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FINDING HIDDEN PATTERN OF FINANCIAL TIME SERIES BASED ON SCORE MATRIX IN SEQUENCE ALIGNMENT

Yong Shi[1]
Ye-Ran Tang[2]
Wen Long[3]+
Ying-Jie Tian[4]
Wen-Ning Yang[5]

[1]*School of Economics & Management, University of Chinese Academy of Sciences, Beijing 100190 P.R. China; Research Center on Fictitious Economy & Data Science, Chinese Academy of Sciences, Beijing, 100190 P.R. China; Key Laboratory of Big Data Mining & Knowledge Management, Chinese Academy of Sciences, Beijing, 100190 P.R. China; College of Information Science and Technology, University of Nebraska at Omaha, Omaha, NE 68182, USA*
Email: yshi@ucas.ac.cn Tel: +86-10-82680698
[2,3,4,5]*School of Economics & Management, University of Chinese Academy of Sciences, Beijing 100190 P.R. China; Research Center on Fictitious Economy & Data Science, Chinese Academy of Sciences, Beijing, 100190 P.R. China; Key Laboratory of Big Data Mining & Knowledge Management, Chinese Academy of Sciences, Beijing, 100190 P.R. China*
[2]*Email: tangyeran14@mails.ucas.ac.cn Tel: +86-18008333092*
[3]*Email: longwen@ucas.ac.cn Tel: +86-10-82680927*
[4]*Email: tyj@ucas.ac.cn Tel: +86-10-82680997*
[5]*Email: wenningyang@126.com Tel: +86-10-82680927*

(+ Corresponding author)

ABSTRACT

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This paper applies sequence alignment method of bioinformatics to financial analysis to find hidden pattern from financial markets. Results of simulation suggest that sequence alignment method can be used to identify key points to inset, delete and replace data in time series, to find lead-lag relationship between two time series, and to analyze matching patterns. We further propose a new score matrix named similarity-oriented matrix which is designed based on the characteristics of financial time series, and apply it to China's stock market. The empirical analysis verifies the validity of our proposed score matrix, and tests the sensitivity for different threshold values of symbols definition.

Contribution/ Originality: This study is one of very few studies which have investigated score matrix in financial markets. The paper's primary contribution is finding that sequence alignment method of bioinformatics can be used to find hidden pattern of financial time series.

1. INTRODUCTION

Recognizing hidden patterns from financial time series has a wide application. Risk management, portfolio construction, asset pricing, and stock price prediction can all benefit from studies of the sequence characteristics and the relationship between variables. The prior literatures use a variety of models to describe the relationship of financial time series, including ARMA, GARCH, VAR, and Copula (Kim, 2001; He and Gong, 2009; Baele *et al.*, 2010; Garcia and Tsafack, 2011; Gallegati, 2012; Gupta and Guidi, 2012). Each of these methods has its applicability and limitations, including: (1) little tolerance for noise, which would probably over fitting and lead to unreliable results; (2) based on certain assumptions, for instance, time series should obey a certain distribution; (3) when analyzing lead-lag relationship between two time series, its order is usually fixed; (4) if it contains missing data in time series, it is difficult to identify the missing place; (5) complex models are hard to understand and apply for investors. In these cases, some researchers attempt to use physics or biology methods to extract hidden patterns from financial time series.

In bioinformatics, sequence alignment method is to find similar structure of biological sequences, such as DNA, RNA or protein, by matching their counterpoints (Needleman and Wunsch, 1970; Smith and Waterman, 1981; Pevsner, 2005). Using sequence alignment method, one can identify maximum base pairing (DNA sequence alignment) or residues (protein sequence alignment), and its results reflect similarity between two series. The aim of sequence alignment method in bioinformatics is similar with the financial time series we analyze. Using sequence alignment method to compare similar financial sequence, we can find hidden pattern of financial time series without prior assumptions related to distribution. It can also be used to analyze lead-lag relationships and to find missing data, which will increase the tolerance for noise. However, since sequence alignment designed for DNA and protein is to analyze discrete data, while financial time series, such as stock price in financial markets, are continuous, it cannot be directly used in financial field. Thus, in this paper, we first discuss how to discretize continuous time series in financial markets to get corresponding symbol data for sequence alignment. Then, use sequence alignment method to construct financial sequence alignment model to recognize key points, lead-lag relationship, and hidden pattern of financial time series. It is meaningful for both financial time series analysis and application field extension of sequence alignment method.

The rest of this paper is organized as follows. Section 2 is the literature review for sequence alignment method and its application in financial markets. Section 3 introduces the model of sequence alignment for financial time series. Section 4 proposes a score matrix we called similarity-oriented matrix in order to find hidden patterns in financial time series. Section 5 conducts simulation to test application of sequence alignment method in different cases of financial markets. Section 6 conduct empirical analysis to study characteristics and relationship between two stock markets in China (Shanghai Composite Index and Shenzhen Component Index), and sensitive analysis of different threshold values of symbols definition. Section 7 concludes the main results in this paper and provides research expectation.

2. LITERATURE REVIEW

In biology, similarity of DNA or protein can be measured by similarity of nucleic acid or amino acid sequence. Since function and structure mainly depend on its sequence, finding similar sequence can help to find similar structure and function, and can even speculate evolutionary relationship of the gene. Thus, sequence alignment is a common method to compare sequence of DNA or protein, and find their similarity and difference patterns. Researches on sequence alignment mainly can be divided into two parts: the one is to improve its algorithm accuracy and computation speed (Gibbs and McIntyre, 1970; Pearson and Lipman, 1988; Altschul *et al.*, 1990; Lambert *et al.*, 2003; Altschul *et al.*, 2008; Dickson and Gloor, 2012; Khazanov *et al.*, 2012; Herman *et al.*, 2015; Mirarab, 2015) and the other is to apply it to study similar structure of the sequences to speculate their evolutionary relationship (Li *et al.*, 2008; Jangam *et al.*, 2009; Li *et al.*, 2010; Di Tommaso *et al.*, 2011; Mirarab *et al.*, 2015; Nguyen, 2016; Yamada *et al.*, 2016). In this paper, we mainly concern about the application of sequence alignment beyond biological field, especially in financial analysis. The literatures applying sequence alignment method to financial markets are as follows.

Takuya Yamano used sequence alignment method to analyze financial markets (Yamano *et al.*, 2008). In empirical analysis, they studied similarity of Brazil index and the Dow Jones industrial average. They suggested using sequence alignment method to analyze financial time series can recognize similar characteristics in different markets. Besides, this method can tolerate abnormal data and time-lag.

Xu combined fuzzy logic theory and sequence alignment method (Xu, 2010). Opening price, closing price, maximum and minimum price were encoded into K-chart, which then can be recognized by sequence alignment. Xu used financial time series in Chinese markets from 1990 to 2006 to predict its trend in 2007-2008. The results suggested that some of the patterns can be used as trading signal, while some other patterns do not have such function.

Xu combined K-nearest and sequence alignment method to predict stock price (Mei, 2013). First, Shanghai Composite Index and Shenzhen Component Index were symbolized. Then, using sequence alignment method, k subsequences were obtained for stock price prediction by K-nearest method.

Yih-Wenn Laih combined GARCH-Copula and sequence alignment method to calculate rank correlation coefficient of financial time series, and analyze correlation of stock index in Four Asian Tigers (Laih, 2014). Empirical results suggested rank correlation coefficient based on sequence alignment method is larger than other methods.

There is a few of literatures applied sequence alignment method in financial markets, and they mainly focus on the correlation between financial time series or stock price prediction. Actually, besides these, the applications of sequence alignment method in financial research can be more extensive, such as lead-lag relationship recognition and missing data finding. Moreover, when prior researches applied sequence alignment in financial time series analysis, the score matrix they use is usually setting a certain value for symbol pairs, which we called simple matrix in this paper. Since simple matrix ignores match probability contained in historical data, pattern, which means probability of symbols occurring in two sequences at the same time, cannot be recognized. This paper will learn from the methods of constructing PAM and BLOSUM matrix in biology, and propose a similarity-oriented score matrix to extract match patterns from financial time series. It not only provides a new method to find hidden pattern of financial time series, but also extends application fields of sequence alignment method.

3. MODEL OF SEQUENCE ALIGNMENT

In bioinformatics, sequence for alignment is a series of characters which refer to DNA, RNA or protein. Sequence alignment is to match symbols according to a scoring rule. When two sequences are placed in two lines, similar symbols are placed in the same column, while different symbols are set as mismatch or gaps. Thus, there are three cases in alignment results, as follows:

(1) Match: corresponding positions have similar symbols in different sequences.

(2) Mismatch: corresponding positions have different symbols in different sequences.

(3) Gap: insert several gaps in one sequence to make them correspond to the symbols in the other sequence.

Thus, sequence alignment is a matching algorithm to maximize similar corresponding symbols. Since we can set each case (match, mismatch and insert gap) a score, sequence alignment is to use such scoring rule to get the optimal (most similar) arrangement of the symbols in two sequences.

Let $S = s_1s_2 \dots s_m$ and $T = t_1t_2 \dots t_m$as the two sequences in a certain character set Ω. For DNA sequence, character set $\Omega = \{A, G, C, T\}$. For protein sequence, character set $\Omega = \{A, R, \dots, V\}$, which refer to 20 kinds of amino acid for protein construction.

When analyzing sequences S and T, S_i refers to the *i*-th character in sequence S, and $|S|$ refers to the number of the characters in sequence S. It is similar for sequence T. Define $\sigma(s, t)$ as score function, which refers to the score of alignment results for symbol S_i and T_i . S' and T' refers to the new sequences updated from sequences S and T

after inserting gaps "$-$". Thus, the symbols in sequences S' and T' belong to the limited character set $\sum = \Omega \cup \{-\}$. Define A as the sequence alignment of sequences S and T, which can be calculated by match of corresponding symbols in sequences S' and T', where $|S'| = |T'|$. The score of sequence alignment A is:

$$Score(A) = \sum_{i=1}^{l} \sigma(S_i', T_i'), (l = |S'| = |T'|) \qquad (3.1)$$

For sequences S and T, the optimal results is the maximum $Score(A)$. In other words, sequence alignment is to optimize sequences S' and T' in order to make $Score(A)$ maximum.

Score system of sequence alignment contains score matrix and gaps penalty. For gaps penalty, inserting gaps will deduct a certain score. For symbol replacement, score matrix is to measure matching score of the two symbols. Score function $\sigma(x,y)$ means the matching score of symbols in *y*-th row (*y*-th symbols in sequence *T*) and *x*-th column (*x*-th symbols in sequence *S*) of the score matrix. It can be seen that the result of sequence alignment depends on score matrix. Thus, score matrix design is important, and is one of our main focus in this paper.

4. SIMILARITY-ORIENTED SCORE MATRIX

In bioinformatics, the common score matrixes for sequence alignment are Point Accepted Mutation (PAM) (Dayhoff, 1972; Pevsner, 2009; Sung, 2009) and BLOSUM matrix (Henikoff and Henikoff, 1992; Pertsemlidis and Fondon, 2001; Eddy, 2004). PAM matrix is according to conversion rate of the amino acids in protein sequence. If the conversion rate of two amino acids is high, the matching score of them is high, and corresponding value in score matrix is large. Thus, the value of *i*-th row and *j*-th column in PAM matrix reflects conversion probability of *i*-th and *j*-th amino acid in two sequences. BLOSUM matrix is also calculated from conversion rate of the amino acids in protein sequence with a different method.

When applying sequence alignment model to financial time series analysis, prior researches mainly use simple score matrix, such as Unitary matrix or BLAST matrix, which set a fixed positive score when symbols in two sequences are the same, and set a fixed negative score (or 0) when they are different. However, such score matrix cannot reflect the relationship of different symbols, for example, the similarity level of the two different symbols. Thus, patterns (probability of symbols occurring in two sequences at the same time) cannot be recognized. Inspired by score matrix in bioinformatics, this paper proposes similarity-oriented matrix as score matrix to analyze financial time series, which can be used to extract match patterns from financial time series according to relationship of symbols in time series.

Suppose the length of two sequences are same, and symbols in both sequences are alignment. Define the first sequence as main chain, and the second sequence is auxiliary chain. Score matrix proposed in this paper called similarity-oriented matrix can be calculated as follows:

(1) Calculate co-occurrences probability matrix

Suppose the length of both sequences is N, and $n(j)$ is count of occurrence for *j*-th symbol in main chain. $n(i)$ is count of occurrence for *i*-th symbol in auxiliary chain. $A(i,j)$ is count of co-occurrences for *j*-th symbol in main chain and *i*-th symbol in auxiliary chain, and $M(i,j)$ refers to the occurrence frequency of *i*-th symbol in auxiliary chain under the condition that *j*-th symbol occurs in main chain, where $M(i,j) = \frac{A(i,j)}{n(j)}$. We can then approximate frequency $M(i,j)$ to probability, and denote it as M.

(2) Standardize probability matrix

If value of $M(i,j)$ is close to zero, which may be caused by rare occurrence of *i*-th symbol in auxiliary chain, probability matrix M should be standardized. Define $f(j)$ as frequency of *j*-th symbol in main chain, and $f(i)$ is frequency of *i*-th symbol in auxiliary chain. Then, $f(j) = \frac{n(j)}{N}$, and $f(i) = \frac{n(i)}{N}$. Thus, standardized value is $\frac{M(i,j)}{f(i)}$. To explain its meaning, we conduct following mathematical transformation:

$$\frac{M(i,j)}{f(i)} = \frac{f(j)M(i,j)}{f(i)f(j)} \qquad (4.1)$$

Where $f(i)f(j)$ refers to co-occurrences probability of *j*-th symbol in main chain and *i*-th symbol in auxiliary chain if they are independent. In this case, their co-occurrence is a random event. $M(i,j)$ is a conditional probability which refers to occurrences probability of *i*-th symbol in auxiliary chain under the condition that *j*-th symbol in main chain is at the corresponding position. $f(j)M(i,j)$ refers to co-occurrences probability of *j*-th symbol in main chain and *i*-th symbol in auxiliary chain. Thus, if $\frac{M(i,j)}{f(i)} = 1$, their co-occurrence is a random event. If $\frac{M(i,j)}{f(i)} < 1$, their co-occurrence probability is even less than a random event. If $\frac{M(i,j)}{f(i)} > 1$, their co-occurrence probability is larger than a random event.

(3) Calculate log odds matrix

For mismatching penalty, we calculate log odds matrix, denoted as m, and $m = log\frac{M(i,j)}{f(i)}$. If $\frac{M(i,j)}{f(i)} = 0$, $m(i,j)$ will be set as $-\infty$. If $m(i,j) < 0$, which means rare co-occurrences of *j*-th symbol in main chain and *i*-th symbol in auxiliary chain. We consider such situation as mismatch. If $m(i,j) > 0$, we consider *j*-th symbol in main chain and *i*-th symbol in auxiliary chain are match.

Following is an example of above three steps to calculate score matrix:

Suppose a main chain
S=GACCAGCTCATTAAACTTTTGGTGTCCAGTAGGCGGCAGGGGTCTATGGACGCGAACGCAGGGG
TCCCCGCCGCCATTCTGCCGGCGCTGCACCGATGTATCGATAGCACAGGTGGGCGGTGTGCTCTCG
GCTGGACTGCCCGGAAGTTGCCCAGAGGTGGCGACAATCCACGGCCTAAAGACGCATGCTCGAGTT
GGTCGTCGCCGCCTCAGAGTGGGGGAGCACGCAAACCTCCAGGAACTT,
and an auxiliary chain
T=GCCGAAGTCATTAAAGTTTGGATGTGGCCGATCCGGCAGGGCGCTACAGACTGGAACCGAGTCG
TGCGATCCACAAGTATTCCGAGCCGGCACAACCTGCTGCAGCGAAAAGCTTGGCTGTGGGGGCTGT
GACCTAGTCACCCCCACGTGGACAGATGTGCCCCAACTCCAGCCAGTAAACAAGGCTGCGACACTTTC
TCGTTGCCGCCTGACAGCCTCTTATAACGCCAACATGCACGAACGT.

(1) Calculate co-occurrences probability matrix:

$$M(i,j) = \begin{bmatrix} 0.7872 & 0.2113 & 0.0741 & 0 \\ 0.2128 & 0.4930 & 0.3086 & 0.0889 \\ 0 & 0.2817 & 0.4198 & 0.2667 \\ 0 & 0.0141 & 0.1975 & 0.6444 \end{bmatrix}$$

(2) Standardize probability matrix:

$$\frac{\mathrm{M}}{\mathrm{f}} = \begin{bmatrix} 3.3118 & 0.8888 & 0.3116 & 0 \\ 0.7016 & 1.6254 & 1.0177 & 0.2931 \\ 0 & 1.0414 & 1.5518 & 0.9859 \\ 0 & 0.0747 & 1.0478 & 3.4184 \end{bmatrix}$$

(3) Calculate log odds matrix:

$$m = \begin{bmatrix} 1.1975 & -0.1179 & -1.1660 & -\infty \\ -0.3545 & 0.4858 & 0.0175 & -1.2273 \\ -\infty & 0.0406 & 0.4394 & -0.0142 \\ -\infty & -2.5942 & 0.0467 & 1.2292 \end{bmatrix}$$

5. SIMULATION

Because sequence alignment method is firstly used to analyze biological sequence which is discrete, when it is applied to financial field where have different data characteristics, we conduct 3 simulations to test validity of the sequence alignment method used in the time series analysis. The simulation contains following steps. First, generate datasets for simulation, which is to get discrete data from a certain function. Next, symbolize datasets, which is to classify datasets according to its characters, and define each of class a symbol, such as G, P, T and N in amino acids. Then, use sequence alignment method to analyze two sequences. Since trigonometric function with uncomplicated range has good characteristics, which can be analyzed combining unit circle, and the values appears repeatedly in the domain of definition, this paper uses trigonometric function to generate datasets for simulation.

5.1. Simulation I: Recognize Key Points in Sequence

First dataset for simulation generates from trigonometric function $y = sin(\frac{3\pi}{11}x)$, and x is the integer in range of [1, 500]. Size of the dataset is 500.

We first symbolize the dataset according to the sign (positive or negative) of its value and slope. Thus, the dataset can be divided into 8 classes. We also divide central angle into 8 parts, and each part is $\frac{3\pi}{11}x$. Define these 8 classes as different symbols in amino acids, which is shown in Table 1 and Fig.1.

Table-1. Characters of the dataset and its corresponding symbols for simulation I.

Range of $\frac{3\pi}{11}x$	Value	Slope	Symbol
$(\frac{\pi}{8}+2k\pi,\frac{3\pi}{8}+2k\pi]$	+	+	G
$(\frac{3\pi}{8}+2k\pi,\frac{5\pi}{8}+2k\pi]$	+	0	P
$(\frac{5\pi}{8}+2k\pi,\frac{7\pi}{8}+2k\pi]$	+	-	T
$(\frac{7\pi}{8}+2k\pi,\frac{9\pi}{8}+2k\pi]$	0	-	S
$(\frac{9\pi}{8}+2k\pi,\frac{11\pi}{8}+2k\pi]$	-	-	N
$(\frac{11\pi}{8}+2k\pi,\frac{13\pi}{8}+2k\pi]$	-	0	Q
$(\frac{13\pi}{8}+2k\pi,\frac{15\pi}{8}+2k\pi]$	-	+	W
$(-\frac{\pi}{8}+2k\pi,\frac{\pi}{8}+2k\pi]$	0	+	L

Note: *k* is the natural number, "+" refers to above 0, "-"refers to below 0, and "0" refers to approximate to 0.

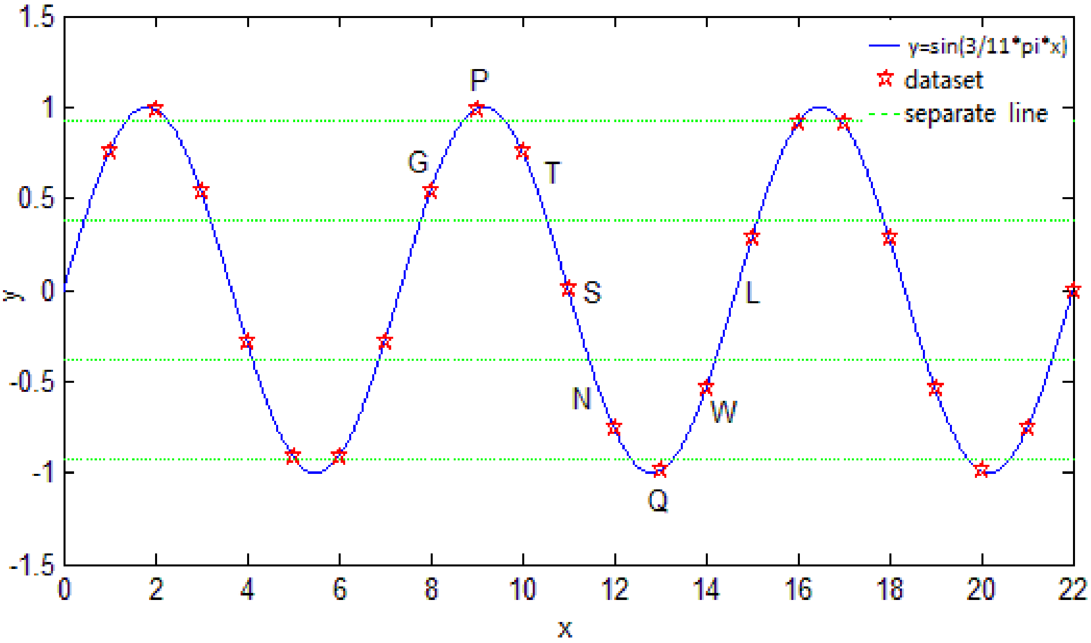
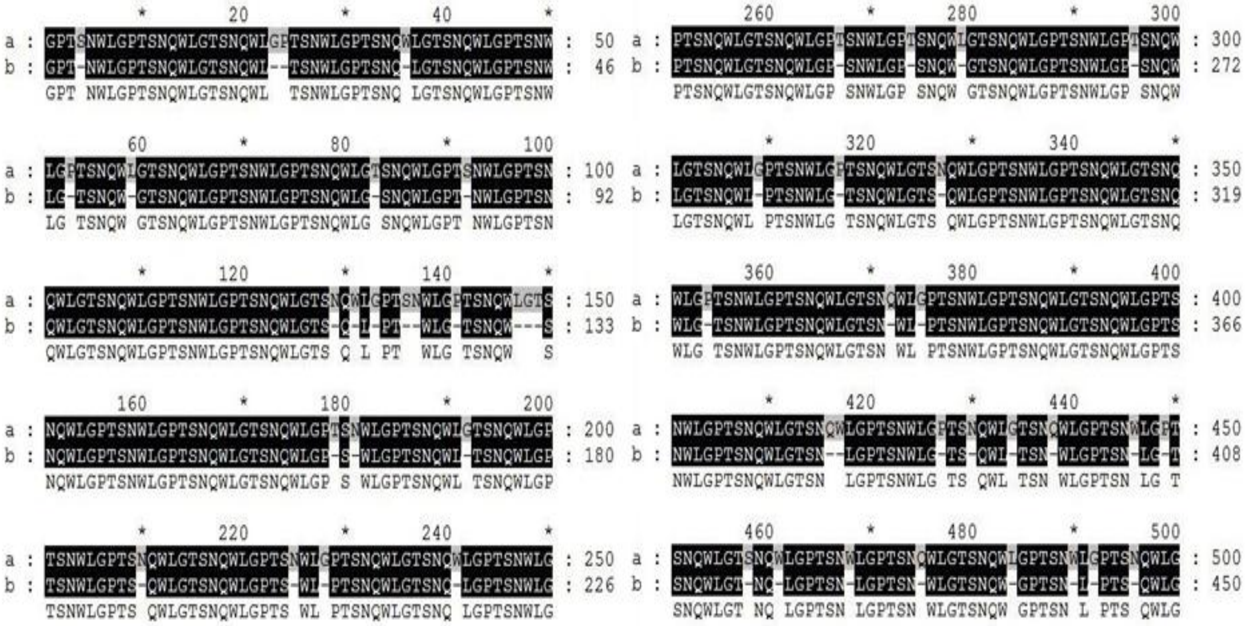


Fig-1. Characters of the dataset and its corresponding symbols for simulation I.

For sequence alignment of the two sequences, define dataset in Fig.1 as sequence *a*, which contains 500 symbols. Random delete 50 characters in sequence *a*, and get sequence *b*. We use simple score matrix for sequence alignment of sequence *a* and *b*, that is, the score will get 1 point if the symbols at the same position of the two sequences are the same, otherwise get 0. This score matrix is also called unitary matrix. Suppose no gap penalty here. The results are shown in Fig.2. It can be seen that several gaps are inserted into sequence *b* so that two sequences are matched. Moreover, if sequence *b* is generated by replacing some symbols in sequence *a*, the alignment results will find the mismatch position.



```
             *        20         *        40         *
a : GPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNW :  50
b : GPT-NWLGPTSNQWLGTSNQWL--TSNWLGPTSNQ-LGTSNQWLGPTSNW :  46
    GPT NWLGPTSNQWLGTSNQWL  TSNWLGPTSNQ LGTSNQWLGPTSNW

            60         *        80         *       100
a : LGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSN : 100
b : LG-TSNQW-GTSNQWLGPTSNWLGPTSNQWLG-SNQWLGPT-NWLGPTSN :  92
    LG TSNQW GTSNQWLGPTSNWLGPTSNQWLG SNQWLGPT NWLGPTSN

             *       120         *       140         *
a : QWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTS : 150
b : QWLGTSNQWLGPTSNWLGPTSNQWLGTS-Q-L-PT--WLG-TSNQW---S : 133
    QWLGTSNQWLGPTSNWLGPTSNQWLGTS Q L PT  WLG TSNQW   S

           160         *       180         *       200
a : NQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGP : 200
b : NQWLGPTSNWLGPTSNQWLGTSNQWLGP-S-WLGPTSNQWL-TSNQWLGP : 180
    NQWLGPTSNWLGPTSNQWLGTSNQWLGP S WLGPTSNQWL TSNQWLGP

             *       220         *       240         *
a : TSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLG : 250
b : TSNWLGPTS-QWLGTSNQWLGPTS-WL-PTSNQWLGTSNQ-LGPTSNWLG : 226
    TSNWLGPTS QWLGTSNQWLGPTS WL PTSNQWLGTSNQ LGPTSNWLG

           260         *       280         *       300
a : PTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQW : 300
b : PTSNQWLGTSNQWLGP-SNWLGP-SNQW-GTSNQWLGPTSNWLGP-SNQW : 272
    PTSNQWLGTSNQWLGP SNWLGP SNQW GTSNQWLGPTSNWLGP SNQW

             *       320         *       340         *
a : LGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQ : 350
b : LGTSNQWL-PTSNWLG-TSNQWLGTS-QWLGPTSNWLGPTSNQWLGTSNQ : 319
    LGTSNQWL PTSNWLG TSNQWLGTS QWLGPTSNWLGPTSNQWLGTSNQ

           360         *       380         *       400
a : WLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTS : 400
b : WLG-TSNWLGPTSNQWLGTSN-WL-PTSNWLGPTSNQWLGTSNQWLGPTS : 366
    WLG TSNWLGPTSNQWLGTSN WL PTSNWLGPTSNQWLGTSNQWLGPTS

             *       420         *       440         *
a : NWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPT : 450
b : NWLGPTSNQWLGTSN--LGPTSNWLG-TS-QWL-TSN-WLGPTSN-LG-T : 408
    NWLGPTSNQWLGTSN  LGPTSNWLG TS QWL TSN WLGPTSN LG T

           460         *       480         *       500
a : SNQWLGTSNQWLGPTSNWLGPTSNQWLGTSNQWLGPTSNWLGPTSNQWLG : 500
b : SNQWLGT-NQ-LGPTSN-LGPTSN-WLGTSNQW-GPTSN-L-PTS-QWLG : 450
    SNQWLGT NQ LGPTSN LGPTSN WLGTSNQW GPTSN L PTS QWLG
```

Fig-2. Results of the sequence alignment for simulation I.

The results in simulation I suggest if two sequences are similar, we can use sequence alignment method to find insert, delete, and replace points in one sequence by comparing with the other, which is useful for financial time series analysis, because in practice, original financial time series may contain abnormal data or missing data. In that case, we can use sequence alignment method to find the position of these abnormal or missing data if we find a sequence highly similar to the original financial sequence.

5.2. Simulation II: Recognize Lead-Lag Relationship of the Sequences

For the second datasets, sequences *a* and *b*are generated from function $y = \sin\left(\frac{3\pi}{50}x\right)$ and $y = \cos\left(\frac{3\pi}{50}x\right)$ respectively. x is the integer in range of [1, 1000]. Size of the two datasets are both 1000.

In simulation II, we use the same method as simulation I to symbolize the two datasets. We also divide central angle into 8 parts, and each part is $\frac{3\pi}{11}x$. Define these 8 classes as different symbols in amino acids, which is shown in Table 2 and Fig.3. Random delete 50 characters in sequence *a* and sequence *b* respectively.

Table-2. Characters of the dataset and its corresponding symbols for simulation II.

Range of $\frac{3\pi}{50}x$	$y = \sin\left(\frac{3\pi}{50}x\right)$			$y = \cos\left(\frac{3\pi}{50}x\right)$		
	Value	**Slope**	**Symbol**	**Value**	**Slope**	**Symbol**
$(\frac{\pi}{8}+2k\pi,\frac{3\pi}{8}+2k\pi]$	+	+	G	+	-	T
$(\frac{3\pi}{8}+2k\pi,\frac{5\pi}{8}+2k\pi]$	+	0	P	0	-	S
$(\frac{5\pi}{8}+2k\pi,\frac{7\pi}{8}+2k\pi]$	+	-	T	-	-	N
$(\frac{7\pi}{8}+2k\pi,\frac{9\pi}{8}+2k\pi]$	0	-	S	-	0	Q
$(\frac{9\pi}{8}+2k\pi,\frac{11\pi}{8}+2k\pi]$	-	-	N	-	+	W
$(\frac{11\pi}{8}+2k\pi,\frac{13\pi}{8}+2k\pi]$	-	0	Q	0	+	L
$(\frac{13\pi}{8}+2k\pi,\frac{15\pi}{8}+2k\pi]$	-	+	W	+	+	G
$(-\frac{\pi}{8}+2k\pi,\frac{\pi}{8}+2k\pi]$	0	+	L	+	0	P

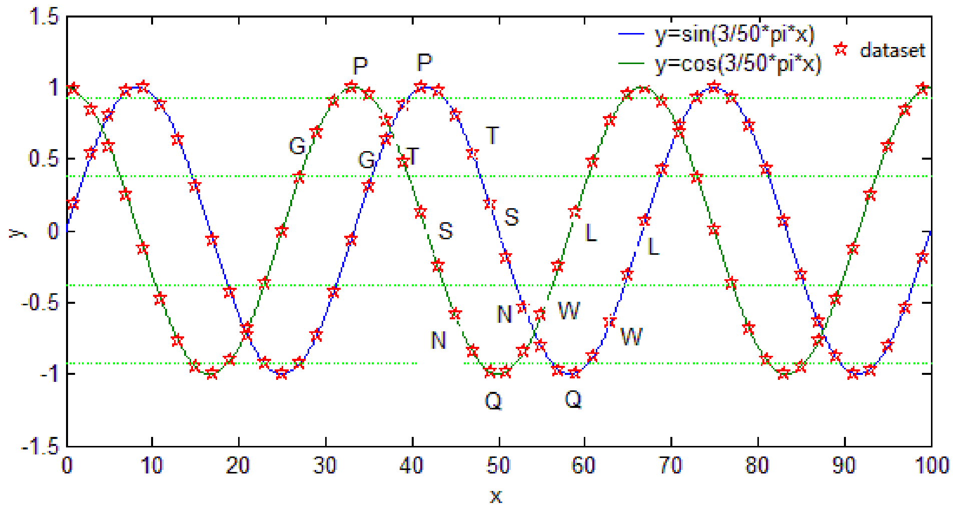
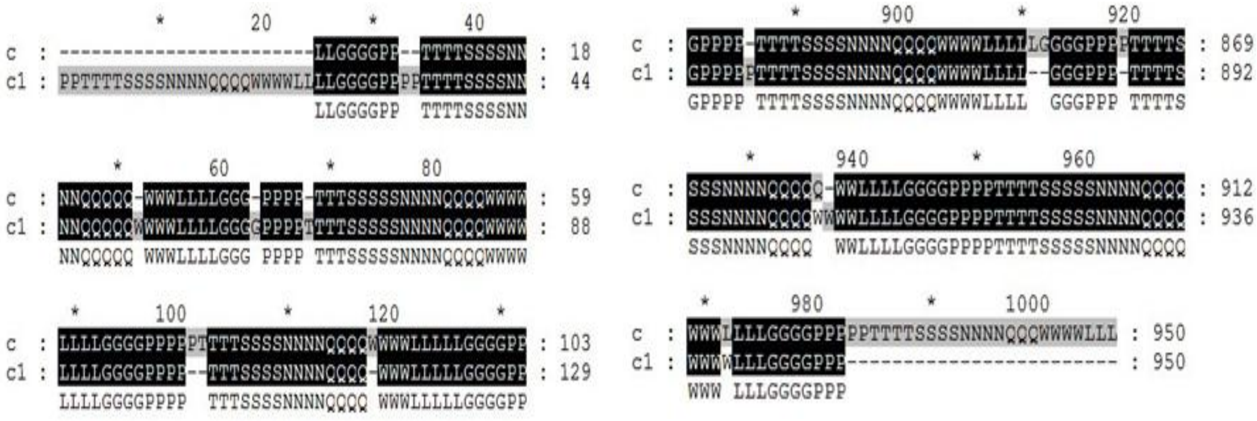


Fig-3. Characters of the dataset and its corresponding symbols for simulation II.

For sequence alignment, we use the same method as simple score matrix in simulation I. In Fig.3, it can be seen that function $y = \cos\left(\frac{3\pi}{50}x\right)$ is lead of function $y = sin\left(\frac{3\pi}{50}x\right)$, which means sequence *b* is lead of sequence *a*. Alignment results in Fig.4 suggest that some gaps inserted into sequence *a* where sequence *b* is leading, so that two sequences are matched.



```
                 *        20         *        40
c  : ------------------------LLGGGGPP--TTTTSSSSNN :  18
c1 : PPTTTTSSSSNNNNQQQQWWWWLLLLGGGGPPPPTTTTSSSSNN :  44
                             LLGGGGPP  TTTTSSSSNN

             *        60         *        80
c  : NNQQQQQ-WWWLLLLGGG-PPPP-TTTSSSSSNNNNQQQQWWWW :  59
c1 : NNQQQQQWWWWLLLLGGGGPPPPTTTTSSSSSNNNNQQQQWWWW :  88
     NNQQQQQ WWWLLLLGGG PPPP TTTSSSSSNNNNQQQQWWWW

         *       100         *       120         *
c  : LLLLGGGGPPPPPTTTTSSSSNNNNQQQQWWWWLLLLLGGGGPP : 103
c1 : LLLLGGGGPPPP--TTTSSSSNNNNQQQQ-WWWLLLLLGGGGPP : 129
     LLLLGGGGPPPP  TTTSSSSNNNNQQQQ WWWLLLLLGGGGPP
```

(a) Beginning fragment.

```
                 *       900         *       920
c  : GPPPP-TTTTSSSSNNNNQQQQWWWWLLLLLGGGGPPPPTTTTS : 869
c1 : GPPPPPTTTTSSSSNNNNQQQQWWWWLLLL--GGGPPP-TTTTS : 892
     GPPPP TTTTSSSSNNNNQQQQWWWWLLLL  GGGPPP TTTTS

             *       940         *       960
c  : SSSNNNNQQQQQ-WWLLLLGGGGPPPPTTTTSSSSSNNNNQQQQ : 912
c1 : SSSNNNNQQQQWWWWLLLLGGGGPPPPTTTTSSSSSNNNNQQQQ : 936
     SSSNNNNQQQQ  WWLLLLGGGGPPPPTTTTSSSSSNNNNQQQQ

         *       980         *      1000
c  : WWWLLLLGGGGPPPPPTTTTSSSSNNNNQQQWWWWLLL : 950
c1 : WWWWLLLGGGGPPP------------------------ : 950
     WWW LLLGGGGPPP
```

(b) End fragment.

Fig-4. Beginning and end fragments of the sequence alignment result for simulation II.

The results in simulation II suggest sequence alignment method can make numbers of matching symbols as large as possible by inserting gaps. In financial studies, this method can be used to analyze lead-lag relationship between the two financial time series.

5.3. Simulation III: Recognize Similar Patterns of the Sequences

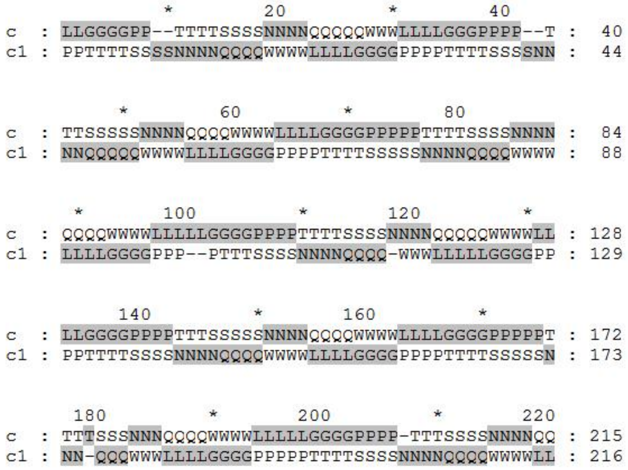
In simulation III, datasets and symbolization methods are the same as simulation II. In Fig.3, it can be seen that symbol G in sequence *a* is always corresponding with symbol T in sequence *b*, and symbol P in sequence *a* is always corresponding with symbol S in sequence *b*. It seems that there are some stable patterns between these two sequences. Thus, we apply similarity-oriented score matrix proposed in section 4 in simulation III to recognize such similar patterns.

The results of standardized probability matrix are shown in Table 3. Correspondence of symbols in two sequences is different according to different symbols. For example, standardized probability of G in sequence *a* with T in sequence *b* is 5.24, with P in sequence *b* is 2.53, and with S in sequence *b* is 0.32, which suggest symbols in the two sequences do have some stable relations.

Table-3. Standardized probability matrix for simulation III.

Sequence *b*	**Sequence *a***							
	G	**P**	**T**	**S**	**N**	**Q**	**W**	**L**
G	0	0	0	0	0	0.2777	5.4934	2.4869
P	2.5296	0	0	0	0	0	0.1402	5.1252
T	5.2432	2.3985	0	0	0	0	0	0.3331
S	0.3224	5.1238	2.3571	0	0	0	0	0
N	0	0.2642	5.3087	2.4632	0	0	0	0
Q	0	0	0.3381	5.0831	2.4771	0	0	0
W	0	0	0	0.4029	5.3756	2.4083	0	0
L	0	0	0	0	0.2752	5.2724	2.5441	0

We introduce similarity-oriented scoring matrix for sequence alignment. In this simulation, set 3 points as penalty point for inserting gaps, because all of the standardized probability of symbols in Table 3 is below 3 except respective maximum matching value of each symbol. Thus, this penalty point ensures that gaps will not be inserted for matching two symbols if co-occurrence probability of the two symbols is not the maximum. Results of sequence alignment are shown in Fig.5. It suggests that G, P, T, S, N, Q, W, L in sequence *a* are matching with T, S, N, Q, W, L, G, P in sequence *b* respectively.



```
              *        20         *        40
c  : LLGGGGPP--TTTTSSSSNNNNQQQQQWWWLLLLGGGPPPP--T :  40
c1 : PPTTTTSSSSNNNNQQQQWWWWLLLLGGGGPPPPTTTTSSSSNN :  44

          *        60         *        80
c  : TTSSSSSNNNNQQQQWWWWLLLLGGGGPPPPPTTTTSSSSNNNN :  84
c1 : NNQQQQQWWWWLLLLGGGGPPPPTTTTSSSSSNNNNQQQQWWWW :  88

      *       100         *       120         *
c  : QQQQWWWWLLLLLGGGGPPPPTTTTSSSSNNNNQQQQQWWWWLL : 128
c1 : LLLLGGGGPPP--PTTTSSSSNNNNQQQQ-WWWLLLLLGGGGPP : 129

          140         *       160         *
c  : LLGGGGPPPPTTTSSSSSNNNNQQQQWWWWLLLLGGGGPPPPPT : 172
c1 : PPTTTTSSSSNNNNQQQQWWWWLLLLGGGGPPPPTTTTSSSSSN : 173

      180         *       200         *       220
c  : TTTSSSNNNQQQQWWWWLLLLLGGGGPPPP-TTTSSSSNNNNQQ : 215
c1 : NN-QQQWWWLLLLGGGGPPPPPTTTTSSSSNNNNQQQQWWWWLL : 216
```

Fig-5. Fragment of the sequence alignment result for simulation III.

The results in simulation III show that we can recognize matching patterns using similarity-oriented score matrix. The sequences for alignment not only can be the sequences with lead-lag relationship like datasets in simulation III, but also sequences with some other matching patterns, such as a set of sequences defined by cosine function and sawtooth wave function respectively, shown in Fig.6. In financial analysis, as long as there are some stable matching patterns between two sequences, we can use sequence alignment method with proposed similarity-oriented score matrix to find them.

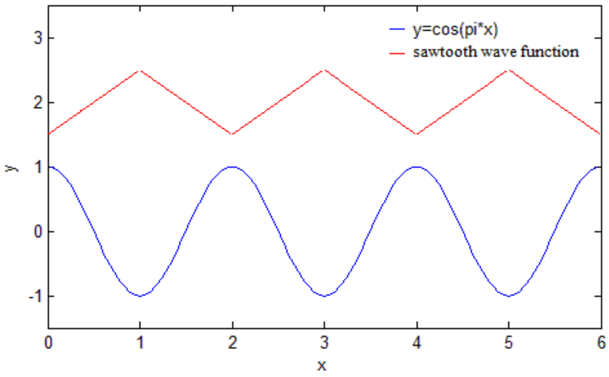


Fig-6. Cosine function and sawtooth wave function.

To sum up, we verify sequence alignment and proposed similarity-oriented score matrix can be used to analyze financial time series in different cases. In simulation I, the results suggest sequence alignment method is useful for data missing problem. In simulation II, it suggests that sequence alignment method can be used to analyze lead-lag relationship of financial time series. In simulation III, we can use proposed similarity-oriented score matrix to find stable matching patterns between two sequences. The similarity-oriented score matrix is not only proposed for sequences alignment, but also for hidden pattern finding. As shown in Fig.6, peaks in trigonometric function are always corresponding to valleys in sawtooth wave function, which is a kind of matching patterns, and vice versa.

6. EMPIRICAL ANALYSIS

We use sequence alignment method and score matrix we proposed to analyze characters and correlation of the two markets in China, whose representative are Shanghai composite index (SH) and Shenzhen component index (SZ) respectively. Because both of the two indices reflect Chinese stock market and their constituent stocks are different, these two indices are highly correlated but not completely same. Unlike traditional methods such as Pearson correlation coefficient to get an overall coefficient to reflect their correlation, the methods in this paper more concern about their matching patterns under certain correlation. For example, we attempt to find sharply drop of one index is always corresponding to which status of the other index, and to find whether co-occurrence of drop is more frequent than rise for the two indices. We also use different threshold to separate stock market index into several bullish and bearish intervals for sensitive analysis.

6.1. Sample and Datasets

Shanghai composite index is the weighted price of all the stocks listed in Shanghai Stock Exchange (SSE). Shenzhen composite index is the weighted stock price index of 500 representative listed companies in Shenzhen Stock Exchange (SZSE). Compared with SSE, SZSE contains more small and medium-size stocks. For example, in 2015, the weight of the small and medium-size stocks is 34% and weight of growth enterprise stocks is 16% in Shenzhen composite index.

Samples we use are time series of close prices of these two composite indices from May 31, 2005 to December 31, 2013.We define returns of the index as $r_t = \ln p_t - \ln p_{t-1}$ and get 2089 observed data. The Pearson correlation coefficient of the two indices is 0.926. Our target is to use proposed similarity-oriented score matrix to find intrinsic hidden patterns under this high correlation.

6.2. Symbolization of Returns Series

In order to analyze characters of the two markets in China, we symbolize returns series as several intervals to reflect bullish and bearish. We define top 100 returns as sharply rise, called T, define last 100 as sharply drop, called A, define returns no less than 0 and except top 100 as weakly rise, called G, and define returns below 0 and except last 100 as weakly drop, called C. Symbols and its frequency in two markets are shown in Table 4. It can be seen that the value of quantile of sharply drop A is larger than sharply rise T in both markets, which suggests that drop rate is larger than rise. Besides, both absolute values of quantile T and A in Shenzhen are larger than Shanghai, which implies that volatility of Shenzhen is more than Shanghai. It is reasonable because compared with Shanghai, there are more small and medium-size stocks in Shenzhen.

Table-4. Symbols and its frequency for index returns series

Symbol	SH frequency	SH interval	SZ frequency	SZ interval
A	0.0479	(-∞,-2.96%)	0.0479	(-∞,-3.19%)
C	0.4119	[-2.96% , 0)	0.4248	[-3.19% , 0)
G	0.4923	[0,2.66%)	0.4794	[0,3.16%)
T	0.0479	[2.66%,+∞)	0.0479	[3.16%,+∞)

6.3. Analysis Based on Similarity-Oriented Score Matrix

Define symbolized returns series of Shanghai as main chain, and that of Shenzhen as auxiliary chain. Then we use method proposed above to calculate score matrix.

(1) Calculate co-occurrences probability matrix, which refers to probability of returns in Shenzhen is i if returns of index in Shanghai is j. Thus, the sum of the value in each column in this matrix is 1. Probability matrix are shown in Table 5.

Table-5. Probability matrix for symbolized index returns.

$M(i,j)$		Symbolized index returns in SH			
		A	**C**	**G**	**T**
Symbolized index returns in SZ	A	0.7900	0.0244	0	0
	C	0.2100	0.8442	0.1362	0
	G	0	0.1314	0.8356	0.2900
	T	0	0	0.0282	0.7100

(2) Standardize probability matrix above, and the results are shown in Table 6.

Table-6. Standardize probability matrix for symbolized index returns.

$\frac{M}{f}$		Symbolized index returns in SH			
		A	**C**	**G**	**T**
Symbolized index returns in SZ	A	16.4952	0.5099	0	0
	C	0.4943	1.9872	0.3206	0
	G	0	0.2741	1.7430	0.6049
	T	0	0.0000	0.5890	14.8248

(3)Calculate log odds matrix, and the results are shown in Table 7.

Table-7. Logarithmic probability matrix for symbolized index returns.

m		Symbolized index returns in SH			
		A	**C**	**G**	**T**
Symbolized index returns in SZ	A	2.8031	-0.6736	-∞	-∞
	C	-0.7045	0.6867	-1.1376	-∞
	G	-∞	-1.2943	0.5556	-0.5027
	T	-∞	-∞	-0.5293	2.6963

It can be seen that the score become positive only when corresponding symbols are same based on the matrix in Table 7 for sequence alignment, which indicates synchronism of the two indices. The value of A in Shanghai (Shenzhen) and G or T in Shenzhen (Shanghai) is -∞, because there is no sample that A and G (or T) are co-occurrence in this time period. As for absolute value, the score for symbol A is larger than symbol T, and symbol C is larger than symbol G, which suggests concurrent decrease of the two indices is more common than rise. Besides, the score for symbol A is larger than symbol C, and symbol T is larger than symbol G, which suggests extreme volatility leads to much more co-movement of the two indices.

6.4. Sensitive Analysis

We use different threshold to separate stock market index into several bullish and bearish interval for sensitive analysis. We expand samples to November 24, 2015, and get 2550 observed data.

(1) Symbolization of returns series

We use three cases for analysis. Definition of quantile in first case is the strictest. We define the highest 5% returns as sharply rise, called T, define the lowest 5% as sharply drop, called A, define returns no less than 0 and except the highest 5% as weakly rise, called G, and define returns below 0 and except the lowest 5% as weakly drop, called C. In second case, we release such quantile. Define the highest 10% and lowest 10% as T and A respectively. In third case, we further release it. Define the highest 15% and lowest 15% as T and A respectively. Rule for definition of C and G is ditto. Symbols and its interval in different quantile for the two markets are shown in Table 8.

Table-8. Symbols and its interval in different quantile.

Quantile	Symbol	A	C	G	T
5%	SH interval	(-∞, -2.9521%)	[-2.9521%, 0)	[0,2.6734%)	[2.6734%, +∞)
	amount	128	1031	1263	128
	SZ interval	(-∞, -3.1936%)	[-3.1936%, 0)	[0, 3.1602%)	[3.1602%, +∞)
	amount	128	1072	1222	128
10%	SH interval	(-∞, -1.9180%)	[-1.9180%, 0)	[0, 2.0103%)	[2.0103%, +∞)
	a□ount	255	904	1136	255
	SZ interval	(-∞, -2.1774%)	[-2.1774%, 0)	[0, 2.3594%)	[2.3594%, +∞)
	amount	255	945	1095	255
15%	SH interval	(-∞, -1.4035%)	[-1.4035%, 0)	[0, 1.5496%)	[1.5496%, +∞)
	amount	383	776	1008	383
	SZ interval	(-∞, -1.6114%)	[-1.6114%□ 0)	[0, 1.8222%)	[1.8222%, +∞)
	amount	383	817	967	383

It can be seen that absolute returns of the highest 5% and lowest 5% in Shanghai is more than 2.67%, and in Shenzhen is more than 3.16%. It is similar with quantile of top and end 100 in section 6.3. When quantile is 10% or 15%, the absolute returns is not large enough, so that we called big drop for symbol A, and big rise for symbol T in these two cases.

Absolute returns of the lowest 5% is larger than the highest 5% in both markets, which indicates drop rate is larger than rise. However, absolute returns of the highest 10% and 15% is larger than the lowest 10% and 15% respectively, which suggests distribution of index return is more concentrated in big rise (not sharply rise) than big drop (not sharply drop). Besides, in all the three cases, absolute returns at quantile in Shenzhen is larger than Shanghai. It suggests compared with Shanghai, Shenzhen which contains more small and medium-size stocks has more sharply volatility.

(2) Analysis Based on Score Matrix

Using quantile above to symbolize returns series in two markets, we define Shanghai as main chain, and Shenzhen as auxiliary chain. We use method proposed in section 4 to calculate score matrix, standardized probability matrix, and logarithmic probability matrix. The results are shown in Table 9, 10, and 11.

Table-9. Results of sensitive analysis for 5% quantile symbolization.

		Symbolized index returns in SH			
Probability matrix		**A**	**C**	**G**	**T**
Symbolized index returns in SZ	A	0.7969	0.0252	0	0
	C	0.2031	0.8400	0.1425	0
	G	0	0.1348	0.8274	0.2969
	T	0	0	0.0301	0.7031
Standardized matrix		A	C	G	T
Symbolized index returns in SZ	A	15.8752	0.5024	0	0
	C	0.4832	1.9980	0.3390	0
	G	0	0.2813	1.7266	0.6195
	T	0	0	0.5994	14.0076
Logarithmic matrix		A	C	G	T
Symbolized index returns in SZ	A	2.7648	-0.6884	-∞	-∞
	C	-0.7274	0.6922	-1.0817	-∞
	G	-∞	-1.2682	0.5461	-0.4788
	T	-∞	-∞	-0.5118	2.6396

Table-10. Results of sensitive analysis for 10% quantile symbolization.

		Symbolized index returns in S□			
Probability matrix		**A**	**C**	**G**	**T**
Symbolized index returns in SZ	A	0.7922	0.0586	0	0
	C	0.2039	0.7887	0.1549	0.0157
	G	0.0039	0.1515	0.7852	0.2549
	T	0	0.0011	0.0599	0.7294
Standardized matrix		A	C	G	T
Symbolized index returns in SZ	A	7.9216	0.5863	0	0
	C	0.5503	2.1283	0.4181	0.0423
	G	0.0091	0.3529	1.8286	0.5936
	T	0	0.0111	0.5986	7.2941
Logarithmic matrix		A	C	G	T
Symbolized index returns in SZ	A	2.0696	-0.5340	-∞	-∞
	C	-0.5974	0.7553	-0.8721	-3.1623
	G	-4.6959	-1.0415	0.6035	-0.5215
	T	-∞	-4.5042	-0.5132	1.9871

Table-11. Results of sensitive analysis for 15% quantile symbolization.

		Symbolized index returns in SH			
Probability matrix		**A**	**C**	**G**	**T**
Symbolized index returns in SZ	A	0.8094	0.0889	0.0040	0
	C	0.1828	0.7358	0.1687	0.0157
	G	0.0078	0.1740	0.7431	0.2089
	T	0	0.0013	0.0843	0.7755
Standardized matrix		A	C	G	T
Symbolized index returns in SZ	A	5.3890	0.5920	0.0264	0
	C	0.5704	2.2966	0.5264	0.0489
	G	0.0207	0.4588	1.9595	0.5508
	T	0	0.0086	0.5614	5.1630
Logarithmic matrix		A	C	G	T
Symbolized index returns in SZ	A	1.6844	-0.5242	-3.6336	-∞
	C	-0.5613	0.8314	-0.6417	-3.0181
	G	-3.8798	-0.7792	0.6727	-0.5964
	T	-∞	-4.7583	-0.5773	1.6415

It can be seen that in all of the three cases, only when corresponding symbols are same does the score become positive, which verifies the results that two indices are synchronism. Besides, absolute score for symbol A is larger than symbol T, and symbol C is larger than symbol G, which suggests concurrent decrease of the two indices is more common than rise. The score for symbol A is larger than symbol C, and symbol T is larger than symbol G, which suggests extreme volatility leads to much more co-movement of the two indices. These results are similar with results in section 6.3, and prove the robustness of the results.

Besides, we also find when define the lowest 5% of the returns as A, the value of A in Shanghai (Shenzhen) with G or T in Shenzhen (Shanghai) is -∞, because there is no sample that A and G (or T) are co-occurrence in this time period. While define the lowest 15% of the returns as A, the value of A in Shanghai (Shenzhen) with G in Shenzhen (Shanghai) may not be -∞, because with release of extreme symbol's definition, some absolute returns assigned to symbol A (or T) are not significantly higher than those of C (or G). Except correlation coefficient, proposed similarity-oriented score matrix helps us to find hidden patterns in these two correlated series.

6.5. Summary

Here we summarize hidden patterns we find in Chinese stock index SSE and SZSE under their high correlation in empirical analysis. (1) Rise and decrease are approximately synchronous in two indices. (2) Simultaneous decrease of the two indices is more common than rise. (3) Extreme volatility leads to much more co-movement of the two indices.

The difference between our method in this paper and traditional correlation analysis in financial time series is that our goal is not to value how similar of the two series. Traditional correlation analysis like Pearson correlation coefficient calculate an overall coefficient to reflect their correlation, while the similarity-oriented score matrix we propose is to find intrinsic hidden pattern between two highly correlated series.

The idea of proposed similarity-oriented score matrix is based on PAM matrix in sequence alignment program. They both use known sequences to calculate frequency of aligned pairs to approximate its probability. Compared with PAM which reflect evolutionarily related of each aligned residue pair, similarity-oriented score matrix is to find co-occurs symbol pairs in different time series. For example, in above empirical analysis, the score for symbols representing decrease is larger than symbols representing rise suggests concurrent decrease of the two indices happens more than concurrent rise.

7. CONCLUSIONS

This paper discussed the application of sequence alignment for financial time series. A few of literatures use sequence alignment method to analyze financial series. Most of these previous literatures focus correlation analysis, and commonly used score matrix is simple matrix, which is to set a fix value subjectively. This paper suggests sequence alignment method and its score matrix can be used to more fields in financial series analysis. In simulation, we have verified simple matrix can be used to find key points, including insert, delete, and replace points, and to analyze lead-lag relations in first two simulations. Further, based on methods of calculating PAM matrix, we propose a similarity-oriented score matrix to find hidden patterns and adopt it in both simulation and empirical analysis.

We apply similarity-oriented score matrix to study characteristics and relationship between two stock markets in China. Since data characteristics for biological sequence and financial series are different, sequence alignment method cannot be directly used in financial analysis. We first symbolize financial time series as several intervals to reflect bullish and bearish. Then, use proposed similarity-oriented score matrix to find matching patterns of these two indices under their high correlation. The results suggest co-occurrence of the volatility in the two markets, and more co-movement in extreme volatility. In sensitive analysis, we get the similar results for different threshold values of symbols definition, and further evidence of co-movement in extreme cases. These results are meaningful for both financial time series analysis and application field extension of sequence alignment method.

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