Exponentially few RNA structures are designable

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ABSTRACT

The problem of RNA design attempts to construct RNA sequences that performs a predefined biological function, identified by several additional constraints. One of the foremost objective of RNA design is that the designed RNA sequence should adopt a predefined target secondary structure preferentially to any alternative structure, according to a given metrics and folding model. It was observed in several works that some secondary structures are undesignable, *i.e.* no RNA sequence can fold into the target structure while satisfying some criterion measuring how preferential this folding is compared to alternative conformations.

In this paper, we show that the proportion of designable secondary structures decreases exponentially with the size of the target secondary structure, for various popular combinations of energy models and design objectives. This exponential decay is, at least in part, due to the existence of undesignable motifs, which can be generically constructed, and jointly analyzed to yield asymptotic upper-bounds on the number of designable structures.

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1 INTRODUCTION

RiboNucleic Acids are ubiquitous biomolecules equipped with a capacity of performing a wide variety of functions, both as a messenger enabling gene synthesis (mRNAs), as a regulator of gene expression (miRNAs…) or as a direct performer of a large collection of enzymatic activities (ncRNAs) [28]. For a large subset of ncRNA family, the adoption of a predefined structure is instrumental to the function(s) of individual molecules [46], and even, at times, the survival of its hosts organisms [20]. Accordingly, the evolutionary pressure on RNA families induced by RNA structure, at the secondary structure level, is at the core of most approaches for the identification of novel ncRNA families [47]. Improved characterizations of this pressure for individual represents a key challenge of RNA Bioinformatics and the object of current work, for instance in the case of the elusive long non-coding RNAs (lncRNAs) [39].

This strong connection between RNA structure and function has motivated the continuous development of mature computational methods for structure prediction [24, 35, 50]. More recently, researchers have attempted to harness the success of folding prediction approaches, and tackled a *de novo* design of structured RNAs. In its historic setting [24], the RNA Design, or inverse folding, consists in designing a sequence of nucleotides, folding into a predefined structure according to a criterion which can computed using available computational methods. RNA design is now an established problem in RNA bioinformatics, motivated by applications ranging from synthetic biology [43] to RNA therapeutics [48] through systems biology [14] and nanotechnologies [21].

Computationally, RNA design is a hard problem [3], motivating the development of several design methodologies [6] relying on exact exponential algorithms (constraint-programming [19], SAT solving) on heuristics (local search [1, 2, 4, 5, 24, 49], genetic algorithms [13, 33], ant colony [30], sampling [38]…). While the former methods are limited in their scope of applications by their extreme computational demands, methods of the latter category have encountered numerous applied successes [23], and enjoy a growing popularity. Historic objectives of design include the adoption, by the produced sequence, of a structure having energy as close as possible to the Minimal Free-Energy (MFE) achieved by the sequence. Modern formulations also include the minimization of defects, properties of the thermodynamic equilibrium that indicate a notion of distance to the expectation of a perfect design [9]. Those include the *probability defect* [9], the probability of not folding into the target structure, or the *ensemble defect* [49], the expected base pair distance to the target at the thermodynamic equilibrium.

However, not all secondary structures may admit a solution to the design problem. This fact was first observed by Aguirre-Hernández *et al* [1], where the authors exhibited two *undesignable* structure motifs, motifs for which alternative motifs would always be preferred by the usual Turner energy models [44]. This claim was later generalized to simple base-pair based energy models by a study of a combinatorial version of RNA design [22], exhibiting motifs whose presence within any structure precludes the designability of the structure. However, the prevalence, in the folding space, of such undesignable motifs and their impact on the overall combinatorics of designable structures, was never been assessed to date. Moreover,

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a characterization of undesignable structures would allow for sanity checks within design methods, avoiding the costly execution of a heuristics-based algorithm. Such an execution would indeed be wasteful in a context where it cannot distinguish between hard and impossible instances, and being able to test the absence of solution sequences would avoid a waste of computational resources, and motivate a redefinition of more realistic design objectives.

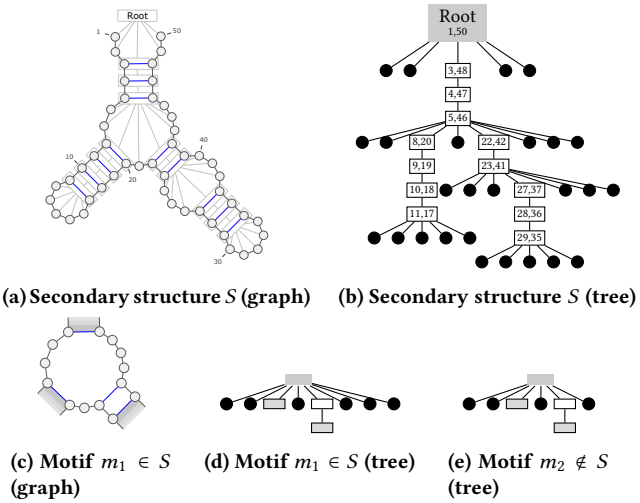
Another motivation for this work pertains to theoretical evolutionary studies, where the RNA sequence to structure relationship represents an attractive model of neutral network [18], and a crucial conceptual framework to quantify the evolvability of species [10]. Indeed, the sequence/structure relationship in RNA enables the existence of, possibly large and highly diverse, subsets of sequences (genotype) folding into the same structure (phenotype), thus achieving the same fitness level. Studies of RNA neutral networks [17, 41] often require an enumeration of accessible phenotypes, *i.e.* the number of RNA secondary structures of a given size which are adopted as the most stable structure for *some* sequence. Since no exact method is known to compute this quantity, studies rely on available asymptotic estimates for the number of all secondary structures [45]. Such an implicit assumption of universal designability may bias studies [27, 29] of the underlying evolutionary dynamics, by artificially inflating the cardinality of structural ensembles. It is thus crucial to provide more precise (approximate) expressions for the number of designable structures.

In this work, we show that the existence of small undesignable motifs, which we call *local obstructions*, constitutes an intrinsic feature of RNA design objectives. An enumeration of the secondary structure that avoid those motifs thus represents an upper bound on the number of designable structures. A direct consequence of this observation is that the proportion of designable secondary structures is typically negligible beyond a certain sequence sizes. Indeed, a tree motif perspective on the problem, coupled with classic results in analytic combinatorics [16] imply that the proportion of designable structures over n nucleotides scales like α^n, where $\alpha < 1$ can be numerically computed from any collection of local obstructions. As a side product of our automated method for computing local obstructions, we are also able to establish a list of likely candidate sequences for each motifs of a given size.

After dedicating Section 2 to formal definitions for the key concepts, and state our main result, we describe in Section 3 the application of our general strategy on a simple combinatorial version of RNA design. We then show in Section 4 how small local obstructions can be computed, for any combination of defect, tolerance and energy models. Section 5 introduces a generic specification for enumerating secondary structures that avoid a collection of local obstructions, and describes a simple numerical procedure to derive asymptotic equivalents for the number of such structures. Section 5 presents the results of our analysis of different design objectives, using the realistic Turner energy model.

2 BACKGROUND AND RESULTS OVERVIEW

RNA secondary structure. An RNA can be abstracted as a sequence $w \in \Sigma^*, \Sigma := \{A, C, G, U\}$, of nucleotides, having length $n := |w|$. For a sequence w of length n, a secondary structure is a set S of base pairs $(i, j), i < j \in [1, n]$, representing the interaction



(a) Secondary structure S (graph) (b) Secondary structure S (tree)

(c) Motif $m_1 \in S$ (graph) (d) Motif $m_1 \in S$ (tree) (e) Motif $m_2 \notin S$ (tree)

Figure 1: RNA secondary structure of size 50, representation as a classic planar graph (1a), and as a tree (1b). (1c) and (1d) depicts a motif m_1 of size 14, having 2 paired leaves. The motif m_1 occurs in the example, *i.e.* it is a subtree, rooted at the node $(5, 46)$, of the example structure. Subfigure (1e) depicts another motif m_2, having size 12 and 2 paired leaves. Although m_2 resembles m_1, misses two unpaired nodes to occur at position $(5, 46)$.

of nucleotides at positions i and j through hydrogen bonding, such that:

(1) Base pairs are pairwise non-crossing, *i.e.* $\nexists (i, j), (k, l) \in S$ such that $i < k < j < l$;
(2) A minimal distance of θ is ensured between interacting positions, *i.e.* $\forall (i, j) \in S, j - i > \theta$;
(3) Any given position of $[1, n]$ is involved in at most one base pair.

Positions of $[1, n]$ that are not involved in any base pair are called *unpaired*. In the following, we will denote by $\mathcal{S}$ the entire set of secondary structures, and by $\mathcal{S}_n$ its restriction to structures of length n.

Under the above conditions, a secondary structure S of length n can be unambiguously represented as a rooted ordered tree $T = (V := V_i \cup V_j, E)$, whose nodes are either intervals $[i, j] \in V_i$, $i < j$, representing base paired positions (i, j) in S, or singletons $\{i\} \in V_j$, representing an unpaired position i in S. Note that leaves of such tree represent only singletons. Any edge $(u \rightarrow v) \in E$ connects intervals such that $u \subset v$ and $\nexists v' \in V_i$ such that $u \subset v' \subset v$. See Fig. 1.

Energy model. An energy model assigns a free-energy value to each pair (w, S), where w is an RNA sequence and S is a secondary structure for w. Popular energy models for RNA folding prediction, such as *Nussinov* base-pair maximization and the *Turner* nearest-neighbors models, can be computed by summing contributions associated with the *shallow subtrees*, *i.e.* subtrees of depth 1, of S and their respective nucleotides assignments.

Hence, an *energy model* is a function $E : \Sigma^* \times \mathcal{S} \to \mathbb{R} \cup \{+\infty\}$ such that

$$E(w, S) = \sum_{T = \overset{p}{a\ \overset{|}{b}\ c\ \cdots}} \in S \Delta G\left(T, \{p \to w_p, a \to w_a, b \to w_b \ldots\}\right)$$

where $\Delta G\,(T, m)$ is the free-energy, expressed in kcal.mol^{-1} associated with the assignment m of concrete nucleotides from w to the (pairs of) positions in the subtree T. In practice, values taken by ΔG are tabulated or extrapolated from experimentally-measured values.

RNA Folding. RNA structure modeling aims, given a sequence w, to find one or several folding(s) of w into RNA secondary structure(s). Several paradigms exist, associated to different objective functions measuring the quality of a folding. In the energy minimization setting, the main algorithmic question is to compute *minimum free energy* (MFE) structures:

$$\mathrm{MFE}(w) = \left\{ S \in \mathcal{S}_{|w|} \mid E(w, S) = \min_{S' \in \mathcal{S}_{|w|}} E(w, S') \right\}.$$

The MFE structure corresponds to the most stable secondary structure(s).

A second, increasingly popular, paradigm strives to predict structures that are representative of the Boltzmann ensemble of low energy structures. Under the hypothesis of a Boltzmann equilibrium, statistical mechanics postulates that, for a given sequence w, the putative secondary structures follow a Boltzmann distribution

$$\mathbb{P}(S \mid w) = \frac{\mathcal{B}(w, S)}{\mathcal{Z}_w}$$

with

$$\mathcal{B}(w, S) = e^{\frac{-E(w,S)}{RT}} \text{ and } \mathcal{Z}_w := \sum_{S' \in \mathcal{S}_{|w|}} \mathcal{B}(w, S')$$

where R is the Boltzmann constant, T is the temperature, $\mathcal{B}(w, S)$ is called the *Boltzmann factor* of w and S, and $\mathcal{Z}_w$ the *partition function* of w. Similarly, the probability of a base pair is defined as

$$p_w(i, j) = \sum_{\substack{S \in \mathcal{S}_n \\ (i,j) \in S}} \mathbb{P}(S \mid w)$$

and $p(i, i)$ represents the probability of i being left unpaired.

Note that, while an MFE structure has maximum probability in the Boltzmann ensemble, its probability can be arbitrary low, so achieving a high probability is not reducible to being an MFE. In fact, modern approaches typically elect structures that are, on average, maximally similar (MEA [32], centroids [8]) to random structures in the Boltzmann ensemble.

Defects and negative RNA design. Given a *target secondary structure* S^*, the *negative RNA design* problem, also called inverse folding, consists in producing one or several RNA sequences w that folds into S^* while avoiding alternative folds of similar quality for the chosen energy model.

The avoidance of alternative structures is captured by a notion of *defect*, defined as a function $\mathcal{D} : \Sigma^* \times \mathcal{S} \to \mathbb{R}$. RNA design methods usually consider one of the three following defects:

(1) The *Suboptimal Defect* $\mathcal{D}_S$ of a sequence w is defined as the energy distance to the first suboptimal, such that

$$\log \mathcal{D}_S(w, S^*) := - \min_{\substack{S \in \mathcal{S}_{|w|} \\ S \neq S^*}} E(w, S) - E(w, S^*);$$

(2) The *Probability Defect* $\mathcal{D}_P$ represents the probability of folding into any other structure than S^*:

$$\mathcal{D}_P(w, S^*) := \sum_{\substack{S \in \mathcal{S}_{|w|} \\ S \neq S^*}} \mathbb{P}(S \mid w) = 1 - \mathbb{P}(S^* \mid w);$$

(3) The *Ensemble Defect* $\mathcal{D}_E$ is the expected base pair distance between S^* and a random structure, generated with respect to the Boltzmann probability distribution:

$$\mathcal{D}_E(w, S^*) := \sum_{S \in \mathcal{S}_{|w|}} \mathbb{P}(S \mid w) \cdot |S \triangle S^*| = |w| - \sum_{(i,j) \in S^*} p_w(i, j)$$

with $|S \triangle S'|$ a shorthand for the set symmetric distance, also known as base pair distance.

Now we can define the *main objectives of negative RNA design*. Given a real-valued threshold $\varepsilon \geq 0$ and a defect $\mathcal{D}$, a sequence w is a *(negative)* $(\mathcal{D}, \varepsilon)$*-design* for a structure S^* if and only if

$$\mathrm{MFE}(w) = \{S^*\} \quad \text{and} \quad \mathcal{D}(w, S^*) \leq \varepsilon. \tag{1}$$

Similarly, we call $(\mathcal{D}, \varepsilon)$-designable a secondary structure that does admit at least a valid design. Note that the defect definition also depends on the chosen energy model, but we chose to make this dependency implicit for the sake of simplicity.

Motifs and local defect. A *motif* is a rooted ordered tree, similar to a secondary structure, but whose leaves may represent base paired positions. We say *a motif m occurs in a secondary structure S (resp. a motif m')* or *a secondary structure S (resp. a motif m') contains a motif m* if m is a subtree of S (resp. m'), rooted at any base paired node in S (resp. m') and obtained by deleting all the children for a subset of its base paired nodes. In other words, a node in m either has exactly all of its children within S (resp. m'), or none. See Fig. 1 for an example.

Consider a motif m, having a root base-pair (i, j) and paired leaves $(i_1, j_1), \ldots, (i_l, j_l)$, and let w, $|w| = n$, be an assignment of nucleotides to the positions of m. We define the *local defect* $\mathcal{D}^L(w, m)$ similarly as $\mathcal{D}$, by replacing $\mathcal{S}_n$ with

$$\mathcal{S}_m := \{S \in \mathcal{S}_n \mid (i, j) \in S \text{ and } (i_\ell, j_\ell) \in S, \forall \ell \in [1, l]\}$$

a restricted set of structures where both the root, and all the paired leaves, of m appear as base pairs. A crucial observation, which we formally prove in Supp. Mat. A, is stated in the following proposition.

Proposition 1. *For any defect $\mathcal{D} \in \{\mathcal{D}_S, \mathcal{D}_P, \mathcal{D}_E\}$, sequence w, $|w| = n$, and structure $S \in \mathcal{S}_n$, one has*

$$\mathcal{D}(w, S) \geq \mathcal{D}^L(w_m, m), \forall m \in S$$

where w_m is the restriction of w to the positions in m.

Corollary 1. *If there exists a motif $m \in S^*$ such that*

$$\mathcal{D}^L(w, m) \geq \varepsilon, \forall w \in \Sigma^{|m|},$$

then S^* cannot be $\mathcal{D}$-designed.

In other words, the presence in the target structure S^* of a motif that cannot be designed *locally* is sufficient to forbid the existence of a sequence w that would constitute a design for S^*.

Problem statement and results overview. In this work, we address the following question: *Given an energy model, a design criterion, how many secondary structures of a given length actually admit a negative design?* Our main result is summarized by the following theorem.

Theorem 1. *For any energy model, defect $\mathcal{D} \in \{\mathcal{D}_S, \mathcal{D}_P, \mathcal{D}_E\}$ and tolerance $\varepsilon \geq 0$, only an exponentially small fraction of the secondary structures in $\mathcal{S}_n$ are $(\mathcal{D}, \varepsilon)$-designable.*

3 BASIC COMBINATORIAL DESIGN

Here, we consider the special case of the 0-dominance criterion in the simplest energy model, the Nussinov model, considered in a previous work [22]. In this setting, the design problem simplifies into finding an RNA sequence admitting a unique folding maximizing the number of base pairs, such that this folding coincides with the given target secondary structure.

Theorem 2. *Let d_n be the number of secondary structures that are designable in the Nussinov model with $\theta = 1$. Then*

$$d_n \in O\left(\frac{\alpha^n}{n\sqrt{n}}\right) \tag{2}$$

where $\alpha = 2.35\ldots$ is the smallest positive real root of

$$5z^8 - 14z^7 + 13z^6 - 8z^5 + 6z^4 - 2z^3 + 4z^2 - 4z + 1.$$

Corollary 2. *The probability that a uniform random secondary structure of length n, with $\theta = 1$, is designable in the Nussinov model for the 0-dominance criterion is in $O(\beta^n)$, where $\beta = \alpha(3-\sqrt{5})/2 < 1$.*

To prove Theorem 2, we rely on analytic combinatorics techniques, widely used in analysis of algorithms [15] and bioinformatics [42], exposed in [16]. Their application in this context involves the following steps:

(1) Identify a collection of secondary structure motifs $\mathcal{M}$ whose occurrence in S implies that S is not designable in the Nussinov model for the 0-dominance criterion;
(2) Design a grammar for the set $\mathcal{S}^{\overline{\mathcal{M}}}$ of all RNA secondary structures excluding this motif;
(3) Derive and solve a system of functional equations satisfied by the generating function $S^{\overline{\mathcal{M}}}(z) = \sum_{n\geq 0} s_n z^n$, where s_n is the number of structures of $\mathcal{S}^{\overline{\mathcal{M}}}$ of length n;
(4) Use singularity analysis to obtain an asymptotic equivalent for s_n, in particular the coefficient α of (2) in Theorem 2, called the *growth factor*, that drives the exponential growth of s_n as a function of n.

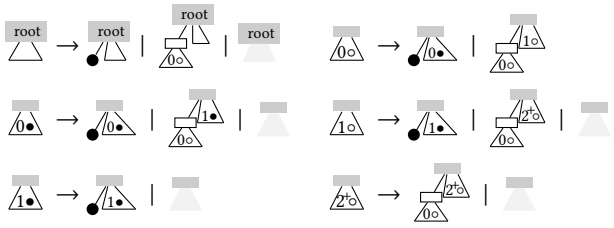
Corollary 2 follows from Theorem 2 and the fact that, when $\theta = 1$, the asymptotic number t_n of secondary structures of length n is such that

$$t_n \in \Theta\left(\frac{\left(2/\left(3-\sqrt{5}\right)\right)^n}{n\sqrt{n}}\right). \tag{3}$$

The exponential decrease in the number of designable secondary structures follows from $2/\left(3-\sqrt{5}\right) = 2.62\ldots > \alpha = 2.35\ldots$.

We now turn to the proof of Theorem 2. For step (1) of the approach outlined above, we rely on the recent paper [22], where it was proved that a secondary structure cannot be designed if its tree representation includes an internal node whose children set contain ≥ 2 internal nodes and at least one leaf (the collection of motifs $\mathcal{M}$ discussed above).

The set of tree representations of the secondary structure avoiding this local motif can be generated by the context-free grammar given below.



Intuitively, this grammar keeps track of properties of the structural elements generated for the current internal node. Except for the root, each non-terminal is indexed by pairs taken from $(i, u) \in \{0, 1, 2^+\} \times \{\circ, \bullet\}$ where, within the current siblings, i represents the number of internal nodes/base pairs, and u expresses whether ($\bullet$) or not ($\circ$) a leaf has been generated. Notice that the grammar implicitly excludes structures having a three siblings composed of two internal nodes and one leaf ($(i, u) = (2^+, \bullet)$), i.e. the motif $\mathcal{M}$.

Following standard enumerative combinatorics techniques that links combinatorial specifications to the calculus of generating functions [16], one obtains that the ordinary generating function $S^{\overline{\mathcal{M}}}(z)$ is defined by the system of functional equations below.

$$\begin{aligned}
S^{\overline{\mathcal{M}}}(z) &= z \times S^{\overline{\mathcal{M}}}(z)(z) + z^2 \times S_{0\circ}(z) \times S^{\overline{\mathcal{M}}}(z) + 1\\
S_{0\bullet}(z) &= z \times S_{0\bullet}(z) + z^2 \times S_{0\circ}(z) \times S_{1\bullet}(z) + 1\\
S_{1\bullet}(z) &= z \times S_{1\bullet}(z) + 1\\
S_{0\circ}(z) &= z \times S_{0\bullet}(z) + z^2 \times S_{0\circ}(z) \times S_{1\circ}(z)\\
S_{1\circ}(z) &= z \times S_{1\bullet}(z) + z^2 \times S_{0\circ}(z) \times S_{2^+\circ}(z) + 1\\
S_{2^+\circ}(z) &= z^2 \times S_{0\circ}(z) \times S_{2^+\circ}(z) + 1
\end{aligned}$$

Solving the system using algebraic elimination, followed by a careful choice of the right conjugate, one obtains a closed form for the generating function $S^{\overline{\mathcal{M}}}(z)$:

$$S^{\overline{\mathcal{M}}}(z) = -\frac{P(z)\sqrt{R(z)}}{Q(z)}$$

where

$$P(z) = 2z^5 - 7z^4 + 7z^3 - 6z^2 + 4z - 1$$

$$Q(z) = 2z(z-1)(z^4 - 4z^3 + 3z^2 - 3z + 1)$$

$$R(z) = 5z^8 - 14z^7 + 13z^6 - 8z^5 + 6z^4 - 2z^3 + 4z^2 - 4z + 1.$$

It follows from classic transfer theorems [15] that the singularity of this generating function is of square-root type, leading to the

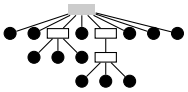


Figure 2: The minimal completion structure of the motif Fig. 1d.

following asymptotic expansion for its coefficients,

$$s_n \in \Theta\left(\frac{{\rho_{\mathcal{M}}}^{-n}}{n\sqrt{n}}\right).$$

where $\rho_{\mathcal{M}}$ is the dominant singularity of $S_{\mathrm{r}}(z)$, *i.e.* the smallest root of $R(z)$, and can be numerically evaluated at $\rho_{\mathcal{M}} = 0.4262\ldots$.

Theorem 2 follows from $\alpha = 1/\rho_{\mathcal{M}}$ and the fact that $d_n \leq s_n$. Indeed, while it is necessary for a designable secondary structures to avoid $\mathcal{M}$, this condition is not sufficient.

4 LOCAL OBSTRUCTIONS

In this section, we describe an algorithm to compute local obstruction, motifs whose presence within a secondary structure forbids its design with respect to some predefined design objectives. Fig. 3 describes the main workflow of this study.

4.1 Emulating a local defect with constraints

The *minimal completion* a motif m for a nucleotide assignment w is a pair (S_m, w_m) such that:

- S_m is the secondary structure obtained from m by adding θ unpaired nodes (leaves) under each paired leaf node;
- w_m is the sequence obtained by inserting θ occurrence of the letter A under paired leaves.

In this study, we set $\theta = 1$ for the *Nussinov* model and $\theta = 3$ for the *Turner* model. Let us consider the motif in Fig. 1d, a motif with two paired leaves. We obtain the minimal completion structure by replacing those a paired leaf by  in the *Turner* model (Fig. 2).

Given a length k, a *folding constraint* C is a set consisting of positions from $[1, k]$ and pairs from $[1, k]^2$, respectively representing positions forced to remain unpaired and paired to a specific partner. The *constrained defect* $\mathcal{D}_C(w, S)$ can be defined by restricting the computation to structures compatible with the constraint C. Such constraints are supported by all reference implementations of the energy-minimization and partition-function algorithms in complex energy models, and can be easily enforced in simpler energy models.

Now consider a motif m and its minimal completion (S_m, w_m). We define the *induced constraint* C_m of a motif m as consisting of:

- the root base pair of S_m;
- the base pairs in S_m stemming from the paired leaves in m;
- the unpaired positions introduced by the completion.

Intuitively, such a constraint will limit the alternative conformations, considered by the defect computation, to be consistent with the boundaries of the initial motif. A *truncation* operation is defined as the inverse of the completion, and allows to recover a motif m from its completion S_m.

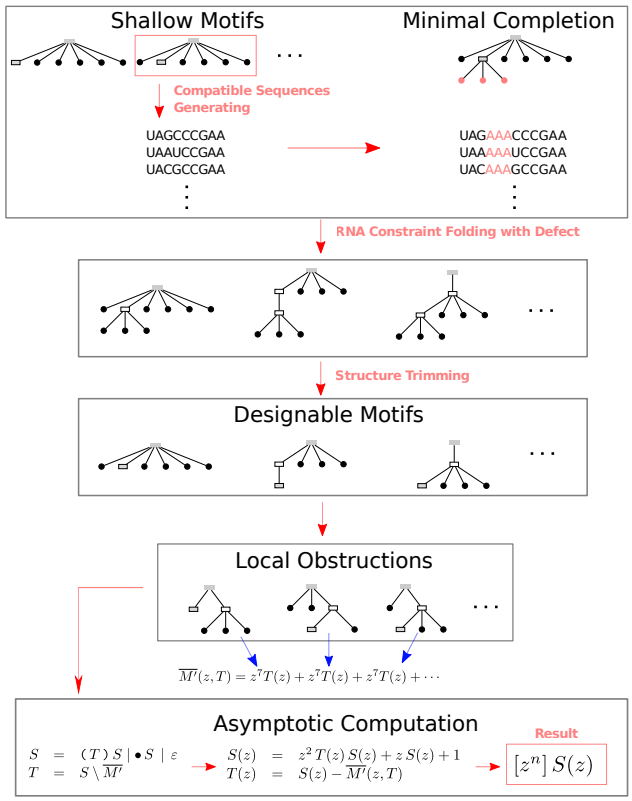


Figure 3: Workflow

Proposition 2. *For every defect $\mathcal{D}$ and energy model considered in this work, one has $\mathcal{D}^L(w, m) = \mathcal{D}_{C_m}(w_m, S_m)$.*

In other words, the local defect of a motif can be practically computed by executing a constrained version of a, suitably constrained, global off-the-shelf algorithm (energy-minimization for $\mathcal{D}_S$, base-pair probability for $\mathcal{D}_P$ and $\mathcal{D}_E$) on the minimal completion of the motif. In particular, motifs that represent local obstructions to design, associated with large local defect, can be detected using this property as shown below. The proof of the proposition is provided in Supp. Mat. B.

4.2 Computing local obstructions

We now tackle the problem of computing the list of *local obstructions* over k nucleotides, motifs whose presence within any secondary structure implies that the overall defect exceeds a predefined *tolerance* $\varepsilon \geq 0$.

In principle, one could compute all possible motifs and nucleotides assignments, followed by an evaluation of the local defect, as described in the previous section. Then we simply consider as local obstructions any motif which, for any sequence assignment, fails to satisfy the ε threshold on local defect. Indeed, any motif whose local defect exceeds ε for all sequence assignments cannot be part of a secondary structure having defect less than ε (Prop. 1), and thus represents a local obstruction. Since motifs are essentially secondary structures over k nucleotides (with $\theta = 0$), the complexity of

this approach is in $O(3^k \cdot 4^k \cdot P(k))$, with $P(n)$ the complexity of the (constrained) energy minimization/partition function algorithm.

This complexity can be further reduced by restricting the above computation to *shallow motifs*, motifs having tree height 1 consisting of paired and unpaired nodes underneath a root node. For any sequence assignment to such a motif, running a constrained energy minimization algorithm on the minimal completion of the sequence either returns one, or multiple co-optimal solutions. In the case of multiple solutions, the sequence admits several alternative local MFE folds, and is thus not suitable for any *refinement* of the shallow motif, *i.e.* any motif that includes the pairs of the shallow motif. Conversely, a unique MFE solution is provably a refinement of the shallow motif, and one concludes that the motif is designable. Since every motif over k nucleotides is a refinement of some shallow motif, this strategy produces the same output as the above-described one. Its complexity, however, is reduced to $O(\varphi^k \cdot 4^k \cdot P(k))$, where $\varphi := (1+\sqrt{5})/2 \approx 1.62$ is the golden ratio, observing that shallow motifs are counted by the Fibonacci numbers.

Overall, for a given defect $\mathcal{D}$, restricted to a value ε, a given motif size k, our algorithm can be summarized as:

- Enumerate all the *shallow motifs* m° of depth 1, involving k nucleotides.
- For any such motif m°, consider any assignment w° consistent with the paired nodes in m°:
  - Build the minimal completion (S°_m, w°_m) of (m°, w°), and execute on w°_m a constrained MFE folding algorithm, using the induced constraint C_{m°;
  - If the resulting MFE is unique, consider the motif m' obtained by removing from the MFE structure the nucleotides introduced for the completion (m' is a refinement of m°, and a unique optimum for w°);
  - Evaluate the local defect and, if $\mathcal{D}^L(w^\circ, m') \leq \varepsilon$, add m' to the list $\mathcal{M}$ of designable motifs;
- Return $\overline{\mathcal{M}}$, the set of all motifs of size k not in $\mathcal{M}$.

A detailed version of the procedure is described in Algorithm 1.

Algorithm 1: Computing local obstructions of a given size

Input : A motif size k, an energy model E, a defect definition $\mathcal{D}$, and a tolerance $\varepsilon \geq 0$
Output : $\overline{\mathcal{M}}$ a, possibly empty, set of local obstructions of length k

$\mathcal{M} \leftarrow \varnothing$;
$\mathcal{Q}_k \leftarrow$ Set of all shallow motifs of size k;
foreach $m^\circ \in \mathcal{Q}_k$ **do**
  foreach $w^\circ \in \Sigma^k$ *(compatible with* m°*)* **do**
    $C_{m^\circ} \leftarrow$ Induced constraint of m°;
    $(S^\circ_m, w^\circ_m) \leftarrow$ Minimal completion of (m°, w°);
    $\mathcal{O} \leftarrow \mathsf{MFE}(w_m \mid C_{m^\circ})$ w.r.t. energy model E;
    if $|\mathcal{O}| = \{S'\}$ **then**
      if $\mathcal{D}_{C_{m^\circ}}(w^\circ, S') \leq \varepsilon$ **then**
        $m' \leftarrow$ truncation of S' ;
        $\mathcal{M} \leftarrow \mathcal{M} \cup \{m'\}$
  $\mathcal{R}_k \leftarrow$ Complete set of all motifs of size k;
  return $\overline{\mathcal{M}} = \mathcal{R}_k - \mathcal{M}$

Proposition 3. *Any motif returned by Algorithm 1 is a local obstruction.*

Proof. Fist, let us consider the properties of a motif m returned by the algorithm. Note that there exists only a single shallow motif m°, of which m is a refinement. Since $m \notin \mathcal{M}$ then, for each sequence w°, either a lower constrained MFE fold was found, or the local defect exceeded ε. In the latter case, Proposition 1 implies that any pair (S, w), where S features m, and sequence w having nucleotide assignment w° on the motif positions, has defect greater than ε, thus w is not a design for S. In the former case where an alternative motif m' is preferred to (or equally stable as) m for w°, then for any structure S containing m and sequence w, having nucleotide assignment w° on the positions of m, a competitor to S for w can be constructed by replacing m by m' in S. One concludes that, if $m \notin \mathcal{M}$, any structure S, $m \in S$, and sequence w does not represent a $(\mathcal{D}, \varepsilon)$-design. □

The exhaustivity, for a given size k, of the list of motifs produced by Algorithm 1 remains unclear. Indeed, a motif is disregarded as a local obstruction as soon as its minimal completion folds correctly (with admissible defect) under suitable constraints for some sequence. Thus, there is no formal guarantee that a sequence would adopt this motif with an acceptable defect in the absence of constraints. However, we empirical observed that motifs not returned by the algorithm can overwhelmingly be included in design and, in particular, that the sequence of their minimal completion is a design for the completed structure. Moreover, the possible omission of some local obstructions is not overly critical, since our main goal is to provide upper bounds on the number of designable structures.

5 ENUMERATION OF SECONDARY STRUCTURES AVOIDING LOCAL OBSTRUCTIONS

Next, we turn to the computation of asymptotic equivalent for the number of secondary structures that avoid a collection of local obstructions, computed using the algorithm outlined in the previous section. We first start by eliminating redundant motifs, *i.e.* motifs that merely extend another motif, as shown in Figure 4, which can be done by running a classic tree alignment algorithm [26] in a pairwise fashion.

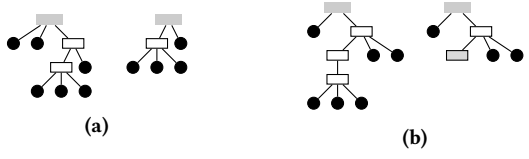


Figure 4: Two examples of pairs of redundant motifs. In both cases, the set of secondary structures rooted on the right motif strictly includes that of the right one, and we discard the left one from our computations.

5.1 Specification and generating function

Our approach represents an instance of the symbolic method [16], and is similar in essence to the detailed example of Section 3.

We establish that the set of all secondary structures avoiding a set $\mathcal{M}$ of local obstructions is generated by the following specification:

$$\begin{aligned} S &= (\,T\,)\,S \mid \bullet\, S \mid \varepsilon \\ T &= S \setminus \overline{M'} \end{aligned}$$

The first line essentially builds the set of all secondary structures ($\theta = 0$), and is highly reminiscent of Waterman's seminal decomposition [45]. The second line, however, subtracts the contributions of secondary structures which, when completed with a root, feature an occurrence of a local obstruction. In other words, M' denotes the set of enclosed forests built from the inner part of local obstructions

$$\overline{M'} := \{m' \mid \forall m \in \overline{\mathcal{M}}, m = (\,m'\,)\}.$$

Therefore, the system of generating functions can be written as

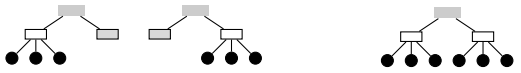
$$\begin{aligned} S(z) &= z^2\, T(z)\, S(z) + z\, S(z) + 1 \\ T(z) &= S(z) - \overline{M'}(z, T) \end{aligned} \tag{4}$$

where $\overline{M'}(z, T)$ denotes the Ordinary Generating Function (OGF) of the set of enclosed structure of motifs, defined as

$$\overline{M'}(z, T) = \sum_{m' \in \overline{\mathcal{M}'}} z^{\gamma(m')}\, T^{\delta(m')} - c(z, T)$$

where $\gamma(m')$ (resp. $\delta(m')$) is the size (resp. number of paired leaves) of the motif m', and $c(z, T)$ is a correcting term to account for potential overlaps.

Indeed, in rare cases, some secondary structures may be counted in the OGF associated to two or more motifs. Such structures would therefore be subtracted several times by the grammar, leading to an error while computing the singularity. Therefore, a correcting term $c(z, T)$ is introduced, as described in Figure 5 to counterbalance the overcounting in such (rare) situations. Given the scarcity of such situations, we computed those terms manually for each pair of motifs. A more systematic solution could be implemented, using ideas from Collet *et al* [7], but the lack of immediate needs led us to leave this for an extended version of this extended abstract.



(a) Two overlapping motifs **(b) Common structure**

Figure 5: Both motifs in (5a) represent local obstructions, each of them contributing $z^7\, T$ to the OGF $\overline{M'}(z, T)$. However, those motifs are overlapping, and any structure in the intersection, such as (5b), will be subtracted twice. We work around this issue by including a correcting term z^{10} in $c(z, T)$.

5.2 Computing the dominant singularity

In general, one could use a symbolic calculus software (`Maple`) to solve the system (4), using some specialized package (`gfun` [40]) to extract the dominant singularity. However, in our case, such a approach turns out to scale poorly with the number of motifs and, more critically, paired leaves in the motifs (*i.e.* the degree of $T(z)$ in $\overline{M'}(z, T)$). Therefore, we consider an alternative approach which combines an elementary symbolic calculus with a numerical determination of the dominant singularity.

Indeed, rewriting the system shows that $T(z)$ is a solution of $G(z, y) = 0$ where

$$G(z, y) = z^2 y^2 + y(z^2 \overline{M'}(z, y) + z) + (z - 1)\, \overline{M'}(z, y) + 1.$$

As $\overline{M'}(z, T)$ depends of $T^{\delta^\star}(z)$, for $\delta^\star = \max_{m' \in \overline{\mathcal{M}'}} \delta(m')$, the degree of G with respect to y might be greater than 2, and the problem is not directly amenable to the techniques developed in Section 3. Nevertheless, it follows from this smooth implicit-function schema that $T(z)$ is analytic. It is aperiodic and its dominant singularity, denoted ρ, is a non-zero root of $R(z)$ defined as the resultant of two polynomials in y, namely:

$$\begin{cases} P(z, y) &= G(z, y) - y \\ Q(z, y) &= \partial_y P(z, y) \end{cases}$$

The solution is easily derived by a numeric approach. The generating function $S(z)$ shares the same dominant singularity as $T(z)$. Thus, coefficients of $S(z)$ satisfy

$$[z^n]\, S(z) \in \Theta\left(\frac{\rho^{-n}}{n\sqrt{n}}\right)$$

.

Example. Let $\overline{\mathcal{M}}$ be restricted to the single motif (▭▭●), a special case of the local obstructions in the *Nussinov* Model described in [22]. Then, the O.G.F. of the set $\overline{\mathcal{M}'}$ with $\theta = 1$ is $1 + z^5 T^2(z)$ and

$$G(z, y) = z + y(z + z^2) + y^2(z^2 - z^5 + z^6) + y^3 z^7$$

Next, we compute the resultant of the polynomial $P(z, y)$ and its partial derivation on y

$$\begin{aligned} P(z, y) &= z^7 y^3 + (z^6 - z^5 + z^2) y^2 + (z^2 + z - 1) y + z \\ Q(z, y) &= 3z^7 y^2 + 2(z^6 - z^5 + z^2) y + (z^2 + z - 1) \end{aligned}$$

A numerical resolution of system locates the dominant singularity at $\rho = 0.3834$. We conclude that

$$[z^n]\, S(z) \in \Theta\left(\frac{2.6082^n}{n\sqrt{n}}\right).$$

6 RESULTS

We implemented Algorithm 1, and the numerical procedure to compute the dominant singularity described in Section 5, in `Python3` using the `pandas` library and `SymPy` [36], a Python library for symbolic computing. Our implementation is available at:
http://www.lix.polytechnique.fr/~ponty/?page=countingdesigns

6.1 Recovering the total number of secondary structures ($\theta = 3$)

As a first test, we ran Algorithm 1, using the suboptimal defect $\mathcal{D}_E$ as our objective and no tolerance for suboptimality ($\varepsilon := 0$), based on `RNAfold` [31] (version 2.4.12 with default parameters), in order to detect local obstructions of small sizes ($k \in [2, 4]$). Unsurprisingly, but still reassuringly, our implementation returned three local obstructions, (), (●), and (●●), corresponding to the $\theta = 3$ minimal distance enforced by `RNAfold`.

Such local obstructions lead to a generating function

$$\overline{M'}(z) = 1 + z + z^2,$$

Defect	ε	#Local obstructions	ρ	Asymptotic equivalent	Equivalent	Proportion of designable structures* (upper bound) $P_{10}(\%)$	P_{50} (%)	P_{100} (%)	P_{200} (%)	P_{500} (%)	P_{1000} (%)
$\mathcal{D}_E$	0	104	0.44917	$\Theta\left(\frac{2.226^n}{n\sqrt{n}}\right)$	0.973^n	76.1	25.4	6.48	$4.19 \cdot 10^{-1}$	$1.14 \cdot 10^{-4}$	$1.30 \cdot 10^{-10}$
$\mathcal{D}_P$	.5	120	0.44964	$\Theta\left(\frac{2.224^n}{n\sqrt{n}}\right)$	0.972^n	75.3	24.2	5.84	$3.41 \cdot 10^{-1}$	$6.81 \cdot 10^{-5}$	$4.64 \cdot 10^{-11}$
$\mathcal{D}_P$	.1	155	0.45967	$\Theta\left(\frac{2.176^n}{n\sqrt{n}}\right)$	0.95^n	59.9	7.69	0.59	$3.51 \cdot 10^{-3}$	$7.27 \cdot 10^{-10}$	$5.29 \cdot 10^{-21}$
$\mathcal{D}_P$	.01	177	0.48127	$\Theta\left(\frac{2.078^n}{n\sqrt{n}}\right)$	0.908^n	38.1	0.80	$6.44 \cdot 10^{-3}$	$4.14 \cdot 10^{-7}$	$1.10 \cdot 10^{-19}$	$1.22 \cdot 10^{-40}$

Table 1: Collections of local obstructions of size up to 12, and their consequences on the proportion of actually designable secondary structures. * Proportions of designable sequences computed using an assumption of equal constants for the asymptotic leading terms of the number of secondary structures, respectively allowing and forbidding local obstructions.

and an application of our method produces the following asymptotic upper bound for the number of designable secondary structures of size n:

$$[z^n]\, S(z) = s_n \in \Theta\left(\frac{2.289^n}{n\sqrt{n}}\right). \tag{5}$$

Note that the singularity matches the value reported by Hofacker *et al* [25].

6.2 Refined estimates for the phenotype space

We pushed our analysis further by using Algorithm 1 to compute the local obstructions of sizes up to 12 (#Paired leaves $\in [0, 5]$). After removing the redundant motifs from the set, we manually computed the correcting terms $c(z, T)$ to avoid double-counting structures compatible with several obstructions. Then, we applied the methodology of Section 5 to produce the dominant term of the asymptotics, along with an first-order estimate of the proportion of designable structures. Our results are summarized in Table 1.

6.2.1 Inverse folding. In the classic setting of RNA design, the inverse folding, one attempts to design a sequence which admits a target structure as its unique MFE structure. This corresponds to choosing a suboptimal defect with $\varepsilon = 0$.

Our analysis reveal the existence of 104 motifs (after removal of redundant ones), an overwhelming majority of which contain isolated base pairs. Such motifs are expected, as they are heavily penalized, yet not explicitly forbidden (unless specified), by folding algorithms. Consecutive bulges, alternating on the 5' and 3' ends of an helix, also seem systematically suboptimal for the Turner model, a large interior loop being systematically favored as a candidate for the MFE. Finally, hairpin loops directly stemming from a multiloop are systematically discriminated, and a structure consisting of a larger unpaired stretch in the multiloop seem systematically favored.

Computing the dominant singularity yields $\rho = 0.44917$, which implies the following asymptotic upper bound on the number of secondary structures

$$[z^n]\, S(z) = s_n \in \Theta\left(\frac{2.22632^n}{n\sqrt{n}}\right). \tag{6}$$

The probability for a secondary structure of size n, taken uniformly at random, to be designable is upper-bounded by $P_n \in \Theta(0.973^n)$. Assuming the identity of constants involved in the leading terms of Equations (5) and (6), one concludes that, while about 3/4 of the structures of size 10 can be designed, this proportion quickly drops to less than 0.5% for RNAs of size 200, and reaches infinitesimal proportions (10^{-10}%) for very large RNAs of size 1 000.

6.2.2 Designing structures with large probabilities. Next, we analyze the probability defect $\mathcal{D}_P$, and investigate the impact of ε on the proportion of designable secondary structures. We consider 3 thresholds, $\varepsilon \in \{.5, 0.1, 0.01\}$, associated with Boltzmann probabilities for the motif greater than 50%, 90% and 99% respectively. Executing Algorithm 1, followed by a removal of redundant motifs, led to the identification 120, 155 and 177 local obstructions respectively.

Interestingly, the $\varepsilon = 50\%$ case induces a dominant singularity of 0.44964, leading to a slightly slower asymptotic growth

$$[z^n]S(z) = s_n \in \Theta\left(\frac{2.22400^n}{n\sqrt{n}}\right)$$

than in the case of the inverse folding. This is not entirely unexpected, since our definition of a valid design requires the target structure to be the sole MFE for the sequence, and thus the set of secondary structures satisfying any probability defect is a strict subset of the solutions to the inverse folding problem. However, the fact that the singularities do not strictly coincide suggests that an exponentially small proportion (albeit with growth factor very close to 1) of MFE designs have Boltzmann probability greater than 50%.

For defect thresholds of 0.1 and 0.01 on the probability, the departure from the MFE design is much more pronounced, with respective singularities at 0.45967 and 0.48127 respectively, leading to asymptotic equivalents in

$$\Theta\left(\frac{2.1754^n}{n\sqrt{n}}\right) \quad \text{and} \quad \Theta\left(\frac{2.07783^n}{n\sqrt{n}}\right).$$

Again, assuming the equality of constants, we obtain proportions of designable structures bounded by $P_n = 0.95^n$ and $P_n = 0.908^n$ respectively. Those estimates support the notion of an extreme sparsity of designable structures in the folding space, with only three out of 10^{-5} (resp. 4 out of 10^{-9}) structures being designable for $\varepsilon = 0.1$ (resp. $\varepsilon = 0.01$). These abysmal proportions are consistent with the popular belief, which rigorously holds for the homopolymer model [12], that the Boltzmann probability of the MFE structure decreases exponentially with the sequence length in a random, uniformly distributed, RNA sequence.

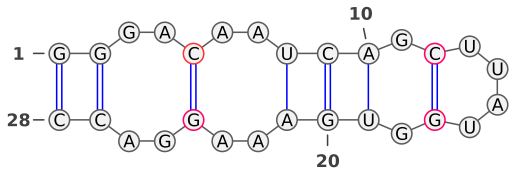


Figure 6: Example of secondary structure with isolated base pairs. The MFE structure of RNA sequence GGGACAAUCAGCUUAUGGUGAAAGGACC has two isolated base pairs (related bases are marked in red).

7 CONCLUSION

In this work, we have addressed the designability of RNA structures for a variety of design paradigms, thresholds and energy models. We have described a procedure for computing a list of local motifs whose presence represents an obstruction to the design task. This procedure is largely agnostic to the exact objectives of design, and holds for any design under mild assumptions (monotonicity of defects over loops). Using enumerative and analytic combinatorics techniques, we were able to automate the computation of asymptotic upper-bounds, revealing an overall sparsity of designable structures within the space of all conformations in the Turner model.

This work sets the stage for further analyses of designable structures, and unlocks a systematic way to address many further questions. For instance, the popular ensemble defect [49], could benefit from a more refined treatment using bivariate generating functions. Indeed, the ensemble defect is defined as an expectation, and is therefore fully additive on the Turner loops of the target secondary structures. One could therefore determine, through a trivial modification of Equation (4), the bivariate generating function $S(z,u) = \sum_{n,k\geq 0} s_{n,v} z^n u^k$, $s_{n,v}$ being an upper bound for the number of structures of size n having v ensemble defect. An application of the famous Drmota theorem [11] would then very likely provide sharper estimates, by accounting the accumulation of local defects rather than only consider the worst one, as currently done in this work.

Enumerative aspects of this work could also easily be extended to secondary structures including algebraic types of pseudoknots. Indeed, multiple grammars have been shown to capture major pseudoknot classes while, at the same time, allowing for a characterization of generating functions [37]. An enumeration of designable structures would greatly help in the parametrization of free-energy models, a key aspect of pseudoknot prediction programs which has so far greatly hindered the development of predictive methods [34].

Regarding the complexity of our method for building local obstructions, we strongly believe its exponential nature may be intrinsic to the problem. More precisely, we believe that the list of local obstructions may generically grow exponentially with the length of investigated motifs. Since structures are also motifs in our definitions, then a polynomially-bounded list of local obstructions would imply a polynomial-time algorithm for the natural decision problem associated with RNA design. Unfortunately, the problem has recently been shown to be NP-hard [3], which appears to ruling out any hope of a polynomial-time alternative to Algorithm 1.

On a more positive note, Algorithm 1 can easily be modified to keep the list of suitable candidate sequences for each and every designable motif. This allows to greatly restrict the search space of classic design algorithms, but also suggests a promising strategy for hard design instances. As an illustration, while investigating our database of local obstructions, we discovered that lonely base pairs appear in a few designable motifs, usually considered unstable in the *Turner* model and difficult to design for. For example, the structure `(((.(....).)))` is the MFE structure of the RNA sequence UCAGCUUAUGGUGA. We also found that the motif `((..(*)..))` could be designable for some collection of sequences. Combining sequences adopting these two motifs, we could verify that an RNA sequence

GGGACAAUCAGCUUAUGGUGAAAGGACC

is predicted by `RNAfold` to adopt an MFE structure of

`((..(..(((.(....).)))..)..))`

featuring two isolated base pairs, and a free-energy of -6.4kcal.mol^{-1} that was not matched across several runs of `RNAfold` and `Nupack` [49]. This observation remains anecdotal, and its validation on traditional design tasks requires to be confirmed by further analyses.

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A PROOF OF PROPOSITION 1

Proposition. *For any defect $\mathcal{D} \in \{\mathcal{D}_S, \mathcal{D}_P, \mathcal{D}_E\}$, sequence w, $|w| = n$, and structure $S \in \mathcal{S}_n$, one has*

$$\mathcal{D}(w, S) \geq \mathcal{D}^L(w_{[|m|]}, m), \forall m \in S$$

where w_m is the restriction of w to the positions in m.

Proof. Let constraint C be the set of all (un)paired positions of $S \setminus m$ plus the paired leaves and the root of m and $\mathcal{S}_C \subset \mathcal{S}$ denotes the set of secondary structures of size n that are compatible with the constraint C. Then, we have the follow inequality,

$$\begin{aligned}\mathbb{P}(S \mid w) &= \frac{\mathcal{B}(w,S)}{\sum_{S' \in \mathcal{S}_n} \mathcal{B}(w,S')} \\ &\leq \frac{\mathcal{B}(w,S)}{\sum_{S' \in \mathcal{S}_C} \mathcal{B}(w,S')} \\ &= \frac{\mathcal{B}(w_{[|m|]},m)}{\sum_{m' \in \mathcal{S}_m} \mathcal{B}(w_{[|m|]},m')} \\ &= \mathbb{P}(m \mid w_{[|m|]})\end{aligned}$$

Therefore, $\mathcal{D}_P(w, S) \geq \mathcal{D}_P^L(w_{[|m|]}, m)$.

Similarly,

$$\begin{aligned}\sum_{S' \in \mathcal{S}_n} \mathbb{P}(S' \mid w) \cdot |S' \triangle S| &\geq \sum_{S' \in \mathcal{S}_C} \mathbb{P}(S' \mid w) \cdot |S' \triangle S| \\ &= \sum_{m' \in \mathcal{S}_m} \mathbb{P}(m' \mid w_{[|m|]}) \cdot |m' \triangle m|\end{aligned}$$

Thus, the inequality for $\mathcal{D} = \mathcal{D}_E$

For the case $\mathcal{D} = \mathcal{D}_S$, we consider m' such that,

$$m' := \underset{\substack{x \in \mathcal{S}_m \\ x \neq m}}{\operatorname{argmin}} E(w_{[|m|]}, x) - E(w_{[|m|]}, m)$$

A such m' exists since the set $\mathcal{S}_m$ is finite. Let $S' \in \mathcal{S}_C$ be the secondary structure containing m' at the position of m. We have,

$$E(w_{[|m|]}, m') - E(w_{[|m|]}, m) = E(w, S') - E(w, S)$$

In addition, we have, by definition, $\mathcal{D}_S(w, S) \geq e^{-(E(w,S')-E(w,S))}$, which implies the inequality $\mathcal{D}_S(w, S) \geq \mathcal{D}_S^L(w_{[|m|]}, m)$ □

B PROOF OF PROPOSITION 2

Proposition. *For every defect $\mathcal{D}$ and energy model considered in this work, one has $\mathcal{D}^L(w, m) = \mathcal{D}_{C_m}(w_m, S_m)$.*

Proof. The schema of proof is similar to the above one. Let $\mathcal{S}_{C_m}$ be the set of secondary structures of length $|S_m|$ that are compatible with the folding constraint C_m. One can observe that the way to make the completion structure is a bijection from $\mathcal{S}_m$ to $\mathcal{S}_{C_m}$. Let m' be a motif equivalent to m and $S_{m'} \in \mathcal{S}_{C_m}$ be its minimum completion structure. The energy of the structure S_m (resp. $S_{m'}$) is the sum of the energy contribution with the motif m (resp. m') and with the constrained part, which is the same for both structures. The later one is a constant for a given sequence. For the reason of simplicity, we denote it by E_C. Then, for a given sequence w and its minimum completion w_m, we have

$$E(w_m, S_{m'}) - E(w_m, S_m) = E(w, m') - E(w, m)$$

This proves the proposition for the case where $\mathcal{D} = \mathcal{D}_S$

For the case of the Probability Defect $\mathcal{D}_P$,

$$\begin{aligned}\mathbb{P}(S_m \mid w_m) &= \frac{e^{-E(w_m,S_m)/RT}}{\sum_{S_{m'} \in \mathcal{S}_C} e^{-E(w_m,S_{m'})/RT}} \\ &= \frac{e^{-E(w,m)/RT} e^{-E_C/RT}}{\sum_{m' \in \mathcal{S}_m} e^{-E(w,m')/RT} e^{-E_C/RT}} \\ &= \frac{e^{-E(w,m)/RT}}{\sum_{m' \in \mathcal{S}_m} e^{-E(w,m')/RT}} \\ &= \mathbb{P}(m \mid w)\end{aligned}$$

Thus, the equality.

Furthermore, for any motif $m' \in \mathcal{S}_m$ and its minimal completion $S_{m'}$, the base pair distance are equal between motifs m' and m and between their minimal completion structures, $|m' \triangle m| = |S_{m'} \triangle S_m|$, because the completion part is same for both motifs. Therefore, the equality for the case of the ensemble defect $\mathcal{D} = \mathcal{D}_E$ □