# Computing maximal generalized palindromes

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#### Abstract

Palindromes are popular and important objects in textual data processing, bioinformatics, and combinatorics on words. Let S = XaY be a string, where X and Y are of the same length and a is either a single character or the empty string. Then, there exist two alternative definitions for palindromes: S is said to be a palindrome if:

**Reversal-based definition:** S is equal to its reversal  $S^R$ ;

Symmetry-based definition: its left-arm X is equal to the reversal of its right-arm  $Y^R$ .

It is clear that if the "equality" ( $\approx$ ) used in both definitions is exact character matching (=), then the two definitions are the same. However, if we apply other string-equality criteria  $\approx$ , including the complementary model for biological sequences, the parameterized model [Baker, JCSS 1996], the order-preserving model [Kim et al., TCS 2014], the Cartesian-tree model [Park et al., TCS 2020], and the palindromic-structure model [I et al., TCS 2013], then are the reversal-based palindromes and the symmetry-based palindromes the same? To the best of our knowledge, no previous work has considered or answered this natural question. In this paper, we first provide answers to this question, and then present efficient algorithms for computing all maximal generalized palindromes that occur in a given string. After confirming that Gusfield's offline suffix-tree based algorithm for computing maximal symmetry-based palindromes can be readily extended to the aforementioned matching models, we show how to extend Manacher's online algorithm for computing maximal reversal-based palindromes in linear time for all the aforementioned matching models.

## 1 Introduction

*Palindromes* are popular and important objects in textual data processing, bioinformatics, and combinatorics on words (see e.g. [25, 1, 16, 9, 10, 21, 26, 14, 6, 15, 24, 5, 13, 29, 8] and references therein). Let us remind the readers of the two following common definitions for palindromes: Let S = XaY be a string, where X and Y are of the same length and a is either a single character or the empty string. Then, S is said to be a palindrome if:

**Reverse-based definition:** S is equal to its reversal  $S^R$ ;

Symmetry-based definition: its left-arm X is equal to the reversal of its right-arm  $Y^R$ .

It is clear that if the "equality" ( $\approx$ ) used in both definitions is exact character matching (=), then the two definitions are the same, meaning that a string S is a reverse palindrome iff S is a symmetric palindrome. Observe this with some examples such as **racecar** and **noon**. Now we pose the following question: If we apply other string-equality criteria  $\approx$ , including the *complementary model* for biological sequences, the *parameterized model* [3], the *order-preserving model* [23], and the *Cartesian-tree model* [28], then are the reverse palindromes and the symmetric palindromes the same? This question is interesting because, while the symmetry-based palindrome definition requires only  $X \approx Y^R$ , the reversal-based palindrome definition requires more strict matching under  $\approx$ , so that  $S \approx S^R \Leftrightarrow XaY \approx (XaY)^R \Leftrightarrow XaY \approx Y^RaX^R$ . Thus, these two types of palindromes can be quite different for some matching criterion  $\approx$  (see also Figure 3 in the following section). To the best of our knowledge, somewhat surprisingly, no previous work has considered or answered this natural question. In this paper, we first provide quick answers to this question, and present efficient algorithms for computing such generalized palindromes that occur in a given string.

One of the well-studied topics regarding palindromes is maximal palindromes, which are substring palindromes whose left-right extensions are not palindromes. It is interesting and important to find all maximal palindromes in a given string T because any substring palindrome of T can be obtained by removing an equal number of characters from the left and the right of some maximal palindrome. Hence, by computing all maximal palindromes of a string, we obtain a compact representation of all palindromes in the string.

Manacher [25] showed an elegant algorithm for finding all maximal palindromes in a given string T. Manacher's algorithm works in an online manner (processes the characters of T from left to right), and runs in O(n) time and space for general (unordered) alphabets, where n is the length of the input string T. Later, Gusfield [16] showed another famous algorithm for computing all maximal palindromes. Gusfield's algorithm uses the suffix tree [34] built on a concatenation of T and its reversal  $T^R$  that is enhanced with an LCA (lowest common ancestor) data structure [30]. Gusfield's method is offline (processes all the characters of T together), and works in O(n) time and space for linearly-sortable alphabets including integer alphabets of polynomial size in n. We remark that Gusfield's algorithm uses only the symmetry-based definition for computing maximal palindromes. That is, computing the longest common prefix (LCP) of T[c..n] and  $(T[1..c-1])^R$  for each integer position c in T gives us the maximal palindrome of even length centered at c - 0.5. Maximal palindromes of odd lengths can be computed analogously. On the other hand, Manacher's algorithm (which will be briefly recalled in a subsequent section) uses both the reversal-based and symmetry-based definitions for computing maximal palindromes.

In this paper, we propose a new framework for formalizing generalized palindromes, which we call Substring Consistent Symmetric and Two-Transitive Relations (SCSTTRs) that include the complementary-matching model and Substring Consistent Equivalence Relations (SCERs) [27]. We note that SCERs include the parameterized model [3], the order-preserving model [23], the Cartesian-tree model [28], and the palindromic-structure model [19]. As far as we are aware, the existing algorithms are designed only for computing standard maximal palindromes based on exact character matching, and it is not clear how they can be adapted for the aforementioned generalized palindromes. We first confirm that Gusfield's framework is easily extensible for generalized palindromes: if one has a suffix-tree like data structure that is built on a suitable encoding for a given matching criterion  $\approx$  enhanced with the LCA data structure, then one can readily compute all maximal symmetric generalized palindromes in O(n) time. Thus, the construction time for the suffix-tree like data structure dominates the total time complexity (see Table 1). On the other hand, extending Manacher's algorithm for generalized palindromes is much more involved, and the main contribution of this paper is to design Manacher-type algorithms which compute all maximal reverse palindromes in O(n) time for all types of generalized palindromes considered in this paper Table 1: Summary of the time complexities of algorithms for computing each type of palindromes, where n denotes the length of the input string,  $\sigma$  is the (static) alphabet size, and  $\pi$  is the size of the parameterized alphabet for parameterized matching. The time complexities are valid under some assumptions for the alphabet, which are designated in the parentheses. The space complexity of each of the algorithms is O(n).

Type	Symmetric Palindromes	Reverse Palindromes		
Erroct	O(n) time [16]	O(n) time [25]		
Exact	(linearly sortable)	(general unordered)		
Complementary	O(n) time	O(n) time		
Complementary	(linearly sortable)	(general unordered)		
Parameterized	$O(n\log(\sigma+\pi))$ time	O(n) time		
1 arameterizeu	(linearly sortable)	(linearly sortable)		
Order Preserving	$O(n \log \log^2 n / \log \log \log n)$ time	O(n) time		
Older-f leserving	(linearly sortable)	(general unordered)		
Cartosian Troo	$O(n \log n)$ time	O(n) time		
Cartestan-11ee	(general ordered)	(linearly sortable)		
Palindromic Structure	$O(n\min\{\sqrt{\log n}, \log \sigma / \log \log \sigma\})$ time	O(n) time		
i annuronne-structure	(general unordered)	(general unordered)		

(see Table 1).

## 2 Preliminaries

#### 2.1 String Notations

Let  $\Sigma$  be an *alphabet*. An element of  $\Sigma^*$  is called a *string*. The length of a string T is denoted by |T|. The empty string  $\varepsilon$  is the string of length 0, namely,  $|\varepsilon| = 0$ . For a string T = xyz, x, y and z are called a *prefix*, *substring*, and *suffix* of T, respectively. For a string T and an integer  $1 \leq i \leq |T|, T[i]$  denotes the *i*-th character of T, and for two integers  $1 \leq i \leq j \leq |T|, T[i...j]$ denotes the substring of T that begins at position i and ends at position j. For convenience, let  $T[i...j] = \varepsilon$  when i > j. The reversal of a string T is denoted by  $T^R$ , i.e.,  $T^R = T[|T|] \cdots T[1]$ .

For two strings X and Y, let lcp(X, Y) denote the length of the longest common prefix of X and Y. Namely,  $lcp(X, Y) = \max\{\ell \mid X[1..\ell] = Y[1..\ell]\}$ . A rightward longest common extension (rightward LCE) query on a string T is to compute lcp(T[i..|T|], T[j..|T|]) for given two positions  $1 \leq i < j \leq |T|$ . Similarly, a leftward LCE query is to compute  $lcp(T[1..i]^R, T[1..j]^R)$ . Then, an outward LCE (resp. inward LCE) query is, given two positions  $1 \leq i < j \leq |T|$ , to compute  $lcp(T[1..i]^R, T[j..|T|])$  (resp.  $lcp(T[i..|T|], T[1..j]^R)$ ).

#### 2.2 Palindromes

A string T is called a *palindrome* if  $T = T^R$ . We remark that the empty string  $\varepsilon$  is also considered to be a palindrome. A non-empty substring palindrome T[i..j] is said to be a *maximal palindrome* in T if  $T[i-1] \neq T[j+1]$ , i = 1, or j = |T|. For any non-empty substring palindrome T[i..j] in  $T, \frac{i+j}{2}$  is called its *center*. It is clear that for each center  $c = 1, 1.5, \ldots, n - 0.5, n$ , we can identify the maximal palindrome T[i..j] whose center is c (namely,  $c = \frac{i+j}{2}$ ). Thus, there are exactly 2n - 1 maximal palindromes in a string of length n (including empty strings which occur at non-integer centers c when  $T[c-0.5] \neq T[c+0.5]$ ). Manacher [25] showed an online algorithm that computes all maximal palindromes in a string T of length n in O(n) time. An alternative offline approach is to use outward LCE queries for 2n-1 pairs of positions in T. Using the suffix tree [34] for string  $T^{*}T^{*}$ enhanced with a lowest common ancestor data structure [17, 30, 4], each outward LCE query can be answered in O(1) time where \$ and # are special characters that do not appear in T. Preprocessing for this approach takes O(n) time and space [12, 16] when alphabet  $\Sigma$  is linearly-sortable.

#### 2.3 Substring Consistent Symmetric and Two-Transitive Relation (SCSTTR)

A Substring Consistent Equivalence Relation (SCER) is an equivalence relation  $\approx_{\text{SCER}}$  such that  $X \approx_{\text{SCER}} Y$  for two strings X, Y of equal length means that  $X[i..j] \approx_{\text{SCER}} Y[i..j]$  holds for all  $1 \le i \le j \le |X| = |Y|$ . Matsuoka et al. [27] defined the notion and considered the pattern matching problems with SCER. Afterward, several problems over SCER have been considered (e.g., [18, 22, 20]).

In this paper, we treat a more general relation; Substring Consistent Symmetric and Two-Transitive Relation (SCSTTR). An SCSTTR is a relation  $\approx_{\text{SCSTTR}}$  that satisfies the following conditions for strings  $W, X, Y, Z \in \Sigma^n$ :

- 1. Satisfies the symmetric law; namely, if  $X \approx_{\text{SCSTTR}} Y$ , then  $Y \approx_{\text{SCSTTR}} X$  also holds.
- 2. Satisfies the two-transitive law; namely, if  $W \approx_{\text{SCSTTR}} X$ ,  $X \approx_{\text{SCSTTR}} Y$ , and  $Y \approx_{\text{SCSTTR}} Z$ , then  $W \approx_{\text{SCSTTR}} Z$  also holds.
- 3. Satisfies the substring consistency; namely, if  $X \approx_{\text{SCSTTR}} Y$ , then  $X[i..j] \approx_{\text{SCSTTR}} Y[i..j]$ holds for all  $1 \le i \le j \le n$ .

We remark that any SCER is also an SCSTTR. Our aim for introducing SCSTTRs is to deal with the complementary matching model including the Watson-Crick (WK) model [33] for  $\Sigma = \{A, C, G, T\}$  that is *not* an SCER. For each of the SCSTTR matching models below, encodings with which the matching can be reduced to exact matching are known.

#### Complementary Matching [10, 21]

Let f be a function on  $\Sigma$  that has the two following properties: (1) f(uv) = f(u)f(v) for all strings  $u, v \in \Sigma^*$ , and (2)  $f^2$  equals the identity. Two strings X and Y are said to complementary match if there is a function f satisfying X = f(Y). For example, if f(A) = T, f(C) = G, f(T) = A, and f(G) = C on  $\Sigma = \{A, T, G, C\}$ , then X = AGCTAT and Y = TCGATA complementary match. For strings X and Y, we write  $X \approx_{\rm rc} Y$  iff X = f(Y). Reversal-based palindromes under complementary matching have been studied as  $\theta$ -palindromes [10, 21]<sup>-1</sup>. In this paper, we consider both the reverse and symmetric definitions and call them Theta rev-palindromes and Theta sym-palindromes, respectively.

#### Parameterized Matching [2]

Let  $\Sigma$  and  $\Pi$  be disjoint sets of characters, respectively called a static alphabet and a parameterized alphabet. Two strings X and Y are said to parameterized match if there is a renaming bijection over the alphabet  $\Pi$  which transforms X into Y. For example, if  $\Sigma = \{\mathsf{C}\}$  and  $\Pi = \{\mathsf{a}, \mathsf{b}, \mathsf{d}\}$ ,

<sup>&</sup>lt;sup>1</sup>In these references,  $\theta$ -palindromes are defined by the function  $\theta$  that is not morphic but is antimorphic. However, we use the morphic function f for simplicity of discussion since they can be treated as the same in this paper.

X = aabaCbC and Y = ddadCaC parameterized match since there is a bijection f such that f(a) = d and f(b) = a. We write  $X \approx_{para} Y$  iff strings X and Y parameterized match.

For a string T, the previous encoding  $\mathsf{PE}_T$  is a string of length |T| defined as follows:

$$\mathsf{PE}_{T}[i] = \begin{cases} T[i] & \text{if } T[i] \in \Sigma;\\ i - \max_{1 \le j < i} \{j : T[j] = T[i]\} & \text{if } T[i] \in \Pi \text{ and such } j \text{ exists};\\ 0 & \text{otherwise.} \end{cases}$$

For any two strings X and Y,  $X \approx_{\text{para}} Y$  iff  $\mathsf{PE}_X = \mathsf{PE}_Y$  [2]. For example, again consider two strings  $X = \mathsf{aabaCbC}$  and  $Y = \mathsf{ddadCaC}$ , which satisfy  $X \approx_{\text{para}} Y$ , then  $\mathsf{PE}_{X=\mathsf{aabaCbC}} = 0102\mathsf{C3C} = \mathsf{PE}_{Y=\mathsf{ddadCaC}}$ . For simplicity, we assume in the rest of this paper that the string consists only of characters from  $\Pi$ . Only trivial modifications to our algorithms are required when considering characters from  $\Sigma$  as well.

#### Order-preserving Matching [23]

For ordered alphabets, two strings X and Y are said to order-preserving match if the relative orders of X correspond to those of Y. Namely,  $X[i] \preccurlyeq X[j] \Leftrightarrow Y[i] \preccurlyeq Y[j]$  for all  $1 \le i, j \le |X| = |Y|$ . For example, X = cecag and Y = hohbr order-preserving match with the standard lexicographical order of characters. We write  $X \approx_{\text{op}} Y$  iff strings X and Y order-preserving match.

Let  $\alpha_T[i]$  (resp.  $\beta_T[i]$ ) be the rightmost occurrence of the predecessor (resp. the successor) of T[i] in T[1..i-1]. Namely,

$$\alpha_T[i] = \begin{cases} \max_{1 \le j < i} \{j : T[j] \text{ is the largest element satisfying } T[j] \preccurlyeq T[i] \} & \text{if such } j \text{ exists;} \\ 0 & \text{otherwise,} \end{cases}$$

and

$$\beta_T[i] = \begin{cases} \max_{1 \le j < i} \{j : T[j] \text{ is the smallest element satisfying } T[j] \succcurlyeq T[i] \} & \text{if such } j \text{ exists;} \\ 0 & \text{otherwise.} \end{cases}$$

Let  $\mathsf{Code}_T$  be a pairwise sequence such that  $\mathsf{Code}_T = (\alpha_T[1], \beta_T[1]), \ldots, (\alpha_T[|T|], \beta_T[|T|])$  holds. For any two strings X and Y,  $X \approx_{\mathrm{op}} Y$  iff  $\mathsf{Code}_X = \mathsf{Code}_Y$  holds [7]. For example, again consider two string  $X = \mathsf{cecag}$  and  $Y = \mathsf{hohbr}$ , which satisfy  $X \approx_{\mathrm{op}} Y$ , then  $\mathsf{Code}_{X=\mathsf{cecag}} = (0,0)(1,0)(1,1)(0,3)(2,0) = \mathsf{Code}_{Y=\mathsf{hohbr}}$ .

#### Cartesian-tree Matching [28]

The Cartesian tree CT(T) of a string T is the ordered binary tree recursively defined as follows [32]:

- 1. If T is the empty string, CT(T) is empty.
- 2. If T is not empty, let T[i] be the leftmost occurrence of the smallest character in T. Then, the root of CT(T) is T[i], the left-side subtree of CT(T) is CT(T[1..i 1]), and the right-side subtree of CT(T) is CT(T[i + 1..|T|]).

We say that two strings X and Y Cartesian-tree match and denote it by  $X \approx_{ct} Y$  if CT(X) and CT(Y) are isomorphic as unlabeled ordered trees. For example,  $X \approx_{ct} Y$  holds for two strings X = cabdcf and Y = eaacbc (See Fig. 1).



Figure 1: Illustration for Cartesian trees of  $X = \mathsf{cabdcf}$  and  $Y = \mathsf{eaacbc}$ . Since they are isomorphic except their node labels,  $X \approx_{\mathrm{ct}} Y$  holds.

For a string T, the parent distance  $\mathsf{PD}_T$  is an integer sequence of length |T| that is defined as follows:

$$\mathsf{PD}_{T}[i] = \begin{cases} i - \max_{1 \le j < i} \{j : T[j] \preccurlyeq T[i]\} & \text{if such } j \text{ exists;} \\ 0 & \text{otherwise.} \end{cases}$$

For any two strings X and Y,  $X \approx_{ct} Y$  iff  $\mathsf{PD}_X = \mathsf{PD}_Y$  [28]. For example, again consider two string  $X = \mathsf{cabdcf}$  and  $Y = \mathsf{eaacbc}$ , which satisfy  $X \approx_{ct} Y$ , then  $\mathsf{PD}_{X=\mathsf{cabdcf}} = 001121 = \mathsf{PD}_{Y=\mathsf{eaacbc}}$ .

#### Palindrome (Palindromic-structure) Matching [19]

Two strings X and Y are said to palindromic-structure match if the length of the maximal palindrome at each center position in X is equal to that of Y. For example, X = aabacdca and Y = ccacdadc palindrome match (See Fig. 2). We write  $X \approx_{pal} Y$  iff strings X and Y palindromic-

$$X = aabacdca \approx_{pal} Y = ccacdadc$$

Figure 2: Illustration for palindromic-structures of X = aabacdca and Y = ccacdadc, which satisfy  $X \approx_{pal} Y$ . Each arrow depicts a maximal palindrome of length at least two.

structure match.

Let  $\operatorname{\mathsf{LPal}}_T$  be the integer sequence of length |T| such that  $\operatorname{\mathsf{LPal}}_T[i]$  stores the length of the longest suffix palindrome of the position i in T. For any two strings X and Y,  $X \approx_{\operatorname{pal}} Y$  iff  $\operatorname{\mathsf{LPal}}_X$  is equal to  $\operatorname{\mathsf{LPal}}_Y$  [19]. For example, again consider two string  $X = \operatorname{\mathsf{aabacdca}}$  and  $Y = \operatorname{\mathsf{ccacdadc}}$ , which satisfy  $X \approx_{\operatorname{pal}} Y$ , then  $\operatorname{\mathsf{LPal}}_{T=\operatorname{\mathsf{aabacdca}}} = 12131135 = \operatorname{\mathsf{LPal}}_{T=\operatorname{\mathsf{ccacdadc}}}$ .

#### 2.4 Our Problems

In this paper, we consider the following two definitions:

**Definition 1** (SCSTTR symmetry-based palindromes). A string P is called an SCSTTR sympalindrome if  $(P[1..\lfloor|P|/2\rfloor])^R \approx_{\text{SCSTTR}} P[\lceil|P|/2\rceil..|P|]$  holds.

**Definition 2** (SCSTTR reversal-based palindromes). A string P is called an SCSTTR rev-palindrome if  $P \approx_{\text{SCSTTR}} P^R$  holds.

As for palindromes under the exact matching, the above two definitions are the same. However, as for generalized palindromes, these definitions are not equivalent. For example, ATTGAAT is not a WK rev-palindrome but is a WK sym-palindrome. Also, CACB is not a parameterized rev-palindrome but is a parameterized sym-palindrome.

In this paper, we consider problems for computing maximal SCSTTR (complementary, parameterized, order-preserving, Cartesian-tree, and palindromic-structure) palindromes for the two definitions. Firstly, we notice that SCSTTR rev-palindromes have symmetricity:

**Lemma 1.** Let P be an SCSTTR rev-palindrome. If a substring P[i..j] of P is an SCSTTR rev-palindrome, then the substring at the symmetrical position is also an SCSTTR rev-palindrome, namely, P[|P| - j + 1..|P| - i + 1] is an SCSTTR rev-palindrome.

*Proof.* Since *P* is an SCSTTR rev-palindrome, *P*[*i..j*] ≈<sub>SCSTTR</sub> *P*[|*P*| − *j* + 1..|*P*| − *i* + 1]<sup>*R*</sup> and  $P[i..j]^R \approx_{SCSTTR} P[|P| - j + 1..|P| - i + 1]$  hold. Also, since P[i..j] is an SCSTTR rev-palindrome,  $P[i..j] \approx_{SCSTTR} P[i..j]^R$  holds. Combining these three equations under SCSTTR, we obtain  $P[|P| - j + 1..|P| - i + 1] \approx_{SCSTTR} P[|P| - j + 1..|P| - i + 1]^R$  from the symmetric law and two-transitive law. Therefore, P[|P| - j + 1..|P| - i + 1] is an SCSTTR rev-palindrome.

This lemma allows us to design a Manacher-like algorithm of computing maximal SCSTTR rev-palindromes in Section 4.

Next, we notice that the Cartesian tree matching is not closed under reversal; namely,  $X \approx_{ct} Y$  does not imply  $X^R \approx_{ct} Y^R$ . For instance, aaaa  $\approx_{ct}$  abcd but aaaa  $\not\approx_{ct}$  dcba. Hence, there are cases where the Cartesian-tree sym-palindrome obtained by extending outward direction is not equal to that obtained by extending inward direction for the same center position c. Therefore, we introduce the two following variants for the Cartesian-tree sym-palindromes:

**Definition 3** (outward Cartesian-tree sym-palindromes). A string P is an outward Cartesian-tree sym-palindrome if and only if  $(P[1..|P|/2|])^R \approx_{ct} P[[|P|/2]..|P|]$  holds.

**Definition 4** (inward Cartesian-tree sym-palindromes). A string P is an inward Cartesian-tree sym-palindrome if and only if  $P[1..\lfloor|P|/2\rfloor] \approx_{\text{ct}} (P[\lceil|P|/2]..|P|])^R$  holds.

	Symmetric Palindromes		Reverse Palindromes				
Exact	abcbbdbbcba		a b c b b d b b c b a				
Complementary	ΑΑΤСGGΑΤΤ		ACCTGCAGGT				
Parameterized	abccbbddbc		abccbaddab				
Order-Preserving	accbabcddb		accbaabcca				
Cartesian-Tree	b b d a c d b c b d	(outward)	doofodbda				
	b a d b c d b c b d	(inward)	ueclaubuc				
Palindromic-Structure	baacabbabdbb	C	abbcbadbabbc				

We give examples of SCSTTR sym-/rev-palindromes in Figure 3.

Figure 3: This figure shows examples of each generalized palindrome. A bijection f such that  $f(\mathbf{a}) = \mathbf{c}$ ,  $f(\mathbf{b}) = \mathbf{b}$ ,  $f(\mathbf{c}) = \mathbf{d}$ ,  $f(\mathbf{d}) = \mathbf{a}$  gives the parameterized sym-palindrome. A bijection f such that  $f(\mathbf{a}) = \mathbf{b}$ ,  $f(\mathbf{b}) = \mathbf{a}$ ,  $f(\mathbf{c}) = \mathbf{d}$ ,  $f(\mathbf{d}) = \mathbf{c}$  gives the parameterized rev-palindrome. In the palindromic-structure sym-palindrome, though palindromes **bb**, **abba**, and **bab** exist, these palindromes are ignored in this symmetric condition.

# 3 Algorithms for Computing Maximal SCSTTR Symmetry-based Palindromes

In this section, we consider algorithms for computing maximal SCSTTR sym-palindromes. The main idea is the same as Gusfield's algorithm; to use the outward LCE query on the matching model in SCSTTR for each center position. Then, the complexity of the algorithm can be written as  $O(nq + t_{\text{SCSTTR}})$  time and  $O(n + s_{\text{SCSTTR}})$  space, where q is the outward LCE query time,  $t_{\text{SCSTTR}}$  is the construction time of the data structure for the LCE query on the matching model, and  $s_{\text{SCSTTR}}$  is the space of the data structure. Then, we obtain the following results for several matching models in SCSTTR.

**Theorem 1.** All maximal SCSTTR sym-palindromes can be computed in the following complexities and matching models:

- 1. For linearly sortable alphabets, all maximal Theta sym-palindromes can be computed in O(n) time with O(n) space.
- 2. For linearly sortable alphabets, all maximal parameterized sym-palindromes can be computed in  $O(n \log(\sigma + \pi))$  time with O(n) space.
- 3. For linearly sortable alphabets, all maximal order-preserving sym-palindromes can be computed in  $O(n \log \log^2 n / \log \log \log n)$  time with O(n) space.
- 4. For ordered alphabets, all outward/inward maximal Cartesian-tree sym-palindromes can be computed in  $O(n \log n)$  time with O(n) space.
- 5. For general unordered alphabets, all maximal palindromic-structure sym-palindromes can be computed in  $O(n \min\{\sqrt{\log n}, \log \sigma / \log \log \sigma\})$  time with O(n) space.

These results can be obtained by using SCSTTR suffix trees [12, 16, 3, 23, 28, 19]. All the details and proofs omitted due to lack of space can be found in Appendix A.

# 4 Algorithms for Computing Maximal SCSTTR Reversal-based Palindromes

In this section, we consider algorithms for computing maximal SCSTTR rev-palindromes. If we were to use the SCSTTR suffix tree and outward LCE queries as in the previous section, how to choose the starting positions of outward LCE queries is unclear. Therefore, a naïve approach would require O(n) inward LCE queries for each center position, and the total complexity will be  $O(n^2 + t_{\text{SCSTTR}})$  time and  $O(n+s_{\text{SCSTTR}})$  space. By combining inward LCE queries and binary search, we can further achieve  $O(n \log n + t_{\text{SCSTTR}})$  time and  $O(n + s_{\text{SCSTTR}})$  space with this approach. In this section, we show O(n) time algorithms without constructing SCSTTR suffix trees.

#### **Outline of Computing SCSTTR Reversal-based Palindromes**

At first, we show a framework for computing maximal SCSTTR rev-palindromes, which is a generalization of Manacher's algorithm [25]. For the sake of simplicity, we denote SCSTTR rev-palindromes by just *palindromes* in the description of the framework below. In the following, we describe how to compute all odd-lengthed maximal palindromes. Even-lengthed maximal palindromes can be obtained analogously.



Figure 4: Illustration for two sub-cases in  $c \leq e$ .

We consider finding the odd-lengthed maximal palindromes in ascending order of the center position. Let  $\mathsf{MPal}[c]$  denote the interval corresponding to the odd-lengthed maximal palindrome centered at position c. The length of  $\mathsf{MPal}[1]$  is always one. Assuming that all odd-lengthed maximal palindromes whose center is at most c-1 have been computed and let  $\mathsf{MPal}[c'] = [b, e]$  be the longest interval whose ending position e is largest among  $\{\mathsf{MPal}[1], \ldots, \mathsf{MPal}[c-1]\}$ . Further let P' = T[b..e]. Also, let d be the distance between c' and c; namely, d = c - c'. See also Fig. 4 for illustration.

If T[i-1..j+1] is a palindrome, we say palindrome T[i..j] can be extended. Also, we call computing the length of MPal[(i+j)/2] computing the extension of T[i..j].

Now, we consider how to compute  $\mathsf{MPal}[c]$ . If  $c \leq e$ , we compute  $\mathsf{MPal}[c]$  as in the following two cases according to the relationship between P' and  $\mathsf{MPal}[c'-d]$ .

- 1. If the starting position of  $\mathsf{MPal}[c'-d]$  is larger than b, then  $|\mathsf{MPal}[c]| = |\mathsf{MPal}[c'-d]|$  holds (by Lemma 1). Thus we copy  $\mathsf{MPal}[c'-d]$  to  $\mathsf{MPal}[c]$  with considering symmetry.
- 2. Otherwise, the ending position of  $\mathsf{MPal}[c]$  is at least e. Then we compute the extension of T[2c e..e], and P' is updated to  $\mathsf{MPal}[c]$  if T[2c e..e] can be extended.

Otherwise (i.e., e < c holds), then c = e + 1 holds. We compute  $\mathsf{MPal}[c]$  by computing the extension of T[e + 1..e + 1].

Note that, in the exact matching model, the behavior of this framework is identical to that of Manacher's algorithm. The framework includes two non-trivial operations; copying and extension-computing. How many times both operations are called can be analyzed in the same manner as for Manacher's algorithm, i.e., O(n). Also, each copying operation can be done in constant time. Thus, if we can perform each extension-computing in (amortized) constant time, the total time complexity becomes O(n). The following sections focus only on how to compute an extension in (amortized) constant time under each of the five matching models.

#### 4.1 Maximal Theta Reversal-based Palindromes

In the complementary matching model, the correspondence of matching characters, although different, is predetermined, and naïve character comparisons can be done in constant time. Thus, the following result can be obtained immediately.

**Theorem 2.** For general unordered alphabets, all maximal Theta rev-palindromes can be computed in O(n) time with O(n) space.

k	 i-1										j+1	
T[k]	 с	а	а	С	а	е	b	d	b	b	d	
k'	1			p							j-i+3	
$PE_{T[i-1j+1]}[k']$	0	0	1	3	2	0	0	0	2	1	3	
$\hat{k}$	 n-j										n-i+2	
$T^R[\hat{k}]$	 d	b	b	d	b	е	а	с	а	а	с	
$\hat{k'}$	1			q							j-i+3	
$PE_{T[i-1,i+1]R}[\hat{k'}]$	0	0	1	3	2	0	0	0	2	1	3	

Table 2: An example for the computation of whether the parameterized palindrome T[i..j] can be extended.

#### 4.2 Maximal Parameterized Reversal-based Palindromes

Now we consider how to determine whether the parameterized palindrome T[i..j] can be extended by one character at each end. If  $T[i - 1..j + 1] \approx_{\text{para}} T[i - 1..j + 1]^R$  holds, then  $\mathsf{PE}_{T[i-1..j+1]} = \mathsf{PE}_{T[i-1..j+1]^R}$ . Since T[i..j] is a parameterized palindrome,  $\mathsf{PE}_{T[i..j]} = \mathsf{PE}_{T[i..j]^R}$ . Now, it is not difficult to see that the number of positions in which values of  $\mathsf{PE}_{T[i-1..j+1]}$  can differ from  $\mathsf{PE}_{T[i..j]}$ when aligned at the center, is at most three; The first and last elements of  $\mathsf{PE}_{T[i-1..j+1]}$  (which do not exist in  $\mathsf{PE}_{T[i..j]}$ ), and the position of the first element of T[i..j] that equals T[i-1], if such exists. From the symmetricity, the same can be said for values of  $\mathsf{PE}_{T[i-1..j+1]^R}$  from  $\mathsf{PE}_{T[i..j]^R}$ . Then, to determine whether T[i - 1..j + 1] is a parameterized palindrome, we only have to consider (1) the equality between the first elements of  $\mathsf{PE}_{T[i-1..j+1]}$  and  $\mathsf{PE}_{T[i-1..j+1]^R}$ , (2) the equality between the last elements of  $\mathsf{PE}_{T[i-1..j+1]}$  and  $\mathsf{PE}_{T[i-1..j+1]^R}$ , and (3) the equality between the first positions pin T[i..j] and q in  $T[i..j]^R$  that respectively equals T[i-1] and T[j+1]. In other words, given that T[i..j] is a parameterized palindrome, T[i-1..j+1] is a parameterized palindrome if and only if all three equalities hold. See also Table 2.

The equality of (1) always holds, since  $\mathsf{PE}_{T[i-1..j+1]}[1]$  and  $\mathsf{PE}_{T[i-1..j+1]^R}[1]$  are always 0 by definition of PE. Next, we show that the equality of (2) implies equality of (3). Since the last elements of  $\mathsf{PE}_{T[i-1..j+1]}$  and  $\mathsf{PE}_{T[i-1..j+1]^R}$  are equal, this implies that the last position in T[i..j] and  $T[i..j]^R$  that respectively equals T[j+1] and T[i-1] are the same. By reversing the string, these correspond to the first position in  $T[i..j]^R$  and T[i..j] that respectively equals T[j+1] and T[i..j] that respectively equals T[j+1] and T[i..j] and T[i..j] therefore implying (3).

Thus, we need only check the equality of (2). Given  $\mathsf{PE}_T$ ,  $\mathsf{PE}_{T[i..j]}[k]$  for any  $1 \le k \le j - i + 1$  can be computed in constant time, i.e.,  $\mathsf{PE}_{T[i..j]}[k] = \mathsf{PE}_T[i + k - 1]$  if  $\mathsf{PE}_T[i + k - 1] < k$  and 0 otherwise. Hence, the computation time of the extension of T[i..j] by one character at each end is O(1). Also, since  $\mathsf{PE}_T$  can be precomputed in O(n) time for linearly sortable alphabets, we obtain the following result:

**Theorem 3.** For linearly sortable alphabets, all maximal parameterized rev-palindromes can be computed in O(n) time with O(n) space.

#### 4.3 Maximal Order-preserving Reversal-based Palindromes

From the definition, an order-preserving rev-palindrome P satisfies that  $P[\lceil c \rceil - d] \preccurlyeq P[\lfloor c \rfloor + d]$  and  $P[\lfloor c \rfloor + d] \preccurlyeq P[\lceil c \rceil - d]$  for integer d with  $1 \le d \le \lceil c \rceil - 1$  where  $c = \frac{1+|P|}{2}$  is the center of P. This means that any order-preserving rev-palindrome must be a palindrome under the exact matching.

k	 i-1										j+1	
T[k]	b	е	с	а	е	b	d	а	е	f	С	
<i>k</i> ′		1								j-i+1		
$PD_{T[ij]}[k']$		0	0	0	1	2	1	4	1	1		
<i>k''</i>	1										j-i+3	
$PD_{T[i-1j+1]}[k'']$	0	1	2	0	1	2	1	4	1	1	3	

Table 3: An example for the difference between  $\mathsf{PD}_{T[i..j]}$  and  $\mathsf{PD}_{T[i-1..j+1]}$ .

Therefore, maximal order-preserving rev-palindromes in T can be computed in O(n) time by using Manacher's algorithm.

**Corollary 1.** For general unordered alphabets, all maximal order-preserving rev-palindromes can be computed in O(n) time with O(n) space.

#### 4.4 Maximal Cartesian-tree Reversal-based Palindromes

Here, we consider how to compute the extension of a maximal Cartesian-tree rev-palindrome T[i..j]. We consider the difference between  $\mathsf{PD}_{T[i..j]}$  and  $\mathsf{PD}_{T[i-1..j+1]}$ . There are three types of positions of  $\mathsf{PD}_{T[i-1..j+1]}$  in which values differ from  $\mathsf{PD}_{T[i..j]}$ ; the first and last positions (which don't exist in  $\mathsf{PD}_{T[i..j]}$ ), and each position k such that  $\mathsf{PD}_{T[i..j]}[k] = 0$  and  $T[i-1] \preccurlyeq T[k]$  with  $i \le k \le j$  (i.e.,  $\mathsf{PD}_{T[i-1..j+1]}[k+1] \ne 0$ ). Let  $m_{[i..j]}$  be the leftmost occurrence position of the smallest value in T[i..j]. Then, k' such that  $\mathsf{PD}_{T[i..j]}[k'] = 0$  is always to the left or equal to  $m_{[i..j]}$ . However, since the number of such positions is not always constant, the time required for computing the extension from T[i..j] to T[i-1..j+1] can be  $\omega(1)$ . See also Table 3. We will consider the total number of updates of such positions through the entire algorithm.

Let c be the center of T[i..j] and T[b..e] be the maximal Cartesian-tree rev-palindrome centered at c. Also, let  $Z_c$  be the number of 0's in  $\mathsf{PD}_{T[i..j]}$ ,  $E_c$  be the length of the extension of T[i..j] (i.e.,  $E_c = i-b$ ), and  $U_c$  be the number of updates of positions of 0 from  $\mathsf{PD}_{T[i..j]}$  to  $\mathsf{PD}_{T[b..e]}$ . Let T[i'..j']be the next palindrome of center c' which we have to compute the extension of, after computing the extension of T[i..j]. Namely, T[i'..j'] is the longest proper suffix palindrome of T[b..e] if |T[b..e]| > 1. Otherwise, T[i'..j'] = T[e + 1..e + 1] holds.

As the first step to considering  $\sum U_c$ , we consider the simpler case such that each character is distinct from the other in the string. We call this case permutation-Cartesian-tree matching.

In this case,  $c = m_{[i..j]}$  holds since  $T[m_{[i..j]}]$  is the only smallest value in T[i..j] and  $m_{[i..j]}$  is the root of  $\mathsf{CT}(T[i..j])$  and  $\mathsf{CT}(T[i..j]^R)$ . Also,  $m_{[i..j]} = m_{[b..e]}$  holds. Now we consider the starting position of the next palindrome T[i'..j'].

**Lemma 2.** Let T[i'..j'] be the next palindrome. Then,  $i' > m_{[i..j]}$  holds.

Proof. The next palindrome T[i'..j'] is either T[e+1..e+1] or the longest proper suffix palindrome of T[b..e]. Since the former case is obvious, we consider only the latter in the following. For the sake of contradiction, we assume that  $i' \leq m_{[i..j]}$ . Then  $T[m_{[i'..j']}] < T[m_{[i..j]}]$  holds. Since  $m_{[i'..j']} \in [b..e]$ , this leads to a contradiction with  $m_{[i..j]} = m_{[b..e]}$ .

From Lemma 2, 0s in  $\mathsf{PD}_{T[i.j]}$  and 0s in  $\mathsf{PD}_{T[i'.j']}$  all correspond to different positions in T. Hence,  $\sum Z_c \leq n$  holds. Also,  $U_c \leq Z_c + E_c$  and  $\sum E_c \leq n$  holds. Therefore, we obtain  $\sum U_c \leq \sum Z_c + \sum_{E_c} \leq 2n$ . Now we have shown the total number of updates  $\sum U_c$  is at most O(n). Similar to the maximal parameterized palindromes,  $\mathsf{PD}_{T[i..j]}[k]$  can be accessed in constant time



Figure 5: Illustration for Cartesian-tree palindromes.

by precomputing  $PD_T$ . Also, since  $PD_T$  can be precomputed in O(n) time for linearly sortable alphabets, we obtain the following result:

**Theorem 4.** For linearly sortable alphabets, all maximal permutation-Cartesian-tree rev-palindromes can be computed in O(n) time with O(n) space.

Now we consider  $\sum U_c$  in the general case. As for the relationship between  $Z_c$  and  $Z_{c'}$ , we show the following lemma:

**Lemma 3.** As for the number of 0's in  $PD_{T[i'..j']}$ ,  $Z_{c'} \leq Z_c + E_c - U_c$  holds.

*Proof.* The next palindrome T[i'..j'] is either T[e+1..e+1] or the longest proper suffix palindrome of T[b..e]. Since the former case is obvious, we consider only the latter in the following. The number of 0's in  $\mathsf{PD}_{T[i'..j']^R}$  is  $Z_{c'}$ . Also, the number of 0's in  $\mathsf{PD}_{T[b..e]}$  is equal to  $Z_c + E_c - U_c$ . For the sake of contradiction, we assume that  $Z_{c'} > Z_c + E_c - U_c$ . Then, the number of 0's in  $\mathsf{PD}_{T[b..e]^R}$  is at least  $Z_{c'}$ , and this leads to a contradiction with T[b..e] being a maximal Cartesian-tree palindrome.  $\Box$ 

See also Figure 5. From Lemma 3,  $U_c \leq Z_c - Z_{c'} + E_c$  holds. Therefore, the total number of updates  $\sum U_c \leq \sum \{Z_c - Z_{c'}\} + \sum E_c \leq n$ . Hence, we obtain the following result:

**Theorem 5.** For linearly sortable alphabets, all maximal Cartesian-tree rev-palindromes can be computed in O(n) time with O(n) space.

#### 4.5 Maximal Palindromic-structure Reversal-based Palindromes

Now we consider how to determine whether the palindromic-structure palindrome T[i..j] can be extended by one character at each end. The changes from the set of maximal palindromes in T[i..j] to that of T[i-1..j+1] are prefix palindromes and suffix palindromes of T[i-1..j+1]. Therefore, if the set of prefix palindromes is equal to the set of suffix palindromes, then T[i-1..j+1] is a palindromic-structure palindrome. To efficiently compute whether this condition is satisfied, we rewrite the condition as follows:

- 1. Among maximal palindromes in T[1..n], the set of maximal palindromes starting at i whose length is at most j - i is equal to the set of maximal palindromes ending at j whose length is at most j - i.
- 2. The presence or absence of "a prefix palindrome of length two beginning at position i-1" and "a suffix palindrome of length two ending at position j+1" correspond.



Figure 6: Illustration for palindromic structures. Solid arrows are maximal palindromes starting at i or ending at j, and dotted arrows are prefix or suffix palindromes. The set of suffix palindromes of T[i-1..j+1] is a union of the set of the extensions of suffix palindromes of T[i..j] and the set of suffix palindromes of lengths one and two. Note that the prefix/suffix palindrome of length one always exists.

Since a suffix palindrome of j + 1 is either a suffix palindrome of j + 1 whose length is at most two or an extension of a suffix palindrome of j which is not a maximal palindrome ending at j, the above rewrites hold. See also Figure 6. Condition 2 can be computed easily; hence, we show how to compute condition 1 below. First, we precompute all maximal palindromes in T[1..n] by using Manacher's algorithm. Then, we construct an ascending sequence of lengths of maximal palindromes with the same ending (starting) position, concatenated with a delimiter character  $\$_i$ , where i is the ending (starting) position. For example, the sequence as for the ending position for a string abaaa is  $1\$_1\$_213\$_32\$_4123\$_5$ . By using these sequences for starting/ending position and LCE data structure, condition 1 can be computed in constant time. The length of the sequence is O(n)since the number of maximal palindromes is 2n - 1. Then we obtain the following theorem:

**Theorem 6.** For general unordered alphabets, all maximal palindromic-structure rev-palindromes can be computed in O(n) time with O(n) space.

Note that the concept of the palindromic structure can be generalized from maximal palindromes to maximal SCSTTR palindromes. From the above results, maximal SCSTTR palindromicstructure rev-palindromes can be computed in O(n) time and space.

## 5 Conclusion and Future Work

In this paper, we dealt with the problems of computing all maximal palindromes in a string under several variants of string matching models. We first showed two distinct definitions of generalized palindromes: symmetric and reverse. For maximal sym-palindromes, we proposed suffix-tree-based algorithms that work in their construction time and O(n) space. Also, for maximal rev-palindromes, we showed that Manacher's algorithm can be generalized to the matching models we consider, and presented O(n) time and space algorithms.

Our future work includes the following: (1) Can we efficiently compute maximal palindromes under other string matching models? For example, can we extend our algorithm to a structural matching model [31], which is a generalization of a parameterized matching? (2) It is known that any string of length n can contain at most n + 1 distinct palindromes [11], and all distinct palindromes can be computed in O(n) time [15]. It is interesting to study distinct palindromes under SCSTTRs. Rubinchik and Shur [29] claimed that their *eertree* data structure for computing distinct palindromes can be extended to computing distinct WK-palindromes. We are unaware whether the computed palindromes are symmetric-based or reversal-based. (3) While there can be  $\Omega(n)$  suffix palindromes in a string of length n, their lengths can be compactly represented with  $O(\log n)$  arithmetic progressions [1, 26]. Can suffix sym-/rev-palindromes under SCSTTRs be represented compactly in a similar way?

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# A Appendix

In this section, we show the details of SCSTTR suffix trees and how to compute the SCSTTR LCE query. First, we show some properties that each SCSTTR suffix tree has.

- 1. Each leaf node corresponds one-to-one to the encoding of each suffix.
- 2. The string depth of the LCA of two leaves corresponds to the value of LCP of the encodings of the suffixes.

Since these properties hold, we can compute the LCP value of encodings of two suffixes by computing the LCA.

In the following, we show the details of each SCSTTR suffix tree.

#### A.1 Maximal Theta sym-palindromes

An outward complementary LCE for the center position c in T can be computed by comparing T[[c+1]..n] and  $f(T[1..[c-1]]^R)$ . By constructing the suffix tree of the string  $T$f(T^R)#$  with delimiter characters \$ and #, the above operation can be done in constant time.

**Lemma 4.** The complementary suffix tree can be constructed in O(n) time and space for linearly sortable alphabets. Also, an outward complementary LCE query can be answered in O(1) time by using this data structure.

From Lemma 4, we obtain the following theorem.

**Theorem 7.** For linearly sortable alphabets, all maximal Theta sym-palindromes can be computed in O(n) time with O(n) space.

#### A.2 Maximal parameterized sym-palindromes

The definition of a parameterized suffix tree is as follows:

**Definition 5** ([3]). The parameterized suffix tree of a string T[1..n] is a compacted trie that stores the set  $\{\mathsf{PE}_{T[i..n]} \mid 1 \leq i \leq n\}$ .

Therefore, by constructing the parameterized suffix tree of  $T^T \#$  and computing the LCP value of  $\mathsf{PE}_{T[\lfloor c+1 \rfloor ..n]}$  and  $\mathsf{PE}_{T[1..[c-1]]^R}$ , we can compute the length of the maximal parameterized palindrome for each center position c.

**Lemma 5** ([3]). The parameterized suffix tree can be constructed in  $O(n \log(\sigma + \pi))$  time and O(n) space for linearly sortable alphabets. Also, an outward parameterized LCE query can be answered in O(1) time by using this data structure.

From Lemma 5, we obtain the following theorem.

**Theorem 8.** For linearly sortable alphabets, all maximal parameterized sym-palindromes can be computed in  $O(n \log \sigma)$  time with O(n) space.

#### A.3 Maximal order-preserving sym-palindromes

An order-preserving suffix tree is defined as follows:

**Definition 6** ([7]). The complete order-preserving suffix tree of a string T[1..n] is a compacted trie that stores  $\mathsf{Code}_{T[i..n]}$  for all  $1 \leq i \leq n$ . Also, the incomplete order-preserving suffix tree is a compacted trie such that some of the edge labels of the complete order-preserving suffix tree are missing.

By using the (incomplete) order-preserving suffix tree, maximal order-preserving sym-palindromes can be computed the same as with maximal parameterized palindrome.

**Lemma 6** ([7]). The (incomplete) order-preserving suffix tree can be constructed in  $O(n \log \log^2 n / \log \log \log n)$  time and O(n) space for linearly sortable alphabets. Also, an outward order-preserving LCE query can be answered in O(1) time by using this data structure.

From Lemma 6, we obtain the following theorem.

**Theorem 9.** For linearly sortable alphabets, all maximal order-preserving sym-palindromes can be computed in  $O(n \log \log^2 n / \log \log \log n)$  time with O(n) space.

#### A.4 Maximal Cartesian-tree sym-palindromes

As for a Cartesian suffix tree, the definition and the construction time are as follows:

**Definition 7** ([28]). The Cartesian suffix tree of a string T[1..n] is a compacted trie constructed with  $\mathsf{PD}_{T[i..n]} \cdot \$$  for every  $1 \le i \le |T|$ , where  $\$ \notin \Sigma$  and  $\$ \prec c$  hold for any character  $c \in \Sigma$ .

**Lemma 7** ([28]). The Cartesian suffix tree of a string of length n can be constructed in  $O(n \log n)$  time with O(n) space for ordered alphabets. Also, an outward/inward Cartesian-tree LCE query can be answered in O(1) time by using this data structure of T<sup>\$T<sup>R</sup>#.</sup>

From Lemma 7, we obtain the following theorem.

**Theorem 10.** For ordered alphabets, all outward maximal Cartesian-tree sym-palindromes can be computed in  $O(n \log n)$  time with O(n) space.

As for the case of inward maximal Cartesian-tree sym-palindromes, it is unclear where is the starting position of inward LCE queries. By combining the LCE queries and the binary search, we obtain the following theorem:

**Theorem 11.** For ordered alphabets, all inward maximal Cartesian-tree sym-palindromes can be computed in  $O(n \log n)$  time with O(n) space.

#### A.5 Maximal palindromic-structure sym-palindromes

The definition of a palindromic suffix tree is as follows:

**Definition 8.** The palindromic suffix tree of a string T[1..n] is a compacted trie that represents  $\mathsf{LPal}_{T[i..n]}$  of suffix T[i..n] for all  $1 \le i \le n$ .

Also, the following result is known:

**Lemma 8** ([19]). The palindromic suffix tree of a string of length n can be constructed in  $O(n \min\{\sqrt{\log n}, \log \sigma / \log \log \sigma\})$  time with O(n) space for general unordered alphabets, where  $\sigma$  is the number of distinct characters in the string. Also, an outward palindromic-structure LCE query can be answered in O(1) time by using this data structure of  $T^T^R \#$ .

From Lemma 8, we obtain the following theorem.

**Theorem 12.** For general unordered alphabets, all maximal palindromic-structure sym-palindromes can be computed in  $O(n \min\{\sqrt{\log n}, \log \sigma / \log \log \sigma\})$  time with O(n) space.