pseudo-Code

CALL: traceback(1, n)

Procedure traceback(i, j)

if $j \leq i$ **then**

return

else if $N_{ij} = N_{ij-1}$ **then**

 traceback($i, j - 1$);

return

else

for all $k : i \leq k < j$, S_k and S_j complementary **do**

if $N_{ij} = N_{ik-1} + N_{k+1j-1} + 1$ **then**

 print (k, j);

 traceback($i, k - 1$); traceback($k + 1, j - 1$);

return

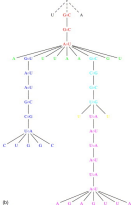
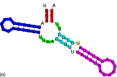
end if

end for

end if

Remarks

- Complexity of trace-back $O(n^2)$ time
- How to get all optimal nc structures?
- How to trace-back non-recursively?
- How to output / represent structures?
 - Dot-bracket
 - 2D-layout
 - Tree-like
- Why doesn't it work for crossing structure?



Limitations of the Nussinov Algorithm

- Base pair maximization does not yield biologically relevant structures:
 - no stacking of base pairs considered
 - loop sizes not distinguished
 - no special scoring of multi-loops
- only one structure predicted
 - base pair maximization can not differentiate structures sufficiently well: possibly many optima
 - no sub-optimal solutions
- crossing structures cannot be predicted

However:

- shows pattern of RNA structure prediction by DP (simple+instructive)
- energy minimization (Zuker) will have similar algorithmic structure
- “only one solution”-problem can be overcome (suboptimal: Wuchty)
- prediction of (restricted) crossing structure can be seen as extension

Disadvantages of Nussinov

Nussinov doesn't determine biologically relevant structures since:

- there are several possibilities to form base pairs, where Nussinov finds only one:

$A-U$ versus $G-C$

- Stacking of base pairs not considered \Rightarrow difference in structure and stability of helices

$G-C$ and $G-C$
 $C-G$ $G-C$

- size of internal loops not considered

unstable



stable



unstable

