Improved Deterministic Length Reduction

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Abstract

This paper presents a new technique for deterministic length reduction. This technique improves the running time of the algorithm presented in [?] for performing fast convolution in sparse data. While the regular fast convolution of vectors $V_1, V_2$ whose sizes are $N_1, N_2$ respectively, takes $O(N_1 \log N_2)$ using FFT, using the new technique for length reduction, the algorithm proposed in [?] performs the convolution in $O(n_1 \log^2 n_1)$, where $n_1$ is the number of non-zero values in $V_1$. The algorithm assumes that $V_1$ is given in advance, and $V_2$ is given in running time. The novel technique presented in this paper improves the convolution time to $O(n_1 \log^2 n_1)$ deterministically, which equals the best running time given achieved by a randomized algorithm.

The preprocessing time of the new technique remains the same as the preprocessing time of [?], which is $O(n_1^2)$. This assumes and deals the case where $N_1$ is polynomial in $n_1$. In the case where $N_1$ is exponential in $n_1$, a reduction to a polynomial case can be used. In this paper we also improve the preprocessing time of this reduction from $O(n_1^4)$ to $O(n_1^3 \text{polylog}(n_1))$.

1 Introduction

The $d$-Dimensional point set matching problem serves as powerful tools in numerous application domains. In the $d$-Dimensional point set matching problem, two sets of points $T, P \in \mathbb{N}^d$ consisting of $n, m$ points, respectively, are given. The goal is to determine if there is a rigid transformation

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under which all the points in $P$ are covered with points in $T$. Among the important application domains to which this problem contributes are model based object recognition, image registration, pharmacophore identification, and searching in music archives. For an explanation of the uses of the point-set matching problem in these domains see [2].

The point-set matching problem has been studied in the literature in many variation, not the least of which in the algorithms literature. In [3] Cardoze and Schulman used a randomized algorithm to reduce the space size of $T, P$ and then apply solve the problem in the reduced space. In [1] Cole and Hariharan proposed a solution to the d-Dimensional Sparse Wildcard Matching. This is a generalization of the d-Dimensional point set matching problem where every point in $\mathbb{N}^d$ is associated with a value. A match is declared if the values of coinciding points are equal. The Cole and Hariharan solution consists of two steps. The first step is a Dimension Reduction where the inputs $T, P$ are linearized into raw vectors $T', P'$ of size polynomial in the number of non-zero values. The second step was a Length Reduction where each of the raw vectors $T', P'$ was replaced by $\log n$ short vectors of size $O(n)$ where $n$ is the number of non-zeros. The idea is that the mapping to the short vectors preserves the distances in the original vectors, thus the problem is reduced to a matching problem of short vectors, to which efficient solutions exist. The problem with the length reduction idea is that more then one point can be mapped into the same location, thus it is no longer clear whether there is indeed a match in the original vectors. The proposed solution of Cole and Hariharan was to create a set of $\log n$ pairs of vectors using $\log n$ hash function rather then a single pair of vectors. Their scheme reduced the failure probability.

In [2], the first deterministic algorithm for finding $\log n$ hash functions that reduce the size of the vectors to $O(n \log n)$ was presented. The algorithm guaranteed that each non-zero value appears with no collisions in at least one of the vectors, thus eliminating the possibility of an error. The length reduction idea was used to solve the Sparse Convolution problem posed in [3], where the aim is to find the convolution vector $W$ of two vectors $V_1, V_2$ whose sizes are $N_1, N_2$, with $n_1, n_2$ non-zero elements respectively (where $n_1 > n_2$). It is assumed that the two vectors are not given explicitly, rather they are given as a set of (index, value) pairs. Using the Fast Fourier Transform (FFT) algorithm, the convolution can be calculated in running time $O(N_1 \log N_2)[2]$. In our context, though, the vectors $V_1, V_2$ are sparse. The aim of the algorithm is to compute $W$ in time proportional to the number of non-zero entries in $W$, which may be significantly smaller than $O(N_1)$. Clearly, this can be easily done in time $O(n_1 n_2)$.

The goal of the length reduction is as follows: Given two vectors $V_1, V_2$ whose sizes are $N_1, N_2$, with $n_1, n_2$ non-zero elements respectively (where $n_1 > n_2$), obtain two vectors $V'_1, V'_2$ of size $O(n_1)$ such that all the non-zero in $V_1$ and in $v_2$ will appear as singletons in $V'_1$ and in $V'_2$ respectively while maintaining the distance property.

The distance property which need to be maintained is defined as follows: If $V'_2[f(0)]$ is aligned with $V'_1[f(i)]$, then $V'_2[f(j)]$ will be aligned with $V'_1[f(i + j)]$.

This goal was not reached yet, rather a set of $O(\log n_1)$ vectors of size $O(n_1 \log n_1)$ where obtained in [2], where each non-zero in the text appears at least once as a singleton in the set of vectors. This length reduction gave an $O(n_1 \log^3 n_1)$ algorithm for convolution in sparse data. In this paper we go one step forward and reduce the size of the obtained vectors to $O(n_1)$. This length reduction technique improves the running time of the fast convolution presented in [2] to $O(n_1 \log^2 n_1)$, which is the running time for the randomized algorithm presented in [1].
2 Preliminaries and Notations

Throughout this paper, a capital letter (usually $N$) is used to denote the size of the vector, which is equivalent to the largest index of a non-zero value, and a small letter (usually $n$) is used to denote the number of non-zero values. It is assumed that the vectors are not given explicitly, rather they are given as a set of $(index, value)$ pairs, for all the non-zero values.

A convolution uses two initial functions, $v_1$ and $v_2$, to produce a third function $w$. We formally define a discrete convolution.

**Definition 1** Let $V_1$ be a function whose domain is $\{0, ..., N_1 - 1\}$ and $V_2$ a function whose domain is $\{0, ..., N_2 - 1\}$. We may view $V_1$ and $V_2$ as arrays of numbers, whose lengths are $N_1$ and $N_2$, respectively. The discrete convolution of $V_1$ and $V_2$ is the polynomial multiplication

$$W[j] = \sum_{i=0}^{N_2-1} V_1[j + i] V_2[i].$$

In the general case, the convolution can be computed by using the Fast Fourier Transform (FFT) [2]. This can be done in time $O(N_1 \log N_2)$, in a computational model with word size $O(\log N_2)$. In the sparse case, many values of $V_1$ and $V_2$ are 0. Thus, they do not contribute to the convolution value. In our convention, the number of non-zero values of $V_1$ and $V_2$ is $n_1$ and $n_2$, respectively. The question posed by Muthukrishnan [3] is whether the convolution can be computed in time $o(n_1 n_2)$. Cole and Hariharan’s suggestion was to use length reduction. Suppose we can map all the non-zero values into a smaller vector, say of size $O(n_1 \log n_1)$. Suppose also that this mapping is alignment preserving in the sense that applying the same transformation on $V_2$ will guarantee that the alignments are preserved. Then we can simply map the the vectors $V_1$ and $V_2$ into the smaller vectors and then use FFT for the convolutions on the smaller vectors, achieving time $O(n_1 \log^2 n_1)$.

The problem is that to-date there is no known mapping with that alignment preserving property. Cole and Hariharan [4] suggested a randomized idea that answers the problem with high probability. The reason their algorithm is not deterministic is the following: In their length reduction phase, several indices of non-zero values in the original vector may be mapped into the same index in the reduced size vector. If the index of only one non-zero value is mapped into an index in the reduced size vector, then this index is denoted as *singleton* and the non-zero value is said to appear as a *singleton*. If more then one non-zero value is mapped into the same index in the reduced size vector, then this index is denoted as *multiple*. The multiple case is problematic since we can not be sure of the right alignment. Fortunately, Cole and Hariharan showed a method whereby in $O(\log n_1)$ tries, the probability that some index will always be in a multiple situation is small. In [5], a deterministic solution to the multiple problem was presented. That solution utilized number theoretic ideas. The new idea of this paper is to improve the reduction size by using *polynomials* to represent the location of the non-0 elements of the given vectors.
3 The New Length Reduction Technique for the Polynomial Case

The proposed technique deals with the case that $N_1$ is polynomial in $n_1$, thus the indices are bounded by $n_1^c$. In the case where, $N_1$ is exponential in $n_1$, the reduction to a polynomial case can be used.

The main idea of the algorithm is to derive a set of unique polynomials from each non-zero index in $V_1$, and one polynomial for each non-zero in $V_2$. Each assignment for the polynomials in $\mathbb{F}_q$, where $q$ is a prime number of size $\Theta(n_1)$ will give a different mapping of the non-zeros in $V_1$ and in $V_2$ to vectors of size $q$. The convolution will be performed between the vectors obtained from $V_1$ and $V_2$ under the same assignments.

The first step of the algorithm is to choose a prime number of size $\Theta(n_1)$, and create a polynomial for each non-zero index in $V_1$. The created polynomial of index $i$ will be denoted as the base polynomial of $T[i]$. The creation of the polynomial is done by representing the index as a number in base $\frac{(q-1)}{2}$. Each digit is interpreted as a coefficient of the polynomial. For example: If $q = 13$, then index 95 in base 10 is 235 in base $\frac{(13-1)}{2} = 6$ which is represented by the polynomial $2X^2 + 3X + 5$.

Since the indices in $V_1$ are bounded by $n_1^c$, and $q$ is $\Theta(n_1)$, then the degree of the polynomials which created in this step is bounded by $c$. In the next step, from each polynomial we create $2^c$ polynomials. This is done by giving to choices for each coefficient of the polynomial: (1) Leave it as is. (2) Add $\frac{(q-1)}{2}$ to the coefficient and decrease by 1 the coefficient of the higher degree. We do this for all the coefficients of the polynomial except for the coefficient of the highest degree.

Example 1 Suppose we have a non-zero index 95, using $q = 13$ we get the base polynomial $2X^2 + 3X + 5$. After the second step we will obtain 4 polynomials: $2X^2 + 3X + 5$, $2X^2 + 2X + 11$, $X^2 + 9X + 5$, $X^2 + 8X + 11$.

The first polynomial is the base polynomial. The second polynomial was obtained by adding 6 to the first coefficient and decreasing the second coefficient by one. The 3rd and the 4th polynomials were created by adding 6 to the second coefficient of the first and second polynomials respectively, and decreasing the third coefficient by one.

The duplication of the polynomials was made to meet the distance preserving requirement from the length reduction specified in the following Lemma:

Lemma 1 For any assignment of $X$, if $V_2[0]$ is aligned with the base polynomial representing $V_1[i]$, then $V_2[j]$ will be aligned with one of the polynomials representing $V_1[i+j]$.

Proof: Let $q$ be the chosen prime number. Index 0 in $V_2$ is represented by the polynomial 0, and index $j$ in $V_2$ is represented by the polynomial $A = a_cX^c + a_{c-1}X^{c-1} + ... + a_0$. Index $i$ in $V_1$ is represented by a polynomial of the form $B = b_cX^c + b_{c-1}X^{c-1} + ... + b_0$, and index $i + j$ in $V_1$ is represented by a polynomial $D = d_cX^c + d_{c-1}X^{c-1} + ... + d_0$. Note that the coefficients $a_i$ and $b_i$ are smaller then $\frac{(q-1)}{2}$.

Clearly, if $V_2[0]$ is aligned with $V_1[i]$, then for any assignment of $X$, $V_2[j]$ will be aligned with the polynomial $A + B = (a_c + b_c)X^c + (a_{c-1} + b_{c-1})X^{c-1} + ... + (a_0 + b_0)$. Now lets look at the
first coefficient of $D$, since $a_0$ and $b_0$ are smaller than $\frac{(q-1)}{2}$, then there are only two cases: (1) $(a_0 + b_0) < \frac{(q-1)}{2}$, thus $d_0 = a_0 + b_0$. (2) $(a_0 + b_0) \geq \frac{(q-1)}{2}$, thus $d_0 = a_0 + b_0 - \frac{(q-1)}{2}$ which is covered by the polynomial where $\frac{(q-1)}{2}$ was added to the first coefficient.

In the later case, one was added to the second coefficient, thus we decrease the next coefficient whenever we add $\frac{(q-1)}{2}$ to the current coefficient. The same cases exist also in all the coefficient, but a polynomial was created for each possible case ($2^c$ cases), thus one of the created polynomials will be equal to the polynomial $A + B$. □

Note that all the $2^c \times n_1$ created polynomials are unique, and in $\mathbb{F}_q$. Assigning a value to the polynomials in $\mathbb{F}_q$ will give a vector of size $q$.

**Lemma 2** Any two polynomials can be mapped to the same location in at most $c$ assignments.

**Proof:** The distance between any two polynomials gives a polynomial, where the degree of the difference polynomial is bounded by $c$. Since both polynomials give the same index under the selected assignment, then the assigned value is a root of the difference polynomial. The degree of this polynomial is bounded by $c$, thus it can have at most $c$ different roots in $\mathbb{F}_q$. □

Since any polynomial can be mapped into the same location with at most $2^c \times n_1 - 1$ other polynomials, and with each of them at most $c$ times, due to Lemma 2 then we get the following Corollary:

**Corollary 1** Any polynomial can appear as a multiple in not more then $c \times 2^c \times n_1$ vectors.

The last step of the length reduction algorithm is to find a set of $O(\log n_1)$ assignments which will ensure that each polynomial will appear as a singleton at least once.

The selection of the $O(\log n_1)$ assignments is done as follows: Construct table $A$ with $2^c \times n_1$ columns and $c \times 2^{c+1} \times n_1$ rows. Row $i$ correspond to an assigned value $a_i$ and the corresponding reduced length vector $V_{1,i}$. A column corresponds to a polynomial $P_j$. The value of $A_{ij}$ is set to 1 if polynomial $j$ appears as a singleton in vector $V_{1,i}$. Due to Corollary 1 the number of zeros in each column can not exceed $c \times 2^c \times n_1$. Thus, in each column there are $1$’s in at least half of the rows, which means that the table is at least half full. Since the table is at least half full there exists a row in which there is one in at least half of the columns. The assignment value which generated this row is chosen, and all the columns where there was a 1 in the selected row are deleted from the table.

Recursively another assignment value is chosen and the table size is halved again, until all the columns are deleted. Since at each step at least half of the columns are deleted, the number of prime number chosen can not exceed $\log(2^c \times n_1) = c \log n_1$.

**Time:** Creating vector $V_{1,i}$ (row $i$) takes $O(n_1)$ time. Since we start with a full matrix of $O(n_1)$ rows then the initialization takes $O(n_1^2)$ time. Choosing the $O(\log n_1)$ assignment values is done recursively. The recurrence is:

$$t(n_1^2) = n_1^2 + t\left(\frac{n_1^2}{2}\right)$$

The closed form of this recurrence is $O(n_1^2)$. 


4 The New Algorithm for The Exponential Case

In this case, as proposed in [7], each of the vectors $V_1$ and $V_2$ is reduced into a single vector of size $O(n_1^4)$, where all the non-zeros appear as singletons. The reduction is performed using the modulus function with a prime number $q$ of size $O(n_1^4)$. It was already proven there that there are at most $n_1^3$ prime numbers of size $O(n_1^4)$, which generate at least one multiple. Thus, by testing $n_1^3 + 1$ prime numbers we ensure that at least one of them produce a vector with no multiples.

In order to find such a prime number, we find $n_1^3 + 1$ of size $O(n_1^4)$. Then we multiply all the prime numbers to receive a large number $Q$. In addition we have at most $n_1^2$ different distances between any two non-zeros. We multiply all of them to receive the large number $D$. The next step is to find the greatest common divider ($GCD$) between $Q$ and $D$. Since there is at least one prime number in $Q$ which does not divide $D$, then $GCD(Q, D)$ is less then $Q$. Dividing $Q$ by the $GCD(Q, D)$ will give $P$ which is the multiplication of all the prime numbers that create only singletons. The last step is to find at least one of them. This is done using a binary search on the prime numbers. We take the multiplication of half of the prime numbers $Q'$, and find the $GCD(Q', P)$. If $GCD(Q', P) > 1$ we continue with this set of prime numbers and multiply half of them iteratively. Otherwise, we continue with the other half of the prime numbers. After $O(\log n_1)$ iterations we will find one prime number which will generate only singletons.

The algorithm appears in detail below.

\begin{algorithm}
1. Find $n_1^3 + 1$ prime numbers of size $O(n_1^4)$.
2. Multiply all the prime numbers to obtain $Q$.
3. Multiply all the difference between any two non-zero indices to obtain $D$.
4. Set $P = \frac{Q}{GCD(Q, D)}$.
5. Let $S$ be the set of all prime numbers.
6. While the size of $S$ is larger than 1 do:
   a. Let $S'$ be a set of the first half of prime numbers in $S$.
   b. Set $Q'$ to be the multiplication of all the prime numbers in $S'$.
   c. If $GCD(Q', P) > 1$ then set $S = S'$, otherwise set $S = S/S'$.
\end{algorithm}

**Correctness:** Immediately follows from the discussion.

**Time:** Step 1 is performed in time $O(n_1^4 \text{polylog}(n_1))$ using the primality testing described in [7]. Step 2 is done by building a binary tree of multiplication where each node contain the multiplication of the two number in the lower level. This tree has $O(\log n_1)$ levels. In the leaves there are $n_1^3$ prime numbers with $\log n_1$ bits, so the total number of bits in each level is $O(n_1^3 \log n_1)$. A multiplication of two numbers can be computed in time $O(b \log b \log \log b)$ [4], where $b$ is the
number of bits. Thus each level can be computed in time \(O(n_1^3 \text{polylog}(n_1))\) and the total time for step 2 is \(O(n_1^3 \text{polylog}(n_1))\). Step 3 is performed in the same way, but this time in the leaves there are \(n_1^2\) numbers with \(n_1\) bits, thus each level has \(n_1^3\) bits and the time for this step is \(O(n_1^3 \log n_1)\). In step 4 we calculate the \(GCD\) of two numbers with \(O(n_1^3 \log n_1)\) bits. This can be calculated in time \(O(n_1^3 \text{polylog}(n_1))\) using \[\text{?}\]. The calculation for step 6(b) was already performed in step 2, and step 6(c) can be calculated in time \(O(n^3 \text{polylog}(n_1))\), thus the time of step 6 is \(O(n_1^3 \text{polylog}(n_1))\). Following this discussion the total time of this algorithm is \(O(n_1^3 \text{polylog}(n_1))\).

5 Conclusion and Open Problems

Improved deterministic algorithms for Length Reduction and Sparse Convolution where presented in this paper. These can be used as tools to provide faster algorithms for several well known problems. The deterministic time achieved for convolving input patterns with a fixed text is the same as the best known randomized algorithm.

An important problem remains: Can the Length Reduction and Sparse Convolution problems be solved in real time without the need of the preprocessing step, or alternately, can the preprocessing time be reduced from quadratic?

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