1 APPLICATION OF SEMI-LOCAL LCS TO STRING APPROXIMATE MATCHING*

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Abstract. We present an application of semi-local lcs to approximate string matching by developing a new algorithm and improving the existing one. Our result is based on the utilization of the underlying algebraic structure of semi-local lcs with the usage of the novel data structure for submatrix maximum queries in Monge matrices. This gives two algorithms with the following running time and space complexity. TODO. The improvement of the existing algorithm not only preserves all properties but also outperforms in practice.

In addition, we show that the algorithm for semi-local lcs based on sticky braid multiplication is not perform well with the current complex recursive structure.

Key words. semi-local lcs, monge matrix, range queries, approximate matching, near-duplicate detection

AMS subject classifications. 68Q25, 68R10, 68U05

1. Introduction. Approximate string matching is an important task in many fields such as computational biology, signal processing, text retrieval and etc. It also refers to a duplicate detection subtask.

In general form it formulates as follows: Given some pattern p and text t need to find all occurrences of pattern p in text t with some degree of similarity.

There are many algorithms that solve the above problem. Nonetheless, the number of algorithms sharply decreases when the algorithm needs to meet some specific requirements imposed by running time, space complexity or specific criterion for the algorithm itself. For example, recently there was developed an approach for interactive duplicate detection for software documentation [2]. The core of this approach is an algorithm that detects approximate clones of a given user pattern with a specified degree of similarity. The main advantage of the algorithm is that it meets a specific requirement of completeness. Nonetheless, it has an unpleasant time complexity.

The algorithm for approximate detection utilizes mainly algorithm for solving the longest commons subsequence (LCS) problem. The longest common subsequence is a well-known fundamental problem in computer science that also has many applications of its own. The major drawback of it that it shows only the global similarity for given input strings. For many tasks, it's simply not enough. The approximate matching is an example of it.

There exist generalization for LCS called $semi-local\ LCS$ [] which overcome this constraint. The effective theoretical solutions for this generalized problem found applications to various algorithmic problems such as bla bla add cited. For example, there has been developed algorithm for approximate matching in the grammar-compresed strings[].

Although the algorithms for *semi-local LCS* have good theoretical properties, there is unclear how they would behave in practice for a specific task and domain.

To show the applicability of semi-local lcs on practice we developed several algorithms based mainly on it and the underlying algebraic structure. As well as developed

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oping new algorithms we improve and significantly outperform the existing one for interactive duplicate detection for software documentation []. It should be noted that improvement preserves all properties of this algorithm. Do we need to state that ant algo is slow for current structue of algorithm

The paper is organized as follows. Blablabla ??, our new algorithm is in ??, experimental results are in ??, and the conclusions follow in ??.

2. Preliminaries.

- 2.1. Approximate matching. Describe approximate matching formally
- **2.2. Semi-local lcs.** Describe semi-local lcs (definition), algorithms that solves (steady and and braid reducing)
 - 2.3. Monge matrix. Describe monge property

Say about range queries (about soda12, soda14 and new result that we will be used)

- 2.4. Near-duplicate detection algorithm. Describe luciv algo
- 3. Related work. ?????

could mention about approximation. Need discuss

- 4. Algorithm for near duplicate detection. We now describe an improved version of Luciv et.al. algorithm [2] by utilizing a *semi-local sa* solution. Then we present proof that improved version preserves completnesess property. It is achieved by imitating all phases of the algorithm.
- **4.1.** Algorithm description. The algorithm comprises three phases as in [2]. At phase one (Lines 1-3) semi-local sa problem is solved for the pattern p against whole text t. This solution provides access to the string-substring matrix $H_{p,t}^{str-sub}$ which allows performing fast queries of sa score for pattern p against every substring of text t. We apply implicitly transposition and inverse operation on $H_{p,t}^{str-sub}$:

68 (4.1)
$$M[j,i] := -H_{p,t}^{str-sub}[i,j]$$

Note that, inverse operataion preserves (anti) Monge property whereas inverse operation make anti Monge matrix Monge and vice versa. So, matrix M is Monge matrix.

The second phase consist of several steps (Lines 4-6). First, we want to obtain for each prefix of the text t a longest suffix that have a highest similarity with given pattern p with following constarint. The lengths of obtained suffixies should be in $|p|*k...\frac{|p|}{k}$ interval where $k\in [\frac{1}{\sqrt{3}},1]$. It could be done in several way. For example, direct pass through diagonal with width $w:=\frac{|p|}{k}-|p|*k=|p|(\frac{1}{k}-k)$ in $H_{p,t}^{str-sub}$ (see fig) or in M (see fig). The other approach is following. Note that in M is M is M in M is quare windows of size M in M is a sliding window of step 1 that goes diagonally. Due to length constraint we only interesting in elements that lies in main diagonal and below it. Each of this M is M in M is M in M is M also totally monotone. If we set to M in that lies above diagonal that matrix will remain totally monotone. Thus, we can apply M algorithm to this matrix to find leftmost element that has minimum in a given row with corresponding column position. For our case leftmost means that for each prefix algorithm will detect longest suffix (remember that M is transposed M is transposed M is transposed M in M is M in M is transposed M in M is M in M in M is M in M in M in M is M in M

Second step, it is simply one way pass through these suffixes with sliding window of size $\frac{|p|}{t}$ to find for each window most similar suffix with the longest length. Then resulting set is filtered out that remaining suffixes have score greater or equal to given the shold $-k_{di}$.

The third phase is same as in [2] (Lines 8-12).

Algorithm 4.1 PATTERN BASED NEAR DUPLICATE SEARCH ALGORITHM VIA SEMI-LOCAL SA

Input: pattern p, text t, similarity measure $k \in [\frac{1}{\sqrt{3}}, 1]$ Output: Set of non-intersected clones of pattern p in text t

(4.2)
$$k_{di} = |p| * (\frac{1}{k} + 1)(1 - k^2)$$

$$(4.3) L_w = \frac{|p|}{k}$$

(4.4)
$$w = |p|(\frac{1}{k} - k)$$

Pseudocode:

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1: W = semilocalsa(p,t) {1st phase}
2: H_{p,t}^{str-sub} = semilocalsa(p,t).stringSubstringMatrix
3: M[j,i] = -H_{p,t}^{str-sub}[i,j]
4: sufixes = processDiagonal(M,L) {2d phase}
5: W_2 = SuffixMaxForEachWindow(sufixes,L_w)
6: filter(W_2,k_{di})
7: W_3 = UNIQUE(W_2) {3rd phase unchanged}
8: \mathbf{for} \ w \in W_3 \ \mathbf{do}
9: \mathbf{if} \ \exists w' \in W_3 : w \subset w' \ \mathbf{then}
10: remove \ w \ from \ W_3
11: \mathbf{end} \ \mathbf{if}
12: \mathbf{end} \ \mathbf{for}
13: \mathbf{return} \ W_3
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Theorem 4.1. Algorithm 4.1 could be solved in O(|p| * |t|) where p is pattern, t is text.

Proof it

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$$D = \operatorname{diag}(d_1, \ldots, d_n)$$

Theorem 4.2. Algorithm 4.1 preserves completnesses property of algorithm [2].

Proof it

$$D = \operatorname{diag}(d_1, \ldots, d_n)$$

5. CutMax a new approximate mathing algorithm. We now describe several algorithms that heavily based on semi-local lcs and it's underlying algebraic structure.

The first algorithm 5.2 refers to following constraint. There should be found all non-intersected clones τ_i of pattern p from text t that has the highest similarity score on the uncovered part of the text t i.e algorithm should perform greedy choice at each

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step. This is a more intuitive approach i.e like looking for the most similar one every time. Formally:

107 (5.1)
$$\tau_i = \underset{l,r \in (t \cap (\cup_{j=1}^{i-1} \tau_j), l < r, t_{l,r} \cap (\cup_{j=1}^{i-1} \tau_j) = \emptyset}{\arg \max} sa(t_{l,r}, p)$$

The algorithm proceeds as follows. First, upon string-substring Monge matrix M of semi-local solution is built data structure for performing range queries on it denoted by rmq2D (Lines 1).

Second, algorithm make recursive call to subroutine greedy. The greedy routine perfoms greedy choice of τ_i with maximal alignment within the current uncovered part of the text $t_{i,j}$. More precisely, it refers to searching maximum value with corresponding position (row and column) in matrix M within $t_{i,j}$ (starting at ith position and ending at jth position of text t. It is solved via range queries. When detected interval has alignment score less then threshold it means that no clones of pattern p are presented in this part of text $t_{i,j}$, and further processing should be skipped. Otherwise, the founded clone is added to final result and the current part of the text splits on two smaller parts and processed in the same way. Finally, the algorithm outputs a set of the non-intersected intervals of clones of pattern p in text t.

Algorithm 5.1 Greedy subroutine

Input: rmq2D— range maximum query data structure for perfoming range queries on monge matrix M, h— the shold value, i, j— start and end positions of current text $t_{i,j}$

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Output: Set of non-intersected intervals from t_{i,j}
Pseudocode:
greedy(rmq2D, h, i, j, t_{i,j}):
 1: interval = rmq2D.query(i, j, i, j)
 2: result = \emptyset
 3: if interval.score < h then
      return result
 5: end if
 6: if interval.i - i \ge 1 then
      cl = greedy(rmq2D, h, t_{i,interval.i})
      result.add(cl)
 8:
 9: end if
10: if j - interval. j \ge 1 then
      cl = greedy(rmq2D, h, t_{j,interval.j})
12:
      result.add(cl)
13: end if
14: return result
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Algorithm 5.2 GREEDY-PATTERN BASED NEAR DUPLICATE SEARCH ALGORITHM

Input: monge matrix M that correspond to string-substring matrix for pattern p and text t, the shold value h

Output: Set of non-intersected clones of pattern p in text t

Pseudocode:

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GreedyMathing(M, h, t)

- 1: rmq2D = buildRMQStructure(M)2: result = greedy(rmq2D, 0, |t|, t)
- 3: return result

The second algorithm 5.3 uses a less sophisticated approach and a more light-weight one but found fewer duplicates of pattern p(see example ??). The algorithm also follows a greedy approach but instead of looking at the uncovered part of text t at each step it looks at the text t and chooses the first available substring with the highest score that doesn't intersect with already taken substrings. More formally, it approximates algorithm 5.2.

Algorithm description. First, the semi-local sa problem is solved (Line 1). Then we solve complete approximate matching problem (Line 3) i.e for each prefix of text t we find the shortest suffix that has the highest similarity score with pattern p (Line 3):

132 (5.2)
$$a[j] = \max_{i \in 0..j} sa(p, t[i, j]), j \in 0..|t|$$

Further, we remove suffixes whose similarity is below the given threshold h (Line 4). Then remaining suffixes are sorted in descending order (Line 5) and the interval tree is built upon them (Lines 7-11). The building process comprises from checking that current substring *candidate* not intersected with already added substrings to tree and adding it to tree. Finally, algorithm output set of non-intersected substrings (clones) of pattern p in text t.

Algorithm 5.3 Greedy approximate

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Input: pattern p, text t, the shold value h
Output: Set of non-intersected clones of pattern p in text t
Pseudocode:

1: sa = semilocalsa(p, t)
2: matrix = sa.getStringSubstringMatrix()
3: colmax = smawk(matrix)
4: colmax = colmax.filter(it.score >= h)
5: colmax = colmax.sortedByDescending(it.score)
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- 6: tree = buildIntervalTree()7: $\mathbf{for}\ candidate \in colmax\ \mathbf{do}$ 8: $\mathbf{if}\ candidate \cap tree = \emptyset\ \mathbf{then}$ 9: tree.add(candidate)10: $\mathbf{end}\ \mathbf{if}$
- 11: end for
- 12: result = tree.toList()
- 13: return result

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 Theorem 5.1. Algorithm 5.3 could be solved in $\max(O(|p|*|t|*|v|), O(|t|*\log^2|t|v))$ time with $O(|t|*v*\log|t|*v)$ space when |p| < |t| where p is pattern, t is text and v is denominator of normalized mismatch score for semi-local sequence alignment $w_{normalized} = (1, \frac{\mu}{r}, 0)$ assuming we are storing solution matrix implicitly.

First phase. As shown in section 2 the time complexity of solving semi – localsa is O(|p|*|t|*|v|). The space complexity of storing monge matrix of semi-local solution is $O(|t|*v*\log|t|*v)$ at most due to fact that v – subbistochastic matrix has at most v non-zeros in each row and upon these v*|t| points we build two dimensional range tree data structure with $|t|*v*\log|t|*v$ nodes that have report range sum queries in $O(\log^2|t|v)$ time.

Second phase. SMAWK algorithm requires O(|t|*q) time where q stands for time complexity of random access of monge matrix. Thus, the total time complexity of line 3 is $O(|t|*\log^2|t|v)$. Filtering and sorting have at most O(|t|) and $O(|t|*\log|t|)$ time complexity. In Line 6 simple intialization of interval tree is performed that requires O(1).

Third phase colmax array has as worst case O(|t|) elements when filtering does not eliminate any substrings. Thus, adding to interval tree (both operation at most require $O(\log |t|)$ time) as well as intersection in (Lines 8-9) will be performed at most O(|t|). Thus, the total complexity of last phase is $O(|t| * \log t)$.

As we see, the third phase is dominated by the second phase in terms of running time and second phase is dominated by the space complexity of third phase. Thereby, the total time and space complexity is $\max(O(|p|*|t|*|v|), O(|t|*\log^2|t|v))$ and $O(|t|*v*\log|t|*v)$ respectively.

COROLLARY 5.2. Algorithm 5.3 could be solved in $\max(O(|p|*|t|), O(|t|*\log|t|))$ when v = O(1).

When v = O(1) we will use simple range tree for orthogonal range queries with $O(\log|t|)$ query time.

COROLLARY 5.3. Algorithm 5.3 could be solved in O(|p| * |t|).

When amount of clones is relatively small and threshold value is set high then after filtering out t intervals (Line 4) sorting is performed on s small set of elements. Thus, this part is dominated by calculating semi-local sa solution.

Theorem 5.4. Algorithm 5.2 could be solved in $\max(O(|p|*|t|*v), O(|t|*\log|t|))$ time with $O(|t|\log|t|)$ space when |p| < |t| where p is pattern, t is text and v is denominator of normalized mismatch score for semi-local sequence alignment $w_{normalized} = (1, \frac{\mu}{n}, 0)$.

On the first phase of alg

The first phase of algorithm requires O(|p|*|t|*v) with O(|t|*v) additional space for stroring monge matrix implicitly. We denote this matrix, specifically it's lower-left quadrant that refers to string-substring solution as M with size $|t| \times |t|$.

Theorema 3.4 First, note that

Building structure for rmq queries for staircase matrix requires Theorem 5.8. Given an n n partial Monge matrix M, a data structure of size O(n) can be constructed in $O(n \log n)$ time to answer submatrix maximum queries in $O(\log \log n)$ time.

Proof it

$$D = \operatorname{diag}(d_1, \dots, d_n)$$

COROLLARY 5.5. Algorithm 5.2 could be solved in $\max(O(|p|*|t|), O(|t|*\log|t|))$ when v = O(1).

6. Evaluation.

Semi-local algorithms. Show perfomance between lcs and semi-local lcs??? and poor perfomance of recursive algorithm based on steady ant?

Approximate matching algorithms. Show outperforming for different cases between luciv and our algorithm.

Show quality betwee our new algo and luciv algo (our should be better)

Show that sparse table bad when large?

7. Conclusion. Say may be successfully be applied on practice (showed by algorithm luciv updated)

Open problem.— >

Say that need to implement with monge2020 (what we not finished)

Improve algo based on recursive steady ant. Because it's critical for algos based on it.

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