

Detecting Variable Length Anomaly Patterns in Time Series Data

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Abstract. The anomaly detection algorithm, developed by Leng et al. (2008), can detect anomaly patterns of variable lengths in time series. This method consists of two stages: the first is segmenting time series; the next is calculating anomaly factor of each pattern and then judging whether a pattern is anomaly or not based on its anomaly factor. Since the lengths of patterns can be different from each other, this algorithm uses Dynamic Time Warping (DTW) as distance measure between the patterns. Due to DTW, the algorithm leads to high computational complexity. In this paper, to improve the above mentioned algorithm, we apply homothetic transformation to convert every pair of patterns of different lengths into the same length so that we can easily calculate Euclidean distance between them. This modification accelerates the anomaly detection algorithm remarkably and makes it workable on large time series.

Keywords: time series, anomaly detection, segmentation, anomaly factor.

1 Introduction

Anomaly detection is a challenging topic, mainly because we need to obtain the lengths of anomaly patterns before detecting them. There has been an extensive study on time series anomaly detection in the literature. Some popular algorithms for time series anomaly detection include window-based methods such as brute-force and HOT SAX by Keogh et al. (2005) [4] and WAT by Bu et al. (2007) [2]; a method based on neural-network by Oliveira et al. (2004) [8]; a method based on segmentation and Finite State Automata by Salvador and Chan (2005) [10]; a method based on time series segmentation and anomaly scores by Leng et al. (2008) [6]; and a method based on Piecewise Aggregate Approximation bit representation and clustering by Li et al. (2013) [7]. Most of these above-mentioned algorithms for time series anomaly detection ([2], [4], [7], [8]) require the user to specify the length of anomaly pattern as an input parameter, but this length is often unknown.

Among these algorithms, the method proposed by Leng et al. [6] is the first one in the literature that can detect anomaly patterns of variable lengths in time series and hence does not require the length of the anomaly pattern as a parameter supplied by user. This method consists of two stages. The first is segmenting time series using a quadratic regression model. The next is discovering all the anomaly patterns by calculating anomaly factor of each pattern and then judging whether a pattern is

anomaly or not based on its anomaly factor. Since in this algorithm, the lengths of patterns can be different from each other, Leng et al. suggested that Dynamic Time Warping (DTW) distance ([1]) should be used to calculate the distances between the patterns in this algorithm. Due to this suggestion, the algorithm proposed by Leng et al. becomes a very complicated algorithm with high computational complexity and is not suitable to work on large time series.

In this work, to improve the algorithm proposed by Leng et al., we apply homothetic transformation to convert every pair of patterns of different lengths into the same length so that we can easily calculate Euclidean distance between them. In addition, we reduce the number of distance calculations in building the distance matrix by constraining the possible alignments between each pair of patterns. These two modifications bring out a remarkable improvement for the original anomaly detection algorithm in time efficiency while maintaining the same detection accuracy. Besides, we try to apply in our proposed anomaly detection algorithm another method of time series segmentation which is based on important extreme points instead of quadratic regression model.

Experimental results on eight real world time series datasets demonstrate the effectiveness and efficiency of our proposed methods in detecting anomaly patterns of variable lengths in time series.

2 Background

2.1 Some Definitions

A time series $T = t_1, t_2, \dots, t_m$ is an ordered set of m real values measured at equal intervals. Given a time series T of length m , a subsequence C is a sampling of length $n < m$ of contiguous positions from T , i.e., $C = t_p, t_{p+1}, \dots, t_{p+n-1}$, for $1 \leq p \leq m-n+1$. Sometimes, C is denoted as (s_p, e_{p+n-1}) , where $s_p = t_p$ and $e_{p+n-1} = t_{p+n-1}$.

Definition 1. *Distance function:* $Dist(C, M)$ is a positive value used to measure the difference between two time series C and M , based on some measure method.

Definition 2. *k-distance of a pattern:* Given a positive integer k , a pattern set D and a pattern $P \in D$, the k -distance of P , denoted as $k-dist(P)$, is defined as the distance between P and a pattern $Q \in D$ such that.

- i) For at least k patterns $Q' \in D$ it holds that $Dist(D, Q') \leq Dist(D, Q)$.
- ii) For at most $k-1$ patterns $Q' \in D \setminus \{Q\}$ it holds that $Dist(D, Q') < Dist(D, Q)$.

Definition 3. *Non-Self Match:* Given a time series T , its two subsequences P of length n starting at position p and Q starting at position q , we say that Q is a non-self-match to P , if $Dist(P, Q) \geq e$ or $|p - q| \geq n$, where e is a given value of distance threshold.

Definition 4. *Anomaly factor:* For any pattern set D and a pattern $P \in D$, $k-dist(D)$ denotes all $k-dist$ of patterns, anomaly factor of pattern P defined as the ratio of $k-dist(P)$ to $median(k-dist(D))$.

Definition 5. Anomaly Pattern: Given any pattern set D , a pattern $P \in D$, P is anomaly only if its anomaly factor is larger than a , where a is the threshold of anomaly pattern.

2.2 Detecting Variable Length Anomaly Patterns in Time Series based on Segmentation and Anomaly Factors

Leng et al. [6] proposed the algorithm for detecting anomaly patterns in time series. This algorithm consists of two phases: segmenting time series and detecting anomaly patterns based on anomaly factors.

Leng et al. used quadratic regression model to segment time series. Regression function is defined as $f(t) = \beta_0 + \beta_1 t + \beta_2 t^2$, where the t values, the values of time domain are real values. The segmentation algorithm searches for a segment $S = t_p, \dots, t_{p+m+1}$ of a given time series T , starts at t_p and end at t_{p+m+1} , such that the sum of squared errors, is less than ε_l , where $f(t) = \beta_0 + \beta_1 t + \beta_2 t^2$ and ε_l is a threshold specified by the user. We can extract all the patterns in the time series T by applying repeatedly this search procedure.

The segmentation procedure is described as follows.

1. Let $s_l = 1$ denote the start position of the first segment, l denote the initial length of each segment, $m = s_l$ and then update this segment, the updating procedure is as follows. Calculate the values of β_0 , $\beta_1 t$, and β_2 and the sum of squared errors:

$$SSE = \sum_{i=p}^{p+l-1} (f(i) - t_i)^2$$

2. If $SSE < \varepsilon_l$ let $l = l + 1$, go to step 1, else goto step 3.
3. Let (s_l, e_l) denote this segment, e_l denotes the end position of this segment and $e_l = l - 1$.
4. Let $i = 1$, if $Dist((s_l, e_l), (s_l + i, e_l + i)) \leq \varepsilon_2$, increment i by 1, calculate it, repeat this procedure until $Dist((s_l, e_l), (s_l + i, e_l + i)) > \varepsilon_2$ or $i > (e_l - s_l)$, let $s_2 = e_l + i$, the s_2 is the start position of the next segment.
5. Let $m = s_2$, calculate e_2 using the steps 1-3, and then obtain the second segment (s_2, e_2) .
6. Calculate s_j using the step 4, let $m = s_j$, calculate the value of e_j using the steps 1 - 3, and then obtain the j -th segment (s_j, e_j) .
7. Repeat the above procedure until the end position of the segment is n .

Notice that the segmentation procedure uses Dynamic Time Warping (DTW) as distance measure for the patterns and Step 4 aims to eliminate the trivial matches. The parameter ε_l determines the length of each segment. The parameter ε_2 (called *non-self match threshold*) helps in removing trivial matches and hence it has impact on the number of extracted segments.

The procedure for Anomaly Pattern Detection is described as follows.

1. Find the maximum value, l_{max} and minimum value l_{min} of the lengths of all extracted segments.
2. Calculate the distance matrix $D = (d_{ij})_{m \times m}$ of segments:

$$d_{ij} = \min_{l_{min} \leq l \leq l_{max}} Dist((s_i, e_i), (s_j, s_j + l)) \quad (1)$$

where $1 \leq i, j \leq m$ and $i \neq j$.

3. Compute k-distance of each segments based on the distance matrix, let $k\text{-dist}(D)$ denote the set of all these distances.
4. Calculate $\text{median}(k\text{-dist}(D))$
5. Calculate anomaly factor of each segment, and determine whether each segment is an anomaly pattern or not basing on the anomaly factor threshold a .
6. Given two anomaly patterns (s_i, e_i) and (s_j, e_j) , if they are overlapped, merge them into one pattern.

Notice that in Step 2, we need to compute $(l_{\max} - l_{\min} + 1)$ DTW distances when calculating the DTW distance between (s_i, e_i) and (s_j, e_j) , and the algorithm selects the minimum value of them as the real DTW distance of (s_i, e_i) and (s_j, e_j) . Step 6 helps to merge two anomaly patterns if they are overlapped and this can weaken the influence of ε_j if the value of ε_i is smaller than its real value.

3 The Proposed Algorithms

The main idea of our method for detecting anomaly patterns of variable lengths in time series is to apply homothetic transformation to convert each pair of patterns of different lengths into the same length so that we can easily calculate Euclidean distances between them rather than using computationally complicated DTW distance. We call our proposed method VL_QR|HT (Variable Length anomaly pattern detection based on Quadratic Regression and Homothety).

3.1 Homothetic Transformation

Homothety is a transformation in affine space. Given a point O and a value $k \neq 0$. A homothety with center O and ratio k transforms the point M to the point M' such that $\overrightarrow{OM'} = k \times \overrightarrow{OM}$.

Homothety can transform a time series T of length n ($T = \{y_1, y_2, \dots, y_n\}$) to time series T' of length n' by performing the following steps. First, compute $Y_MAX = \text{MAX}(y_1, \dots, y_n)$, $Y_MIN = \text{MIN}(y_1, \dots, y_n)$. Second, set the center I of homothety with the coordinates $X_C = n/2$, $Y_C = (Y_MAX + Y_MIN)/2$. Next, perform the homothety with the center I and the ratio n'/n .

To compute Euclidean distance of two time series, first we check their lengths. If the two lengths are similar, we can compute their distance right away. Otherwise, we apply homothety to convert them to the same length and then compute their Euclidean distance. Here we select the average length of the two time series as the length to which we convert the two time series using homothety.

Besides, we note that two 'similar' subsequences will not be recognized where a vertical difference exists between them. To make the Euclidean distance calculation in the anomaly pattern detection algorithm able to handle not only uniform scaling but also shifting transformation along vertical axis, we modify our Euclidean distance by using Modified Euclidean Distance as a method of negating the differences caused

through vertical axis offsets. Details of Modified Euclidean Distance are given in our previous work; interested reader can refer to [11].

3.2 Reducing the Number of Distance Calculations in Building the Distance Matrix

In the procedure for detecting anomaly patterns of variable lengths proposed by Leng et al. [6], to compute the distance between two patterns (s_i, e_i) and (s_j, e_j) , we need to compute $(l_{max} - l_{min} + 1)$ times of distance calculations, where l_{min} and l_{max} are the maximum and minimum length of all the patterns extracted from the original time series (see Eq. 1 in Subsection 2.2). When l_{max} is much larger than l_{min} , the algorithm has to perform so many distance calculations in order to determine the real distance between two patterns and this might bring out the pathological cases in which a very short segment can match with a very long segment.

In order to reduce the number of distance calculations as well as to prevent pathological alignments between two patterns, in our proposed algorithm, we modify Eq. 1 by adding the parameter r and replace l_{max} and l_{min} with l_{upper} and l_{lower} respectively. The lower bound l_{lower} and the upper bound l_{upper} are defined by:

$$l_{upper} = \lfloor l_{avg}(1 + r) \rfloor \quad l_{lower} = \lceil l_{avg}(1 - r) \rceil$$

where l_{avg} is the average length of all the segments extracted from the original time series. Now, the formula to compute the distance between two patterns i and j is:

$$d_{ij} = \min_{l_{lower} \leq l \leq l_{upper}} Dist((s_i, e_i), (s_j, s_j + l)) \quad (2)$$

By the parameter r , we limit how far the length of the pattern j may differ from the average length of all the extracted patterns. The parameter r (called *length difference width*) should be chosen in order that the difference between l_{upper} and l_{lower} is not high while still maintaining the accuracy of the algorithm. Through experiment, we find out that r should vary in the range 0.05 to 0.25.

3.3 Other Issue: Using Some Alternative Segmentation Method

Using the same framework of VL_QR|HT, we can develop another anomaly detection algorithm by replacing the segmentation method based on quadratic regression with another time series segmentation method. The other segmentation method we selected here is based on the concepts of Important Extreme Points, proposed by Pratt and Fink [9]. This time series segmentation consists of two following steps. First, we extract all important extreme points of the time series T . The result of this step is a sequence of extreme points $EP = (ep_1, ep_2, \dots, ep_l)$. Secondly, we compute all the candidate patterns iteratively. A candidate pattern $CP_i(T)$, $i = 1, 2, \dots, l-2$ is the subsequence of T that is bounded by extreme points ep_i and ep_{i+2} . Candidate patterns are subsequences that may have different lengths. To be able to calculate distance between them, we bring them to the average length by using homothety.

After segmentation stage, we calculate anomaly factor for each candidate pattern in the same way as in VL_QR|HT. We call this anomaly detection algorithm VL_EP|HT (Variable Length anomaly pattern detection based on Extreme Points and

Homothety). Note that in identifying important extreme points of a time series, we need the parameter R , called *compression rate*, which is greater than one and an increase of R leads to selection of fewer important extreme points ([9]). To set a lower bound for the length of all extracted subsequences, we introduce the parameter min_length , the minimum time lag between two adjacent important extreme points. When a candidate pattern is extracted, its length must be greater than or equal to $2*min_length$.

4 Experimental Evaluation

We implemented all four algorithms: VL_QR|DTW (the original algorithm proposed by Leng et al.), VL_QR|HT, VL_EP|HT and HOT SAX. The first experiment aims to compare VL_QR|HT to original VL_QR|DTW in terms of time efficiency. The second experiment aims to compare VL_QR|HT and VL_EP|HT to HOT SAX in terms of time efficiency and anomaly detection accuracy.

Our experiments were conducted over the datasets from the UCR Time Series Data Mining Archive for discord discovery [5]. There are 8 datasets used in these experiments. The datasets are from different areas (finance, medicine, manufacturing, science). The names and lengths of the eight datasets are: ECG108 (17500 points), ECG308 (1300 points), ERP (5000 points), Memory (6875 points), Power_Italy (7000 points), Power_Dutch (9000 points), Stock20 (5000 points) and TEK1 (5000 points).

Table 1. Parameter values in the three algorithms for each dataset

Datasets	VL_QR HT	VL_EP HT	HOT SAX
ECG108	$\varepsilon_1 = 5.0, \varepsilon_2 = 0.3, a = 3.5, r = 0.1$	$R = 1.04, min_length = 50, a = 4, r = 0.1$	$n = 600, PAA_size = 60$
ERP	$\varepsilon_1 = 3.0, \varepsilon_2 = 1.0, a = 3.0, r = 0.15$	$R = 1.42, min_length = 10, a = 3.5, r = 0.1$	$n = 100, PAA_size = 10$
Memory	$\varepsilon_1 = 8.0, \varepsilon_2 = 0.1, a = 2.2, r = 0.1$	$R = 1.1, min_length = 40, a = 1.6, r = 0.1$	$n = 100, PAA_size = 20$
Power_Italy	$\varepsilon_1 = 100000, \varepsilon_2 = 100, a = 2.5, r = 0.1$	$R = 1.8, min_length = 20, a = 3.0, r = 0.1$	$n = 300, PAA_size = 30$

For each dataset, we have to set the required parameters for each of the three algorithms: VL_QR|HT, VL_EP|HT and HOT SAX. For VL_QR|HT, the parameters are regression error threshold ε_1 , non-self match threshold ε_2 , anomaly factor threshold a and the length difference width r . For VL_EP|HT, the parameters are compression rate R , the minimum length of extracted subsequence min_length , anomaly factor a and the length difference width r . For HOT SAX, the parameters are the discord length n and the length of PAA segment PAA_size . The values of parameters in the three algorithms for some datasets are shown in Table 1.

4.1 Experiment 1: Comparing VL_QR|HT to VL_QR|DTW.

This experiment aims to compare the efficiency of our proposed algorithm, VL_QR|HT to that of the algorithm proposed by Leng et al. (VL_QR|DTW). Over 8 datasets, we found out that the anomaly pattern detected by VL_QR|HT is exactly the same as the one detected by VL_QR|DTW. Table 2 shows the run times (in seconds) of the two algorithms over 8 datasets. Since VL_QR|DTW performs extremely slowly, we have to limit the lengths of the eight datasets to less than 3000 data points. Besides, to accelerate the DTW distance calculation, we employed a multithreading method, proposed by Huy in 2015 [3], in computing this distance.

The experimental results in Table 2 demonstrate that with all the datasets, the VL_QR|HT is remarkably faster than VL_QR|DTW while brings out the same accuracy. The speedup of our proposed algorithm over to the original algorithm by Leng et al. varies from 4 (dataset Memory) to 97 times (dataset Stock20) and in average is about 33.6.

Table 2. Run times (in seconds) of VL_QR|HT and VL_QR|DTW over eight datasets

Dataset	VL_QR HT	VL_QR DTW
ECG 108 (1000 points)	1	14
ECG 308 (1300 points)	1	11
ERP (1000 points)	1	5
Memory (1000 points)	1	4
Power_Italy (3000 points)	6	200
Power_Dutch (3000 points)	1	24
Stock20 (3000 points)	2	194
TEK16 (2000 points)	1	81

4.2 Experiment 2: Comparing VL_QR|HT and VL_EP|HT to HOT SAX

In the second experiment we compare VL_QR|HT and VL_EP|HT to HOT SAX in terms of time efficiency and anomaly detection accuracy. The HOT SAX [4] is used as the baseline algorithm in this experiment. The HOT SAX is selected for comparison since it is the most cited algorithm for detecting time series discords up to date and has been applied in many applications.

In order to compare with HOT SAX which always brings out the top-anomaly pattern in a time series, in this experiment, we set the parameter k in k -distance for patterns to 1 for both VL_QR|HT and VL_EP|HT.

Over 8 datasets, we found out that the anomaly pattern detected by VL_QR|HT or VL_EP|HT is exactly the same as the one detected by HOT SAX.

Additionally, we measured the execution times of the three algorithms over 8 datasets. From the experimental results we can see that:

- VL_QR|HT and VL_EP|HT perform remarkably faster than HOT SAX in all the tested datasets.

- The speedup of VL_QR|HT over HOT SAX varies from 8 to 302 times and is about 71.9 times in average. The speedup of VL_EP|HT over HOT SAX varies from 6 to 94 times and is about 27.8 times in average.
- The run time of VL_QR|HT is always lower than that of VL_EP|HT over all the datasets.

5 Conclusions

We have introduced the two proposed algorithms which are improved variants of the method for variable length anomaly pattern detection in time series proposed by Leng et al. [6]. These two algorithms, called VL_QR|HT and VL_EP|HT, hinge on using homothetic transformation to convert each pair of patterns of different lengths into the same length so that we can easily calculate Euclidean distances between them. This modification that avoids using DTW distance brings out a remarkable improvement for the original algorithm in time efficiency without compromising anomaly detection accuracy.

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