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| Genetics and population analysis  IEPSM: An improved exact string matching method for genomic sequencing data  Lin Dai1,\*, Li Wang1 and Zhang Zhang 2,\*  1 Department of Computer Science, Beijing Institute of Technology, Beijing, China.  2 CAS Key Laboratory of Genome Sciences and Information, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China  Received on XXXXX; revised on XXXXX; accepted on XXXXX  Associate Editor: XXXXXXX |

[[1]](#footnote-2)\*abstract

**Summary:** String matching algorithm plays a vital role in bioinformatics. Here we present IEPSM, an improved exact packed string matching algorithm that is dedicated for biological sequences. IEPSM features optimized word-size packed strings and adopts a big hash value to decrease byte-by-byte comparisons. Comparative results on multiple empirical datasets show that IEPSM achieves better efficiency by comparison with existing algorithms. Thus, IEPSM is of broad utility for searching a specific pattern in the era of big biological data.

**Availability and implementation:** IEPSM is available through Bioconductor. It is released under the GPL-2 license. [link]

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**Supplementary information:** Supplementary data are available at Bioinformatics online.

# introduction

String matching is an important problem that has been thoroughly studied in computer science, with broad applications in bioinformatics as well as natural language processing, information retrieval, etc. For example, it is used to find similar sequence or locate a segment in a long sequence (Senapati, Sandip and Sahoo, 2012). Currently, several string matching algorithms are used on biological sequences, such as tvsbs (Thathoo, Virmani, Lakshmi, Balakrishnan and Sekar, 2006), graspm (Deusdado and Carvalho, 2009) etc. With the rapid development of high-throughput sequencing technologies, it has become easier and cheaper to obtain vast quantities of biological sequences, accordingly posing great challenges in searching for a specific pattern (viz., sequence or segment) within a large volume of biological sequences. Therefore, it is of fundamental importance to design more effective string matching algorithms to address this challenge (Eric, Leena and Jorma, 2011).

There are several algorithms that have developed for exact string matching in the past years (Navarro and Raffinot, 2002). Among them, an algorithm called EPSM (Faro and Kulekei, 2013) obtained better performance by comparison with others. It uses exact packed string matching technique (Frediksson, 2002), in which multiple characters are packed into one block-character, so that the characters can be compared in bulk rather than individually. EPSM computes fingerprint values by a hash function using Single Instruction Multiple Data instructions, which supports parallel execution of some operations via a set of special instructions. However, EPSM is developed for general purposes, without considering features of biological sequences. The max shift distance of EPSM algorithm is *m*-8, where *m* is the length of the given pattern. This is not the optimal shift distance because the theoretical safe maximum shift distance should be *m*[**王力**添加bm算法引文]. Here we take good account of biological sequences features and propose an improved EPSM (IEPSM) by adopting more shift distances and less byte-by-byte comparison calls.

# methods

EPSM algorithm stores all the 8 bytes substrings of the pattern and their position in a hash table. In the searching phase, it checks the last 8 bytes of the current searching window using the hash table to find possible matches. It then checks all the possible positions byte-by-byte. Since the SIMD instructions are used to calculate hash value of packed string, the size of packed strings is set as 8 bytes. When finishing the examination of current window, it jumps forward by *m*-8 bytes to perform next examination, where *m* is the length of the pattern.

IEPSM is developed based on EPSM with specialized improvements for string matching in biology sequences. Specially, its basic idea to achieve higher efficiency for matching a specific pattern in biological sequences is to get larger jumping distance and less byte-by-byte comparisons. Our improvements are as follows.

1) Optimizing the size of packed strings for biological sequences. In fact, shift distance of EPSM is *m*-*B*, where *B* is the size of packed strings. If a smaller *B* is adopted, we can achieve larger shift distance. In the meantime, however, smaller *B* also results in more hash conflicts and more possible matches, which incur more additional examinations. We decide the optimal *B* experientially.

2) Reducing byte-by-byte comparison between pattern and text. EPSM uses a 32bit hash value to determine the entry of hash table and the entrance of byte-by-byte comparison. Intuitively, taking bigger numbers as the byte-by-byte comparison entrance condition will trigger less byte-by-byte comparison. We introduce a 64bit numbers as the byte-by-byte entrance condition. In practice, we add a new field *fingerprint* to the definition of the structure of the hash table node. These fingerprints are initialized during pre-processing phase. In searching phrase, before calling *memcmp* to perform byte-by-byte comparison, the algorithm examines the 64bit fingerprint of current window against that of the pattern. By this way, we avoid lots of *memcmp* calls.

# results

## Experimental Settings

IEPSM was implemented using C. All experiments were conducted on a PC with Intel(R) Xeon E3-1230 V2 at3.30GHz, 4G memory, running Linux Mint 13. The size of the hash table in IEPSM equals to that of EPSM algorithm, i.e., 2048.

We compared IEPSM against five state-of-art string matching algorithms, viz., Tvsbs (Thathoo, Virmani, Lakshmi, Balakrishnan and Sekar, 2006), Ufndmq (Durian, Holub, Peltola and Tarhio, 2009), Hashq (Lecroq, 2007), Fsbndmq (Peltola and Tarhio, 2011) and EPSM (Faro and Kulekei, 2013). All the algorithms were tested on four different data sets, i.e., *Escherichia coli*, *Rice*, *human genome*, *coli amino acid* (ftp？？？章老师这个怎么给). The pattern strings were randomly extracted from the text. All the experiment were executed 10 times and the average results are recorded.

## Optimal packed string size

The optimal packed string size is essential to the algorithm’s performance. The optimal size would be affected by the length of pattern and the alphabet of the sequences. To determine the optimal size, we tested different lengths of packed string on different pattern sizes on different data sets. According to the experimental results, the optimal packed string sizes are as follows, which will be used in the following experiments.

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用表格列出优化的参数。

## Efficiency

We evaluated IEPSM by comparing it to five different algorithms on four data sets. It is evident that across all tested data sets, IEPSM outperforms other algorithms by achieving less matching time. The result on human nucleotide and human protein

E:\Documents\human_dna.tifE:\Documents\human_dna.tif

Fig.1. Comparisons of IEPSM against five popular algorithms on human nucleotide and human protein.

When pattern strings are long enough so that IEPSM and EPSM take the same size of packed string, the performance improvement is attributable to the filtering by using big fingerprints. This filter avoids lots of byte-by-byte comparison. When pattern strings are short, the performance improvement also benefits from the increment of shift distances. The shorter the pattern string is, IEPSM is capable of getting larger shift distance than EPSM. Therefore, in the experiments with shorter pattern string, IEPSM outperforms other algorithms by obtaining extraordinary improved performance.

【m<16时候如何解释？忽略这种情况还是同样思路可以优化？】

At the same time, we can observe that IEPSM and EPSM obviously outperform other algorithms. This is because the use of SIMD instructions and these results are consistent with the literature (Faro and Kulekei, 2013).

# Conclusions

We presented an improved algorithm based on EPSM for string matching problem on biological sequences. Based on characteristics of biological sequences, IEPSM took the optimized size of the packed string to generate the hash table. Besides, IEPSM used a 64bit number as a fingerprint of string, the fingerprint was generated by 8 bytes string. We used the fingerprint filtering many comparisons before taking byte-by-byte comparison. And the experiment results proved that by using these two optimized strategies, IEPSM is more efficient than EPSM.

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