

Kinwalker - Kinetic Backtracking of RNA folding

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1 Introduction

2 Algorithm

- Setup
- Extending the Structure
- Saddle Height

3 Results

- Toy problem
- E. coli Phenylalanin
- E. coli Tryptophane
- SV11
- Hok

Essential components in simulating RNA folding:

Select a set of states

Model state transitions

Main issue: How to calculate energy barriers between states.

Calculate the suboptimal structures

For $1 \leq i \leq j \leq n$ consider as states the lowest energy structures on a subsequence (i,j) given that bases i and j pair (extremes).

Order the states

Rank extremes by

1. diagonal
2. distance from edge of matrix
3. 5' before 3'

Algorithm

saddleheight = 0

Front F = initial structure

while($F \neq mfE$)

 increment *saddleheight*

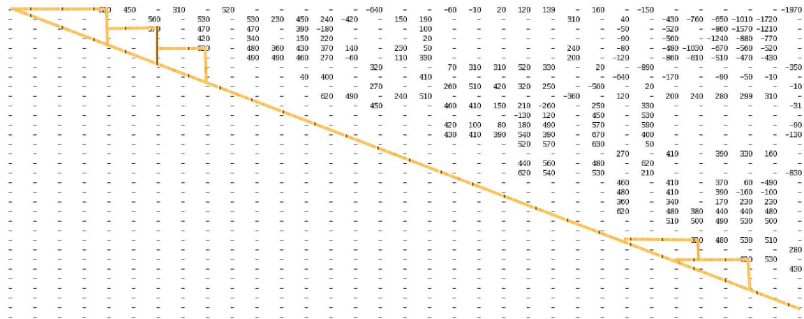
 for x in extremes

 calculate saddle point S between x and F

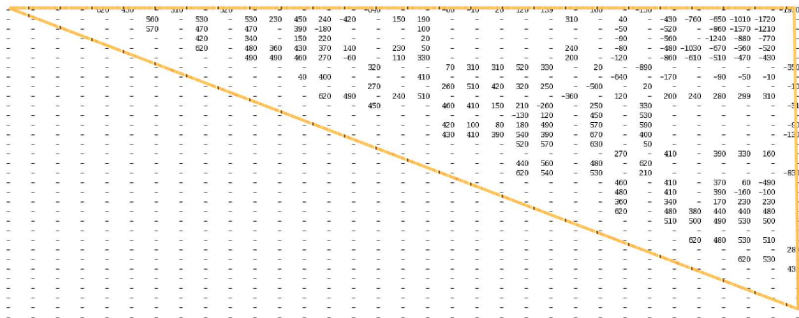
if($E(S) - E(F) < \textit{saddleheight}$)

 extend F by x

Extend Front



Final Front



Conflict

A substructure (i,j) determines how the bases in that subsequence pair. Once (i,j) is part of the front, and a pair (k,l) overlapping with (i,j) is added, they may demand incompatible base pairs in the overlapping region.

Conflict Resolution

1. Add only those basepairs of a conflicting substructure that don't conflict with the current structure.
2. Replace further base pairs if it improves energy.

Saddle Height

To go from conformation A to B, there are $(A\Delta B)!$ direct paths.

The best path does not have to be direct.

The saddle height is the highest energy of the lowest path:

$$S = \min_{P: A \rightarrow B} \max_{x \in P} E(x)$$

Heuristic for Saddle Points:Morgan-Higgs(1998)

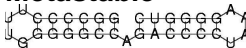
1. Rank the elements in $B \setminus A$ by conflict
2. For each x in $B \setminus A$
 - i) Remove the base pairs in A that conflict with x
 - ii) Add x
 - iii) Add all other elements in $B \setminus A$ that can be added now
 - iv) Record the energies of the traversed states
3. Take the highest recorded energy as saddle energy

Toy problem

MfE



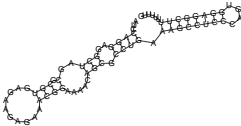
Metastable



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E. coli Phenylalanin

MfE

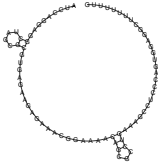


Metastable



Folding Trajectory

State 1



State 2



State 3



State 4



State 5

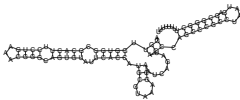


State 6

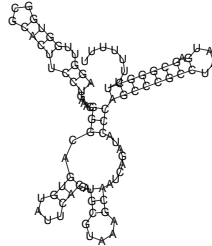


E. coli Tryptophane

MfE



Metastable



Folding Trajectory

State 1



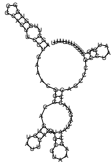
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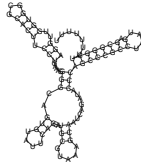
State 3



State 4



State 5

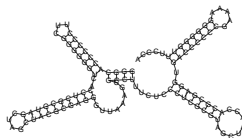


SV11

MfE



Metastable



Folding Trajectory

State 1



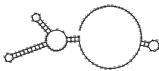
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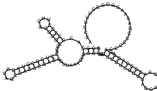
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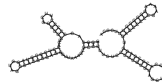
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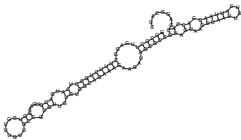
State 5



State 6

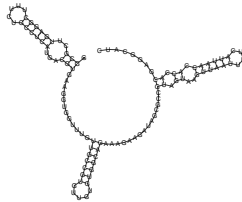


MfE



HOK

Metastable



Folding Trajectory I

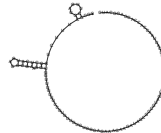
State 1



State 2



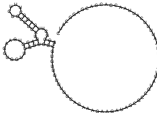
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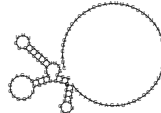
State 4



State 5

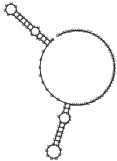


State 6

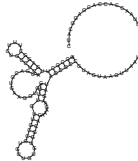


Folding Trajectory II

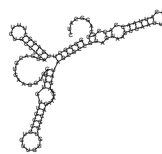
State 7



State 8



State 9



THANK YOU!

Caro Thurner, Christoph Flamm, Peter Stadler