Reconstructing Strings from Substrings:
Optimal Randomized and Average-Case Algorithms

KAZUO IWAMA 1  JUNICHI TERUYAMA 2  SHUNTARO TSUYAMA 3

1RIMS, Kyoto University, Japan; iwama@kuis.kyoto-u.ac.jp
2School of Social Information Science, University of Hyogo, Japan; junichi_teruyama@hq.u-hyogo.ac.jp
3School of Informatics, Kyoto University, Japan; stsuyama@kuis.kyoto-u.ac.jp

Abstract

The problem called String reconstruction from substrings is a mathematical model of sequencing by hybridization that plays an important role in DNA sequencing. In this problem, we are given a blackbox oracle holding an unknown string $X$ and are required to obtain (reconstruct) $X$ through substring queries $Q(S)$. $Q(S)$ is given to the oracle with a string $S$ and the answer of the oracle is Yes if $X$ includes $S$ as a substring and No otherwise. Our goal is to minimize the number of queries for the reconstruction. In this paper, we deal with only binary strings for $X$ whose length $n$ is given in advance by using a sequence of good $S$’s. In 1995, Skiena and Sundaram first studied this problem and obtained an algorithm whose query complexity is $n + O(\log n)$. Its information theoretic lower bound is $n$, and they posed an obvious open question; if we can remove the $O(\log n)$ additive term. No progress has been made until now. This paper gives two partially positive answers to this open question. One is a randomized algorithm whose query complexity is $n + O(1)$ with high probability and the other is an average-case algorithm also having a query complexity of $n + O(1)$ on average. The $n$ lower bound is still true for both cases, and hence they are optimal up to an additive constant.

1 Introduction

Sequencing by hybridization (SBH) [5][10][12] is one of the major approaches to DNA sequencing which was developed in 1980’s and 1990’s. Its basic idea is to construct, for a given set $L$ of (short) strings, a single (long) string $T$ that contains all the strings in $L$ as substrings. Of course a concatenation of all strings in $L$ is a trivial answer. So we usually impose several constraints for $T$, for instance, $T$ should be shortest or $T$ should not include another given set of strings. The problem is certainly interesting from an algorithmic point of view, but unfortunately, many nontrivial versions of the problem were proven as intractable (e.g., [9][2]).

In 1995, Skiena and Sundaram proposed a new approach for SBH which is more interactive [13]. Namely we can ask $T$ whether some string $S$ is its substring or not, sequentially, i.e., by dynamically selecting $S$ in each round. Of course our goal is to select “good” $S$’s by using previously obtained information (yes/no answers of $T$ to the previous queries). More formally they introduced the problem called String reconstruction from substrings. We are given a black-box oracle having a hidden string $X$. If we ask the oracle with a query string $S$, then the oracle gives back an answer Yes if $X$ contains $S$ as a substring and No otherwise. Our goal is to reconstruct the string $X$ using a minimum number of queries. This is an idealized model of SBH, having an excellent simplicity as a mathematical model.

For the case that the alphabet is binary and the length $n$ is known in advance, the authors gave the following elegant algorithm, called SkSu in this paper. [13] also discusses different cases involving a larger alphabet and/or unknown $n$. In this paper, however, we are interested in only this binary, known-$n$ case.) SkSu first obtains the longest 0’s, $0^d$, in $X$ using a simple binary search by spending at most $\log n$ queries (our log in this paper is all base-2). Assume for simplicity that
this 0^d appears in \( \mathcal{X} \) only once. Then we “extend” this 0^d to the right by asking if 0^d1 is a substring (this query is denoted by Query(0^d1)). Note that the answer should be Yes since 0^d is the longest 0’s. Then make Query(0^d11). If the answer is Yes then 0^d11 is confirmed as a substring of \( \mathcal{X} \). Otherwise, 0^d10 should be a substring since our string is binary. Repeat this procedure, namely we add 1 to the current substring and ask the oracle with that string, until the substring arrives at the right end of \( \mathcal{X} \). We then extend it to the left until its length becomes \( n \) (see the next section for more details).

By using a nice mechanism for detecting the right end, they proved SkSu spends at most \( n + \log n + O(1) \) queries and always produces a correct answer. The information theoretic lower bound for this query complexity is \( n \), and hence, the above upper bound is almost optimal. Unfortunately, however, it still has an additive logarithmic gap. An obvious question is if we can remove this gap, which is posed as an open question in [13].

**Our Contribution.** We give two partially positive answers to this open question. Our first algorithm is deterministic which spends \( n + O(1) \) (in fact at most \( n + 6 \) queries on average) and our second one is randomized, which spends \( n + O(1) \) queries with high probability before it outputs an always correct answer. It is straightforward to show that the lower bound for the query complexity is \( n \) for both average case (obvious) and randomized case (using the Yao’s principle). So our algorithm is optimal up to an additive constant.

Both algorithms exploit the following fundamental property of binary strings: Let \( S \) be an arbitrarily fixed string of length \( \log n \). Then a constant fraction of strings of length \( n \) includes \( S \) as its substring, but this proportion decreases rapidly as the length of \( S \) increases. For instance, if a string \( T \) of length \( n \) is randomly selected, it is unlikely for \( T \) to include \( S \) of length \( \log n + 10 \). Similarly, a constant fraction of \( T \) does not include \( S \) of length \( \log n \) as its substring, but the proportion decreases rapidly as the length of \( S \) decreases. Our average-case algorithm is virtually the same as SkSu but we simply include this property in its analysis.

The randomized algorithm is more involved. The easy case is that the oracle string \( \mathcal{X} \) is close to a random string. Then we can fully use the above property. Namely a constant number of queries with random strings of length about \( \log n \) allow us to find a substring and a nonsubstring of length about \( \log n \) whp, which can save \( \log n \) queries of SkSu. Therefore, we can focus ourselves on the case that \( \mathcal{X} \) is far from a random string. It then turns out that we can define two groups such that \( \mathcal{X} \) must belong to either of them. One group consists of strings having a lot of repetitions of same substrings. Intuitively, if we know that a substring \( S0 \) appears in \( \mathcal{X} \) but \( S1 \) does not, then we can save one query whenever we encounter substring \( S \). Thus our profit is large if \( S \) repeats a lot. The other group does not have many repetitions of same substrings. Then we can find a “second seed” other than the first seed (the longest substring of 0’s), which is a bit longer than the first seed, without any extra queries. We can exploit this difference of the length between the first and the second seeds to remove the log \( n \) gap.

**Related Work.** There are various models for string reconstruction from the information of substrings and nonsubstrings. Margaritis and Skiena [11] studied the problem called *String reconstruction from substrings in rounds*. The query model of this problem is exactly the same as above, but (two or more) queries can be performed in a single round. Queries in each round can depend on the answers to the queries and the answers in the previous rounds but not on those in the same round and the goal is to minimize the number of rounds and the number of queries in each round. Margaritis and Skiena [11] gave a trade-off between the number of rounds and the number of queries per round. There are results about several lower bounds of queries [7, 14] in this model, for instance, the lower bound of queries when the number of rounds is one. Frieze and Halldórsson [6] studied a variant of the model, in which for each query, the answer is not binary but ternary. Namely, it is whether the string appears once in the oracle, appears at least twice, or does not appear. Tsur [15] provided algorithms that improve the results of [11] and [6]. Acharya et
The Skiena and Sundaram’s algorithm \cite{13} works as follows: For given \( d > 0 \) such that it is already known that \( 0^d \) is a substring of \( \mathcal{X} \) and \( 0^{d+1} \) is not, the algorithm extends string \( S \) (originally \( S = 0^d \)) to the right by making Query\((S\cdot 1)\). If the answer is Yes, then \( S \) is replaced by \( S1 \) and
by S0 otherwise. (If Query(S, 1) is No, the correct symbol after S should have been \(\overline{T} = 0\) since our strings are always binary.) This extension is obviously correct until the right end of \(\mathcal{X}\) comes. If the extension has gone beyond the right end of \(\mathcal{X}\), all queries after that are answered with No. In other words, if Suffix\(_{d+1}(S) = 0^{d+1}\), then we know that this has happened (recall that 0\(^{d+1}\) is known to be a nonsubstring) and there must be the right end somewhere in 0\(^{d+1}\). Finding it is easy, i.e., if the current S is S\(^{d+1}\), then simply make queries Query(S\(^0\)), Query(S\(^0\)) and so on until the answer becomes No (if Query(S\(^0\)) is Yes and Query(S\(^0\)) is No, then \(\mathcal{X}\) has a suffix of S\(^0\)). Once we have reconstructed the correct suffix, say S\(^0\), then all we have to do is to extend it to the left in a way similar to the above until its length becomes n which we have assumed is given in advance.

Suppose that the correct suffix is S\(^0\). Then the algorithm has spent \(|S'| - d\) queries until the end of S\(^{'}\), then d + 1 ones until we have noticed the right end has been passed, j + 1 ones to find the right end, and n − |S\(^{'}\)| − j ones for the last phase of left extension, which makes
\[
(|S'| - d) + (d + 1) + (j + 1) + (n - |S'| - j) = n + 2
\]
queries in total. Note that we further need queries to obtain the value of d such that 0\(^d\) is a substring of \(\mathcal{X}\) and 0\(^{d+1}\) is not, i.e., \(O(\log n)\) ones in the worst case if we use a simple binary search.

We add a small generalization to this algorithm, by replacing 0\(^d\) and 0\(^{d+1}\) with any (known) substring S and any (known) nonsubstring T of \(\mathcal{X}\), respectively. The new algorithm, Algorithm 1, is very similar: Our extension to the right begins from S as before. Suppose that our current string is S and the last query (= Query(S)) was answered Yes. Then our next query is Query(S T\([1]\)) and if the answer is No, then the next query is Query(S T\([1]\) T\([2]\)). If the answer is again No, then the next query is Query(S T\([1]\) T\([2]\) T\([3]\)), and so on. If the answer is Yes we simply confirm the extension so far, say as S\(^{'}\), and restart with Query(S\(^{'}\) T\([1]\)). Again if the suffix of the current string becomes T (having |T| consecutive No’s), there should have been the right end somewhere in this suffix.

We call this generalized Skiena and Sundaram Basic, which will be used in several occasions in our new algorithms given in the next sections. Its query complexity can be obtained exactly as above, giving us our first theorem, Theorem 1

**Theorem 1.** Basic is correct and its query complexity is \(n - |S| + |T| + 1\).

### 3 Average-Case Algorithm

Our algorithm is simple: We first ask \(\mathcal{X}\) if 0\(^{\log n}\) is a substring. If yes, we ask, for each \(i = 1, 2, \ldots, \log n\), if 0\(^{\log n + i}\) is an \(\mathcal{X}\)-sub until the answer becomes No. Otherwise, we ask, for each \(j = 1, 2, \ldots, \log n - i\), if 0\(^{\log n - j}\) is an \(\mathcal{X}\)-sub until the answer becomes Yes. Thus we can find the integer \(d\) (maybe negative) such that 0\(^{\log n + d}\) is an \(\mathcal{X}\)-sub but 0\(^{\log n + d + 1}\) is not. (For instance, \(d = 1\) means that Query(0\(^{\log n}\)) returns Yes, Query(0\(^{\log n + 1}\)) Yes, and Query(0\(^{\log n + 2}\)) No. Thus we need 3 queries for \(d = 1\). Similarly we need 3 queries for \(d = -2\).) Then we call Basic(0\(^{\log n + d}\), 0\(^{\log n + d + 1}\)), which gives us the final answer \(\mathcal{X}\). Note that Basic(0\(^{\log n + d}\), 0\(^{\log n + d + 1}\)) spends \(n + 1\) queries regardless of the value of \(d\). So our goal is to obtain the total number, \(N\), of queries to obtain \(d\) in the above procedure for all \(2^n\) strings. Let \(X_i\) be the set of length-n binary strings that have substring 0\(^i\) but not 0\(^{i+1}\), and let \(f(i) = |X_i|\). Then \(N\) can be written as

\[
N = f(\log n) \cdot 2 + f(\log n + 1) \cdot (2 + 1) + f(\log n + 2) \cdot (2 + 2) + \cdots + f(n) \cdot (2 + n - \log n) \\
+ f(\log n - 1) \cdot 2 + f(\log n - 2) \cdot (2 + 1) + f(\log n - 3) \cdot (2 + 2) + \cdots + f(0) \cdot (2 + \log n - 1) \\
= 2 \cdot [f(0) + \cdots + f(\log n - 2) + f(\log n - 1) + f(\log n)] + f(\log n + 1) + \cdots + f(n) \\
+ [f(\log n) \cdot 0 + f(\log n + 1) \cdot 1 + f(\log n + 2) \cdot 2 + \cdots + f(n) \cdot (n - \log n)] \\
+ [f(\log n - 1) \cdot 0 + f(\log n - 2) \cdot 1 + f(\log n - 3) \cdot 2 + \cdots + f(0) \cdot (\log n - 1)].
\]
The first sum is obviously $2 \cdot 2^n$. For the second sum, note that for $\ell \geq \log n + 1$, $f(\ell) + f(\ell + 1) + \cdots + f(n)$ is the number of strings that have substring $0^\ell$. Since $0^\ell$ can start from $n - \ell + 1$ different positions in $\mathcal{X}$, by using a union bound, we have

$$f(\ell) + f(\ell + 1) + \cdots + f(n) \leq \alpha(\ell) := (n - \ell + 1) \cdot 2^{n-\ell}.$$  

Obviously $f(\ell) \leq \alpha(\ell)$ (this approximation is not very bad) and it is easy to see that $\alpha(\ell + 1) \leq \alpha(\ell)/2$. Therefore, using $\sum_{i=0}^{\infty} i \cdot 2^{-i} = 2$, the second sum is bounded by

$$\alpha(\log n) \cdot \left( \frac{0}{2^0} + \frac{1}{2^1} + \frac{2}{2^2} + \cdots \right) \leq (n - \log n + 1) \cdot 2^{n-\log n} \cdot 2 \leq 2 \cdot 2^n.$$  

For the third sum, note that for $\ell \leq \log n - 1$, $f(\ell) + f(\ell - 1) + \cdots + f(1)$ is the number of strings that do not have substring $0^{\ell+1}$, which can be bounded as follows due to [8,3].

$$f(\ell) + f(\ell - 1) + \cdots + f(1) \leq \beta(\ell) := \left( 1 - \frac{1}{2^{\ell+1}} \right)^{n-\ell+1} \cdot 2^n.$$  

For a large $n$ and any $\ell \leq \log n - 1$, this $\beta(\ell)$ also decreases exponentially, namely

$$\frac{\beta(\ell - 1)}{\beta(\ell)} = \frac{(1 - \frac{1}{2^{\ell+1}})^{n-\ell+2}}{(1 - \frac{1}{2^{\ell+1}})^{n-\ell+1}} = \left( 1 - \frac{1}{2^{\ell+1} - 1} \right)^{n-\ell+1} \cdot \left( 1 - \frac{1}{2^\ell} \right) < e^{-\frac{n-\log n}{n-1}} < 2^{-1}.$$  

Now, exactly as before, the third sum is bounded by

$$\beta(\log n - 1) \cdot \left( \frac{0}{2^0} + \frac{1}{2^1} + \frac{2}{2^2} + \cdots \right) \leq (1 - 1/2^{\log n})^{n-\log n} \cdot 2^n \cdot 2 \leq (1/e)(1 - 1/n)^{-\log n} \cdot 2^{n+1} \leq 2^n.$$  

Thus $N \leq 5 \cdot 2^n$. Since Basic spends $(n + 1)2^n$ queries as mentioned before, we have

**Theorem 2.** The average complexity for reconstruction from substrings is at most $n + 6$.

**4 Randomized Algorithm**

Here are our basic ideas for the algorithm and its analysis. Our main routine is **DoubleSeed** (see Algorithm 3). As mentioned in the previous section, if we can find an $\mathcal{X}$-sub of length $\log n$ using a constant number of queries, then we are done. This is exactly what we do in **TryEasycase** (see Algorithm 4) at the beginning of **DOUBLESEED**. Note that we seek a substring that is shorter than $\log n$ by a constant $C_1$. (This constant is not harmful since our target complexity has the $O(1)$ term.) If there is no such “easy” substring, we obtain a seed, $0^d$, such that it is an $\mathcal{X}$-sub but $0^{d+1}$ is not, to start the extension with it. Let $d_1$ be the cost for this search. Then it turns out that $2\log d$ is enough for this $d_1$ by using a sort of binary search (we want a smaller cost for a smaller $d$). In **TRYEASYCASE**, we also check if $1^{d+2d_1}$ is an $\mathcal{X}$-sub and if so, we are again done by Theorem 1. The reason why we try to find such a 1’s (not 0’s) substring is related to the repetition structure of $\mathcal{X}$ and will be stated later.

If **TRYEASYCASE** fails, i.e., if it returns with 0, then after setting important values $q, \ell$ and $r_0$ at Line 3, we start extending the seed, $0^d$, to the right, until its length becomes $q = 0.01n$ (Line 6). If we can successfully do it, then we have already achieved our goal, namely we can achieve a query complexity of $n + O(1)$ by continuing with the standard SkSu at Line 24. This is our main claim in the following sections. Let $I_0$ be this extended string of length $q$. If we reach the right end before the length becomes $q$, it means we could not have done what should be done in the main
Algorithm 3: Procedure DoubleSeed

Output: The oracle string $\mathcal{X}$

1. if $\text{TryEasyCase}(Z, d, d_1) = 1$ then
   
   2. return $Z$

3. $q \leftarrow 0.01n$; $\ell \leftarrow d + 2d_1$; $r_0 \leftarrow d_1/(2q)$;

4. Assume Label($S$) has value null for all strings $S$ initially.

5. $I \leftarrow 0^d$ ($0^d$ is the longest substring of 0’s in $\mathcal{X}$)

6. while $|I| < q$ do
   
   7. if $\text{Suffix}_{d+1}(I) = 0^{d+1}$ then
      
      8. return $\text{Exception}(I, d, d_1)$
   
   9. $r \leftarrow$ a uniformly random value in $[0, 1]$; (Do sample at each position with prob. $r_0$.)

10. if $r < r_0$ then

11. $j \leftarrow 0$;

12. while Sibling($\text{Suffix}_{\ell+j}(I)$) $\in \text{Sub}(I)$ do

13. $j \leftarrow j + 1$; (extending $S$ in Fig. 1 to the left until it becomes $I_0$-nonsub)

14. if $\text{Query}(\text{Sibling}(\text{Suffix}_{\ell+j}(I))) = 0$ then (if the position is single-child)

15. Label(Parent($\text{Suffix}_{\ell+j}(I)$)) $\leftarrow$ the last symbol of $I$;

16. else

17. return $\text{2ndSeed}(I, \text{Sibling}(\text{Suffix}_{\ell+j}(I)))$

18. for $j := 0$ to $|I| - \ell$ do

19. if Label($\text{Suffix}_{\ell+j}(I)$) $\neq$ null then (if the next position is registered as single-child)

20. $I \leftarrow \text{TwoExtension}(I, \text{Label}(\text{Suffix}_{\ell+j}(I)))$;

21. break

22. if $j = |I| - \ell$ then

23. $I \leftarrow \text{ExtendRight}(I)$; (the same as $\text{ExtendLeft}$ except the direction)

24. return $\text{Basic}(I, 0^{d+1})$

loop because the seed is located too close to the right end of $\mathcal{X}$ (by chance). So we go to a sort of exception handling routine, Exception (see Algorithm 5), at Line 8, and complete our (failed) job in the main loop with extending the current string to the left. Note that it is easier to do this than the original main loop, since we have no chance of encountering the right end of the oracle.

Each round of the main loop is “sampled” with probability $r_0$ (in Lines 9–10, and Lines 11–17 are skipped if not sampled). Note that “each step” is the same as “each position” of $I_0$. Namely when we say “at each position” it means we have already extended the seed up to $I$ that is a prefix of $I_0$, and we are now looking at the last symbol of $I$. See Fig. 1. At each position, we obtain $S = S'\overline{s}$ (Lines 12–13 where no queries are needed) that is the shortest string such that (i) its sibling, $S'$s, is a suffix of $I$, (ii) its length is at least $\ell$, and (iii) it is an $I$-nonsub. The condition at
Algorithm 4: Procedure TryEasycase(Z, d, d₁)

Output: 1 with the final answer Z or 0 with integers d and d₁ such that 0^d is an x-sub and 0^{d+1} not, and d₁ is the query cost spent in this routine

1. if Query(0^{log n - C₁}) = 1 then (C₁ is a constant related to the error probability)
   2. while true do
      3. Generate a random string X of length log n + C₁
      4. if Query(X) = 0 then
         5. break
      6. Z = Basic(0^{log n - C₁}, X)
      7. return 1
   8. i ← 0

9. if Query(0.5 log n) = 1 then
   10. while Query(0^{log n - C₁ - 2^i}) = 0 do
       11. i ← i + 1
       12. d ← BS(0^{log n - C₁ - 2^i}, 0^{log n - C₁ - 2^i-1}); (BS(0^x, 0^y) returns the value d by using the standard binary search that finds the 0^d in the range of 0^x and 0^y)
       13. d₁ ← # of oracle queries (= (# of queries in BS) + i + 2)
   14. else
   15. while Query(0^{2^i}) = 1 do
      16. i ← i + 1
      17. d ← BS(0^{2^i-1}, 0^{2^i})
      18. d₁ ← # of oracle queries
   19. if d₁ ≤ C₂ then (C₂ is a constant related to the performance)
      20. Z = Basic(0^d, 0^{d+1})
      21. return 1
   22. if Query(1^{d+2d₁}) = 1 then
      23. Z = Basic(1^{d+2d₁}, 0^{d+1})
      24. return 1
   25. return 0

Line 12 must be met eventually since at least Sibling(I) ≠ I. Now we are ready to introduce the two cases.

(1) S (= S'|s) is an x-sub. (2) S is an x-nonsub.

If Case (1) happens, substring S’ can be followed by both 0 and 1 in x, but only 0 or only 1 follows S’ if Case (2) happens. Now we define a single-child position and a double-child position for each position h of I₀: If Case (1) happens, position h is called double-child and otherwise (if Case (2) happens) called single-child.

Suppose that the current position is double-child and is sampled. Then we go to 2ndSeed (see Algorithm 5) at Line 17. Because S = S'|s is an I-nonsub, S should appear on the right side of I or on its left side, as shown in Fig. 1(a) and (b). 2ndSeed does not know which side, but it extends this new seed S to the right in its while loop at Line 2. If S is on the left side (Fig. 1(b)), then its extension hits I and returns at Line 7. Otherwise, the extension hits the right end of x and comes to Line 17. If I and S do not overlap and there is a gap of at least d between them, our task is easy (Lines 17–21): We simply extend I to the left, get to the left end and fill the gap between I and S to obtain the final answer x. Let us look at the bookkeeping on the cost using the notion of “profit” and “loss.” Recall that we obtained the first seed of length d using d₁ queries, where we
**Algorithm 5: Procedure Exception(I, d, d1)**

**Input:** I = I'0d+1 is a string such that I'0m is a suffix of X for some m. d and d1 are the same as those in the main routine

**Output:** The oracle string X

1. q ← 0.01n; ℓ ← d + 2d1; r0 ← d1/(2q);
2. Assume Label(S) has value null for all strings S initially.
3. I ← FindRightEnd(I)
4. k ← |I|
5. while |I| < q + k do
6.   r ← a uniformly random value in [0, 1]; (Do sample at each position with prob. r0.)
7.   if r < r0 then
8.     j ← 0;
9.     while SiblingL(Prefixℓ+j(I)) ∈ Sub(I) do
10.    j ← j + 1;
11.   if Query(SiblingL(Prefixℓ+j(I))) = 0 then
12.     Label(ParentL(Prefixℓ+j(I))) ← the first symbol of I;
13.   else
14.     return 2ndSeed(I, SiblingL(Prefixℓ+j(I)));
15.   end if
16.   for j := 0 to |I| - ℓ do
17.     if Label(Prefixℓ+j(I)) ≠ null then
18.       I ← TwoExtensionL(I, Label(Prefixℓ+j(I))); break
19.   end if
20. end while
21. return Fill(ε, I)

count (i) d as a profit and (ii) d1 as a loss. To know the right and the left ends of X as above, we have a loss (iii) d for each. Furthermore, we spend d1/2 expected queries for the sampling (recall the value of r0), which is not more than (iv) d1 queries whp (a loss). Do not forget that we have obtained the second seed S of length at least (v) d + 2d1 (a profit). Thus our profit is (i)+(v) and our loss is (ii)+(iii)×2+(iv), which balance and means we have spent at most n queries in total. We also need to consider the case that the gap between I and S is small (the if condition at Line 19 is not met and we come to Line 22) and the more messy case that I and S overlap (Fig. 1(c)). Fortunately it turns out that we can enjoy a similar balance for all the cases, namely we can prove that if we go to DoubleSeed, we are done.

If the sampled position is single-child, it means we have found the substring S' such that if S' appears anywhere in X, its next symbol is always s. This information is kept in the database (at Line 15 of DoubleSeed).

Now whether or not the current round is sampled, if we do not go to 2ndSeed, we come to Line 18 of DoubleSeed. Here, if the next position (sometimes denoted as the current position +1) is single-child and that information is already stored in the database, we can make a single extension without a query. Look at Lines 18–22. Here we first search a string S' existing in the database and go to TwoExtension (see Algorithm 7), which is a bit complicated because of the right-end issue and gives us only 1/2 extension for free on average. If we cannot find such S' in the database, then we simply extend the current string by one at Line 22 using a query. Note that we need Case (1) (the position is sampled and double-child) only once to go to 2ndSeed. So, without loss of generality we can assume we encounter a good number of single-child positions. If some of them are sampled and have substrings S' that repeat many times in X, we have a corresponding
amount of profit, hopefully an enough one to recover the several losses mentioned above. It turns out that it is important for this purpose that we set value $\ell$ sufficiently smaller than $\log n$. Details will be given in Sec. 5.

Finally we give a short reason for the importance of the sampling. Suppose that we have 100 single-child and 100 double-child positions in $I_0$. Then if we sample too many, say 100 positions, we would not have any profit since we need an extra query (Line 12) for each sampled position. However if we sample, say, 10 positions at random, this extra cost is only 10 and about one-half of them should be single-child positions. If some of them have strings $S'$ that repeats many times in $I_0$, we have a good chance of getting enough profit. See the next section for details.

Other routines are EXTENDRIGHT which is exactly the same as EXTENDLEFT in Sec. 2 except the direction of extension, FINDRIGHTEND that is already explained and given as Lines 7–9 of BASIC in Sec. 2, FINDLEFTEND that is similar to FINDRIGHTEND and FILL that fills a gap between the given prefix and suffix of $X$, by extending the prefix to the right, until the total length becomes $n$. We omit pseudo codes for those easy routines.
Algorithm 6: $2^\text{ndSeed}(I, S)$

**Input:** Two $\mathcal{X}$-subs $S$ and $I$ s.t. $S$ is an $I$-nonsub and $\text{Sibling}(S) = \text{Suffix}_{|S|}(I)$. Note that $I$ can be written as $0^dZ$.

**Output:** The oracle string $\mathcal{X}$

1. $k \leftarrow |S|$
2. while true do
   1. $S \leftarrow \text{RightExtend}(S)$
   2. if $\text{Suffix}_d(S) = 0^d$ then (S may hit $I$ or the right end)
      1. if $\text{Query}(S \cdot 1 \cdot Z[1])$ is Yes then
         1. return $\text{Basic}(S \cdot 1 \cdot Z, 0^d+1)$
      2. else if $\text{Query}(S \cdot 1 \cdot Z[1])$ is No then
         1. if $\text{Query}(S \cdot 1)$ is Yes then
            1. $S \leftarrow S \cdot 1$
         2. else
            1. $S \leftarrow \text{FindRightEnd}(S)$
         3. break
      3. $S \leftarrow S \cdot 1 \cdot Z[1]$
3. while $|I| + |S| \leq n$ do
   1. $I \leftarrow \text{LeftExtend}(I)$
   2. if $\text{Prefix}_{d+1}(I) = 0^d+1$ then
      1. $I \leftarrow \text{FindLeftEnd}(I)$
      2. return $\text{Fill}(I, S)$
   3. if $\text{Query}(I)$ is No then
      1. $I \leftarrow \text{FindLeftEnd}(I)$
      2. return $\text{Fill}(I, S)$
4. for $j \leftarrow k$ to 1 do
   1. if $\text{Suffix}_j(I) = \text{Prefix}_j(S)$ and $\text{Query}(I \cdot \text{Suffix}_{|S| \cdot -j}(S)) = 1$ then
      1. return $\text{Fill}(\epsilon, I \cdot \text{Suffix}_{|S| \cdot -j}(S))$ ($\epsilon$ is the empty string)

Algorithm 7: TwoExtension($I, t$).

**Input:** $t$ is a unique symbol following $I$ in $\mathcal{X}$ unless the right end of $I$ is also that of $\mathcal{X}$.

**Output:** New $I$ with two symbols extended or with $0^d+1$, an indication of the right end

1. $s \leftarrow 0$ or 1 uniformly at random.
2. if $\text{Query}(I \cdot t \cdot s)$ is Yes then return $I \cdot t \cdot s$
3. if $\text{Query}(I \cdot t \cdot \overline{s})$ is Yes then return $I \cdot t \cdot \overline{s}$
4. if $\text{Query}(I \cdot t)$ is Yes then ($I \cdot t$ is the right end of $\mathcal{X}$)
   1. Add 0’s after $I \cdot t$ such that its suffix of length $d+1$ is $0^d+1$.
5. else ($I$ is the right end of $\mathcal{X}$)
   1. Add 0’s after $I$ such that its suffix of length $d+1$ is $0^d+1$.
6. return $I$
5 Analysis of the Algorithm

As mentioned in the previous section, the basic structure of DOUBLESEED is as follows: (1) It first checks if our \( X \) is easy and we are done if so. Otherwise we obtain an \( X \)-sub 0\( d \) as a seed. (2) It extends the seed to the right, where each round is sampled with probability \( r_0 \). (3) If a sampled round is double-child (its position is a double-child position), we go to \( \text{2ndSeed} \) and we are done. (4) If a sample round is single-child, we store the single-child information in the database. (5) If the next position has been known to be single-child, either it is sampled or not, we do not need a query for the extension. Now we start our detailed analysis. It is straightforward to see that DOUBLESEED always returns with a right answer, so our job in this section is to bound the number of queries for several different cases.

**Lemma 1.** If DOUBLESEED ends at Line 2, its query complexity is \( n + \max\{2C_1, C_2\} + 1 \) with failure (i.e., we cannot achieve the complexity) probability at most \( \frac{1}{2} \).

**Proof.** TRYEASYCASE returns with 1 in three cases: (1) 0\( \log n - C_1 \) is an \( X \)-sub. Then we try to find an \( X \)-nonsub of length \( \log n + C_1 \). Since the length of \( X \) is \( n \), the number of different substrings of a fixed length is at most \( n \). Therefore the probability that a random string of length \( \log n + C_1 \) is an \( X \)-sub is at most \( n/2^\log n + C_1 = 1/2^{C_1} \). Then using Basic, our query complexity is \( n + 2C_1 + 1 \) by Theorem 1. (2) The overhead \( d_1 \) is smaller than a constant \( C_2 \). Then this overhead is also an overhead of Basic and our query complexity is \( n + C_2 + 1 \) by Theorem 1. (3) There are an \( X \)-sub 1\( d + 2d_1 \) (string of 1’s, not 0’s) and an \( X \)-nonsub 0\( d+1 \). Note that the cost of obtaining the former is 1 and \( d_1 \) for the latter. So, our query complexity is even less than \( n \) by Theorem 1. Note that Cases (2) and (3) do not use randomness.

**Lemma 2.** Suppose that TRYEASYCASE returns \( 0 \). Then, (i) \( C_2 \leq d_1 \leq 2 \log d + 1 \), and (ii) \( d + 2d_1 \leq \log n - C_1 + 1 \).

**Proof.** Straightforward and omitted.

We postpone the analysis of EXCEPTION at the end of this section. Recall that its role is to do what we cannot do in the rest of the main loop since we encounter the end of the string too early. So it is easier to see its analysis after finishing that of the whole parts of the main loop. Thus, let us move on to the next event of DOUBLESEED; it goes to \( \text{2ndSeed} \). Although it was mentioned above that we are done, we are actually not since the second seed may overlap with the current string \( I \). Recall that \( I_0 \) is the extended string after we finished the while loop. Fix \( I_0 \) as an arbitrary string of length \( q \) and let \( h \) be a position in \( I_0 \) from which \( \text{2ndSeed} \) is called with \( I \) and \( S \). Let \( J(h) \) be the largest integer \( j \) such that, at position \( h \), \( \text{Suffix}_j(I) = \text{Prefix}_j(S) \) and \( I \cdot \text{Suffix}_{|S|-j}(S) \) is an \( X \)-sub or 0 if such a positive \( j \) does not exists. Namely \( I \) and \( S \) overlap with an intersection of length \( J(h) \) and their union is an \( X \)-sub. If \( J(h) \) is large, it effectively shortens the second seed and we may not be able to achieve the profit we have expected. Fortunately, we have the next technical lemma claiming that such a concern is needless and then Lemma 4 which assures that if \( J(h) \) is small, we have a sufficient profit.

**Lemma 3.** The probability that DOUBLESEED samples at a double-child position \( h \) such that \( J(h) > |S| - 4d_1 \) is at most \( 2^{-4d_1} \) (we call such a position a bad position).

**Proof.** We first review the basic property of strings. Suppose that a string \( X \) overlaps with the same \( X \) as illustrated in Fig. 2(1), i.e., \( X = X'Z = ZX'' \) for some \( Z \). Then one can see easily that if the intersection is one-half or more, the string should have a repetition structure, namely, we can write that \( X = \sigma^k\sigma' \), where \( \sigma' \) is a prefix of \( \sigma \). We call \( \sigma \) a block. Next suppose that a string \( Y \) also has a repetition structure with a block \( \gamma \) and that \( k = \max(|\sigma|, |\gamma|) \). Furthermore, suppose that
(1) \[ X = \sigma \sigma \sigma \sigma \sigma \sigma \sigma' \]
\[ X = \sigma \sigma \sigma \sigma \sigma \sigma \sigma' \]
(2) \[ Y = Y_1Y_2Y_3Y_4 \]
\[ Y = Y_1Y_2Y_3Y_4 \]

Figure 2: Periodic structure

\[ h_1 \quad h_2 \quad \ell - 12d_1 \quad h_4 \]

\[
\begin{array}{c}
\sigma \sigma \sigma \sigma \quad 0 \quad 0 \quad 0
\end{array}
\begin{array}{c}
\sigma \sigma \sigma \sigma \quad 0 \quad 0 \quad 0
\end{array}
\begin{array}{c}
\gamma \quad \gamma \quad 0
\end{array}
\begin{array}{c}
\gamma \quad \gamma \quad 0
\end{array}
\]

Figure 3: Intervals of bad positions

\[ X \]
\[ X' \]
\[ S' \]

X and Y overlap with an intersection of length at least \( k' = 2k \), i.e., \( \text{Suffix}_{k'}(X) = \text{Prefix}_{k'}(Y) \). Then we can claim that both strings have the same repetition structure. (The formal proof may be a bit messy, but see Fig. 2 (2) for its sketch. Let \( p \) be a common divisor of \(|\sigma|\) and \(|\gamma|\). Then as shown in the figure, we can write \( \sigma = \sigma_1\sigma_2\sigma_3 \) and \( \gamma = \gamma_1\gamma_2\gamma_3\gamma_4 \) if \(|\sigma| = 3p\) and \(|\gamma| = 4p\), for instance. Then one can see that \( \gamma_1 = \sigma_1 = \gamma_4 \), \( \gamma_2 = \sigma_3 = \gamma_3 \), \( \gamma_3 = \sigma_2 = \gamma_2 \), implying \( \sigma_i \)'s and \( \gamma_j \)'s are all identical. Thus X and Y have the same repetition structure with the same block.)

Now see Fig. 3. Suppose that current position \( h_1 \) is a bad position, namely the second seed \( S \) and \( X = \text{Suffix}_S(I) \) deeply overlap \((h_2)\) is the position of the right end of the union\). Their intersection has length \( J(h_1) > |S| - 4d_1 \) by the condition of the lemma. Since \( S \) and \( X \) are the same strings except for their rightmost symbols, they must have a repetition structure with a block, say \( \sigma \), as mentioned above.

Because of the large length of the intersection, the length, \( g \), between \( h_1 \) and \( h_2 \) is at most \( 4d_1 \). Consider the position \( h_4 \) that is far away from \( h_2 \) by \( \ell - 12d_1 \). Then we can show that there is no bad position between \( h_2 \) and \( h_4 \). Suppose otherwise that \( h_3 \) (see the figure) is a bad position. Then we can define \( X' \) and \( S' \) exactly as we did for \( X \) and \( S \) and they heavily overlap with a block \( \gamma \) whose length is at most \( 4d_1 \). Furthermore, because both \( X \) and \( X' \) are substrings of \( X \) and the distance between \( h_1 \) and \( h_3 \) is at most \( \ell - 8d_1 \), \( X \) and \( X' \) overlap with an intersection of length at least \( 8d_1 \). Thus the two strings satisfy the condition for the above claim, meaning that their blocks should be the same. However, as shown in the figure, this implies a contradiction because the symbol in \( X' \) at position \( h_2 \) cannot be determined uniquely. This means that the number of bad positions is less than \( \frac{4d_1}{\ell - 8d_1}q \). Hence the probability that these bad positions are not sampled at all is at least \( (1 - r_0)^{4d_1} \geq 1 - \frac{4r_0d_1}{\ell - 8d_1} = 1 - \frac{2d_2}{\ell - 8d_1} \). Namely the probability that a bad position is sampled (=the probability of the lemma we want to prove) is at most \( \frac{2d_2}{\ell - 8d_1} \), which is at most \( \frac{2d_2}{2^{(d_1-1)/2} - 6d_1} \) by Lemma 5.2 (i). For \( C_2 \geq 40 \) (implying \( d_1 \geq 40 \) by Lemma 5.2 (i)), we have \( 2^{(d_1-1)/2} - 6d_1 \geq 2^{d_1/2}/2 \) and \( 4d_1^2 \leq 2(3/8)d_1 \), which implies \( \frac{2d_2}{2^{(d_1-1)/2} - 6d_1} \leq 1/2d_1^4/8 \). Thus the lemma is proved.
Lemma 4. If 2ndSeed is called at a position h (called a good position) such that \( J(h) \leq |S| - 4d_1 \), then our profit inside 2ndSeed is at least \(-d + 2d_1\).

Proof. We go to 2ndSeed with two \( \mathcal{X} \)-subs, \( I \) that is the current extension of the first seed and \( S \) a second seed. In the while-loop from Line 2, \( S \) is extended right and if the extension continues, we do not have gain or loss as shown in the small example in the pseudo code (for instance, we obtain two extensions at Line 8 with two queries). We already (in Sec. 4) saw the case that \( S \) is located on the right side of \( I \) and they do not overlap with a relatively large gap. Namely the profit in 2ndSeed is \((v)-(iii)\times2 = -d + 2d_1 \). The case that \( S \) is located on the left side of \( I \) is rather easy, too. In 2ndSeed, we lose \( d \) for detecting the overlap (Line 6) and will lose another \( d \) in BASIC to detect the right end. Since our gain is \( d + 2d_1 \), the overall profit is \(-d - d + 2d_1 = -d + 2d_1 \). The small-gap case is similar.

Now the remaining case is that \( S \) is located on the right side of \( I \) and they overlap. Suppose that the length of the intersection between \( I \) and \( S \) is \( j_0 (\leq |S| - 4d_1 \) by the assumption of the lemma) when 2ndSeed is called, which means if we let \( k = |S| \), we have a new profit of \( k - j_0 \) at this moment (instead of \( d + 2d_1 \) in the non-overlap case), since we can think that the first seed is prolonged by \( k - j_0 \) for free at Line 26. However, we have to spend extra queries to determine this overlap in the for loop of Lines 25–27. Here, observe that this check is done downward from the maximum \( k \), i.e., from the possibility that the intersection is \( S \) itself. Furthermore, if the intersection is more than one-half of \( S \), then as explained in the proof of Lemma 3 \( S \) must have a repetition structure and the length of its block is at least two (recall that the case that \( \mathcal{X} \) has a long 1’s substring is already excluded using TRYEASYCASE). Thus the query at Line 26 occurs at most every other round, i.e., the number of queries is at most \((k - j_0)/2\), assuming that this query is actually done only if the first condition of the if statement is met. If the intersection is less than one-half (i.e., \( j_0 < k/2 \)), the query can start from \( k/2 \). Therefore the number of queries to determine the overlap is at most \( k/2 - j_0 < (k - j_0)/2 \). Thus we still keep a profit of \((k - j_0)/2\) in both cases. Since \( j_0 \leq k - 4d_1 \) by the assumption of the lemma, \((k - j_0)/2\) is at least \( 2d_1 \). Considering the loss of detecting the right end (no loss for the left end) our profit inside 2ndSeed is at least \(-d + 2d_1 \).

Now we have two remaining cases; DoubleSeed’s ending at line 17 and at line 24. For our analysis, we introduce a threshold for the number of double-child positions in \( I_0 \), namely whether it is at least \( q/2^{11} \) or not. If we have that many double-child positions, we can expect at least one of them is sampled at a good position and we are done by Lemma 4. All other possibilities, such as going to 2ndSeed from a bad position and all the double-child positions have missed being sampled (and ending at line 24), are regarded as a failure, whose probability turns out to be sufficiently small.

Conversely suppose that the number of double-child positions is less than \( q/2^{11} \). Then if we go to 2ndSeed (and DoubleSeed ends at line 17), it is still fine; our failure probability due to the bad positions, etc. is small enough similarly as before. However, the probability that we do not go to 2ndSeed (hence eventually ending at line 24) becomes a main issue. Namely we need to assure that we can enjoy a sufficient profit by free extensions at line 20. The idea is that the number of different strings, \( U \), in the database that give us free extensions is much smaller than the number of single-child positions in \( I_0 \). This is because such a string \( U \) should have a (shorter) prefix that has already appeared in \( I \) at a double-child position (and was not sampled since, if sampled, we should have gone to the 2ndSeed). Thus the number of different \( U \)’s is closely related to the number of double-child positions that is now assumed to be small. Thus the same \( U \) appears many times, giving us many free extensions. Details are given in the proof of the following lemma.

Lemma 5. If DoubleSeed ends at line 17 or 24, its query complexity is at most \( n \) with failure probability at most \( 3 \cdot e^{-d_1} \).
Proof. We consider two cases depending on the number of double-child positions in $I_0$.

(Case 1: The number of double-child positions in $I_0$ is at least $q/2^{11}$) First of all, observe Lines 2 and 3 of TWOEXTENSION which is called at Line 20 of DOUBLESEED. Suppose neither $I$ nor $I'$ hits the right end. Then the condition in Line 2 is met with probability $1/2$ and if it is not, the condition in Line 3 must be met. So, $I$ is extended by 1.5 symbols on average. This mechanism means that if a double-child position $P_D$ is preceded by a single-child position $P_S$ and if $P_S$ is extended by TWOEXTENSION, then $P_D$ is skipped regardless of the value of $r_0$ at that round. However, if this actually happens, then TWOEXTENSION gives us a profit of $1/2$ per each on average. Therefore, if a $\delta$ fraction of double-child positions are actually skipped in this mechanism, we can obtain a profit of $\delta q/2^{12}$, which is far more than needed (recall that $q$ includes $n$ as a linear form and what we need as a profit is a logarithm of $n$) and we are done. Thus without loss of generality, we can assume most of the $q/2^{12}$ double-child positions are subject to being sampled.

Our “success” here is only to end at line 17 (if we finish at Line 24 it is counted as failure). Consider the following three conditions: (i) No bad position is sampled. (ii) At least one double-child position is sampled. (iii) The number of samples is at most $d_1$. If (i) and (ii) are met, the sample in (ii) forces us to go to 2NDSEED and that sample is not bad. So, our profit in 2NDSEED is at least $-d + 2d_1$ by Lemma [3] If (iii) is met, our profit before coming to 2NDSEED is at least $d - 2d_1$, so we have a good balance. Namely if all (i) to (iii) are met, DOUBLESEED succeeds. Now let us calculate the failure probability. (i) A bad position is sampled with probability at most $2^{-d_1/8}$ by Lemma [3] (ii) The probability that there is no sample at any double-child position is at most $(1 - \rho_0)q/2^{12} < e^{-\rho_0/2^{12}} = e^{-d_1/8}$. (iii) DOUBLESEED spends $d_1/2$ expected queries for sampling. Thus the probability that this value exceeds $d_1$ is at most $e^{-d_1/4}$ by Chernoff bound. The lemma just takes the largest one among the three failure probabilities, multiplied by three.

(Case 2: The number of double-child positions in $I_0$ is less than $q/2^{11}$) We have further two cases; ending at Line 17 and ending at Line 24. In the former case, (i) and (iii) of Case 1 must be met for the success. In other words, the (conditional) failure probability is $P_1 = e^{-d_1/8} + e^{-d_1/6} < 2 \cdot e^{-d_1/8}$. In the following, we prove that if we end at Line 24, then our (conditional) failure probability is $P_2 = 3 \cdot e^{-d_1/4}$, which suffices for the lemma since $P_2$ is obviously larger than $P_1$.

Fix an arbitrary $I_0$. If a position $h$ is a single-child position, we can determine a unique string, $U_h$ of length at least $\ell - 1$, that is given a label. See Fig. [4](1) for instance, where $V'$ of length $\ell - 1$ appears twice in $I_0$. Since $V'$ is followed by only 0 in $I_0$ and if that is also the case in the entire $X'$, it is given label 0. Here, $U_h = V'$. Let $\mathcal{L} = \{U_h \mid h$ is a single-child position$\}$. We prove that for any $I_0$, $|\mathcal{L}|$ is much smaller than the number of single-child positions and this means that many single-child positions have the same string for $U_h$. We can assume most of the single-child positions are samplable for exactly the same reason as in the preceding lemma. If $U_h = U_h'$, $h'$ comes later than $h$ (see Fig. [4](1)), and $U_h$ is already labeled (by sampling), then TWOEXTENSION is called at position $h' - 1$. Hence if a same $U_h$ repeats, some of them is probably sampled and after that TWOEXTENSION is called for every $U_h$. For the sake of later argument, we divide $\mathcal{L}$ into two parts, $\mathcal{L}_1$ collecting strings in $\mathcal{L}$ of length $\ell - 1$ and $\mathcal{L}_2$ collecting ones of length $\ell$ or more.

Let $V$ be a string satisfying the following three conditions: (i) $|V| \geq \ell$, (ii) there exists a symbol $s \in \{0, 1\}$ such that $Vs$ is an $I_0$-sub and $V\sigma$ is a $I_0$-nonsub, and (iii) $V'0$ and $V'1$ are both $I_0$-sub, where $V' = \text{Suffix}_{|V|-1}(V)$. Let $\mathcal{L}'$ be the set of such $V$'s. We will claim that if $V \in \mathcal{L}_2$, i.e., if DOUBLESEED puts the label to a string $V$ and at Line 15 (namely assuming that the round is sampled) and $|V| \geq \ell$, then this $V$ satisfies these three conditions, i.e., $|\mathcal{L}_2| \leq |\mathcal{L}'|$. (i) and (ii) are obvious and to see (iii) is also met, look at Fig. [4](2). Suppose that DOUBLESEED comes to Line 15 at position $h$ with $\text{Suffix}_e(I) = V_1$ for $\ell \geq \ell$, where $I$ is a prefix of $I_0$ up to position $h$. For this to happen, the condition of the while-loop at Line 12 should have been met for $V'1$ that is the suffix of $V_1$ with length one shorter (otherwise it would come to Line 15 with the shorter $V'1$).
Namely \( \text{Sibling}(V'1) = V'0 \) is an I-sub, that is, \( V'0 \) should have appeared before, at position \( h' \) in the figure. Thus (iii) is indeed met.

Thus \( |L_2| \leq |L'| \). Since the number of binary strings of length \( \ell - 1 \) is \( 2^{\ell - 1} \), we have

\[
|L| = |L_1| + |L_2| \leq 2^{\ell - 1} + |L'|.
\]

We then bound \( |L'| \) from above. By the property (iii), for each \( V \in L' \), there is a double-child position that is the first appearance of \( V'0 \) or \( V'1 \) for \( V' = \text{Suffix}_{|V|-1}(V) \). (In Fig. 4 (2), the position \( h' \) can be this double-child position. If it is sampled then we go to 2NDSEED, but if not, we can get to the single-child position \( h \).) Note that two different \( V \)'s (\( V'0 \) and \( V'1 \)) have the same \( V' \) and hence for two elements in \( L' \), there must be at least one double-child position. In other words, \( |L'| \) is at most twice the number of double-child positions, i.e., at most \( q/2^{10} \) by the assumption of the lemma. Therefore, \( |L| \) is at most \( 2^{\ell - 1} + q/2^{10} < q/2^9 \), because by Lemma 2 (ii), \( 2^{\ell - 1} \leq q/2^9 \) and this is at most \( q/2^{10} \) for \( C_1 \geq 20 \).

Recall that almost all positions are single-child (exactly speaking it is at least \((1 - 2^{-11})q\) by reducing the number of double-child positions, but there is no harm in using \( q \)). For a string \( U \in L \), we denote by \( \text{pos}(U) \) the sequence of positions \( h \) in \( I_0 \) such that \( U_h = U \) and let \( \text{freq}(U) = |\text{pos}(U)| \). Since \( |L| \leq q/2^9 \) as shown above, \( \text{freq}(U) \) is as large as \( 2^9 \) on average. However, \( \text{freq}(U) \) can differ arbitrarily for each \( U \), which is messy for the proof. So we use the following modest approach: \( \text{pos}(U) \) is partitioned into blocks of size \( \gamma \). The last block may be smaller than the others; we call a block of size \( \gamma \) a complete block. We ignore a possible profit from smaller blocks and count only the number of complete blocks for all sequences in \( L \), which is given as

\[
\sum_{U \in L} \left[ \frac{\text{freq}(U)}{\gamma} \right] \geq \sum_{U \in L} \frac{\text{freq}(U)}{\gamma} - |L| > q \left( \frac{1}{\gamma} - \frac{1}{2^9} \right) = \frac{3}{2^8}q
\]

by setting \( \gamma = 2^7 \).

Recall that each position will be sampled with probability \( r_0 \). Our analysis is based on the fact that if the first half of a complete block is sampled then we can enjoy TwoExtension in the second half. (Note that if some block is sampled, then the following blocks having the same \( U \) will automatically go to TwoExtension in the algorithm. But in this (modest) analysis, new samples are also needed in those following blocks.) Consider a single (complete) block. The probability that its first half is sampled is \( 1 - (1 - r_0)^{2^7} > r_0 \gamma/2 - O(r_0^6) > \frac{5}{2^7}r_0 \) for sufficiently large \( n \). Thus the expected number of sampled blocks is \( \left( \frac{2^7}{3}r_0 \right) \left( \frac{3}{2^8}q \right) = (r_0q)/4 = d_1/8 \). Since the sampling is independent for each block, this value is at least, say \( d_1/12 \) with failure probability \( e^{-(d_1/8 - (1 - \delta)2^{7})/2} = e^{-d_1/12} \), by Chernoff bound. If a block is sampled, TwoExtension is called \( \gamma/2 \) times and our profit for each is one with probability \( 1/2 \). Thus the expected profit per sampled block is \( \gamma/4 = 2^5 \) and again by Chernoff bound it is at least a \( 3 \cdot 2^3 \) fraction with failure probability \( e^{-(d_1/12)(1 - (3 \cdot 2^3)/2^{7})/2} = e^{-d_1/20} \). Thus our total profit is at least \((d_1/12)(3 \cdot 2^3) = 2d_1 \) with the total failure probability \( e^{-d_1/12} + e^{-d_1/20} \).

Finally our bookkeeping: Our gain is \( d \) for the first seed and \( 2d_1 \) from TwoExtension as above. Our loss is \( d_1 \) for finding the first seed, \( d \) for detecting the right end and at most \( d_1 \) for the sampling with failure probability \( e^{-d_1/6} \) as in the proof of Case 1. Thus our gain and loss are balanced with failure probability \( e^{-d_1/12} + e^{-d_1/20} + e^{-d_1/6} < 3 \cdot e^{-d_1/12} \), which is smaller than the failure probability stated in the lemma. \( \square \)

Now we are ready to come back to Exception.

**Lemma 6.** If DoubleSeed ends at Line 8, its query complexity is at most \( n \) with failure probability \( 3 \cdot e^{-d_1/2^{13}} \).
Proof. When it is called, we know $I$ has already gone over the right end of $X$. So what we do first is to determine the real right end of $I$ (Line 3). Then we extend $I$ exactly as the main loop of DoubleSeed does. The amount of (new) extension is the same, i.e., $q$. However, the direction of the extension is to the left, so Sibling, Suffix and TwoExtension are replaced by SiblingL, Prefix and TwoExtensionL, respectively. The modification is almost obvious; for a string $S = S[1]S[2] \cdots S[m]$, SiblingL$(I) = S[1]S[2] \cdots S[m]$, and it turns out that TwoExtensionL$(I, t)$ can just return $tI$ without any query, since we do not have to worry about the left end of $X$ within the while loop. Note that we can use 2ndSeed$(I, S)$ as it is, since it covers the case, which is always the case now, that $S$ exists on the left side of $I$.

Our bookkeeping analysis in Lemma 5 is also similar except the following differences; (i) Our loss to detect the right end happens at Line 7 of DoubleSeed and Fill at Line 20 of Exception does not lose anything. Thus this is neutral. (ii) The new TwoExtensionL gives us a profit of one instead of $1/2$ before. Thus our expected total profit is $4d_1$ with the same probability as Case 2 in the proof of Lemma 5. (iii) The loss for the sampling can increase up to $2d_1$ instead of $d_1$ because we have extra $q$ rounds, but this can be compensated for by (ii). Thus the performance does not become worse than the case that the algorithm does not go to Exception. The failure values are virtually the same as those in Lemmas 3–5.

Now we have our main theorem.

**Theorem 3.** For any constant $0 < \delta \leq 1$, our algorithm spends at most $n + 2^{13} \log_e(3/\delta) + 1$ queries with failure probability at most $\delta$.

**Proof.** The procedure DoubleSeed ends at Lines 2, 8, 17 and 24. When it ends at Line 2, it spends at most $n + \max\{2C_1, C_2\} + 1$ queries with failure probability $2^{-C_1}$ by Lemma 1. When DoubleSeed ends at Lines 8, 17 and 24, Lemmas 5 and 6 say that it spends at most $n$ queries with failure probability at most $3 \cdot e^{-d_1/2^{13}}$.

Combining these results, DoubleSeed spends at most $n + \max\{2C_1, C_2\} + 1$ queries with failure probability at most $\max\{2^{-C_1}, 3 \cdot e^{-d_1/2^{13}}\}$. Setting $2C_1 = C_2 = 2^{13} \log_e(3/\delta)$ and using $d_1 \geq C_2$ (see Lemma 2), this failure probability is at most

$$\max\{2^{-C_1}, 3 \cdot e^{-d_1/2^{13}}\} = \max\{2^{-C_1}, 3 \cdot e^{-C_2/2^{13}}\} = \max\left\{\left(\frac{\delta}{3}\right)^{2^{12} \log_e 2}, \delta\right\} = \delta.$$

Note that the proof of Lemmas 3 and 5 require that $C_1 \geq 20$ and $C_2 \geq 40$ hold. Our setting satisfies these conditions for any $0 < \delta \leq 1$.

## 6 Final Remarks

An obvious future work is derandomization of the algorithm of Sec. 4, although it does not seem easy. For example, TryEasyCase is using randomization to find a nonsubstring of length about $n$..
in constant steps. There is no obvious way of doing this deterministically. Another issue is the time complexity. In this paper, we are interested in only the query complexity and in fact our algorithm seems to spend more than linear number of computation steps, but this issue should be easier and we already have some idea to make it linear whp. The failure probability and the constant term of the randomized algorithm could be improved, too.

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