

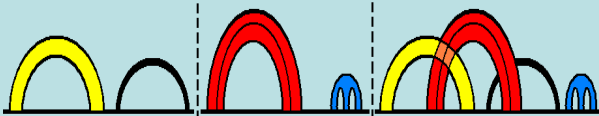


Hierarchical Model for Pseudoknotted RNA Secondary Structure Prediction

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PROBLEM ?

- ▶ develop an efficient algorithm for predicting an **MFE pseudoknotted (PK) secondary structure (SS)**, given a PK-free structure

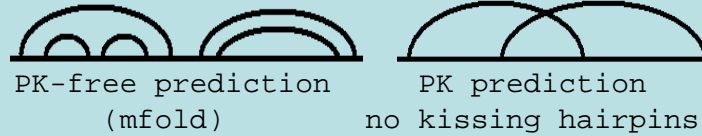


G + **G'** = **R**
 given PK-free $O(n^3)$ added PK-free $O(n^3)$ result bi-sec. $O(n^3)$

- ▶ calculate the **MFE** structure, **R**, for a given sequence s.t. **R**:
 - » contains **G**
 - » has density ≤ 2
 - » **R - G** is PK-free

MOTIVATION

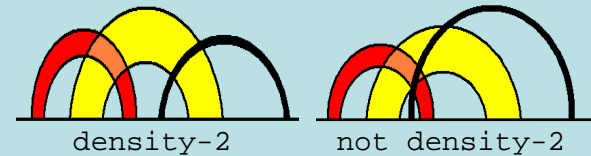
- ▶ SS prediction is key in determining the **function** of RNA molecules
- ▶ costly to find SS experimentally, so **computational methods** preferred
 - » Zuker and Stiegler - $O(n^3)$
 - » Dirks and Pierce - $O(n^5)$



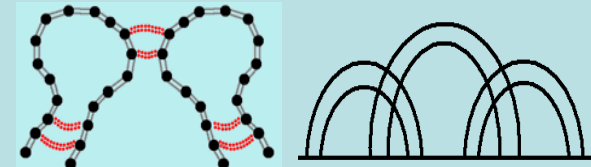
- ▶ many algorithms exist for PK-free
- ▶ algorithms exist for PK but are **costly or restrictive**
- ▶ **hierarchical folding** view:
 - » first folds into a PK-free SS
 - » next folds into a more complex structure (possibly including PK)

ALGORITHM $f(x)$

- ▶ uses several **recurrences** that handle cases relating to PK
- ▶ overall complexity $O(n^3)$
- ▶ predicts **density-2** SS



- ▶ predicts **kissing hairpins**



- ▶ because of hierarchical folding, **R may not be MFE** structure for the sequence

WORK IN PROGRESS

- ▶ **implementation** using Algebraic Dynamic Programming by Giegerich and Meyer [2]
 - » DP algorithm divided into two phases: recognition and evaluation
 - » can more easily change the types of structures allowed and how they are scored



[1] Y.S. Zhao. *Efficient algorithm for RNA pseudoknotted secondary structure prediction given a pseudoknot free structure*. 2005. http://www.cs.ubc.ca/grads/resources/thesis/Nov05/Yinglei_Zhao.pdf

[2] R. Giegerich and C. Meyer. *Algebraic Dynamic Programming. Algebraic Methodology And Software Technology*, pages 349-364. LNCS 2422, 2002, © Springer-Verlag.