A new exact string matching method for genomic sequencing data

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Running head: Improved exact string matching algorithm using SIMD instructions.

### Abstract

String matching algorithm plays a vital role in the Bioinformatics. In this research, we propose an improved pattern matching algorithm for biological sequences. According to the feature of biological sequences, the algorithm uses specialized word-size packed string matching instructions. Furthermore, for each test, the algorithm uses a hash table to decide shift distance, which is independent to matching result. The Intel streaming SIMD extensions (SSE) technology is applied to compute hash value of each testing window. The experimental results show that the algorithm is very efficient when compared to state-of-art algorithms especially when the pattern length is shorter than 64 bytes.

Key words: Exact string matching, streaming SIMD extensions, biological sequence

### Introduction

String matching is an important research subjects that have been thoroughly studied in computer science. It is also applied extensively in bioinformatics. For example, it is used to find similar sequence or locate a segment in a long sequence. Currently, several string matching algorithms are used on biological sequences, such as tvsbs, graspm etc. With the development of sequencing techniques, it has become easy to obtain the sequence, i.e. the linear arrangement of residues (nucleotides or amino-acids), of DNA, RNA, or protein molecules. So it is meaningful to find more effective string matching algorithms to tackle this challenge [1].

Recently, a new algorithm called packed string matching technique [3] has been used in bioinformatics. In the packed string matching technique, multiple characters are packed into one larger word, so that the characters can be compared in bulk rather than individually. And in the modern CPU, SIMD instructions exist in many microprocessors supporting parallel execution of some operations on multiple data simultaneously via a set of special instructions working on limited number of special registers. And epsm [4] had obtain good results, it is based on a simple filtering method and uses a hash function for computing fingerprint values on blocks of 8 characters. The fingerprint values are computed by a hash function using SIMD instructions.The algorithm is shown in Fig. 1. However, the max shift length of epsm algorithm is m-8. It was not a good result for string of middle length. So in this case, we use Intel streaming SIMD extensions (SSE) technology to make the shift distance close to m.

In BM algorithm [2], pattern string moves from left to right, while character is compared from right to left. When it loses matching, the predefined excursion function adopts the max value to decide right shift value. The efficiency of an algorithm depends on two phases: the pre-processing phase and the searching phase. The aim of a good algorithm is to minimize the work done during each attempt and to maximize the length of the shifts.

### Material and methods

##### Algorithm

In this section we describe the improved algorithm. The algorithm is designed to be faster for medium biological sequences. The algorithm is shown in Fig.2. The ideas of the new algorithm are:

First we define a function called hash(p,seed)(line 1-2) for calculating the CRC of a fixed-length string using the following SSE instruction, \_mm\_crc32\_u64().It receive a string of length 8 and a fingerprint values of 64 bits using \_mm\_crc32\_u64 instruction. Then getting a values of 32 bits with a mask 0x7FF.We use this function to calculate the fingerprint values of a string of length 8.And by changing the value of mask, we could get the fingerprint values of different length of string, such as length of 6 and length of 5.

The pre-processing phase(line 1-11):

1). First initialize the array of shift distance, make shift[i] = m.

2). Let i equals from 1 to 8, then find out all the string whose suffix of length i equals the prefix of the pattern string of length i. Then using the hash function to calculate the fingerprint values of 32 bits, say filter. Then let the shift[filter] = m – i.

3). Let i equals from 0 to m-8, then calculate the fingerprint values of the string P+i, if m-i less then shift[filter], then shift[filter] = m-i. And when calculate the string P+m-8, make the shift[filter] = 1, so we could always jump forward in the search phase.

The search phase(line 1-7):

1). Let i equals from 0 to n-8, then calculate the fingerprint values of the string T+i of length 8.

2). If shift[filter] equals to 1, then compare the two string using memcmp function. Otherwise shifting forward the length of shift[filter].

So in most cases, we could jump the distance of m in a great probability. Unlile epsm , it could only jump the distance of m-8 [4].

##### Estimating

We would conduct two experiments, the first one was the comparison between the five representive string matching algorithms, the second one was the comparison between different length of packed string and the third one was the comparison between memcmp function and INT64MEMCMP which compare the string using 64 bits.

We expect the algorithm was faster then the other algorithms for the biological sequences, especially for the medium one(the length of the pattern string was less than 64 bytes and greater than 8 bytes).

##### Data collection

The algorithm was implemented using C. And all experiments were conducted on a PC with Intel(R) Xeon E3-1230 V2@3.30GHz and 4G memory. The host operating system was Linux Mint 13.

In this case, we choose five different types of state-of-art string matching algorithms to conduct comparison experiment.

- Tvsbs [5], which represent the pattern matching algorithm for biological sequences;

- Ufndmq [6], which represent the prefix searching algorithm;

- Hashq [7], which represent the suffix searching algorithm;

- Fsbndmq [8], which represent the substring searching algorithm;

- Epsm [4], which was the fastest pattern matching algorithm at the present.

And the test data suit contained four types of gene data:

- the Escherichia coli, ecoil;

- the rice, OrySat\_Aug2009.fa;

- the gene sequence of the human genome on chromosome 1, chr1.fa;

- the amino acid of the Escherichia coli K12MG1655, NC\_000913.faa.

We assume that these test data and algorithms were representative.

### Results and discussion

##### Efficiency

The experimemtal results shown in the Table 1, Table 2, Table 3 and Table 4 was a comparison between our new algorithm and other five algorithms in four different types of gene data, such as ecoli, rice, human and amino acid.

From these tables, we could see our algorithm perform stablility in different data. And the new algorithm obtained the best performance when m<64 and m>8, beat the other four algorithms such as tvsbs, ufndmq, hashq and fsbndmq in all cases. The only challenger was epsm algorithm, which perform better when m≥64.

This results were as expected. Because of the SIMD instruction, we could obtain great performance when sampling the string. So we could beat the none four algorithms which was not using the SIMD instructions.

And our algorithm could jump the distance of m in a high probability. So the algorithm beat the epsm in middle string, but the results show the epsm beat our algorithm when m≥64. Because the advantage of our algorithm faded when the length of pattern string grew, the probability of shifting distance of m had dropped.

##### Parameter

From the experimental results shown in the Table 5, Table 6 and Table 7, we could find out the influence of length of packed string. Because in general, in guarantee of the read speed, we chose 2048 as a good choice for the array size. But hash function take a string of length 8 by default, which would result in great hash confilct cause of the . So we change the length of packed string, say 5 or 6. And from the results, we did find out that length 6 was a suitable choice when m<64 and 8 was the other way around.

##### INT64

The system function memcmp compare the character one by one. So naturally, we considered add some packed string thoughts into it. By packing string of 8 bytes into a 64 bits number, then compare the unsigned long long number one by one. However this experiments did not obtain good results. Table 8, table 9 and table 10 showed there were no performance difference between INT64MEMCMP and MEMCMP function.

### Conclusions

We presented a new exact string matching algorithm using Intel SSE instructions. Experiments show the algorithm obtained better performance for medium biological sequences.

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### Tables

Table 1.

Experimental results for searching different length of patterns on a ecoli genome sequence using six algorithm. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| new | **146.55** | **95.9** | **72.35** | **58.2** | **49.25** | **43.1** | **38.9** | **35.9** |  |
| epsm | 158.05 | 157.8 | 123.55 | 124.75 | 65.05 | 66.1 | 46.35 | 47.15 |  |
| tvsbs | 531.29 | 409.43 | 372.43 | 325.86 | 292 | 276.29 | 300.43 | 278.86 |  |
| ufndmq | 527.86 | 407.29 | 370 | 324.86 | 291 | 275.57 | - | 262.57 |  |
| hashq | 5022.86 | 1015.71 | 574.43 | 400.86 | 307.71 | 253.14 | 216.14 | 187 |  |
| fsbndmq | 376.57 | 296.14 | 226.14 | 184 | 152.71 | 142.14 | 126.29 | 120.57 |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| new | **33.7** | **32.25** | **30.95** | 29.2 | 26.4 | 41.25 | 32.1 | 17.65 | 11.65 |
| epsm | 37.2 | 37.5 | 31.3 | **25.9** | **21.45** | **17.95** | **13.4** | **10.95** | **9.15** |
| tvsbs | 245 | 256.71 | 244.29 | 268.71 | 277.14 | 293.86 | 270.57 | 301 | - |
| ufndmq | 225 | 274.86 | 286.71 | 243 | 254.57 | 274.86 | 280.43 | 254.71 | - |
| hashq | 167.14 | 149.57 | 138 | 103.86 | 63.71 | 45.29 | 43.71 | 40.29 | 40.29 |
| fsbndmq | 120.57 | 113.86 | 113.14 | 94.14 | 94.29 | 95.86 | 94 | 97.14 | 96.71 |

Table 2.

Experimental results for searching different length of patterns on a rice genome sequence using six algorithm. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| new | **148.05** | **96.3** | **71.95** | **58.5** | **49.8** | **44.05** | **39.6** | **36.4** |  |
| epsm | 161.5 | 164.45 | 122.6 | 124.25 | 65.15 | 65.9 | 46.75 | 47.4 |  |
| tvsbs | 502 | 385.86 | 371.86 | 369.71 | 306.14 | 283 | 281.86 | 260.71 |  |
| ufndmq | 500.29 | 385.57 | 370.29 | 368.43 | 304.14 | 283.29 | - | 293 |  |
| hashq | 5033 | 1016.14 | 570.86 | 399.71 | 308.71 | 252.71 | 213.71 | 186.43 |  |
| fsbndmq | 317 | 280.29 | 224.43 | 180 | 148.14 | 139.71 | 124.57 | 116.57 |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| new | **34.4** | **33.35** | **31.7** | 30 | 26.95 | 42.9 | 32.45 | 18.1 | 11.45 |
| epsm | 37.4 | 38.1 | 31.75 | **26.25** | **21.8** | **18.7** | **13.7** | **11.75** | **9.65** |
| tvsbs | 273.43 | 224 | 216 | 211.57 | 198.43 | 263.43 | 235.71 | 144.86 | - |
| ufndmq | 228 | 239.57 | 219.29 | 247.14 | 213 | 202 | 229.29 | 219.29 | - |
| hashq | 165.29 | 149.86 | 136.71 | 102 | 62.14 | 44.86 | 42.86 | 40 | 39.57 |
| fsbndmq | 121.43 | 117.86 | 107.43 | 93.43 | 92.14 | 94.43 | 91.71 | 91.43 | 93.71 |

Table 3.

Experimental results for searching different length of patterns on a human genome sequence using six algorithm. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| new | **146.5** | **95.9** | **71.75** | **57.85** | **49.25** | **42.9** | **39.05** | **35.9** |  |
| epsm | 163.05 | 159.2 | 123.45 | 125.6 | 65.5 | 66.8 | 47.1 | 47.35 |  |
| tvsbs | 509.71 | 426.86 | 370.86 | 302.86 | 299.71 | 281.86 | 284.29 | 293.71 |  |
| ufndmq | 505.43 | 424.29 | 369 | 301.29 | 297.29 | 280.43 | - | 281.43 |  |
| hashq | 5028.29 | 1015.71 | 571.71 | 400.57 | 308.86 | 252.29 | 214.57 | 186.57 |  |
| fsbndmq | 360.29 | 281.29 | 215.14 | 182.86 | 166.14 | 137.14 | 126.86 | 118.57 |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| new | **34** | **32.2** | **31.2** | 29.7 | 27.2 | 44.1 | 33.1 | 18.3 | 12.15 |
| epsm | 37.9 | 38.2 | 32.1 | **26.65** | **22.25** | **18.85** | **14.05** | **11.75** | **9.9** |
| tvsbs | 293.43 | 241.43 | 229.43 | 237.14 | 231.57 | 169.86 | 211 | 239.29 | - |
| ufndmq | 265.57 | 284.43 | 263.43 | 249.71 | 234.14 | 233.29 | 240.14 | 216.14 | - |
| hashq | 167 | 149 | 137.86 | 102.57 | 62.57 | 44.29 | 43 | 40.29 | 39.57 |
| fsbndmq | 120.14 | 117.14 | 113.43 | 91.14 | 96.29 | 96.14 | 95.43 | 96.29 | 93.43 |

Table 4.

Experimental results for searching different length of patterns on a protein genome sequence using six algorithm. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| new | 128.15 | **84.6** | **64.05** | **52.2** | **44.4** | **39.95** | **36.25** | **33.6** |  |
| epsm | **123** | 122.8 | 122.55 | 125.6 | 64.85 | 65.85 | 46.25 | 46.85 |  |
| tvsbs | 222.29 | 152 | 120.86 | 103.57 | 90.86 | 81.71 | 70.57 | 64.43 |  |
| ufndmq | 222.57 | 152.43 | 120.29 | 103.71 | 90.43 | 81 | - | 66.14 |  |
| hashq | 5018 | 1010.14 | 566.14 | 431.43 | 317.29 | 249.71 | 211.43 | 184.71 |  |
| fsbndmq | 126.86 | 86.86 | 68.57 | 57.86 | 52.14 | 46.57 | 43.57 | 40.29 |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| new | **32** | **30.65** | **29.9** | 28.1 | 29 | 40.4 | 29.6 | 17.05 | 10.8 |
| epsm | 37.25 | 37.6 | 31.5 | **26** | **21.8** | **18.6** | **13.4** | **10.7** | **8.9** |
| tvsbs | 59.14 | 54.71 | 50.86 | 42.14 | 31.57 | 29.29 | 31.57 | 28 | - |
| ufndmq | 60 | 56 | 50 | 43 | 31.86 | 28.71 | 31.43 | 29.14 | - |
| hashq | 163 | 147 | 133.71 | 100.14 | 59.71 | 42.71 | 41.43 | 39.43 | 39.43 |
| fsbndmq | 39.86 | 40.43 | 41.29 | 41.43 | 40.14 | 39.86 | 39.29 | 38 | 39 |

Table 5.

Experimental results for searching different length of patterns on a ecoli genome sequence using different length of packed string. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| 5 | 149.9 | 98.45 | 73.95 | 60.3 | 51.25 | 45.35 | 40.6 | 38.1 |  |
| 6 | **146.55** | **95.9** | **72.35** | **58.2** | **49.25** | **43.1** | **38.9** | **35.9** |  |
| 8 | 163.85 | 99.8 | 72.8 | 58.25 | 49.6 | 43.3 | 39.45 | 36.95 |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| 5 | 35.35 | 34.6 | 32.6 | 30.15 | **26.2** | 42.35 | 44.15 | 37.35 | 32.75 |
| 6 | **33.7** | **32.25** | **30.95** | **29.2** | 27.45 | 41.05 | 35.4 | 21.15 | 15.6 |
| 8 | 34.4 | 32.9 | 31.85 | 29.3 | 26.4 | **41.25** | **32.1** | **17.65** | **11.65** |

Table 6.

Experimental results for searching different length of patterns on a rice genome sequence using different length of packed string. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| 5 | 149.7 | 98.1 | 73.3 | 59.65 | 50.9 | 44.85 | 40.85 | 37.55 |  |
| 6 | **148.05** | **96.3** | **71.95** | **58.5** | **49.8** | **44.05** | **39.6** | **36.4** |  |
| 8 | 163.35 | 99.05 | 72.5 | 58.15 | 49.4 | 43.55 | 39.45 | 36.75 |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| 5 | 35.65 | 33.65 | 32.7 | 30.5 | **26.65** | 44.55 | 44.3 | 35.25 | 30.9 |
| 6 | **34.4** | **33.35** | **31.7** | 30 | 28.55 | 43.95 | 36.05 | 22.1 | 15.7 |
| 8 | 34.85 | 33.35 | 32.1 | **29.4** | 26.95 | **42.9** | **32.45** | **18.1** | **11.45** |

Table 7.

Experimental results for searching different length of patterns on a human genome sequence using different length of packed string. Running times are expressed in millisecond, best results have been boldfaced and padded.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 |  |
| 5 | 149.45 | 97.35 | 73.85 | 59.8 | 51.3 | 45.15 | 40.85 | 38.3 |  |
| 6 | **146.5** | **95.9** | **71.75** | **57.85** | **49.25** | **42.9** | **39.05** | **35.9** |  |
| 8 | 164.35 | 99.45 | 73.05 | 58.7 | 49.65 | 43.75 | 40 | 37.3 |  |
|  |  |  |  |  |  |  |  |  |  |
| m | 40 | 44 | 48 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| 5 | 35.5 | 34.2 | 32.95 | 30.75 | 26.9 | 44.3 | 44.7 | 36.45 | 33 |
| 6 | **34** | **32.2** | **31.2** | **29.7** | 27.9 | **42.75** | 34.9 | 21.4 | 15.05 |
| 8 | 35.1 | 33.7 | 32.5 | 29.95 | **27.2** | 44.1 | **33.1** | **18.3** | **12.15** |

Table 8.

Experimental results for searching different length of patterns on a ecoli genome sequence using two kinds of string comparing function. Running times are expressed in millisecond.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 16 | 32 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| int64cmp | 164.15 | 72.95 | 39.75 | 30 | 27.3 | 43.55 | 32.95 | 18.2 | 11.5 |
| memcmp | 164.4 | 73 | 39.6 | 29.8 | 27.2 | 42.05 | 32.6 | 17.95 | 11.25 |

Table 9.

Experimental results for searching different length of patterns on a rice genome sequence using two kinds of string comparing function. Running times are expressed in millisecond.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 16 | 32 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| int64cmp | 164.3 | 72.9 | 39.7 | 30 | 27 | 43.35 | 32.6 | 17.75 | 12.3 |
| memcmp | 164.45 | 73.05 | 39.5 | 29.65 | 26.7 | 41.7 | 32.2 | 18.1 | 11.6 |

Table 10.

Experimental results for searching different length of patterns on a human genome sequence using two kinds of string comparing function. Running times are expressed in millisecond.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| m | 8 | 16 | 32 | 64 | 128 | 256 | 512 | 1024 | 2048 |
| int64cmp | 164 | 73.1 | 39.85 | 30.55 | 27.25 | 44.5 | 33 | 18.4 | 12.15 |
| memcmp | 164.4 | 73.45 | 39.85 | 30.05 | 27.35 | 43.45 | 32.85 | 18 | 12.35 |

### Figure legends

Fig. 1 The algorithm.

### Figures

Fig. 1

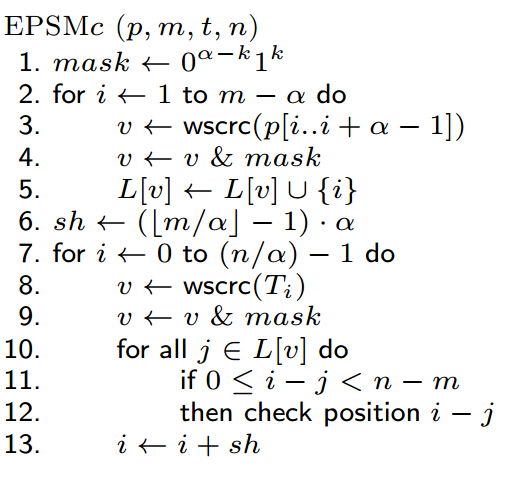


Fig. 2

