# Partition function for circular RNA and Application

Ronny Lorenz ronny@bioinf.uni-leipzig.de

Department of Bioinformatics University of Leipzig

October 30, 2006



- Partition function for linear RNAs
  - Structure decomposition

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- 3 Application
  - Occurence of circular RNAs
  - Metastable Structures

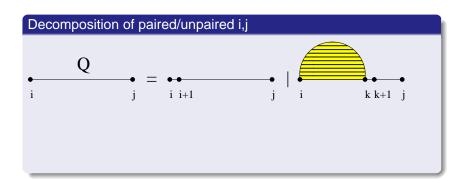
- let S be the set of all possible secondary structures for a given RNA sequence
- each  $s \in S$  is associated with a free energy  $G_s$

### The partition function Q for a given sequence

$$Q = \sum_{S \in S} e^{\frac{-G_S}{RT}}$$
 (1)

- i and j do not pair
- i and j form a hairpin loop, with closing pair [i,j],
- there exist two positions k,l with i < k < l < j so that the subsequence i,j forms an interior loop with closing pairs i,j and k,l
- i and j are the closing pair of a multiloop

dynamic programming approach, that calculates the partition function for all subsequences x[i,j] and ends with the partition function for the whole sequence...



## Decomposition of paired/unpaired i,j

$$\begin{array}{c}
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i \\
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\end{array} = \underbrace{i_{i+1}}_{j} | \underbrace{i_{k+1}}_{j} |$$

$$Q_{i,j} = 1 + \sum_{1 < k < j} Q_{i,k}^b \cdot Q_{k+1,j}$$
 (2)

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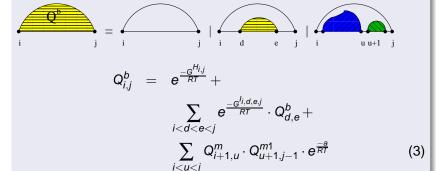
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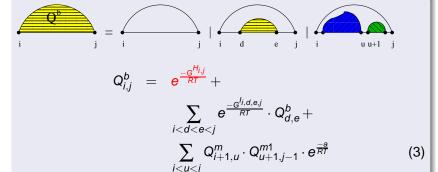
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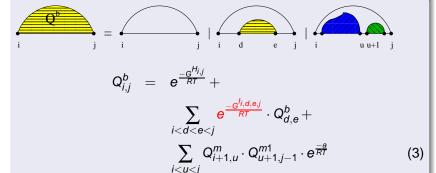
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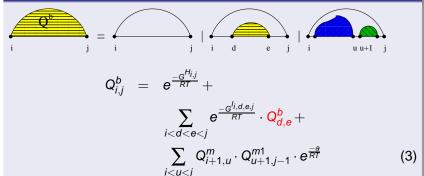
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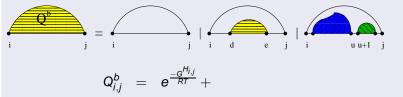






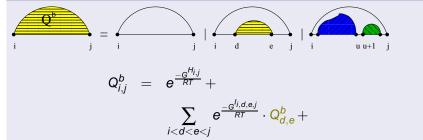




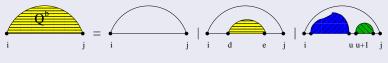


$$Q_{i,j}^{O} = e^{\frac{-RT}{RT}} + \sum_{i < d < e < j} e^{\frac{-G^{l_{i,d,e,j}}}{RT}} \cdot Q_{d,e}^{b} + \sum_{i < u < j} Q_{i+1,u}^{m} \cdot Q_{u+1,j-1}^{m1} \cdot e^{\frac{-a}{RT}}$$

$$(3)$$



$$\sum_{i < u < j} Q_{i+1,u}^{m} \cdot Q_{u+1,j-1}^{m1} \cdot e^{\frac{-a}{RT}}$$
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$$Q_{i,j}^{b} = e^{\frac{-G^{H_{i,j}}}{RT}} + \sum_{i < d < e < j} e^{\frac{-G^{I_{i,d,e,j}}}{RT}} \cdot Q_{d,e}^{b} + \sum_{i < u < j} Q_{i+1,u}^{m} \cdot Q_{u+1,j-1}^{m1} \cdot e^{\frac{-a}{RT}}$$
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$$Q_{i,j}^{m} = Q_{i,j-1}^{m} \cdot e^{\frac{-c}{RT}} + \sum_{i < u < j} e^{\frac{-(u-i-1) \cdot c - b}{RT}} \cdot Q_{u+1,j}^{b} + \sum_{i < u < j} Q_{i,u}^{m} \cdot Q_{u+1,j}^{b} \cdot e^{\frac{-b}{RT}}$$

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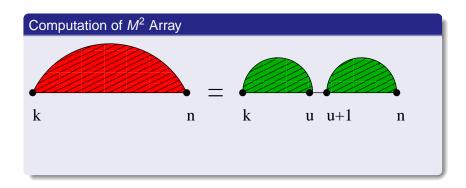
• computing sum of weighted energies for all loops that contain bases  $x_n$  and  $x_1$ 

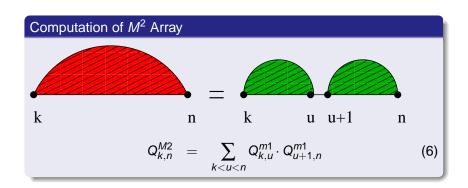
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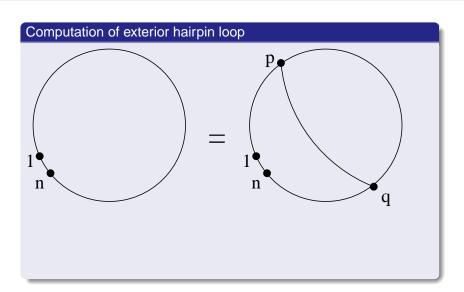
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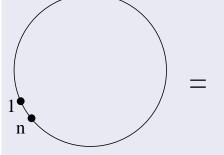
- computing sum of weighted energies for all loops that contain bases  $x_n$  and  $x_1$
- leads to the computation of so called "exterior loops"

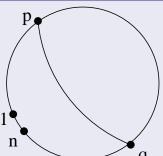




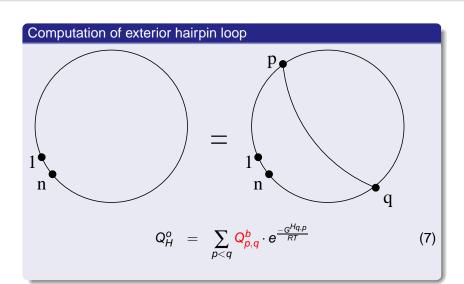


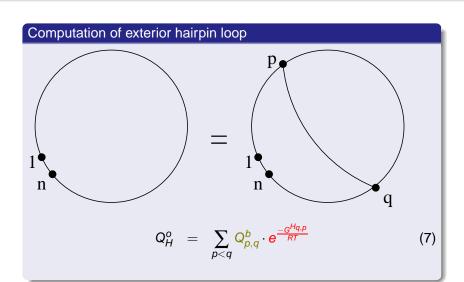
# Computation of exterior hairpin loop

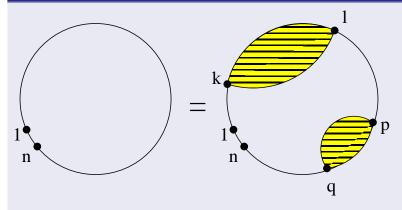


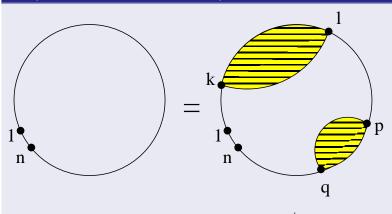


$$Q_{H}^{o} = \sum_{p < q} Q_{p,q}^{b} \cdot e^{\frac{-G^{Hq,p}}{RT}}$$
 (7)

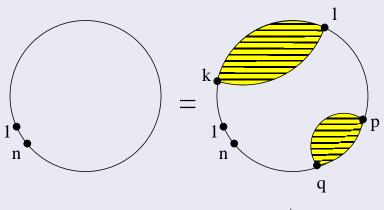






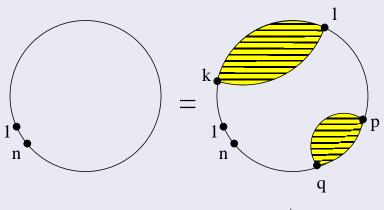


$$Q_{l}^{o} = \sum_{k < l < p < q} Q_{k,l}^{b} \cdot Q_{p,q}^{b} \cdot e^{\frac{-G^{l_{k,l,p,q}}}{RT}}$$
(8)

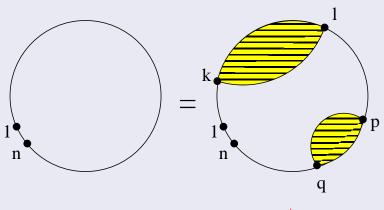


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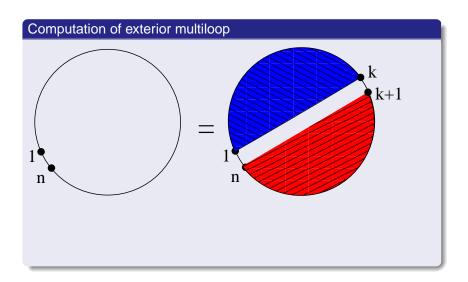


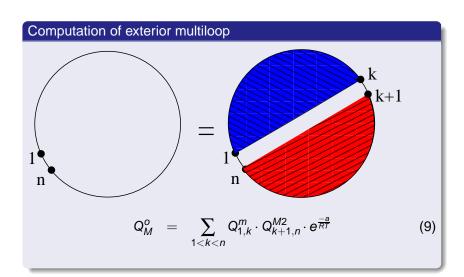


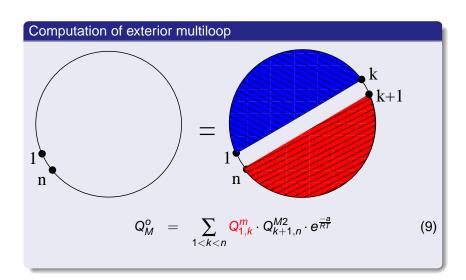
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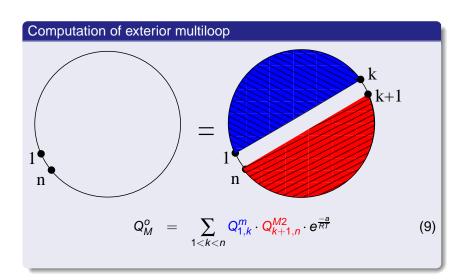


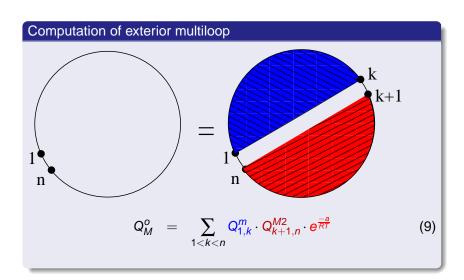
$$Q_{I}^{o} = \sum_{k < I < p < q} Q_{k,I}^{b} \cdot Q_{p,q}^{b} \cdot \mathbf{e}^{\frac{-G^{lk,I,p,q}}{RT}}$$
(8)











#### Partition function for circular case:

$$Q^{o} = Q_{H}^{o} + Q_{I}^{o} + Q_{M}^{o}$$
 (10)

This is the step where i am actually in my diploma thesis

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equations for base pairing probability matrix

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- equations for base pairing probability matrix
- way of backtracking to obtain secondary structures

Most known RNAs are linear and circular RNAs are not found very often
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Viroids and satellite RNAs (sizes arround 300-400 nt)

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In almost all cases, circular RNAs code not for any mRNA but for their own structure

finding metastable structure states

- finding metastable structure states
- better prediction of circular RNA structures

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- other things I did not have thought about yet

Decurence of circular RNAs Metastable Structures

Thank you for your attention