Matching Consecutive Subpatterns Over Streaming Time Series

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Abstract. Pattern matching of streaming time series with lower latency under limited computing resource comes to a critical problem, especially as the growth of Industry 4.0 and Industry Internet of Things. However, against traditional single pattern matching model, a pattern may contain multiple subpatterns representing different physical meanings in the real world. Hence, we formulate a new problem, called "consecutive subpatterns matching", which allows users to specify a pattern containing several consecutive subpatterns with various specified thresholds. We propose a novel representation Equal-Length Block (ELB) together with two efficient implementations, which work very well under all L_p -Norms without false dismissals. Extensive experiments are performed on synthetic and real-world datasets to illustrate that our approach outperforms the brute-force method and MSM, a multi-step filter mechanism over the multi-scaled representation by orders of magnitude.

Keywords: pattern matching, stream, time series

1 Introduction

Time series are widely available in diverse application areas, such as Healthcare [21], financial data analysis [22] and sensor network monitoring [25], and they turn the interests on spanning from developing time series database [6]. In recent years, the rampant growth of Industry 4.0 and Industry Internet of Things, especially the development of intelligent control and fault prevention to complex equipment on the edge, urges more challenging demands to process and analyze streaming time series from industrial sensors with low latency under limited computing resource [24].

As a typical workload, similarity matching over streaming time series has been widely studied for fault detection, pattern identification and trend prediction, where accuracy and efficiency are the two most important measurements to matching algorithms [11]. Given a single or a set of patterns and a pre-defined threshold, traditional similarity matching algorithms aim to find matched subsequences over incoming streaming time series, between which the distance is less than the threshold. However, in certain scenarios, the single threshold pattern model is not expressive enough to satisfy the similarity measurement requirements. Let us consider the following example.





Fig. 1: Diverse patterns of Extreme Operating Gust(EOG). EOG pattern is composed of three subpatterns and users tend to specify a larger threshold for Subpattern 2 comparing with Subpattern 1 and Subpattern 3.

Fig. 2: (a) Pattern P is composed of three subpatterns: $P_1 = P[1:4], P_2 = P[5:11]$ and $P_3 = P[12:15]$.

(b) In ELB representation, if we set block size w = 3, P and W_t are divided into 5 pattern/window blocks.

In the field of wind power generation, Extreme Operating Gust (EOG) [4] is a typical gust pattern which is a phenomenon of dramatic changes of wind speed in a short period. Early detection of EOG can prevent the damage to the turbine [17]. A typical pattern of EOG has three physical phases, where its corresponding shape contains a slight decrease (Subpattern 1), followed by a steep rise, a steep drop (Subpattern 2), and a rise back to the original value (Subpattern 3). Users usually emphasize the shape feature of the second subpattern much more than its exact numeric value. In other words, users tend to specify a larger threshold of distance measurement for Subpattern 2 comparing with Subpattern 1 and Subpattern 3. For instance, all time series in Fig. 1 are regarded as correct matches of EOG, although they have diverse values in their second subpatterns.

In summary, above example shows that a complex pattern is usually composed of several subpatterns representing different physical meanings, and users may want to specify various thresholds for different parts. There are similar situations in other fields like electrocardiogram in Healthcare and technique analysis in the stock market. Therefore, we formulate a new problem, named as *consecutive subpatterns matching* over streaming time series. In this scenario, a pattern contains a list of consecutive subpatterns with different thresholds. A sliding window on stream matches the given pattern only if each of its components matches the corresponding subpattern.

Although many techniques have been proposed for time series similarity matching, they do not aim to solve the problem mentioned above. For streaming time series matching, some recent works take advantage of similarity or correlation of multiple patterns and avoid the whole matching of every single patterns [11,21]. Similarly, most of the previous approaches for subsequence similarity search explore and index the commonalities of time series in database to accelerate the query [14,20]. These approaches are not optimized for the scenario of matching consecutive subpatterns.

In this paper, we propose Equal-Length Block (ELB) representation together with the *lower bounding property*. ELB representation divides both the pattern and a sliding window into equal-length disjoint pattern/window blocks. Then ELB characterizes a pattern block as upper/lower bounds and a window block as a single value. Two ELB implementations are provided which allow us to process multiple successive windows together, so that speed up the matching process dramatically while guaranteeing no false dismissals.

In summary, this paper makes the following contributions:

- We introduce a new model, consecutive subpatterns matching, which allows us to describe pattern more expressively and process streaming time series more precisely.
- We propose a novel ELB representation which accelerate the matching process dramatically under all L_p -norms and guarantees no false dismissals.
- We illustrate the efficiency of our algorithms with sufficient experiments on real-world and synthetic datasets and a comprehensive theoretical analysis.

The rest of the paper is arranged as follows: Sect. 2 gives a brief review of the related work. Sect. 3 formally defines our problem. Sect. 4 proposes ELB representation together with its two implementations. Sect. 5 conducts extensive experiments. Finally, Sect. 6 concludes the paper.

2 Related Work

There are two categories of the related works, multiple patterns matching over streaming time series and subsequence similarity search.

Multiple patterns matching over streaming time series. Traditional single pattern matching over the stream is relatively trivial, hence recent research works put more focus on optimizing the multiple pattern scenario. Atomic wedge [21] is proposed to monitor stream with a set of pre-defined patterns, which exploits the commonality among patterns. Sun et al. [18] extend atomic wedge for various length queries and tolerances. Lian et al. [11] propose a multi-scale segment mean (MSM) representation to detect static patterns over streaming time series. They discuss the batch processing optimization and the case of dynamic patterns in its following work [10]. Lim et al. [12] propose SSM-IS which divides long sequences into smaller windows. Although these techniques are proposed for streaming time series and some of them speed up the distance calculation between the pattern and the candidate, most of them focus on exploring the commonality and correlation among multiple patterns for pruning unmatched

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pattern candidates, which doesn't reduce the complexity brought by the problem of consecutive subpatterns matching.

Subsequence similarity search. FRM [5] is the first work for subsequence similarity search which maps data sequences in database into multidimensional rectangles in feature space. General Match [16] divides data sequences into generalized sliding windows and the query sequence into generalized disjoint windows, which focuses on estimating parameters to minimize the page access. Loh et al. [14] propose a subsequence matching algorithm that supports normalization transform. Lim et al. [13] address this problem by selecting the most appropriate index from multiple indexes built on different windows sizes. Kotsifakos et al. [9] propose a framework which allows gaps and variable tolerances in query and candidates. Wang et al. [20] propose DSTree which is a data adaptive and dynamic segmentation index on time series. This category of researches focuses on indexing the common features of *archived* time series, which is not optimized for pattern matching over the stream.

3 Problem Definition

Pattern P is a time series which contains n number of elements (p_1, \dots, p_n) . We denote the subsequence (p_i, \dots, p_j) of P by P[i : j]. Logically, P could be divided into several consecutive subpatterns which may have varied thresholds of matching deviation. Given a pattern P, P is divided into b number of non-overlapping subsequences in time order, represented as P_1, P_2, \dots, P_b , in which the k-th subsequence P_k is defined as the k-th subpattern and associated with a specified threshold ε_k .

As shown in Fig. 2(a), for instance, pattern P is composed of three subpatterns: $P_1 = P[1:4], P_2 = P[5:11]$ and $P_3 = P[12:15]$. These subpatterns may be specified different thresholds.

A streaming time series S is an ordered sequence of elements that arrive in time order. We denote a sliding window on S which starts with timestamp t by $W_t = (s_{t,1}, s_{t,2}, \dots, s_{t,n})$. We denote the the subsequence $(s_{t,i}, s_{t,i+1}, \dots, s_{t,j})$ in W_t by $W_t[i:j]$. According to the sub-pattern division of P, W_t is also divided into b sub-windows $W_{t,1}, W_{t,2}, \dots, W_{t,b}$. For convenience, we refer to p_i and $s_{t,i}$ as an element pair.

There are many distance functions such as DTW [3], LCSS [19], L_p -norm [23], etc. We choose L_p -norm distance which covers a wide range of applications [1][5][15]. Given two *n*-length sequences where $X = (x_1, x_2, \dots, x_n)$ and $Y = (y_1, y_2, \dots, y_n)$, the L_p -Norm Distance between X and Y is defined as follows:

$$L_p(X,Y) = \left(\sum_{i=1}^{n} |x_i - y_i|^p\right)^{\frac{1}{p}}$$

Since the L_{norm} is a distance function between two equal-length sequences, there are $|W_t| = n$ and $|W_{t,k}| = |P_k|$ for $k \in [1, b]$. In addition, we denote by $L_p[i:j]$ the normalized Euclidean distance between P[i:j] and $W_t[i:j]$. **Problem Statement:** Given a pattern P which contains b number of subpatterns P_1, P_2, \dots, P_b with specified thresholds $\varepsilon_1, \varepsilon_2, \dots, \varepsilon_b$. For a stream S, consecutive subpatterns matching is to find all sliding windows W_t on S, where it holds that $L_p(P_k, W_{t,k}) \leq \varepsilon_k$ for $k \in [1, b]$ (denoted by $W_{t,k} \prec P_k$).

4 Equal-Length Block

In this section, we first sketch a novel representation, Equal-Length Block(ELB), together with *Lower Bounding Property*, which enables us to process several successive windows together while guaranteeing no false dismissals. After that, we will introduce two ELB implementations in turn.

ELB representation is inspired by the following observation. To avoid false dismissals, a naive method is to slide the window over the stream by one element and calculates the corresponding distance, which is computationally expensive. However, one interesting observation is that in most real-world applications, the majority of adjacent subsequences of time series might be similar. This heuristic gives us the opportunity to process multiple successive windows together. Based on this hint, we propose Equal-Length Block (ELB), and the corresponding lower bounding property.

ELB divides the pattern P and the sliding window W_t into several disjoint w-length blocks while the last indivisible part can be safely discarded. The block division is independent of pattern subpatterns. A block may overlap with two or more adjacent subpatterns, and a subpattern may contain more than one block. The number of blocks is denoted by $N = \lfloor n/w \rfloor$. Based on the concept of block, P and W_t are split into $\hat{P} = \{\hat{P}_1, \dots, \hat{P}_N\}$ and $\hat{W}_t = \{\hat{W}_{t,1}, \dots, \hat{W}_{t,N}\}$ respectively, where \hat{P}_j (or $\hat{W}_{t,j}$) is the *j*-th block of P (or W_t), that is, $\hat{P}_j = \{p_{(j-1)\cdot w+1}, p_{(j-1)\cdot w+2}, \dots, p_{j\cdot w}\}$, similarly for $\hat{W}_{t,j}$. As shown in Fig. 2(b), we set w = 3, thus P and W_t are divided into 5 blocks. Based on blocks, each pattern block \hat{P}_j is represented by a pair of bounds, upper and lower bounds, which are denoted by \hat{P}_j^u and \hat{P}_j^l respectively. Each window block $\hat{W}_{t,j}$ is represented by a feature value, denoted by $\hat{W}_{t,j}^f$.

It is worth noting that the ELB representation is only an abstract format description, which doesn't specify how to compute upper and lower bounds of \hat{P}_j and the feature of window $\hat{W}_{t,j}$. We can design any ELB implementation, which just needs to satisfy the following lower bounding property:

Definition 1. (Lower Bounding Property): given \hat{P} and \hat{W}_t , if $\exists i \in [0, w)$, W_{t+i} is a result of consecutive subpatterns matching of P, then $\forall j \in [1, N]$, $\hat{P}_j^l \leq \hat{W}_{t,j}^f \leq \hat{P}_j^u$ (marked as $\hat{W}_{t,j} \prec \hat{P}_j$).

We first provide our matching algorithm based on ELB which satisfies lower bounding property before introducing our ELB implementation. Instead of processing sliding windows one-by-one, lower bounding property enables us to process w successive windows together in the pruning phase. Given N number of window blocks $\{\hat{W}_{t,1}, \dots, \hat{W}_{t,N}\}$, if anyone in them (e.g. $\hat{W}_{t,j}$) doesn't match 6 R. Kang et al.

its aligned pattern block (\hat{P}_j correspondingly), we could skip w consecutive windows, $W_t, W_{t+1}, \cdots, W_{t+w-1}$, together. Otherwise, the algorithm takes these w windows as candidates and calculate exact distances one by one. The lower bounding property enables us to extend the sliding step to w while guaranteeing no false dismissals. The critical challenge is how to design ELB implementation which is both computationally efficient and effective to prune sliding windows.

4.1 Element-based ELB Representation

In this section, we present the first ELB implementation, element-based ELB, denoted by ELB_{ele} . The basic idea is as follows. According to our problem statement, if window W_t matches P, for any subpattern P_k and corresponding $W_{t,k}$, their L_p -Norm distance holds that:

$$L_p(W_{t,k}, P_k) \leqslant \varepsilon_k \tag{1}$$

It's easy to infer that any element pair p_i together with $s_{t,i}$, which falls into the k-th subpattern, satisfies that:

$$|s_{t,i} - p_i| \leqslant \varepsilon_k \tag{2}$$

In other words, if $s_{t,i}$ falls out of the range $[p_i - \varepsilon_k, p_i + \varepsilon_k]$, we know that W_t cannot match P.

Based on this observation, we construct two envelope lines for pattern P, as illustrated in Fig. 3(b). The upper line $U = \{U_1, U_2, \dots, U_n\}$ and the lower line $L = \{L_1, L_2, \dots, L_n\}$ are defined as follows, $1 \leq i \leq n$:

$$\begin{cases} U_i = p_i + \varepsilon_k \\ L_i = p_i - \varepsilon_k \end{cases}$$
(3)

The envelope guarantees that if $s_{t,i}$ falls out of $[L_i, U_i]$, we know that W_t cannot match P.

Now we consider how to construct ELB implementation satisfying the lower bounding property, i.e., how to construct upper/lower bounds of pattern block and the feature of window block so that we could prune w number of successive windows together. We show the basic idea with an example in Fig. 3(a). Assume w = 3 and N = 5. At the sliding window W_t , element $s_{t,9}$ aligns with p_9 . Accordingly, in W_{t+1} (or W_{t+2}), $s_{t,9}$ aligns with p_8 (or p_7). Obviously, if $s_{t,9}$ falls out of all upper and lower envelopes of p_9 , p_8 and p_7 , these 3 corresponding windows can be pruned together. Note that $s_{t,9}$ is the last element of block $\hat{W}_{t,3}$, and only in this case, all three elements of P aligning with $s_{t,9}$ belong to a same pattern block \hat{P}_3 . Based on this observation, we define \hat{P}_i^u , \hat{P}_i^l and \hat{W}_i^f as follows:

$$\begin{cases}
\hat{P}_{j}^{u} = \max_{0 \leq i < w} (U_{j \cdot w - i}) \\
\hat{P}_{j}^{l} = \min_{0 \leq i < w} (L_{j \cdot w - i}) \\
\hat{W}_{t,j}^{f} = last(\hat{W}_{t,j}) = s_{t,j \cdot w}
\end{cases}$$
(4)



Fig. 3: (a) The element $s_{t,9}$ aligns with p_9, p_8 and p_7 at W_t, W_{t+1} and W_{t+2} respectively. (b) \hat{P}_i^u and \hat{P}_i^l are constructed by U and L.

As shown in Fig. 3(b), for each pattern block, its upper and lower bounds are set to the maximum and minimum of its two envelope lines respectively. It's obvious that ELB_{ele} satisfies the lower bounding property.

4.2 Subsequence-based ELB Representation

In this section, we introduce the second ELB implementation, subsequence-based ELB, denoted by ELB_{seq} . Compared to ELB_{ele} , ELB_{seq} has a tighter bound which brings higher pruning power, although it is a little costlier on computing features of window blocks.

Different from ELB_{ele} which uses the tolerance of the whole subpattern to constrain one element pair, in ELB_{seq} , we use the same tolerance to constrain a *w*-length subsequence. Referring to [10], given two sequences $X = (x_1, \dots, x_w)$ and $Y = (y_1, \dots, y_w)$, it holds that:

$$w |\mu_x - \mu_y|^p \leqslant \sum_{i=1}^{w} |x_i - y_i|^p$$
 (5)

where μ_x and μ_y are the mean values of X and Y. This theorem allows us to construct upper/lower envelope with the mean value of the subsequence.

Consider two *w*-length subsequences P[i':i] and $W_t[i':i]$ where i' = i - w + 1 $(i' > 0 \text{ so } i \ge w)$. We first consider the case that all elements in P[i':i](or $W_t[i':i]$) belongs to only one subpattern(like P_k) and the corresponding subwindow(like $W_{t,k}$). If $W_{t,k}$ matches P_k , referring to Eq. 1, we know that:

$$L_p(P[i':i], W_t[i':i])^p = \sum_{j=i'}^i (p_j - s_{t,j})^p \leqslant \varepsilon_k^p \tag{6}$$

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We denote by $\mu_{P[i':i]}$ and $\mu_{W_t[i':i]}$ that the mean value of P[i':i] and $W_t[i':i]$ respectively. By combining Eq. 5 and Eq. 6, we have:

$$|\mu_{P[i':i]} - \mu_{W_t[i':i]}| \leqslant (\frac{1}{w} \varepsilon_k^p)^{1/p}$$
(7)

We construct the envelope of pattern P as follows, $w \leq i \leq n$:

$$\begin{cases} U_i = \mu_{P[i':i]} + (\frac{1}{w}\varepsilon_k^p)^{1/p} \\ L_i = \mu_{P[i':i]} - (\frac{1}{w}\varepsilon_k^p)^{1/p} \end{cases}$$

$$\tag{8}$$

Now we consider the case that the interval [i':i] overlaps with more than one subpattern. Suppose P[i':i] overlaps with $P_{k_l}, P_{k_l+1}, \dots, P_{k_r}$. Due to the additivity of the *p*-th power of L_p -Norm, we deduce from Eq. 6 that:

$$L_p(P[i':i], W_t[i':i])^p = \sum_{j=i'}^{i} (p_j - s_{t,j})^p \leqslant \sum_{k=k_l}^{k_r} \varepsilon_k^p$$
(9)

By combining Eq. 5 and Eq. 9, we have that:

$$|\mu_{P[i':i]} - \mu_{W_t[i':i]}| \leqslant \left(\frac{1}{w} \sum_{k=k_l}^{k_r} \varepsilon_k^p\right)^{1/p} \tag{10}$$

We denoted the right term as $\theta_{seq}(i)$ and provide the general case of the pattern envelope as follows, $w \leq i \leq n$:

$$\begin{cases} U_i = \mu_{P[i':i]} + \theta_{seq}(i) \\ L_i = \mu_{P[i':i]} - \theta_{seq}(i) \end{cases}$$
(11)

Note that Eq. 8 is the special case of Eq. 11.

The construction of upper and lower bounds are very similar to ELB_{ele} , while the feature of window block is adopted to the mean value. We show the basic idea with an example in Fig. 4(a). At the sliding window W_t , the subsequence $W_t[7:9]$ aligns with P[7:9]. Similarly, in W_{t+1} (or W_{t+2}), this subsequence aligns with P[6:8] (or P[5:7]). According to Eq. 11, we know that if the mean value of $W_t[7:9]$ falls out of all upper and lower bounds of P[7:9], P[6:8] and P[5:7], these 3 corresponding windows can be pruned together. Based on this observation, we give the formal implementation of ELB_{seq} as follows:

$$\begin{cases} \hat{P}_{j}^{u} = \max_{0 \leq i < w} (U_{j \cdot w - i}) \\ \hat{P}_{j}^{l} = \min_{0 \leq i < w} (L_{j \cdot w - i}) \\ \hat{W}_{t,j}^{f} = mean(\hat{W}_{t,j}) = \mu_{W_{t}[(j-1) \cdot w + 1 : j \cdot w]} \end{cases}$$
(12)

Note that, the upper and lower bounds of \hat{P}_1 are meaningless according to the definition of the envelope of ELB_{seq} .

Figure 4(b) provides an example of ELB_{seq} implementation. For clarity, we only illustrate the bounds of \hat{P}_3 . The lower bound \hat{P}_3^l is set to the minimum of L_7, L_8 and L_9 and covers 3 successive windows W_t, W_{t+1} and W_{t+2} .



Fig. 4: (a) The subsequence $W_t[7:9]$ aligns with P[7:9], P[6:8] and P[5:7] at W_t, W_{t+1} and W_{t+2} respectively. (b) \hat{P}_i^u and \hat{P}_j^l are constructed by U and L.

4.3 Complexity Analysis

We first analyze ELB_{ele} . For each block $\hat{W}_{t,j}$, the time complexities of computing feature and determining $\hat{W}_{t,j} \prec \hat{P}_j$ are both O(1). Therefore, the amortized pruning cost of ELB_{ele} is O(1/w). Its space complexity is $O(N) = O(\lfloor n/w \rfloor)$. Although ELB_{ele} is very efficient, it constrains one element pair with the tolerance of the whole subpattern, which makes the envelope loose. Its pruning effectiveness is better when thresholds are relatively small, or pattern deviates from the normal stream far enough.

 ELB_{seq} calculates the mean value of each window block with O(w) and determining $\hat{W}_{t,j} \prec \hat{P}_j$ with O(1). Considering a window block appears in several consecutive sliding windows, we store feature values in memory to avoid repeated calculation. Therefore, the amortized pruning cost of ELB_{seq} is reduced to O(1). Same as ELB_{ele} , the space complexity of ELB_{seq} is O(N).

5 Experimental Evaluation

In this section, we first describe datasets and experimental settings in Sect. 5.1 and then present the results of performance evaluation comparing the brute-force approach Sequential Scanning(SS), the classic method MSM [10] and our two approaches based on ELB_{ele} (ELB-ELE) and ELB_{seq} (ELB-SEQ) respectively. As presented in Sect. 2, although there are many works after MSM addressing time series similarity matching, most of them focus on utilizing the commonality among multiple patterns to build indexes, but not speeding up the problem of matching stream with a list of consecutive subpatterns.

Our goal is to:

– Demonstrate the efficiency of our approach on all L_p -Norm distance and different thresholds.

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- Demonstrate the robustness of our approach on different pattern occurrence probabilities.
- Investigate the impact of block size on performance which helps to choose the appropriate parameter.

5.1 Experimental Setup

The experiments are conducted on both synthetic and real-world datasets.

Datasets. Real-world datasets are collected from a wind turbine manufacturer, where each wind turbine has hundreds of sensors generating streaming time series with sampling rate from 20 ms to 7s. Our experimental datasets are from 3 turbines. In each turbine, we collect data of 5 sensors including wind speed, wind deviation, wind direction, generator speed and converter power. We replay the data as streams with total lengths of 10^8 . For each stream, a pattern containing consecutive subpatterns with thresholds is given by domain experts.

Synthetic datasets are constructed based on UCR Archive [7]. UCR Archive is a popular time series repository, which includes a set of datasets widely used in time series mining researches [2,8,10]. To simulate patterns with various lengths, we select four datasets, Strawberry (Straw for short), Meat, NonInvasiveFatalECG_Thorax1 (ECG for short) and MALLAT whose time series lengths are 235, 448, 750 and 1024. Referring to [10], for each selected UCR dataset, we choose the first time series of class 1 as the pattern and divide it into several subpatterns according to its shape and trend. Numbers of subpatterns of these four datasets are 5, 6, 8 and 7 respectively.

Concerning threshold of synthetic datasets, we define *threshold_ratio* as the ratio of the average threshold to the value range of this subpattern. Given a *threshold_ratio* and a subpattern P_k , the L_p -Norm threshold of P_k is defined by:

$$\varepsilon_k = |P_k|^{1/p} \times threshold_ratio \times value_range(P_k)$$

In practice, we observe that *threshold_ratio* being larger than 30% indicates that the average deviation from a stream element to its aligned pattern element is more than 30% of its value range. In this case, the candidate may be quite different from given pattern where similarity matching becomes meaningless. Therefore, we vary *threshold_ratio* from 5% to 30% in Sect. 5.2.

As for streaming data of synthetic datasets, referring to [2], we first generate a random walk time series S with length of 10⁸ for each UCR dataset. Element s_i of S is $s_i = R + \sum_{j=1}^{i} (\mu_j - 0.5)$, where μ_j is a uniform random number in [0,1]. As value ranges of the four patterns are about -3 to 3, we set R as the mean value 0. Then we randomly embed some time series of class 1 of each UCR dataset into corresponding steaming data with certain occurrence probabilities. **Algorithm**. We compare our approaches to SS and MSM [10]. SS matches the sliding window one by one. For each window, SS calculates the L_p -Norm distances between all subpatterns and subwindows sequentially. In our scene, we let MSM build hierarchical grid index for each subpattern. For fair comparison, we adopt its batch version where the batch size is equal to ELB block size. We perform three schemes of MSM to choose the best one: stop the pruning phase at the first level of grid index(MSM-1), the second level (MSM-2), or never early stop the pruning phase(MSM-MAX).

Default Parameter Settings. There are three parameters for datasets: distance function, threshold and pattern occurrence probability. There is a parameter for our algorithm: block size. The default distance function is set to L_2 -Norm (i.e., Euclidean distance). The default value of *threshold_ratio* and pattern occurrence probability are set to 20% and 10^{-4} respectively. We set the default value of block size to 5% of the pattern length. The impact of all above parameters will be investigated in following sections.

Performance Measurement. We regard the brute-force method SS as the baseline and measure the speedup of MSM and our algorithms. Streams and patterns are loaded into memory in advance where data loading time is excluded. To avoid the inaccuracy due to cold start and random noise, we run all algorithms over 10,000 ms and average them by their cycle numbers. All experiments are run on 4.00 GHz Intel(R) Core(TM) i7-4790K CPU, with 8GB physical memory.

5.2 Performance Analysis

In this set of experiments, we first show our algorithms together outperform compared approaches on both synthetic and real-world datasets under different L_p -Norm functions and provide detailed analysis. After that, we perform experiments on diverse synthetic datasets by varying threshold ratio and pattern occurrence probability to demonstrate efficiency and robustness of our approaches. At last, we also evaluate the impact of block size for optimal parameter determination.

Performance under Different L_p -Norm Distance In this section, we report experiments of ELB-ELE and ELB-SEQ comparing to SS and MSM under different distance functions. We performed these experiments on all real-world and synthetic datasets using L_p -Norm where $p = 1, 2, 3, \infty$.

Figure 5 shows the experimental results. For real-world datasets, the results are similar among different turbines, so we only illustrate the wind turbine 1. Our algorithms show a great advantage over MSM and SS. As the distance function varies from L_1 -Norm to L_{∞} -Norm, the advantage of our approaches over other methods gets larger.

We provide the experimental detail on a wind generator dataset in Table 1. The first two columns present the total and pruning time on each sliding window. Column *pruning power* is the percentage of pruned windows. Comparing to SS, our algorithms could prune numerous windows in the pruning phase, while SS has to perform exact matching for each sliding window, resulting in high time cost. Regarding MSM, its pruning power gets better from MSM-ONE to MSM-MAX (increased from 98.20% to 99.96% in L_1 -Norm). Although MSM is more accurate, our pruning phase is much more efficient than MSM. Concerning ELB_SEQ and MSM_TWO (the best one among three MSM schemes) on L_1 -Norm, our approach has slightly lower pruning power (97.16% vs. 99.89%), yet



Fig. 5: Speedup vs. L_p -Norm. s_1 : wind speed, s_2 : wind deviation, s_3 : wind direction, s_4 : generator speed, s_5 : converter power.

Algorithm	L_1 -Norm			L_{∞} -Norm		
	total	pruning	pruning	total	pruning	pruning
	time(ns)	time(ns)	power(%)	time(ns)	time(ns)	power(%)
ELB_SEQ	13.04	0.52	97.16	8.78	0.41	97.43
ELB_ELE	146.10	0.51	6.48	10.78	0.30	96.18
MSM_ONE	556.39	543.15	98.20	691.11	667.34	87.05
MSM_TWO	548.42	547.40	99.89	670.51	668.73	99.21
MSM_MAX	549.43	548.94	99.96	682.40	682.00	99.97
SS	562.84	-	-	413.34	-	-

Table 1: The Detail statistics on wind generator dataset

much more efficient pruning cost(0.52 vs. 547.40). On the whole, ELE_SEQ has an advantage of more than one order of magnitude over MSM_TWO.

Now we analyze the different performance of ELB on different L_p -Norm. From L_1 -Norm to L_{∞} -Norm, the pruning effectiveness of ELB gets better. Although ELB-ELE spends less time on pruning phase than ELB-SEQ, its pruning power is very low at L_1 -Norm (6.48%) due to its too loose bound. As p increases, its bound becomes tighter and performance gets better. In the case of L_{∞} -Norm, its performance has been flat with, and even outperformed ELB-SEQ on several datasets, as shown in Fig. 5(d) and (h). In contrast to ELB-ELE, ELB-SEQ is efficient under all L_p -Norms.

Impact of Distance Threshold In this section, we compare the performance of ELB-ELE, ELB-SEQ, SS and MSM under different thresholds. We vary *threshold_ratio* from 5% to 30% on synthetic datasets, as described in Sect. 5.1.



Fig. 7: Speedup vs. pattern occurrence probability.

The result on synthetic datasets is shown in Fig. 6. The performances of our two algorithms are very similar in synthetic datasets. Both ELB-ELE and ELB-SEQ outperforms MSM and SS by orders of magnitude. As the threshold gets larger, the speedups of ELB-ELE and ELB-SEQ decrease slightly. Nevertheless, our algorithms keep their advantage over other approaches even though threshold_ratio increases to 30%.

Impact of Pattern Occurrence Probability In this section, we further examine the performance by varying the pattern occurrence probability. When the probability becomes lower, more windows are filtered out in the pruning phase. In contrast, when the probability becomes higher, more windows enter the postprocessing phase. A good approach should be robust to these situations.

We perform this experiment on synthetic datasets and vary the occurrence probability over $\{10^{-3}, 5 \times 10^{-4}, 10^{-4}, 5 \times 10^{-5}, 10^{-5}\}$. The largest probability is set to 10^{-3} since in this case, the stream of MALLAT, which has largest pattern length, has been filled up by embedded UCR time series. As illustrated in Fig. 7, Our algorithms outperform MSM and SS in all examined probabilities. Furthermore, our algorithms show a larger speedup when the pattern occurrence probability becomes lower. This experiment demonstrates the robustness of our algorithms over different occurrence probabilities.

Impact of Block Size The block size is an important parameter affecting the pruning power of our approach. In this experiment, we investigate the effect of block size by comparing ELB-ELE, ELB-SEQ and MSM on both synthetic and





Fig. 8: Speedup vs. block_ratio.

real-world datasets. We vary the ratio of the block size to the pattern length from 1% to 40%. A ratio being larger than 50% indicates that the entire pattern contains only one block, which makes ELE-SEQ meaningless.

Figure 8 shows the experimental results on some representative synthetic and real-world datasets while the rest are consistent. A too small or too large block size results in performance degradation. In detail, a smaller block size leads to a tighter bound for each block which improves the pruning effectiveness. Nevertheless, a small block size, corresponding to a small sliding step, results in more block computation and higher cost in the pruning phase. A larger block size may bring less block computation, but a looser bound meanwhile. The loose bound incurs degradation of the pruning effectiveness. In practice, our algorithms achieve the optimal performance when the block ratio is about 5% to 10%.

6 Conclusion

In this paper, we propose a new problem, called "consecutive subpatterns matching", which allows users to specify a pattern containing a list of consecutive subpatterns with different distance thresholds. We present a novel ELB representation to prune sliding windows efficiently under all L_p -Norms. We conduct extensive experiments on both synthetic and real-world datasets to illustrate that our algorithm outperforms the baseline solution and prior-arts.

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