

Analytic properties of RNA secondary structures and their representations

Asymptotics of RNA Shapes

Yann Ponty

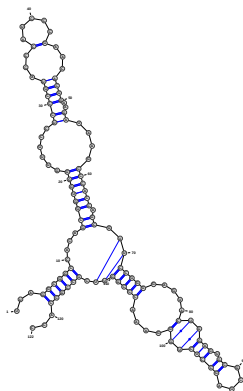
Bioinformatics Team
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April 15, 2014

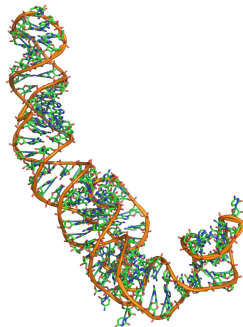
RNA structure

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

Primary structure



Secondary structure



Tertiary structure

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

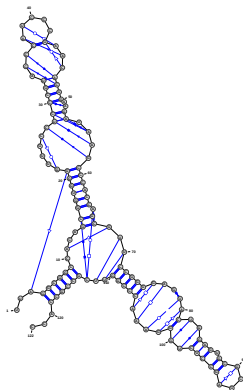
Definition

Secondary structures of RNA =
Maximal non-crossing subset of canonical base-pairs.

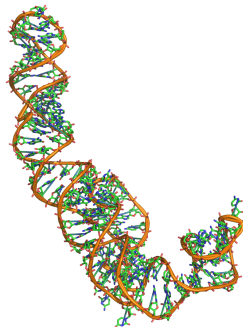
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Primary structure



Secondary⁺ structure



Tertiary structure

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Secondary structures of RNA =
Maximal non-crossing subset of **canonical** base-pairs.

1 Foreword

- Introduction
- Motivation

2 Enumerative/analytic combinatorics 101

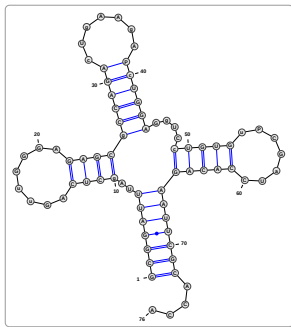
- Generating functions
- DSV/symbolic method
- Singularity analysis

3 RNA shapes

- Presentation
- Motivation
- π shapes

4 Conclusion

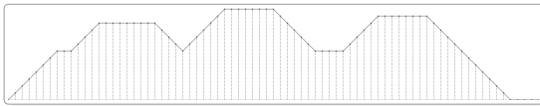
Various representations for a versatile molecule



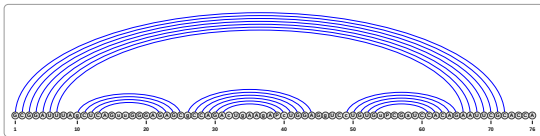
Outer planar graph

(((((.....)))((((.....)))).....((((.....)))))).....

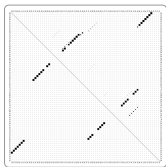
Well-parenthesized expression



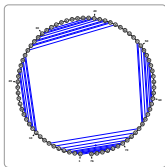
Mountain view



Non intersecting arcs



Dot plot

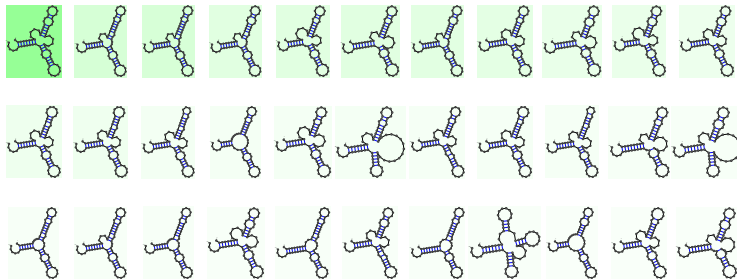


Circular diagram

Different objects
yet
Common combinatorial structure

Why use combinatorics?

Boltzmann ensemble is a (weighted) combinatorial class.



Studying it as such *cleans out the details* and helps:

- Assess asymptotic properties of sec. str.
- Investigate worst and average-case complexities
- Obtain better algorithms for RNA

Generating functions

Let $|\cdot|$ be a **size function** over **objects** (Sequences, trees, ...).
Combinatorial classes are (infinite) sets $\mathcal{C}$ of objects whose restrictions $\mathcal{C}_n$ to objects of size n are of **finite cardinality**.

Definition (Generating functions)

Let $\mathcal{C}$ be a combinatorial class and $c_n = |\mathcal{C}_n|$ the number of objects of size n in $\mathcal{C}$, then the **generating function** of $\mathcal{C}$ is $C(z)$ s. t.

$$C(z) = \sum_{s \in \mathcal{C}} z^{|s|} = \sum_{n \geq 0} c_n z^n$$

Closed forms for $C(z)$ are often easy to find ...

Example (DNA)

$$\mathcal{D} := \{a, c, g, t\}^* \Rightarrow d_n = 4^n$$

and $C(z) = 1 + 4z + 16z^2 + 64z^3 + \dots = \sum_{n \geq 0} 4^n z^n = \frac{1}{1-4z}$

... and very often much simpler than finding closed-form for c_n !!!

DSV/symbolic method

From a **class specification**, one can directly establish the gen. fun.
Historically on languages, stems from Schützenberger's observation
Gen. fun. are commutative images of languages

Grammar	Generating function	Coefficients
$C \rightarrow \varepsilon$	$C(z) = z^0 = 1$	$c_n = \mathbb{1}_{\{0\}}(n)$
$C \rightarrow t$	$C(z) = z^1 = z$	$c_n = \mathbb{1}_{\{1\}}(n)$
$C \rightarrow A \mid B$	$C(z) = A(z) + B(z)$	$c_n = a_n + b_n$
$C \rightarrow A.B$	$C(z) = A(z) \cdot B(z)$	$c_n = \sum_{k=0}^n a_k b_{n-k}$

Remark: Disjoint unions and unambiguous concatenations.

Example (DNA)

DNA = $\{a, c, g, t\}^* \Leftrightarrow D \rightarrow a.D \mid c.D \mid g.D \mid t.D \mid \varepsilon$

$$\Rightarrow D(z) = z \cdot D(z) + z \cdot D(z) + z \cdot D(z) + z \cdot D(z) + 1$$

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Example (DNA)

DNA = $\{a, c, g, t\}^* \Leftrightarrow D \rightarrow a.D \mid c.D \mid g.D \mid t.D \mid \varepsilon$

$$\Rightarrow D(z) = 4z \cdot D(z) + 1$$

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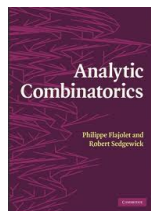
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$$\Rightarrow D(z) = \frac{1}{1 - 4z}$$

Analytic combinatorics: Main principles

Disclaimer

What follows, although true in this context, is **embarrassingly simplistic**. A rigorous presentation can (and should) be sought in the **Flajolet/Sedgewick Bible**.



A **singularity** is a point $z = \rho$ where $C(z)$ is no longer analytic. Asymptotics of coeff c_n are driven by the **singularities** of $C(z)$.

1st principle

Location of the dominant (smallest) singularity ρ dictates the **exponential growth** $\Rightarrow \frac{c_n}{\rho^{-n}} = o(\alpha^n), \forall \alpha > 1$.

Example (DNA)

$$D(z) = 1/(1 - 4z) \Rightarrow \rho = 1/4 \Rightarrow d_n \sim 4^n P(n).$$

Analytic combinatorics: Basic transfer theorem

2nd principle

Nature of ρ dictates **subexponential** part $P(n)$ s.t. $c_n \sim \rho^{-n}P(n)$.

Basic scale: If one can rewrite $C(z)$ as

$$C(z) = f(z) + g(z)(1 - z/\rho)^\alpha$$

where f and g are analytic $\forall |z| < |\rho|$ and non-null at ρ , then

$$c_n \equiv [z^n]C(z) \sim \frac{g(\rho)\rho^{-n}}{\Gamma(-\alpha)n^{\alpha+1}}$$

Example (DNA)

$$D(z) = \frac{1}{1-4z} \Rightarrow c_n \sim 4^n$$

($\rho = 1/4$, $\alpha = -1$, $f(z) = 0$, and $g(z) = 1$)

General methodology

Asymptotic estimates are obtained using a 4 steps meta-algorithm:

1 Find the right model

2 Translate into grammar

3 Translate into system and solve g. f.

4 Singularity analysis yields asymptotics

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Appetizer: Motzkin words

Let us count dot-bracket notations (Motzkin words)

$$1 \quad \text{---} = \text{---} \vee \text{---} \vee \epsilon$$

Appetizer: Motzkin words

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1		=		$\vee$		$\vee$	ϵ
2	M	$\rightarrow$	$\bullet M$		$(M)M$		ϵ

Appetizer: Motzkin words

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$$1 \quad \text{---} = \text{---} \vee \text{---} \vee \epsilon$$

Diagram illustrating the decomposition of a Motzkin word. A wavy line with two dots is equal to a wavy line with three dots, or a wavy line with two dots followed by a loop, or the empty word ϵ .

$$2 \quad M \rightarrow \bullet M \mid (M)M \mid \epsilon$$

Diagram illustrating the recursive decomposition of a Motzkin word M into three cases: a dot followed by M , a pair of parentheses enclosing M followed by M , or the empty word ϵ .

$$3 \quad M(z) = z \cdot M(z) + z \cdot M(z) \cdot z \cdot M(z) + 1$$

$$= \frac{1 - z \pm \sqrt{1 - 2z - 3z^2}}{2z^2}$$

Diagram illustrating the generating function equation for Motzkin words. The equation relates $M(z)$ to its recursive decomposition.

Appetizer: Motzkin words

Let us count dot-bracket notations (Motzkin words)

$$1 \quad \text{---} = \text{---} \vee \text{---} \vee \epsilon$$

Diagram illustrating the decomposition of a Motzkin word starting with a dot. A wavy line with two dots is equal to a wavy line with two dots, or a wavy line with one dot followed by a wavy line with one dot, or the empty word ϵ .

$$2 \quad M \rightarrow \bullet M \mid (M)M \mid \epsilon$$

Diagram illustrating the decomposition of a Motzkin word M . It can be a dot followed by M , or a pair of parentheses enclosing M followed by M , or the empty word ϵ .

$$3 \quad M(z) = z \cdot M(z) + z \cdot M(z) \cdot z \cdot M(z) + 1$$

$$= \begin{cases} \frac{1-z+\sqrt{1-2z-3z^2}}{2z^2} = \frac{1}{z^2} - \frac{1}{z} - 1 - z - 2z^2 + \mathcal{O}(z^3) \\ \frac{1-z-\sqrt{1-2z-3z^2}}{2z^2} = 1 + z + 2z^2 + 4z^3 + 9z^4 + \mathcal{O}(z^5) \end{cases}$$

Diagram illustrating the generating function $M(z)$ for Motzkin words. The equation shows the decomposition of $M(z)$ into three cases: a dot followed by $M(z)$, a pair of parentheses enclosing $M(z)$ followed by $M(z)$, and the empty word 1 . The generating function is then expressed as a sum of two series, each representing a different branch of the decomposition.

Appetizer: Motzkin words

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$$1 \quad \text{---} = \text{---} \vee \text{---} \vee \epsilon$$

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$$3 \quad M(z) = z \cdot M(z) + z \cdot M(z) \cdot z \cdot M(z) + 1$$

$$= \frac{1-z-\sqrt{1-2z-3z^2}}{2z^2}$$

$$4 \quad \rho = 1/3, M(z) = \frac{1-z}{2z^2} - g(z) \cdot \sqrt{1-z/\rho}, \text{ and } g(z) := \frac{\sqrt{1+z}}{2z^2}$$

$$\Rightarrow s_n \equiv [z^n]M(z) \sim \frac{g(\rho)\rho^{-n}}{\Gamma(-\alpha)n^{\alpha+1}} = \frac{3\sqrt{3}}{2\sqrt{\pi}} \cdot \frac{3^n}{n\sqrt{n}} (1 + \mathcal{O}(1/n))$$

RNA secondary structures

Consider RNA secondary structures

[Waterman 78 + Viennot/Vauchaussade de Chaumont 78]

$$1 \cdot \text{---} = \text{---} \vee \text{---} \overset{\geq 1}{\text{---}} \vee \epsilon$$

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Consider RNA secondary structures

[Waterman 78 + Viennot/Vauchaussade de Chaumont 78]

1

$$\bullet \text{---} \bullet = \bullet \text{---} \bullet \text{---} \bullet \vee \bullet \text{---} \bullet \text{---} \bullet \text{---} \bullet \vee \epsilon$$

≥ 1

2

$$S \rightarrow \bullet S \mid (S_{>0}) S \mid \epsilon$$

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Consider RNA secondary structures

[Waterman 78 + Viennot/Vauchaussade de Chaumont 78]

1

$$\bullet \text{---} \bullet = \bullet \text{---} \bullet \text{---} \bullet \vee \bullet \text{---} \bullet \text{---} \bullet \text{---} \bullet \vee \epsilon$$

≥ 1

2

$$\begin{array}{ll} S & \rightarrow \bullet S \mid (\mathbf{T}) S \mid \epsilon \\ \mathbf{T} & \rightarrow \bullet S \mid (\mathbf{T}) S \end{array}$$

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$$S(z) = \frac{1 - z + z^2 - \sqrt{1 - 2z - z^2 - 2z^3 + z^4}}{2z^2}$$

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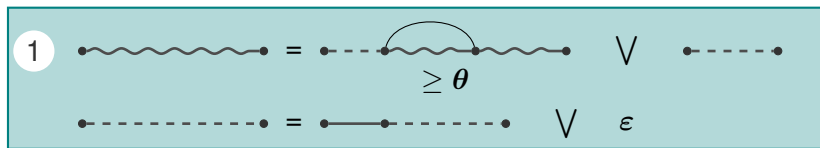
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4

$$\rho = \frac{3 - \sqrt{5}}{2} = 1 - \phi$$
$$[z^n]S(z) = \sqrt{\frac{15 + 7\sqrt{5}}{8\pi}} \cdot \frac{\left(\frac{3 + \sqrt{5}}{2}\right)^n}{n\sqrt{n}} (1 + \mathcal{O}(1/n)) \sim 1.1 \cdot \frac{2.6^n}{n\sqrt{n}}$$

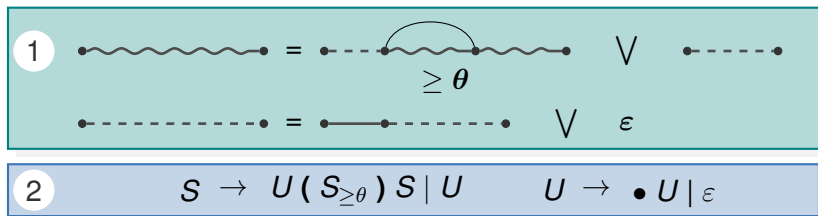
RNA secondary structures

Let us generalize the θ constraint



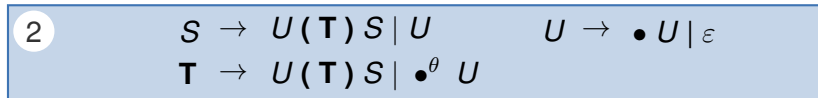
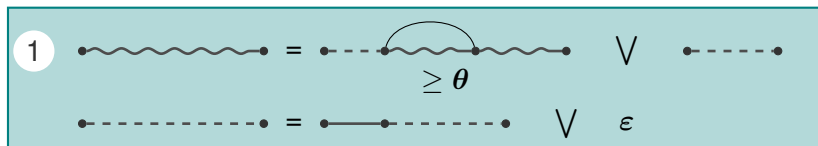
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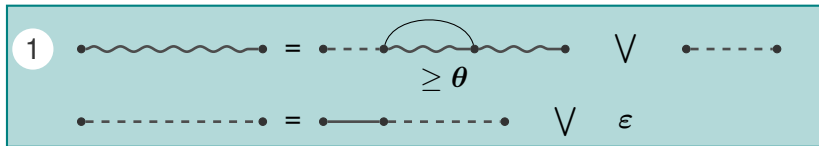
RNA secondary structures

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2

$$S \rightarrow U(\mathbf{T})S \mid U \quad U \rightarrow \bullet U \mid \epsilon$$

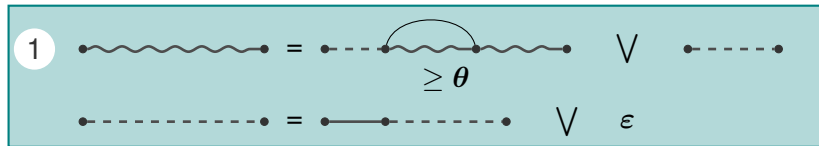
$$\mathbf{T} \rightarrow U(\mathbf{T})S \mid \bullet^\theta U$$

3

$$S(z) = \frac{1 - 2z + 2z^2 - z^{\theta+2} - \sqrt{1 - 4z + 4z^2 - 2z^{\theta+2} + 4z^{\theta+3} - 4z^{\theta+4} + z^{2\theta+4}}}{(1-z)2z^2}$$

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$$S \rightarrow U(T)S \mid U \quad U \rightarrow \bullet U \mid \epsilon$$

$$T \rightarrow U(T)S \mid \bullet^\theta U$$

3

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4

$$s_n \sim K \cdot \frac{\beta^n}{n\sqrt{n}} (1 + \mathcal{O}(1/n))$$

θ	0	1	3	10
β	3.	2.62	2.29	2.02

Half-time report

Message #1

Finding the right decomposition (DP) is a combinatorial task.

Message #2

Applying **automatic theorems** gives **precise** asymptotic equivalents.

Message #3

There is a large exponential number of structures of size n :

Homopolymer model: $\Omega(2^n)$ **Stickiness model:** $\mathcal{O}(1.8^n/n^{3/2})$

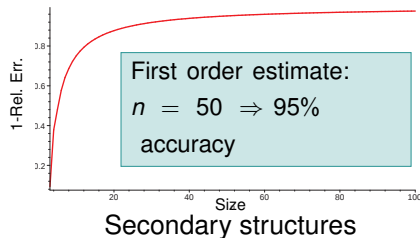
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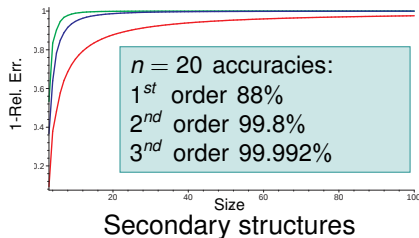
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Presentation

Definition (RNA shapes [Giegerich *et al*])

Coarse-grain representation hierarchy for RNA sec. struct.

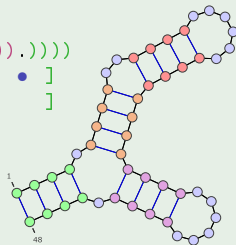
Based on the *underlying backbone* structure.

Example

Sec. str. ((((. ((((. ((((.))))))) ((((.))))))) ((((.)))))))

π' -shape [• [• [•]]] [•] •]

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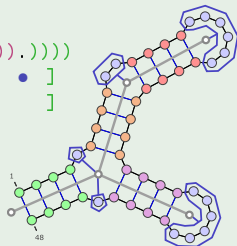
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Sec. str. (((((.((((...(((.....)))))))))(((.....))))).(((

π' -shape [• [• [•]] [•] •]

π -shape [[- -] []]

Contract identical consecutive characters



Presentation

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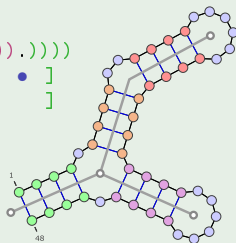
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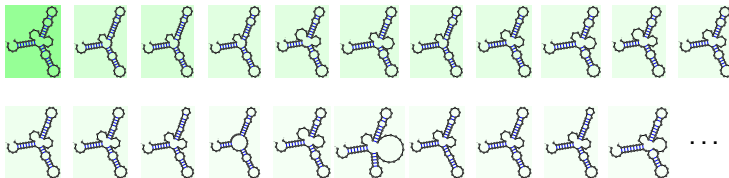
Sec. str.	(((((.((((...(((((...)))))))))(((((...)))...))))))
π' -shape	[• [• [•]]] [•] •]
π -shape	[[- -] []]

Remove unpaired regions
Contract nested helices



Motivation

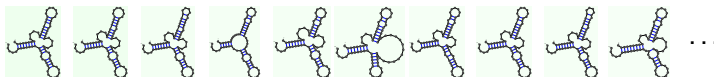
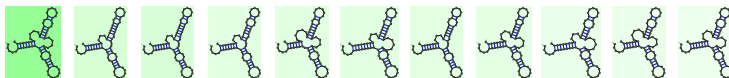
RNA shapes allow for a hierarchical search in the Boltzmann ensemble



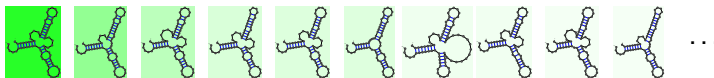
10000 samples $\Rightarrow$ 1727 Secondary structures...

Motivation

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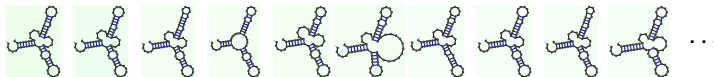
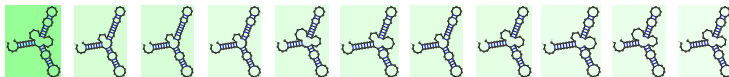
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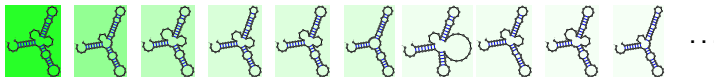
... 406 π' -shapes...

Motivation

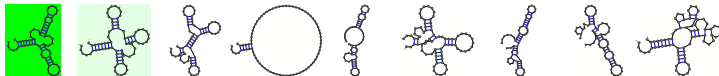
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10000 samples $\Rightarrow$ 1727 Secondary structures...



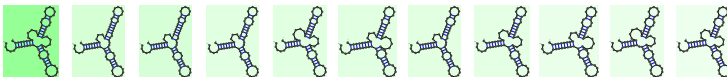
... 406 π' -shapes...



... but only 9 π -shapes!

Motivation

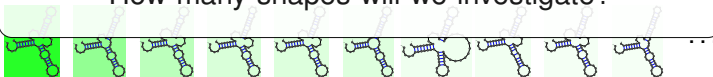
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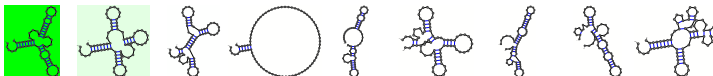
Can we reasonably consider all possible shapes compatible with input structure?

10000 samples $\Rightarrow$ 1727 Secondary structures...

How many shapes will we investigate?



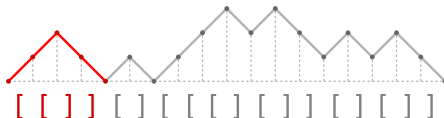
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π -shapes

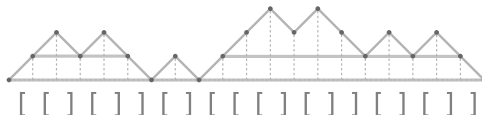
Objective: Count π -shapes with $2n$ parentheses.



1 π -shapes are bracket words avoiding the $[[\dots]]$ motif.

π -shapes

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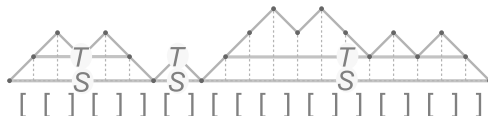


1 π -shapes are bracket words avoiding the $[[\dots]]$ motif.

2 $S \rightarrow [S_{/\{\dots\}}] S \mid [S_{/\{\dots\}}]$

π -shapes

Objective: Count π -shapes with $2n$ parentheses.

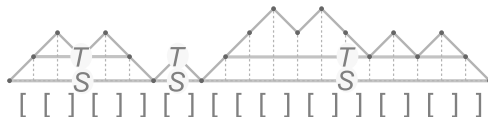


- 1 π -shapes are bracket words avoiding the $[[\dots]]$ motif.

$$2 \quad S \rightarrow [\mathbf{T}] S \mid [\mathbf{T}] \quad \mathbf{T} \rightarrow [\mathbf{T}] S \mid \varepsilon$$

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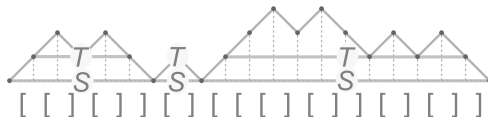
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2 $S \rightarrow [\mathbf{T}]S \mid [\mathbf{T}]$ $\mathbf{T} \rightarrow [\mathbf{T}]S \mid \varepsilon$

3
$$S(z) = \frac{1 - z^2 - \sqrt{1 - 2z^2 - 3z^4}}{2z^2}$$

π -shapes

Objective: Count π -shapes with $2n$ parentheses.



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$$3 \quad S(z) = \frac{1 - z^2 - \sqrt{1 - 2z^2 - 3z^4}}{2z^2}$$

$$4 \quad s_{2n} \sim \frac{\sqrt{3}}{2\sqrt{\pi}} \cdot \frac{3^n}{n\sqrt{\pi}} (1 + \mathcal{O}(1/n)) \quad \text{and} \quad s_{2n+1} = 0$$

Remark: Doesn't this look familiar???

Limitations

Number of π -shapes of size n
 $\neq$
Number of π -shapes compatible with RNA of size n

Reasons:

- 1 Shapes of size $\leq n$ should be considered
- 2 Forming a hairpin loop $[]$ takes at least $\theta + 2$ bases

$$2 \quad S \rightarrow [T]S \mid [T] \quad T \rightarrow [T]S \mid \varepsilon$$

$$3 \quad S(z) = \frac{1 - z^2 - \sqrt{1 - 2z^2 - 3z^4}}{2z^2}$$

$$4 \quad \text{For } n \text{ even: } s_{2n} \sim \frac{3\sqrt{3}}{4\sqrt{\pi}} \cdot \frac{3^n}{n\sqrt{\pi}} (1 + \mathcal{O}(1/n)) \approx 0.48 \cdot \frac{3^n}{n\sqrt{n}}$$

Limitations

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$$\begin{aligned} 2 \quad S &\rightarrow [T]S \mid [T] & T &\rightarrow [T]S \mid \bullet^\theta \\ R &\rightarrow \square S \mid \varepsilon \end{aligned}$$

$$3 \quad R(z) = \frac{1 - z^2 - \sqrt{1 - 2z^2 - 3z^4}}{2z^2(1 - z)}$$

$$4 \quad r_{2n} \sim \frac{3\sqrt{3}}{4\sqrt{\pi}} \cdot \frac{3^n}{n\sqrt{n}} (1 + \mathcal{O}(1/n)) \Rightarrow r_n \approx 2.07 \cdot \frac{1.73^n}{n\sqrt{n}}$$

Limitations

Number of π -shapes of size n
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Number of π -shapes compatible with RNA of size n

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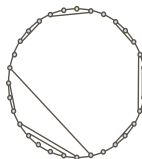
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$$3 \quad R(z) = \frac{1 - z^{\theta+2} - \sqrt{1 - 2z^{\theta+2} - 4z^{\theta+4} + z^{2\theta+4}}}{2z^2(1 - z)}$$

$$4 \quad \theta = 3 \Rightarrow r_n \approx 2.44 \frac{1.32^n}{n\sqrt{n}}$$

A surprising bijection



Theorem

$\# \pi$ shapes of size $n = \# \text{Motzkin words of length } 2n + 2$

Proof.

$$\begin{aligned} S(z) &= \frac{1-z^2-\sqrt{1-2z^2-3z^4}}{2z^2} & M(z) &= \frac{1-z-\sqrt{1-2z-3z^2}}{2z^2} \\ S(z) &= 1 + z^2 M(z^2) & \Rightarrow & S_n = m_{2n+2} \end{aligned}$$



These two classes are in bijection.

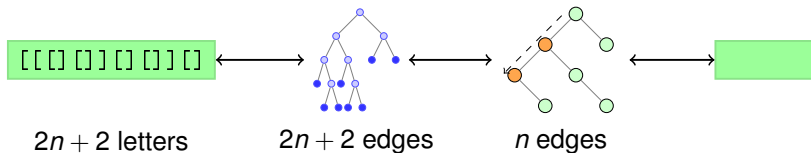
→ **How?** Can we **exploit** it?

Explicit bijection

Let $\psi, \phi : \{ [,] \}^* \rightarrow \{ (,) , \bullet \}$ such that

$$\begin{aligned}\psi((A) B) &= \begin{cases} \phi(A) & \text{If } B = \varepsilon \\ \phi(A) \bullet \psi(B) & \text{Otherwise} \end{cases} \\ \phi((A) B) &= \phi(A)[\psi(B)] \\ \phi(\varepsilon) &= \varepsilon.\end{aligned}$$

Then ψ is a **bijection** between s_{2n+2} and m_n .

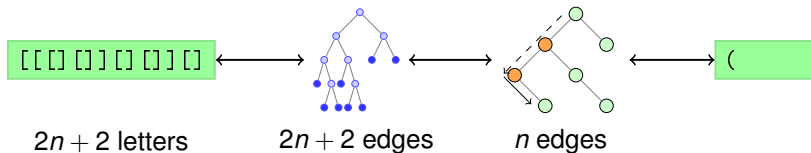


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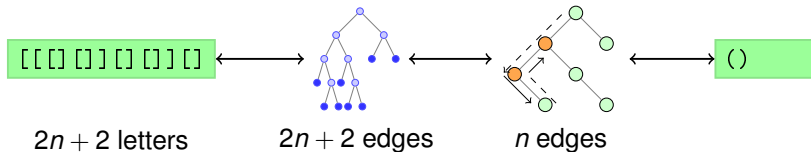


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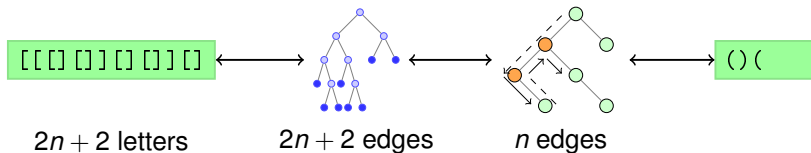


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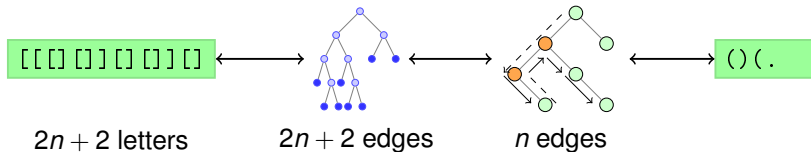


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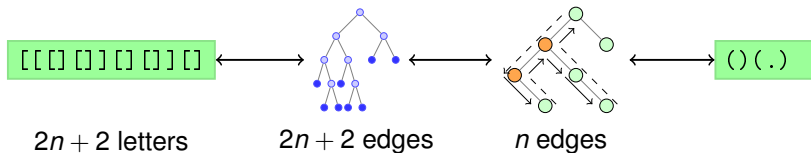


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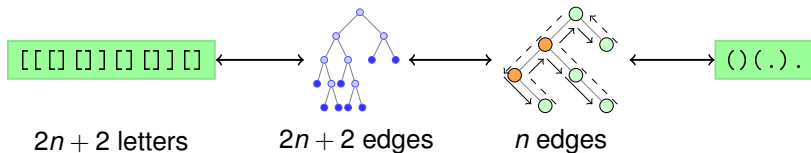


Explicit bijection

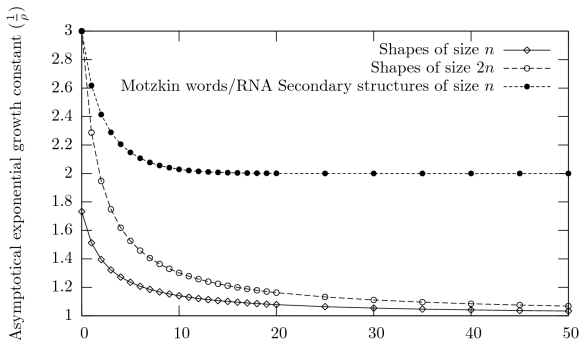
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Then ψ is a **bijection** between s_{2n+2} and m_n .



Limits of the bijection



Impacts of θ on shapes and Motzkin are drastically different.

Theorem

Expectations of number of term. loops in Motzkin words and π -shapes scale like $m_n^t \sim \frac{n}{6} + \mathcal{O}(1)$ and $s_{2n+2}^t \sim \frac{2n}{3} + \mathcal{O}(1)$

π' -shapes

Objective: Count π' -shapes compatible with RNA of length n .

1 π' -shapes = bracket words avoiding motifs $[[\dots]]$ and $\bullet\bullet$

2 $R \rightarrow \square R \mid S \quad S \rightarrow U[T]S \mid U \quad U \rightarrow \diamond \mid \varepsilon$
 $T \rightarrow U[T]U[T]S \mid \diamond[T] \mid [T]\diamond \mid \diamond[T]\diamond \mid \bullet^\theta$

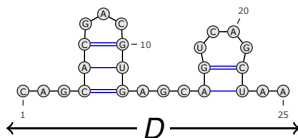
3 $\theta = 3, R(z) = \frac{1+2z^2+2z^3+z^4-z^5-z^6-\sqrt{1-4z^3-2z^4-2z^5+2z^6-7z^8-z^{10}+2z^{11}+z^{12}}}{2z^2(1-z^2)}$

4 $r_n \sim 1.27 \frac{1.81^n}{n\sqrt{n}}$

Summary

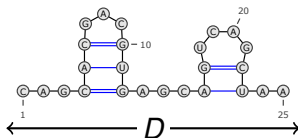
Model	Asymptotic number
Sec. str. on n – Combinatorial	$1.1 \cdot \frac{2.6^n}{n\sqrt{n}}$
Sec. str. on n – Empirical	$0.04 \cdot \frac{1.4^n}{n\sqrt{n}}$
π -shapes of size n	$1.38 \cdot \frac{1.73^n}{n\sqrt{n}}$
π -shapes compatible with sec. str. on n	$2.44 \cdot \frac{1.32^n}{n\sqrt{n}}$
π -shapes – Empirical	$0.21 \cdot \frac{1.1^n}{n\sqrt{n}}$
π' -shapes of size n	$0.99 \cdot \frac{2.41^n}{n\sqrt{n}}$
π' -shapes compatible with sec. str. on n	$1.28 \cdot \frac{1.81^n}{n\sqrt{n}}$

5'-3' Distance: Theory vs Empirical evidences



[Clote-P-Steyaert 12]

5'-3' Distance: Theory vs Empirical evidences

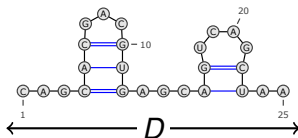


[Clote-P-Steyaert 12]

2

$$\begin{aligned}
 T &\rightarrow [S_{\geq \theta}]T \mid \bullet T \mid \varepsilon & S &\rightarrow (S_{\geq \theta})S \mid \circ S \mid \varepsilon \\
 S_{\geq \theta} &\rightarrow (S_{\geq \theta})S \mid \circ S_{\geq \theta} \mid \circ^{\theta}
 \end{aligned}$$

5'-3' Distance: Theory vs Empirical evidences

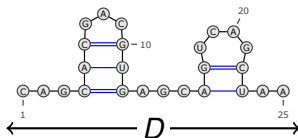


[Clote-P-Steyaert 12]

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 &S_{\geq \theta} && \rightarrow (S_{\geq \theta})S \mid \circ S_{\geq \theta} \mid \circ^{\theta}
 \end{aligned}$$

$$\begin{aligned}
 3 \quad E_{\theta}(z) &= \frac{2 - 9z + 14z^2 - 8z^3 + 2z^5 \\
 &\quad + z^{\theta+2}(-4 + 10z - 10z^2 + 2z^3) + z^{2\theta+4}(2 - z) \\
 &\quad - (2 - 5z + 4z^2 - 2z^{\theta+2} + z^{\theta+3})\sqrt{\Delta_{\theta}}}{2(1 - z)^2 z^4} \\
 \Delta_{\theta} &:= 1 - 4z + 4z^2 - 2z^{\theta+2} + 4z^{\theta+3} - 4z^{\theta+4} + z^{2\theta+4}
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5'-3' Distance: Theory vs Empirical evidences



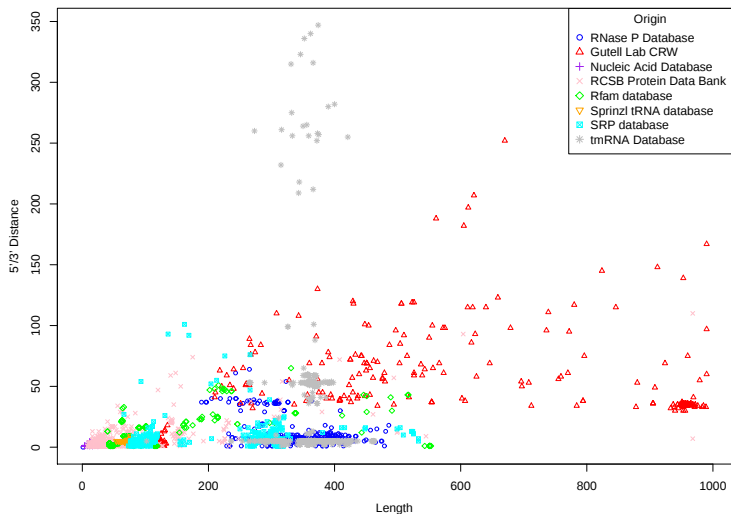
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$$4 \quad D_n \sim \frac{2 - 5\rho + 4\rho^2 - 2\rho^{\theta+2} + \rho^{\theta+3}}{(1 - \rho)\rho^2} - 1, \quad \rho \text{ smallest sol. of } \Delta_{\theta} = 0$$

5'-3' Distance: Theory vs Empirical evidences



Empirical distribution of 5'-3' distance (Strand database)

⇒ Linear correlation Length/Distance [Clote-P-Steyaert 12]...

uh?!

Analytic combinatorics: Limiting distribution

3rd principle (Drmotá-Lalley-Woods)

Strongly connected grammar/specification + Technical conditions

⇒ Dominant singularity in $\sqrt{1 - z/\rho}$

⇒ #Occurrences of any letter t follows **Normal** distribution

Expectation: $\mathbb{E}(\#t) \in \Theta(\mu \cdot n)$ **Variance:** $\mathbb{V}(\#t) \in \Theta(\sigma^2 \cdot n)$

+ μ and σ are easy to compute **symbolically** or **numerically**.

Results robust to **weights**...

...or **almost connected** specifications (subcritical composition)...

...generalizes to **higher dimensions** (joint distribution)...

...but any limiting distrib. can be induced by general grammars!

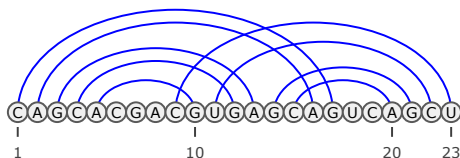
Example (RNA)

Generated by a strongly connected grammar (Nussinov)

⇒ #Base pairs, #Unpaired bases... are Normally distributed

Pseudoknots and partition function

Recursive Pseudoknots, Akutsu-style [Saule et al 10] [Nebel Weinberg 12]



2

$$S \rightarrow (S)S \mid \bullet S \mid \Phi(\text{Seq}(a.a' \mid b.b')) SS \mid \varepsilon$$

Strongly connected grammar

⇒ Partition function approach will always predict PKs for large structures...

...but PK-free structures exist.

Conclusion

- For *context-free* objects, finding gen. fun. is **easy**...
...and **precise asymptotics estimates** follow readily
- **Bijection** between Motkzin words and π -shapes
- **Way less** many shapes than sec. str.!
- Homopolymer model **overestimates** number of shapes
Need for a probabilistic model for base-pairing
But **stickiness** is not enough...

Hammer (analytic combinatorics) $\rightarrow$ **nail** (RNA+homopolymer model)
 $\Rightarrow$ Time for a **new hammer**?

Collaborators: W. A. Lorenz and P. Clote (Boston College), A. Denise (Univ. Paris Sud), J.-M. Steyaert (Ecole Polytechnique)