What Makes the ARC-PRESERVING SUBSEQUENCE Problem Hard?*

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Abstract. Given two arc-annotated sequences (S, P) and (T, Q) representing RNA structures, the ARC-PRESERVING SUBSEQUENCE (APS) problem asks whether (T, Q) can be obtained from (S, P) by deleting some of its bases (together with their incident arcs, if any). In previous studies [3, 6], this problem has been naturally divided into subproblems reflecting intrinsic complexity of arc structures. We show that APS(CROSSING, PLAIN) is **NP**-complete, thereby answering an open problem [6]. Furthermore, to get more insight into where actual border of APS hardness is, we refine APS classical subproblems in much the same way as in [11] and give a complete categorization among various restrictions of APS problem complexity.

Keywords: RNA structures, Arc-Preserving Subsequence, Computational complexity.

1 Introduction

At a molecular state, the understanding of biological mechanisms is subordinated to RNA functions discovery and study. Indeed, it is established that the conformation of a single-stranded RNA molecule (a linear sequence composed of ribonucleotides A , U , C and G , also called *primary structure*) partly determines the molecule function. This conformation results from the folding process due to local pairings between complementary bases ($A-U$ and $C-G$). The RNA secondary structure is a collection of folding patterns that occur in it.

RNA secondary structure comparison is important in many contexts, such as (i) identification of highly conserved structures during evolution which suggest a significant common function for the studied RNA molecules [9], (ii) RNA

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classification of various species (phylogeny)[2], (iii) RNA folding prediction by considering a set of already known secondary structures [13].

Structure comparison for RNA has thus become a central computational problem bearing many challenging computer science questions. At a theoretical level, RNA structure is often modelled as an *arc-annotated sequence*, that is a pair (S, P) where S is a sequence of ribonucleotides and P represents hydrogen bonds between pairs of elements of S . Different pattern matching and motif search problems have been investigated in the context of arc-annotated sequences among which we can mention ARC-PRESERVING SUBSEQUENCE (APS) problem, EDIT DISTANCE problem, ARC-SUBSTRUCTURE (AST) problem and LONGEST ARC-PRESERVING SUBSEQUENCE (LAPCS) problem (see for instance [3, 8, 7, 6, 1]). For other related studies concerning algorithmic aspects of (protein) structure comparison using *contact maps*, refer to [5, 10].

In this paper, we focus on APS problem: given two arc-annotated sequences (S, P) and (T, Q) , this problem asks whether (T, Q) can be exactly obtained from (S, P) by deleting some of its bases together with their incident arcs, if any. This problem is commonly encountered when one is searching for a given RNA pattern in an RNA database [7]. Moreover, from a theoretical point of view, APS problem can be seen as a restricted version of LAPCS problem, and hence has applications in structural comparison of RNA and protein sequences [3, 5, 12]. APS problem has been extensively studied in the past few years [6, 7, 3]. Of course, different restrictions on arc-annotation alter APS computational complexity, and hence this problem has been naturally divided into subproblems reflecting the complexity of the arc structure of both (S, P) and (T, Q) : PLAIN, CHAIN, NESTED, CROSSING or UNLIMITED (see Section 2 for details). All of them but one have been classified as to whether they are polynomial time solvable or **NP**-complete. The problem of the existence of a polynomial time algorithm for APS(CROSSING,PLAIN) problem was mentioned in [6] as the last open problem in the context of arc-preserving subsequences. Unfortunately, as we shall prove in Section 4, APS(CROSSING,PLAIN) is **NP**-complete even for restricted special cases.

In analyzing the computational complexity of a problem, we are often trying to define a precise boundary between polynomial and **NP**-complete cases. Therefore, as another step towards establishing the precise complexity landscape of APS problem, we consider that it is of great interest to subdivide existing cases into more precise ones, that is to refine classical complexity levels of APS problem, for determining more precisely what makes the problem hard. For that purpose, we use the framework introduced by Vialette [11] in the context of 2-intervals (a simple abstract structure for modelling RNA secondary structures). As a consequence, the number of complexity levels rises from 4 to 8, and all the entries of this new complexity table need to be filled. Previous known results concerning APS problem, along with our **NP**-completeness proofs, allow us to fill all the entries of this new table, therefore determining what exactly makes the APS problem hard.

The paper is organized as follows. Provided with notations and definitions (Section 2), in Section 3 we introduce and explain new refinements of the complexity levels we are going to study. In Section 4, we show that $\text{APS}(\{\sqsubset, \emptyset\}, \emptyset)$ is **NP**-complete thereby proving that *classical* $\text{APS}(\text{CROSSING}, \text{PLAIN})$ is **NP**-complete as well. As another refinement to that result, we prove that $\text{APS}(\{\prec, \emptyset\}, \emptyset)$ is **NP**-complete. Finally, in Section 5, we give new polynomial time solvable algorithms for restricted instances of $\text{APS}(\text{CROSSING}, \text{PLAIN})$.

2 Preliminaries

An RNA structure is commonly represented as an arc-annotated sequence (S, P) where S is a sequence of ribonucleotides (or bases) and P is a set of arcs connecting pairs of bases in S . Let (S, P) and (T, Q) be two arc-annotated sequences such that $|S| \geq |T|$ (in the following, $n = |S|$ and $m = |T|$). APS problem asks whether (T, Q) can be exactly obtained from (S, P) by deleting some of its bases together with their incident arcs, if any.

Since the general problem is easily seen to be intractable [3], the arc structure must be restricted. Evans [3] proposed four possible restrictions on P (resp. Q) which were largely reused in subsequent literature: (1) there is no base incident to more than one arc, (2) there are no arcs crossing, (3) there is no arc contained in another and (4) there is no arc.

These restrictions are used progressively and inclusively to produce five different levels of allowed arc structure: UNLIMITED - general problem with no restrictions, CROSSING - restriction (1); NESTED - restrictions (1) and (2); CHAIN - restrictions (1), (2) and (3); PLAIN - restriction (4).

Guo proved in [7] that $\text{APS}(\text{CROSSING}, \text{CHAIN})$ is **NP**-complete. Guo *et al.* observed in [6] that **NP**-completeness of $\text{APS}(\text{CROSSING}, \text{CROSSING})$ and $\text{APS}(\text{UNLIMITED}, \text{PLAIN})$ easily follows from results of Evans [3] concerning LAPCS problem. Furthermore, they gave a $O(nm)$ time algorithm for $\text{APS}(\text{NESTED}, \text{NESTED})$. This algorithm can be applied to easier problems such as $\text{APS}(\text{NESTED}, \alpha)$ and $\text{APS}(\text{CHAIN}, \alpha)$ with $\alpha \in \{\text{CHAIN}, \text{PLAIN}\}$. Finally, Guo *et al.* mentioned in [6] that $\text{APS}(\text{CHAIN}, \text{PLAIN})$ can be solved in $O(n+m)$ time. Observe that UNLIMITED level has no restrictions, and hence is of limited interest in our study. Consequently, from now on we will not be concerned anymore with that level. Until now, the question of the existence of an exact polynomial algorithm for $\text{APS}(\text{CROSSING}, \text{PLAIN})$ remained open. We will show in the present paper that $\text{APS}(\text{CROSSING}, \text{PLAIN})$ is **NP**-complete.

3 Refinement of APS Problem

In this section, we propose a refinement of APS problem. We first state formally our approach and explain why such a refinement is relevant for both theoretical and experimental studies.

3.1 Splitting the Levels.

As we will show soon, $\text{APS}(\text{CROSSING}, \text{PLAIN})$ is **NP**-complete. That result answers the last open problem concerning APS computational complexity with respect to classical complexity levels. However, we are mainly interested in the elaboration of a precise border between **NP**-complete and polynomially solvable cases. Indeed, both theorists and practitioners might naturally ask for more information concerning APS hard cases in order to get valuable insight into what makes the problem difficult. As a next step towards better understanding what makes APS problem hard, we propose to refine classically models used for classifying arc-annotated sequences. Our refinement consists in splitting those models of arc-annotated sequences into more precise relations between arcs. For example, such a refinement provides a general framework for investigating polynomial time solvable and hard restricted instances of $\text{APS}(\text{CROSSING}, \text{PLAIN})$, thereby refining in many ways Theorem 1 (see Section 5).

We use three relations first introduced by Vialette [11] in the context of 2-intervals. Actually, his definition of 2-intervals could almost apply in this paper (the main difference lies in the fact that 2-intervals are used for representing sets of contiguous arcs). Vialette defined three possible relations between 2-intervals that can be used for arc-annotated sequences as-well. They are the following: for any two arcs $A_1 = (i, j)$ and $A_2 = (k, l)$ in P , we will write $A_1 < A_2$ if $i < j < k < l$ (*precedence* relation), $A_1 \sqsubset A_2$ if $k < i < j < l$ (*nested* relation) and $A_1 \bowtie A_2$ if $i < k < j < l$ (*crossing* relation). Two arcs A_1 and A_2 are τ -comparable for some $\tau \in \{<, \sqsubset, \bowtie\}$ if $A_1 \tau A_2$ or $A_2 \tau A_1$. Let $\mathcal{P}$ be a set of arcs and R be a non-empty subset of $\{<, \sqsubset, \bowtie\}$. The set $\mathcal{P}$ is said to be *R-comparable* if any two distinct arcs of $\mathcal{P}$ are τ -comparable for some $\tau \in R$. An arc-annotated sequence (P, A) is said to be an *R-arc-annotated sequence* for some non-empty subset R of $\{<, \sqsubset, \bowtie\}$ if A is *R-comparable*. By abuse of notation, we write $R = \emptyset$ in case $A = \emptyset$. Observe that our model cannot deal with arc-annotated sequences which contain only one arc. However, having only one arc or none can not really affect the problem computational complexity. Just one guess reduces from one case to the other.

As a straightforward illustration of above definitions, classical complexity levels for APS problem can be expressed in terms of combinations of our new relations: **PLAIN** is fully described by $R = \emptyset$, **CHAIN** by $R = \{<\}$, **NESTED** by $R = \{<, \sqsubset\}$ and **CROSSING** by $R = \{<, \sqsubset, \bowtie\}$. The key point is to observe that our refinement allows us to consider new structures for arc-annotated sequences, namely $R \in \{\{\sqsubset\}, \{\bowtie\}, \{<, \bowtie\}, \{\sqsubset, \bowtie\}\}$, which could not be considered using classical complexity levels. Although other refinements may be possible (in particular well-suited for parameterized complexity analysis), we do believe that such an approach allows a more precise analysis of APS complexity. Of course one might object that some of these subdivisions are unlikely to appear in RNA secondary structures. However, it is of great interest to answer, at least partly, the following question: Where is the precise boundary between polynomial and **NP**-complete cases? Indeed, such a question is relevant for both theoretical and experimental studies.

4 Hardness Results

We show in this section that $\text{APS}(\{\sqsubset, \emptyset\}, \emptyset)$ and $\text{APS}(\{\leq, \emptyset\}, \emptyset)$ are **NP**-complete thereby proving that $\text{APS}(\text{CROSSING}, \text{PLAIN})$ is **NP**-complete. That result answers an open problem posed by Gramm, Guo and Niedermeier in [6] which is the last open problem concerning the APS computational complexity with respect to classical complexity levels, *i.e.*, **PLAIN**, **CHAIN**, **NESTED** and **CROSSING**.

Theorem 1. $\text{APS}(\{\sqsubset, \emptyset\}, \emptyset)$ is **NP**-complete.

We prove Theorem 1 by giving a polynomial time reduction from the well known **NP**-complete 3-SAT problem [4]. Due to space considerations, the entire proof is deferred to the full version of the paper.

It follows immediately from Theorem 1 that $\text{APS}(\{\leq, \sqsubset, \emptyset\}, \emptyset)$, and hence $\text{APS}(\text{CROSSING}, \text{PLAIN})$, are **NP**-complete. One might naturally ask for more information concerning hard cases of APS problem in order to get valuable insight into what makes the problem difficult. Another refinement of the hardness of $\text{APS}(\text{CROSSING}, \text{PLAIN})$ is given by the following theorem.

Theorem 2. $\text{APS}(\{\leq, \emptyset\}, \emptyset)$ is **NP**-complete.

The proof is also by reduction from 3-SAT. Due to space considerations, the rather technical proof is also deferred to the full version of the paper.

5 Two Polynomial Time Solvable APS Problems

We prove in this section that $\text{APS}(\{\emptyset\}, \emptyset)$ and $\text{APS}(\{\emptyset\}, \{\emptyset\})$ are polynomial time solvable. In other words, relation $\emptyset$ alone does not imply **NP**-completeness. We need the following notations. Sequences are the concatenation of zero or more elements from an alphabet. We use the period “.” as the concatenation operator, but frequently the two operands are simply put side by side. Let $T = T[1]T[2]\dots T[m]$ be a sequence of length m . For all $1 \leq i \leq j \leq m$, we write $T[i : j]$ to denote $T[i]T[i+1]\dots T[j]$. The *reverse* of T is the sequence $T^R = T[m]\dots T[2]T[1]$. A *factorization* of T is any decomposition $T = x_1x_2\dots x_q$ where $x_1, x_2, \dots, x_q$ are (possibly empty) sequences. Let (T, A) be a $\{\emptyset\}$ -arc-annotated sequence and $(i, j) \in A$, $i < j$, be an arc. We call $T[i]$ a *forward base* and $T[j]$ a *backward base*. We will denote by LF_T the position of the last forward base in (T, A) and by FB_T the position of the first backward base in (T, A) , *i.e.*, $\text{LF}_T = \max\{i : (i, j) \in A\}$ and $\text{FB}_T = \min\{j : (i, j) \in A\}$. By convention, we let $\text{LF}_T = 0$ and $\text{FB}_T = |T| + 1$ if $A = \emptyset$. Observe that $\text{LF}_T < \text{FB}_T$. We begin by proving a factorization result on $\{\emptyset\}$ -arc-annotated sequences.

Lemma 1. *Let S and T be two $\{\emptyset\}$ -arc-annotated sequences of length n and m , respectively. If T occurs as an arc preserving subsequence in S , then there exists a factorization (possibly trivial) $T[\text{LF}_T + 1 : \text{FB}_T - 1] = xy$ such that $T[1 : \text{LF}_T] \cdot x \cdot (y \cdot T[\text{FB}_T : m])^R$ occurs as an arc preserving subsequence in $S[1 : \text{FB}_S - 1] \cdot S[\text{FB}_S : n]^R$.*

Proof. Suppose that T occurs as an arc preserving subsequence in S . Since both S and T are $\{\emptyset\}$ -arc-annotated sequences, then there exist two factorizations $S[1 : \text{LF}_S] = uv$ and $S[\text{FB}_S : n] = zv$ such that: (i) $T[1 : \text{LF}_T]$ occurs in u , (ii) $T[\text{LF}_T + 1 : \text{FB}_T - 1]$ occurs in $w \cdot S[\text{LF}_S + 1 : \text{FB}_S - 1] \cdot z$ and (iii) $T[\text{FB}_T : m]$ occurs in v . Then it follows that there exists a factorization $T[\text{LF}_T + 1 : \text{FB}_T - 1] = xy$ such that x occurs in $w \cdot S[\text{LF}_S + 1 : \text{FB}_S - 1]$ and y occurs in z , and hence $T' = T[1 : \text{LF}_T] \cdot x \cdot (y \cdot T[\text{FB}_T : m])^R$ occurs as an arc preserving subsequence in $S' = S[1 : \text{FB}_S - 1] \cdot S[\text{FB}_S : n]^R$ $\square$

Theorem 3. $\text{APS}(\{\emptyset\}, \{\emptyset\})$ is solvable in $O(nm^2)$ time.

Algorithm 1:

Data : Two $\{\emptyset\}$ -arc-annotated sequences S and T of length n and m , respectively

Result : true iff T occurs as an arc-preserving subsequence in S

begin

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1   $S' = S[1 : \text{FB}_S - 1] \cdot S[\text{FB}_S : n]^R$ 
2  foreach factorization  $T[\text{LF}_T + 1 : \text{FB}_T - 1] = xy$  do
3       $T' = T[1 : \text{LF}_T] \cdot x \cdot (y \cdot T[\text{FB}_T : m])^R$ 
4      if  $T'$  occurs as an arc preserving subsequence in  $S'$  then
5          L return true
6  return false
end
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Proof. Consider Algorithm 1. Correctness of the algorithm follows from Lemma 1. What is left is to prove the time complexity. Clearly, $S' = S[1 : \text{FB}_S - 1] \cdot S[\text{FB}_S : n]^R$ is a $\{\square\}$ -arc-annotated sequence. The key point is to note that, for any factorization $T[\text{LF}_T + 1 : \text{FB}_T - 1] = xy$, the obtained $T' = T[1 : \text{LF}_T] \cdot x \cdot (y \cdot T[\text{FB}_T : m])^R$ is a $\{\square\}$ -arc-annotated sequence as-well. Now let k be the number of arcs in T . So there are at most $m - 2k$ iterations to go before eventually returning false. According to the above, Line 4 constitutes an instance of $\text{APS}(\{\square\}, \{\square\})$. But $\text{APS}(\{\square\}, \{\square\})$ is a special case of $\text{APS}(\{<, \square\}, \{<, \square\})$, and hence is solvable in $O(nm)$ time [6]. Then it follows that the algorithm as a whole runs in $O(nm(m - 2k)) = O(nm^2)$ time. $\square$

Clearly, the proof of Theorem 3 relies on an efficient algorithm for solving $\text{APS}(\{\square\}, \{\square\})$: the better the complexity for $\text{APS}(\{\square\}, \{\square\})$, the better the complexity for $\text{APS}(\{\emptyset\}, \{\emptyset\})$. We have used only the fact that $\text{APS}(\{\square\}, \{\square\})$ is a special case of $\text{APS}(\{<, \square\}, \{<, \square\})$. It remains open, however, whether a better complexity can be achieved for $\text{APS}(\{\square\}, \{\square\})$. Theorem 3, combined with Observation 1, carries out easily to restricted versions.

Corollary 1. $\text{APS}(\{\emptyset\}, \emptyset)$ is solvable in $O(nm^2)$ time.

6 Conclusion

In this paper, we investigated the APS problem time complexity and gave a precise characterization of what makes the APS problem hard. We proved that $\text{APS}(\text{CROSSING}, \text{PLAIN})$ is **NP**-complete thereby answering an open problem posed in [6]. Note that this result answers the last open problem concerning APS computational complexity with respect to classical complexity levels, *i.e.*, **PLAIN**, **CHAIN**, **NESTED** and **CROSSING**. Also, we refined the four above mentioned levels for exploring the border between polynomial time solvable and **NP**-complete problems. We proved that both $\text{APS}(\{\sqsubset, \emptyset\}, \emptyset)$ and $\text{APS}(\{<, \emptyset\}, \emptyset)$ are **NP**-complete and gave positive results by showing that $\text{APS}(\{\emptyset\}, \emptyset)$ and $\text{APS}(\{\emptyset\}, \{\emptyset\})$ are polynomial time solvable. Hence, the refinement we suggest shows that APS problem becomes hard when one considers sequences containing $\{\emptyset, \alpha\}$ -comparable arcs with $\alpha \neq \emptyset$. Therefore, crossing arcs alone do not imply APS hardness. It is of course a challenging problem to further explore the complexity of the APS problem, and especially the parameterized views, by considering additional parameters such as the cutwidth or the depth of the arc structures.

References

1. J. Alber, J. Gramm, J. Guo, and R. Niedermeier. Computing the similarity of two sequences with nested arc annotations. *Theoretical Computer Science*, 312(2-3):337–358, 2004.
2. G. Caetano-Anollés. Tracing the evolution of RNA structure in ribosomes. *Nucl. Acids. Res.*, 30:2575–2587, 2002.
3. P. Evans. *Algorithms and Complexity for Annotated Sequence Analysis*. PhD thesis, U. Victoria, 1999.
4. M. Garey and D. Johnson. *Computers and Intractability: A Guide to the Theory of NP-Completeness*. W. H. Freeman and Company, 1979.
5. D. Goldman, S. Istrail, and C.H. Papadimitriou. Algorithmic aspects of protein structure similarity. In *Proc. of the 40th Symposium of Foundations of Computer Science (FOCS99)*, pages 512–522, 1999.
6. J. Gramm, J. Guo, and R. Niedermeier. Pattern matching for arc-annotated sequences. In *Proc. of the 22nd Conference on Foundations of Software Technology and Theoretical Computer Science (FSTTCS02)*, volume 2556 of *LNCS*, pages 182–193, 2002.
7. J. Guo. Exact algorithms for the longest common subsequence problem for arc-annotated sequences. Master's Thesis, Universitat Tübingen, Fed. Rep. of Germany, 2002.
8. T. Jiang, G.-H. Lin, B. Ma, and K. Zhang. The longest common subsequence problem for arc-annotated sequences. In *Proc. 11th Symposium on Combinatorial Pattern Matching (CPM00)*, volume 1848 of *LNCS*, pages 154–165. Springer-Verlag, 2000.
9. V. Juan, C. Crain, and S. Wilson. Evidence for evolutionarily conserved secondary structure in the H19 tumor suppressor RNA. *Nucl. Acids. Res.*, 28:1221–1227, 2000.

10. G. Lancia, R. Carr, B. Walenz, and S. Istrail. 101 optimal PDB structure alignments: a branch-and-cut algorithm for the maximum contact map overlap problem. In *Proceedings of the 5th ACM International Conference on Computational Molecular Biology (RECOMB01)*, pages 193–202, 2001.
11. S. Vialette. On the computational complexity of 2-interval pattern matching. *Theoretical Computer Science*, 312(2-3):223–249, 2004.
12. K. Zhang, L. Wang, and B. Ma. Computing the similarity between RNA structures. In *Proc. 10th Symposium on Combinatorial Pattern Matching (CPM99)*, volume 1645 of *LNCS*, pages 281–293. Springer-Verlag, 1999.
13. M. Zuker. RNA folding. *Meth. Enzymology*, 180:262–288, 1989.