

A Combinatorial Framework for Designing (Pseudoknotted) RNA Algorithms

Yann Ponty Cédric Saule

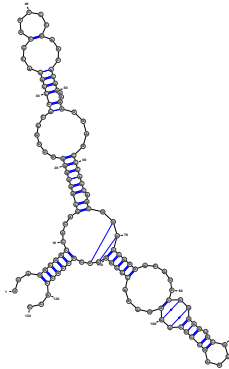
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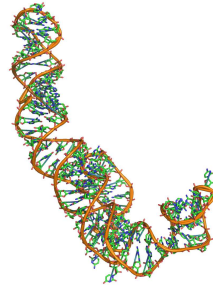
September 5, 2011

```
UUAGGCGGCCACAGC
GGUGGGGUUGCCUCC
CGUACCAUCCCGAA
CACGGAAGAUAGCC
CACCAGCGUCCGGG
GAGUACUGGAGUGCG
CGAGCCUCUGGGAAA
CCCGGUUCGCCGCCA
CC
```

Primary structure



Secondary structure
(Matching)



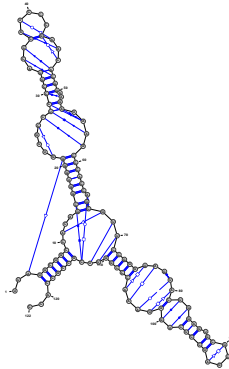
Tertiary structure

Source: 5s rRNA (PDBID: 1K73:B)

Bottom-up approach to molecular biology

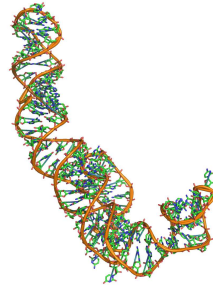
Understand and predict how RNAs fold to decipher their function(s).

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Secondary⁺ structure
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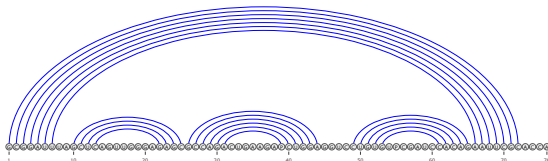
Bottom-up approach to molecular biology

Understand and predict how RNAs fold to decipher their function(s).

Input: RNA sequence ω

Definition (Minimum Free-Energy (MFE) Folding Problem)

Find a partial matching s^* of positions from ω that min(max)-imizes a free-energy function E_{ω, s^*} within some restricted class of matching.



Secondary Structure (Non-crossing) + Additive energies: Easy!

Optimal substructure \Rightarrow Dynamic Programming (DP)

- (Weighted) base-pairs maximization:

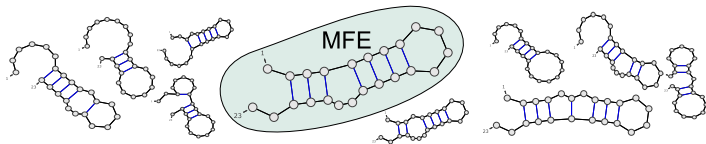
$$\Theta(n^3)$$

[Nussinov and Jacobson, 1980]

- Nearest-neighbor model:

$$\Theta(n^4)/\Theta(n^3)$$

[Zuker and Stiegler, 1981]

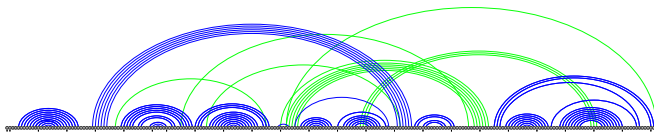


- Energy functions are not **ideally accurate**
- MFE structure might be **isolated**

⇒ Recent thermodynamic studies postulate a **Boltzmann equilibrium**, i.e. admissible conformations exist in a **probability distribution** [McCaskill, 1990]

$$\mathbb{P}(s) = \frac{e^{\frac{-E_s}{RT}}}{\mathcal{Z}} \quad \text{where} \quad \mathcal{Z} = \sum_{s' \in S} e^{\frac{-E_{s'}}{RT}} \quad (\text{Partition function})$$

Observables can be derived, such that the base-pairing prob. [McCaskill, 1990], centroid-structure [Ding and Lawrence, 2003], likelihood of multi-stable RNAs [Voss *et al.*, 2004], confidence in prediction [Mathews, 2004], **moments of the free-energy distribution** [Miklós *et al.*, 2005]. . .



Any matching (crossing): Harder for realistic energy models

- BP maximization: $O(n^3)$ (Max. Weighted Matching)
[Tabaska *et al.*, 1998]
- Nearest-neighbor: NP-complete
[Akutsu, 2000, Lyngsø and Pedersen, 2000]

In practice:

- Heuristics/local search
- Restricted conformational spaces solved exactly (DP) in polynomial time
[Rivas and Eddy, 1999, Lyngsø and Pedersen, 2000, Dirks and Pierce, 2003, Reeder and Giegerich, 2004, Cao and Chen, 2006, Cao and Chen, 2009, Chen *et al.*, 2009, Cao and Chen, 2009, Huang *et al.*, 2009, Theis *et al.*, 2010, Reidys *et al.*, 2011].

Very few of them allow for a transposition to ensemble based approach!

Folding RNAs including pseudoknots remains a challenge:

- Incorporate incoming thermodynamic parameters
- Capture complex topological aspects
- Optimize expressivity/computational complexity tradeoff
- Address ensemble-related questions
- Tackle other problems (RNA-RNA interaction)

Yet developing new DP algorithms is tedious and error-prone:

- Lack of modularity
- Tedious proofs for unambiguity/correctness
- Hard to connect DP equation (product) to decomposition (source)

CS geek: Underlying object to define meta-algorithms/proofs?

Existing abstractions for Dynamic Programming algorithms:

- Giegerich *et (many!) al*: Algebraic Dynamic Programming
 - Folding = Parsing: Based on grammar/algebra pair
 - + Automated (efficient!) code generation
 - + Partially automated (heuristic) ambiguity check
 - + High level: No indices. . .
 - Hacky for context-dependent features (Addressed by Bellmann's GAP?)
- Lefebvre *et al*: Multi-tape attributed grammars
- Roytberg and Finkelstein: Forward hypergraphs

Existing abstractions for Dynamic Programming algorithms:

- Giegerich *et (many!) al*: Algebraic Dynamic Programming
- Lefebvre *et al*: Multi-tape attributed grammars
 - Context-free grammar, coupled with attributes system
 - + Mixed algebras
 - Synchronized multiple tapes for PKs
⇒ Performance degradation...
- Roytberg and Finkelstein: Forward hypergraphs

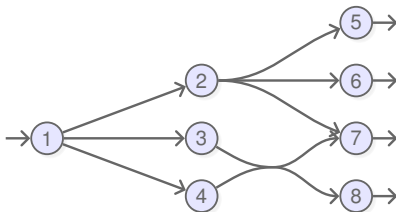
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- Roytberg and Finkelstein: Forward hypergraphs
 - Conformations bijectively associated with hyperpaths (\sim Traces)
 - + Highly expressive
 - Low-level: Explicit indices manipulation

Main Contribution

Considering families of hypergraphs as combinatorial classes will

- Simplify algorithms
- Ease proving their correctness
- Help develop new applications



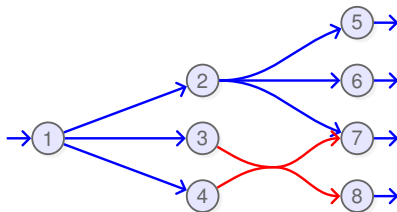
Hypergraphs generalize directed graphs to arcs of arbitrary in/out degrees.

Definition (Hypergraph)

A directed hypergraph \mathcal{H} is a couple (V, E) such that:

- V is a set of vertices
- E is a set of hyperarcs $e = (t(e) \rightarrow h(e))$ such that $t(e), h(e) \subset V$

Forward hypergraphs, or F-graphs, are hypergraphs whose arcs have ingoing degree exactly 1.



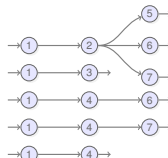
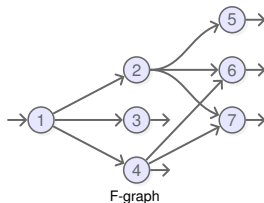
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All F-paths starting from vertex 1

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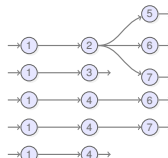
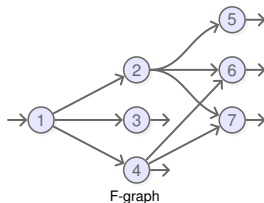
A **F-path** is a tree having root $s \in V$, whose children are F-paths built from the **outgoing vertices** of some arc $e = (s \rightarrow t) \in E$.

Remark: Vertices of out degree 0 ($t = \emptyset$) provide an elegant terminal case.

F-graph is **independent** iff each F-path sees at most once each arc.

A numerical **feature fonction** $\alpha : E \rightarrow \mathbb{R}$ assigns a value to each arc:

- Weight of a path is **the product** of its arcs' values
- Score of a path is **the sum** of its arcs' values



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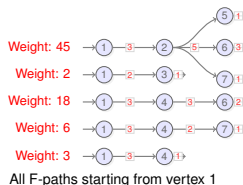
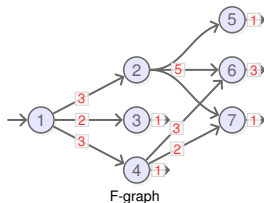
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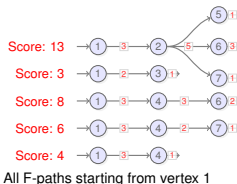
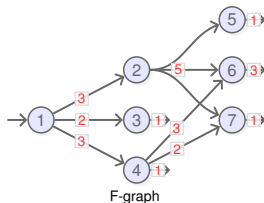
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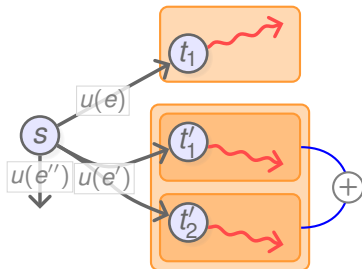
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$\mathcal{H} = (v_0, V, E, \alpha)$: acyclic F-graph v_0 : Init. node α : feature function

$$m_s = \min_{p \in \mathcal{P}_s} \text{Score}(s)$$

$$= \min_{e=(s \rightarrow t)} \left(u(e) + \sum_{u \in t} m_u \right)$$

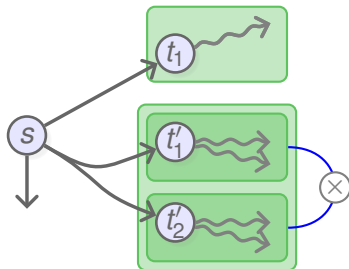


Problem	Recurrence	Time/space (DP)
Min. score	$m_s = \min_{e=(s \rightarrow t)} \left(u(e) + \sum_{u \in t} m_u \right)$	$\Theta(E + V)/\Theta(V)$
Num. paths	$n_s = \sum_{(s \rightarrow t)} \prod_{u \in t} n_u$	$\Theta(E + V)/\Theta(V)$
Total weight	$w_s = \sum_{e=(s \rightarrow t)} u(e) \cdot \prod_{s' \in t} w_{s'}$	$\Theta(E + V)/\Theta(V)$

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$$n_s = |\mathcal{P}_s| = \sum_{p \in \mathcal{P}_s} 1$$

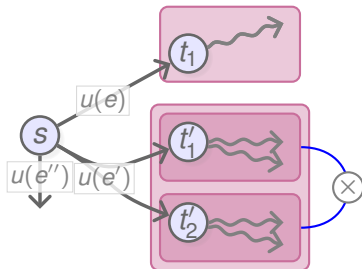
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$$\begin{aligned} w_s &= \sum_{p \in \mathcal{P}_s} \text{Weight}(s) \\ &= \sum_{e=(s \rightarrow t)} u(e) \cdot \prod_{s' \in t} w_{s'} \end{aligned}$$



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Assume a weighted (Boltzmann) probability distribution on F-paths \mathcal{P} :

$$\mathbb{P}(p) = \prod_{e \in p} \alpha(e) / w_{v_0}$$

Problem	Algorithm	Time/space (DP)
Random gen.	Compute w_s ; Starting with $s \leftarrow v_0$, pick an arc $s \rightarrow (t_1, t_2, \dots)$ w.p. $\prod w_{t_i} / w_s$ and recurse on each t_i .	$\Theta(E + V)/\Theta(V)$
Arcs prob.	$p_e = \frac{b_{t(e)} \cdot \prod_{s' \in h(e)} w_{s'}}{w_{v_0}}$ $b_s = (1 +) \sum_{s' \rightarrow (t_1 \dots s \dots)} \alpha(e') b_{s'} \prod_{t_i} w_{t_i}$	$\frac{\Theta(E + V + \sum h(e) ^2)}{\Theta(V)}$

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Given an RNA sequence ω and an energy function E , assume one has:

- **Acyclic hypergraph** \mathcal{H} , whose F-paths are in bijection with the targeted (pseudoknotted) conformations
- **Feature function** α which returns, for each F-path p , the energy $E_{\omega,s}$ of its conformation s_p .

Application		Hypergraph Algorithm	Arguments
MFE folding	\Leftrightarrow	Minimum score	(\mathcal{H}, α)
Partition function	\Leftrightarrow	Total weight	$(\mathcal{H}, e^{-\alpha/RT})$
Statistical sampling	\Leftrightarrow	Random generation	$(\mathcal{H}, e^{-\alpha/RT})$
BP probabilities (dot-plot)	\Leftrightarrow	Arcs prob.	$(\mathcal{H}, e^{-\alpha/RT})$

Message #1

Dynamic programming equations for ensemble applications are by-products of an underlying combinatorial decomposition (\Rightarrow Family of hypergraphs).

How to design such hypergraphs/energy function?

You do it yourself! But combinatorics can help. . .

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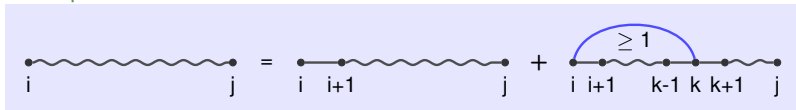
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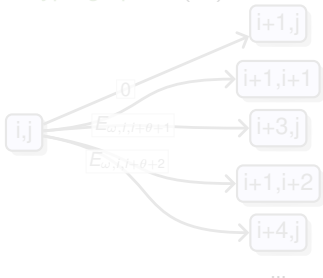
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Example: Base-pairs maximization (Nussinov)

Decomposition:



As an Hypergraph: $\Theta(n^2)$ vertices, $\Theta(n^3)$ arcs ($n = |\omega|$).



Initial vertex

Initial vertex

Terminal vertices

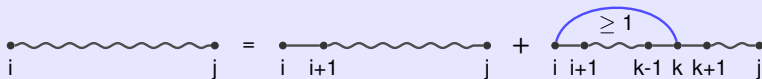
Terminal vertices

$$E_{\omega, i, j} = \begin{cases} 1 & \text{If } \omega_i \text{ base-pairs with } \omega_j \\ +\infty & \text{Otherwise} \end{cases}$$

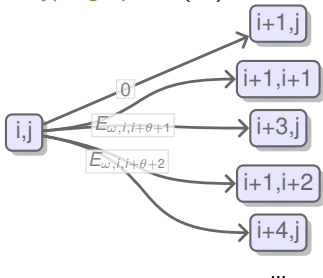
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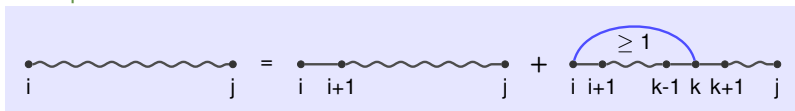
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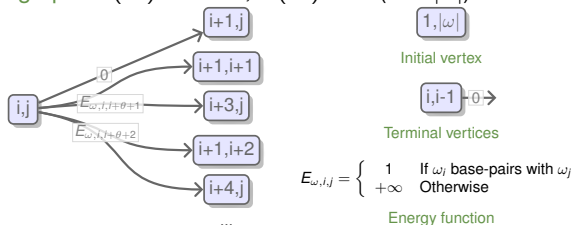
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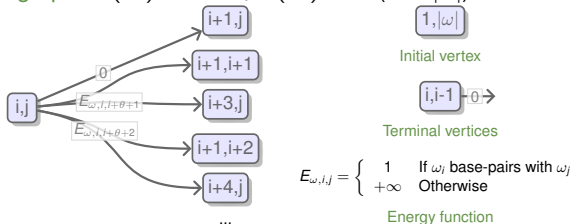


Before applying generic ensemble algorithms, one needs to prove:

- Bijection between F-paths and secondary structures of length n .
Halve the burden through **generating functions** (cf proceedings).
- Free-energy is reflected by weight/score.

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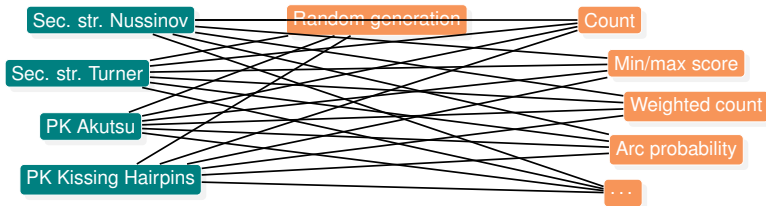
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Application	Algorithm	Feature fun.	Time/Space
Energy minimization	Minimal weight	E	$O(n^3)/O(n^2)$
Partition function	Weighted count	$e^{\frac{-E}{RT}}$	$O(n^3)/O(n^2)$
BP prob.	Arc-traversal prob.	$e^{\frac{-E}{RT}}$	$O(n^3)/O(n^2)$
Stat. sampling (k-samples)	Random gen.	$e^{\frac{-E}{RT}}$	$O(n^3 + kn \log n)$ $O(n^2)$

Message #2 (cf ADP)

Applications of DP could (and should) be detached from the equation, and be expressed at an abstract – combinatorial – level.

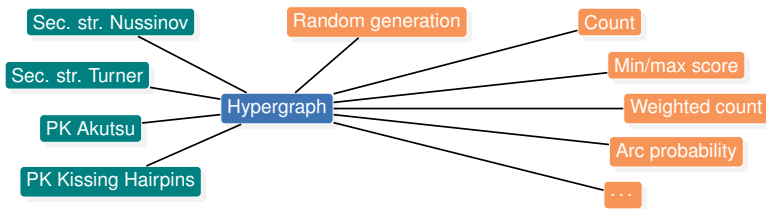


Credits: Roytberg and Finkelstein for Hypergraph DP in Bioinformatics, L. Hwang for algebraic hypergraph DP, R. Giegerich for ADP...

Let us extend applications of DP...

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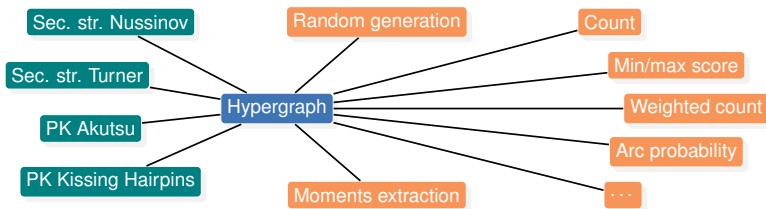


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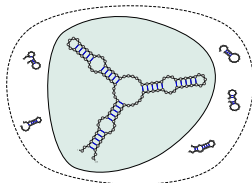
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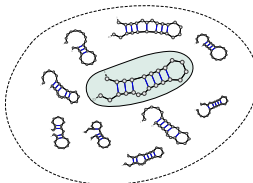


Credits: Roytberg and Finkelstein for Hypergraph DP in Bioinformatics, L. Hwang for algebraic hypergraph DP, R. Giegerich for ADP...

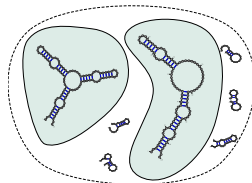
Let us extend applications of DP...



Functional folding?



Ill-defined folding:
mRNA?



Bistable RNA
Kinetics?

Toward ab-initio signatures for ncRNAs, one may have to go beyond average behavior of additive features (#Hairpins, #Multiple Loops, Free-Energy...).

Input:

- An acyclic F-graph \mathcal{H} , defining the set of F-paths (trees) in \mathcal{H} .
- Weight function $w : E \rightarrow \mathbb{R}$, defining a probability distribution.
- Additive feature functions $\alpha_1, \dots, \alpha_k : E \rightarrow \mathbb{R}$.

What can be said about the (joint) distribution of features?
 \Rightarrow (Generalized) moments.

Definition (Generalized moments)

$$\mathbb{E}[\alpha_1^{m_1} \alpha_2^{m_2} \cdots \alpha_k^{m_k}] = \sum_{p \in \mathcal{P}_s} \frac{\pi(p)}{w_s} \prod_{i=1}^k \alpha_i(p)^{m_i}$$

Remark: Single feature + $m_i = 1 \Rightarrow$ **Expectation** in the weighted distribution.

Theorem (Generalized moments extraction (Generalizes Miklos *et al* 2005))

Generalized moments can be computed as $\mathbb{E}[\alpha_1^{m_1} \cdots \alpha_k^{m_k}] = c_s^{\mathbf{m}} / w_s$, where

$$c_s^{\mathbf{m}} = \sum_{e=(s \rightarrow t)} \pi(e) \cdot \sum_{\substack{\mathbf{m}', (\mathbf{m}_1'', \dots, \mathbf{m}_{|t|}'') \\ \text{s. t. } \mathbf{m}' + \sum_j \mathbf{m}_j'' = \mathbf{m}}} \prod_{i=1}^k \binom{m_i}{m_i', m_{1,i}'', \dots, m_{|t|,i}''} \cdot \alpha_i(e)^{m_i'} \cdot \prod_{i=1}^{|t|} c_{t_i}^{\mathbf{m}_i''}$$

Time: $\mathcal{O}\left((|E| + |V|) \cdot k \cdot t^+ \cdot \prod_{i=1}^k m_i^{t^++1}\right)$ **Memory:** $\Theta\left(|V| \cdot \prod_{i=1}^k m_i\right)$
 ($t^+ = \max. \text{ out-degree}$).

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Remark: Single feature + $m_2 = 2$ characterizes **Standard Deviation**.

Theorem (Generalized moments extraction (Generalizes Miklos *et al* 2005))

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Remark: Two features + $m_1 = m_2 = 1$ computes **Pearson product-moment corr. coeff.**

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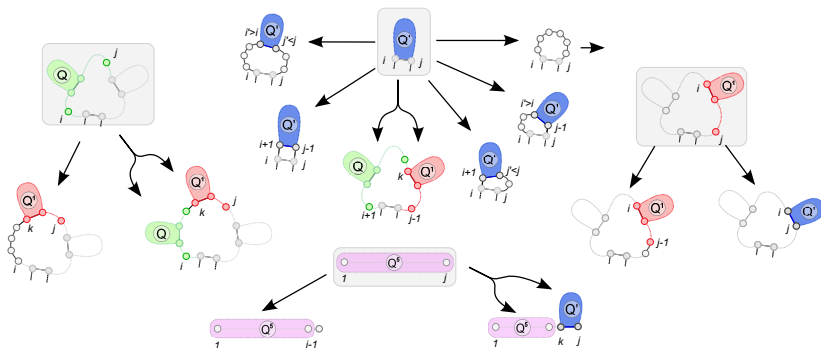
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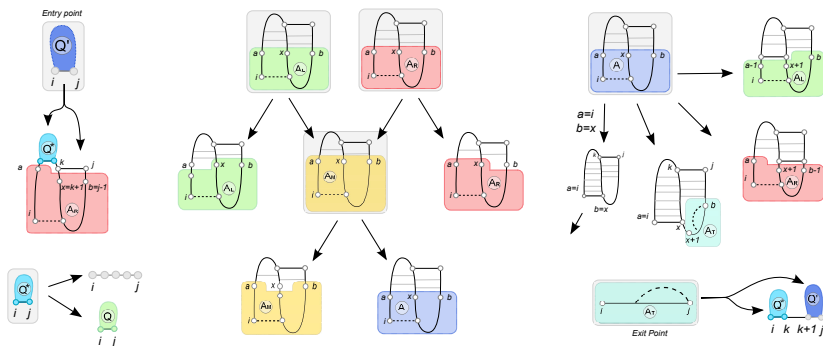
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Mfold/Unafold decomposition

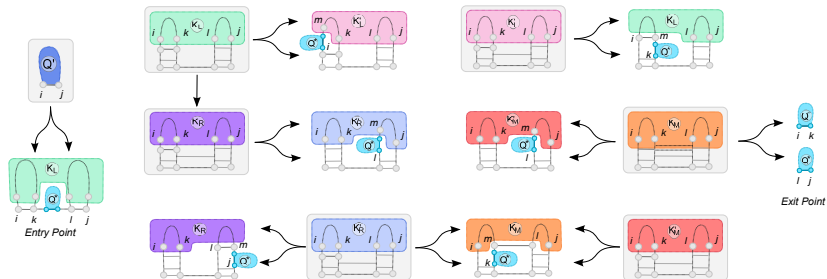


Application	Algorithm	Weight fun.	Time/Space	Ref.
Energy minimization	Minimal weight	π_T	$O(n^{3(4)})/O(n^2)$	[Zuker and Stiegler, 1981]
Partition function	Weighted count	$e^{-\frac{\pi_T}{RT}}$	$O(n^{3(4)})/O(n^2)$	[McCaskill, 1990]
Base-pairing probabilities	Arc-traversal prob.	$e^{-\frac{\pi_T}{RT}}$	$O(n^{3(4)})/O(n^2)$	[McCaskill, 1990]
Statistical sampling (k -samples)	Random gen.	$e^{-\frac{\pi_T}{RT}}$	$O(n^{3(4)} + kn \log n)/O(n^2)$	[Ding and Lawrence, 2003, Ponty, 2008]
Moments of energy (Mean, Var.)	Moments extraction	$e^{-\frac{\pi_T}{RT}}$	$O(n^{3(4)})/O(n^2)$	[Mikiós <i>et al.</i> , 2005]
m -th moment of additive features	Moments extraction	$e^{-\frac{\pi_T}{RT}}$	$O(m^3 \cdot n^{3(4)})/O(m \cdot n^2)$	—
Correlations of additive features	Moments extraction	$e^{-\frac{\pi_T}{RT}}$	$O(n^{3(4)})/O(n^2)$	—



Application	Algorithm	Weight fun.	Time/Space	Ref.
Energy minimization	Minimal weight	π_{bp}	$O(n^4)/O(n^4)$	[Akutsu, 2000]
Partition function	Weighted count	$e^{-\frac{\pi_{bp}}{RT}}$	$O(n^4)/O(n^4)$	$\Theta(n^6)$ [Cao and Chen, 2009]
Base-pairing probabilities	Arc-traversal prob.	$e^{-\frac{\pi_{bp}}{RT}}$	$O(n^4)/O(n^4)$	—
Statistical sampling (k -samples)	Random gen.	$e^{-\frac{\pi_{bp}}{RT}}$	$O(n^4 + kn \log n)/O(n^4)$	—
Moments of energy (Mean, Var.)	Moments extraction	$e^{-\frac{\pi_{bp}}{RT}}$	$O(n^4)/O(n^4)$	—
m -th moment of additive features	Moments extraction	$e^{-\frac{\pi_{bp}}{RT}}$	$O(m^3 \cdot n^4)/O(m \cdot n^4)$	—

Kissing hairpins



Application	Algorithm	Weight fun.	Time/Memory	Ref.
Energy minimization	Minimal weight	π_T	$O(n^5)/O(n^4)$	[Chen <i>et al.</i> , 2009]
Partition function	Weighted count	$e^{-\frac{\pi_T}{RT}}$	$O(n^5)O(n^4)$	—
Base-pairing probabilities	Arc-traversal prob.	$e^{-\frac{\pi_T}{RT}}$	$O(n^5)/O(n^4)$	—
Statistical sampling (k -samples)	Random gen.	$e^{-\frac{\pi_T}{RT}}$	$O(n^5 + k \cdot n \log n)/O(n^4)$	—
Moments of energy (Mean, Var.)	Moments extraction	$e^{-\frac{\pi_T}{RT}}$	$O(n^5)/O(n^4)$	—
m -th moment of additive features	Moments extraction	$e^{-\frac{\pi_T}{RT}}$	$O(m^3 \cdot n^5)/O(m \cdot n^4)$	—

- Implementation issues: Table design, avoid memory consumption, compilation to low-level language. . .
- Generate hypergraph from more abstract description (CFG, Möhl's *split-types*, Nebel's algebraic descriptors)
- Novel sequence-only features \Rightarrow Thermodynamic signatures for ncRNAs, Riboswitches, Pseudoknotted RNAs classifier. . . ?
- Formulate generic optimizations: Sparsification, four-russians. . .
- Extensions: Predicting interactions, RNA design, Simultaneous folding and alignment



Thanks to





Tatsuya Akutsu.

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