TrieMotif

A New and Efficient Method to Mine Frequent K-Motifs from Large Time Series

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Abstract: Finding previously unknown patterns that frequently occur on time series is a core task of mining time series. These patterns are known as time series motifs and are essential to associate events and meaningful occurrences within the time series. In this work we propose a method based on a trie data structure, that allows a fast and accurate time series motif discovery. From the experiments performed on synthetic and real data we can see that our TrieMotif approach is able to efficiently find motifs even when the size of the time series goes longer, being in average 3 times faster and requiring 10 times less memory than the state of the art approach. As a case study on real data, we also evaluated our method using time series extracted from remote sensing images regarding sugarcane crops. Our proposed method was able to find relevant patterns, as sugarcane cycles and other land covers inside the same area.

1 INTRODUCTION

The large volume of time series continually generated by a variety of sensors, climate models and stock markets demands fast methods to take advantage of such amount of data. The information contained in time series databases is a rich source for decision making tasks demanded by the owners of such data. One of the main tasks when mining time series is to find the motifs present therein, that is, to find patterns that frequently occurs in time series. By finding motifs, it is possible to mine association rules aimed at spotting patterns indicating that some events frequently lead to others.

Existing applications involving time series, such as stock market analysis, are not yet able to record all the factors that govern the data organized in the time series, such as political and technological factors. On the contrary, climate variations nowadays have most of its governing factors being recorded, using sensing equipments such as satellites and ground-based weather stations. However, the diversity of data available makes it hard to discover complex patterns that can support more robust analyzes. In this scenario, finding motifs assumes an even greater importance.

In this work we took advantage of real time series extracted from remote sensing imagery containing Normalized Difference Vegetation Index (NDVI) measurements. The NDVI time series present the vegetative strength of the plantation (Rouse et al., 1973). To follow the development of a crop is strategic for agribusiness practices in Brazil, since agriculture is the country's main asset. The accurate monitoring of agriculture in the whole world have become more and more important specially due to climate change impacts. The "food safety" issue has concerned governments from several countries and the development of new technologies for monitoring, as well as the proposition of mitigation and adaptation measures, are crucial. In this sense, remote sensing can be an important tool to improve the fast detection of changes in the land cover besides to aid at monitoring the crop cycle.

Since the volume of time series databases as well as the length of the series is growing at a very fast pace, it is mandatory to develop algorithms and methods that can deal with time series in the scenario of big data. In this paper we present a new method to extract motifs from time series and a new algorithm to index them in a trie data structure that performs well over large time series, which is up to 3 times faster than the state-of-the-art method. We evaluated

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the proposed TrieMotif over both synthetic and real time series and obtained very promising results.

This paper is organized as follows. Section 2 summarizes the main concepts used as the basis to develop our work. Section 3 describes our proposed method and Section 4 discusses its evaluation. Section 5 shows the TrieMotif performance on real data obtained from remote sensing images and Section 6 concludes this paper.

2 BACKGROUND AND RELATED WORKS

A time series motif is a pattern that occur frequently. They were first defined in (Lin et al., 2002) and a generalized definition was given in (Chiu et al., 2003). In this section we recall these definitions and notations, as they will be used in this paper. First we begin with a definition of time series:

Definition 1. *Time Series:* A time series $T = t_1, \ldots, t_m$ is an ordered set of m real-valued variables.

Since we want to find patterns that frequently occur along a time series, we will not work with the whole time series, we are aiming only at parts of a time series, which are called subsequences and are defined as follows.

Definition 2. *Subsequence:* Given a time series T of length m, a subsequence S_p of T is a sampling of length $n < m$ of contiguous positions from T beginning at position p, that is, $S_p = t_p, \ldots, t_{p+n-1}$ for $1 \leq p \leq m-n+1$.

In order to find frequent patterns, we need to define a matching between patterns.

Definition 3. *Match:* Given a distance function $D(S_p, S_q)$ between two subsequences, a positive real number R (*range*) and a time series T containing a subsequence S_p and a subsequence S_q, if $D(S_p, S_q) \leq R$ then S_q is called a *matching* subsequence of S_p.

On subsequences of the same time series, the best matches are probably subsequences that are slightly shifted. Matching between two overlapped subsequences is called a trivial match. Figure 1 illustrates the idea of a trivial match. The trivial match is defined as follows:

Definition 4. *Trivial Match:* Given a time series T, containing a subsequence S_p and a matching subsequence S_q, we say that S_q is a *trivial match* to S_p if either $p = q$ or if there is no subsequence $S_{q'}$ beginning at q' such that $D(S_p, S_{q'}) > R$, and either $q < q' < p$ or $p < q' < q$. That is, if two subsequences overlaps, there must exist a subsequence between them that is not a match.

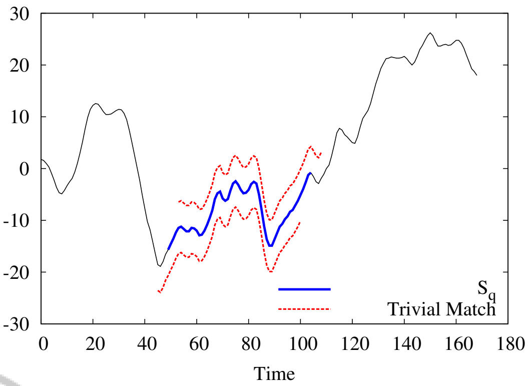


Figure 1: The best matches of a subsequence S_q are probably the trivial matches that occur right before or after S_q.

These definitions allow defining the Frequent K-Motif problem. First, all subsequences are extracted using a sliding window. Then, since we are interested in patterns, each subsequence is z-normalized to have zero mean and one standard deviation (Keogh and Kasetty, 2003). The K-Motif is defined as follows.

Definition 5. *Frequent K-Motifs:* Given a time series T, a subsequence of length n and a range R, the most significant motif in T (*1-Motif*) is the subsequence $F^{\{1\}}$ that has the highest count of non-trivial matches. The K^{th} most significant motif in T (*K-Motif*) is the subsequence $F^{\{K\}}$ that has the highest count of non-trivial matches, and satisfies $D(F^{\{K\}}, F^{\{i\}}) > 2R$, for all $1 \leq i < K$.

The Nearest Neighbor motif was defined by Yankov et al. (Yankov et al., 2007), and it represents the closest pair of subsequences. In our proposed work, we focus on the Frequent K-Motif problem and we will be referring to them as K-Motif. Since the K-Motifs are unknown patterns, a brute-force approach would compare every subsequence with each other. This approach has quadratic computational cost since it requires O(m^2) calls to the distance function.

An approach to reduce the complexity of this problem employs dimensionality reduction and discretization of the time series (Lin et al., 2002). The SAX (Symbolic Aggregate approXimation) technique allows time series of size n to be represented by strings of arbitrary size w ($w < l$) (Lin et al., 2003). For a given time series, SAX consists of the following steps. Firstly, the time series is z-normalized, so that the data follow normal distribution (Goldin et al., 1995). Next, the normalized time series is converted into the Piecewise Aggregate Approximation (PAA) representation, decreasing the time series dimensionality (Keogh et al., 2001). The time series is then replaced with w values corresponding to the average of the respective segment. Thus, in the PAA representation, the time series is divided into w continuous segments of equal length. Finally, the PAA representation is discretized into a string with an alphabet of size $a > 2$. Figure 2 shows an example of a time series subsequence of size $n = 128$ discretized using SAX with $w = 8$ and $a = 3$. It is also possible to compare two SAX time series using the MINDIST function. The MINDIST lower bounds the Euclidean distance (Lin et al., 2007), warranting no false dismissals (Faloutsos et al., 1994).

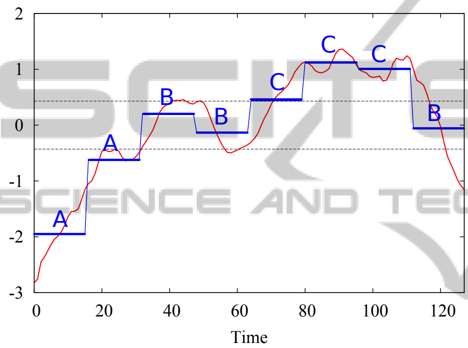


Figure 2: A time series subsequence of size $n = 128$ is reduced to a PAA representation of size $w = 8$ and then is mapped to a string of $a = 3$ symbols *AABBCCCB*.

Chiu et al. proposed a fast algorithm based on Random Projection (Chiu et al., 2003). Each subsequence of a time series is discretized using SAX. The discretized subsequences are mapped into a matrix, where each row points back to the original position of the subsequence on the time series. Then, the algorithm uses the random projection to compute a collision matrix, which counts the frequency of subsequence pairs. Through the collision matrix, the subsequences are checked on the original domain seeking for motifs. Although fast, the collision matrix is quadratic on the length of the time series, requiring a high amount of memory. Also using the SAX discretization, Li and Lin (Li and Lin, 2010; Li et al., 2012) proposed a variable length motif discovery based on grammar induction. Catalano et al. (Catalano et al., 2006) proposed a method that works on the original domain of the data. The motifs are discovered in linear time and constant memory costs using random sampling. However, this approach can lead to poor performance for long time series with infrequent motifs (Mohammad and Nishida, 2009).

Several works proposed to solve the motif discovery problem taking advantage of tree data structures. Udechukwu et al. proposed an algorithm that uses a suffix tree to find the Frequent Motif (Udechukwu et al., 2004). The time series are discretized considering the slopes between two consecutive measures. The symbols are chosen according to the angle between the line joining the two points and the time axis. Although this algorithm do not require to set the length of the motif, the algorithm is affected by noise. A suffix tree was also used to find motifs in multivariate time series (Wang et al., 2010). Keogh et al. solved a similar problem to the motif discovery using a trie structure to find the most unusual subsequence in a time series (Keogh et al., 2007).

Our proposed TrieMotif algorithm is up to 3 times faster and requires up to 10 times less memory than the state-of-the-art approach, because TrieMotif selects only the candidates that are most probably a match to a motif. Using this approach, TrieMotif reduces the number of unnecessary distance calculations.

3 OUR PROPOSAL: TrieMotif ALGORITHM

In this section we present the TrieMotif algorithm, which aims at finding the top K-Motifs. The TrieMotif algorithm consists of three stages:

- First, all subsequences are extracted from the time series and converted into a symbolic representation;
- The subsequences are indexed using a Trie and a list of possible non trivial matches (candidates) are generated for each subsequence using the Trie index;
- The distances between the motif candidates on the original time series are calculated.

On the first stage, all subsequences S_i of size n are extracted using a sliding window and are z-normalized. These subsequences pass through a dimensionality reduction process to reduce the computational cost on the next stage. A subsequence of size n can be represented as a sequence of size w, via the PAA algorithm. On the next step of this stage, subsequences are converted into a symbolic representation. This representation is obtained by dividing the interval of the subsequence values into a equal size bins, where each bin receives a symbol. Each value in the subsequence is converted into the symbol of the corresponding bin. Figure 3 shows an example that converts a subsequence S of size $m = 128$ and values between $[-2.83, 1.36]$ into a string of size $w = 8$

using an alphabet a of 3 symbols. Initially the subsequence passes through a dimensionality reduction via PAA with $w = 8$. Then, assuming $a = 3$, three bins are created: $A = [-2.83, -1.43)$, $B = [-1.43, -0.03)$ and $C = [-0.03, 1.36]$. Notice, that we kept the zero mean and the standard deviation requirements. Finally, the symbolic representation of S is $\hat{S} = ABCBCCCB$.

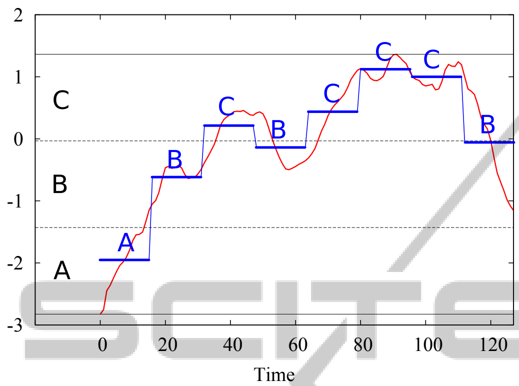


Figure 3: A time series subsequence of size $m = 128$ is converted into a string of $a = 3$ symbols and size $w = 8$.

To find the top K-Motifs, the brute force algorithm would calculate the distance of each subsequence S_q to every other subsequence. Our proposal reduces the number of distance calculations by selecting only candidates S_i that may be a match – the trivial matches are discarded on the next stage. To select the candidates we index all subsequences (already represented as a string) in a trie. For example, consider the subsequences S_1, S_2, S_3 and S_4, $w = 4$ and $a = 4$, as shown in Figure 4. As they are processed in the first stage, they become $\hat{S_1} = AABD$, $\hat{S_2} = BABD$, $\hat{S_3} = ABDA$ and $\hat{S_4} = DCCA$ respectively. Figure 5 shows how the trie is built.

An exact search on the trie would return candidates faster, but some candidates S_i that are a match could be discarded. If we search for candidates of $\hat{S_1}$, although $\hat{S_2}$ is probably a match, it would not be selected. To solve this problem, we modified the exact search on the trie to a range-like search. On the exact search, when the algorithm is processing the j^{th} element of $\hat{S_q}$ ($\hat{S_q}[j]$), it only visits the path of the trie where $Node_{symbol} = \hat{S_q}[j]$. In our proposed approach, we associate numerical values to the symbols. For example, A is equal to 1, B is equal to 2, and so on. Therefore, we can take advantage of closer values to compute the similarity when comparing the symbols. On our modified search, the algorithm also visits paths where $|\hat{S_q}[j] - Node_{symbol}| \leq \delta$. That is, if $\hat{S_q}[j] = B$ and $\delta = 1$, the algorithm visits the paths of A, B and C (one up or one down). As backtracking all possible paths might be computationally expensive, we exploit pruning of unwanted paths by indexing the elements of the strings in a non-sequential order. This approach is interesting, because time series measures over a short period tend to have similar values. For example, if in a given time there is a B symbol, probably the next symbol might be A, B or C (even in large alphabets). Taking that into account, we interleave elements from the beginning and the end of the string, i.e, the first symbol, then the last symbol, then the second and so on.

Figure 5 shows how the modified search behave when searching for candidates to $\hat{S_1}$. On the first level, $\hat{S_1}[1] = A$ and the algorithm will visit the paths of the symbols A and B. On the next level, $\hat{S_1}[4] = D$ and it will visit the paths of C and D. This process is repeated until it reaches a leaf node. In this example, it will return the candidates $\hat{S_1}$ and $\hat{S_2}$, but $\hat{S_3}$ and $\hat{S_4}$ will not be checked. Figures 5 and 6 also show that changing the order of the elements can reduce the backtracking. If the subsequences were indexed using the sequential order, our modified search would also visit the path of $\hat{S_3}$ for at least one more level, while changing the order, this path is never visited.

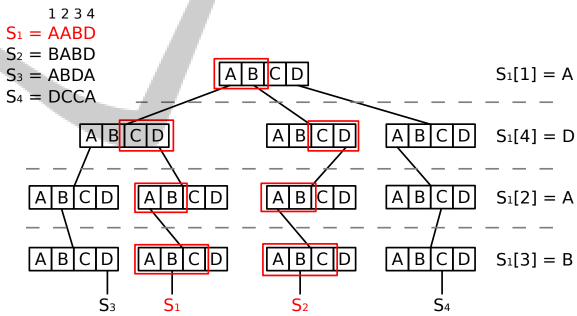


Figure 5: By selecting candidates using our modified search, the algorithm backtracks only on nodes of the paths of the strings $\hat{S_1}$ and $\hat{S_2}$.

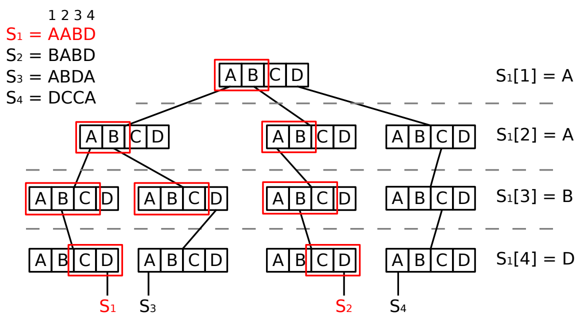
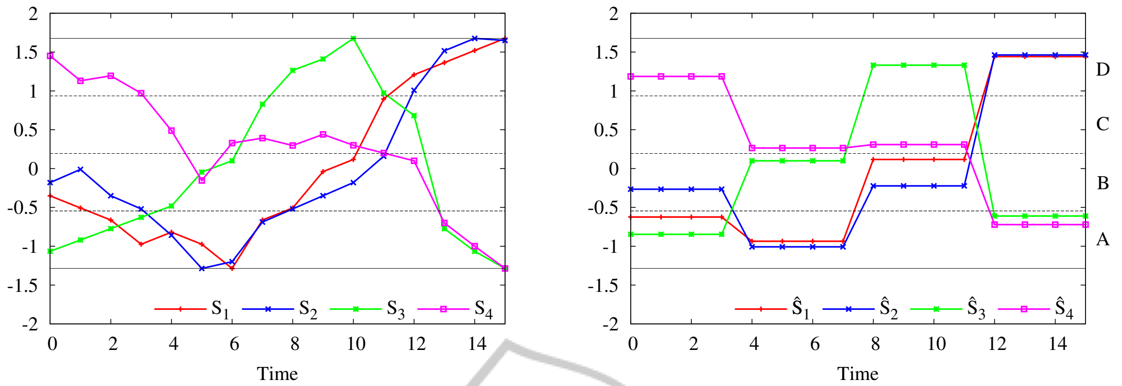


Figure 6: Creating the trie index using normal order increases the backtracking, since the algorithm visits part of the path of the string $\hat{S_3}$.

The basic idea of this stage is shown in Figure 7. Non-trivial matches subsequences S_i might have values near S_q, so basically, the range search algorithm



(a) Original time series. (b) PAA representantion.

Figure 4: Symbolic conversion process of the subsequences S_1, S_2, S_3 and S_4 to the strings $\hat{S_1} = AABD$, $\hat{S_2} = BABD$, $\hat{S_3} = ABDA$ and $\hat{S_4} = DCCA$.

sets an upper and a lower limit to define an area containing these subsequences.

On the last stage, after obtaining a list of candidates for each S_q, we calculate the distance between S_q and S_i on the original time series domain, discarding trivial matches of S_q. On this stage we also make sure that the K-Motifs satisfy Definition 5.

Algorithm 1 shows the TrieMotif algorithm to locate the top K-Motifs. First, all subsequences S_i are converted into a symbolic representation $\hat{S_i}$ and every $\hat{S_i}$ is indexed in the Trie index. Through the Trie index, we can reduce the number of non-trivial match calculations by generating a set C of the possible candidates for every $\hat{S_i}$. Then, we check on the original time series domain if the subsequences C_j in C satisfies $D(S_i, C_j) \leq R$ and it is not a trivial match. Since it is not possible to know the top K most frequent motifs before computing every subsequence, we store the motif on a list ($ListOfMotif$). On the last step of the algorithm, we also need to check if the top K-Motifs satisfies the Definition 5. To do so, we sort the $ListOfMotif$ by the number of non-trivial matches in decreasing order. Thus, the most frequent motifs appear on the beginning of the list. Thereafter we iterate through the sorted $ListOfMotif$ and whenever $F^{\{i\}}$ satisfies the Definition 5, we insert $F^{\{i\}}$ in the result set $TopKMotif$, otherwise $F^{\{i\}}$ is discarded.

To improve the efficiency of the method, we also calculate every distance using the "early abandonment" approach. Note that, although we presented a method to discretize the time series subsequences, the TrieMotif algorithm also support others symbolic discretizations, such as the SAX algorithm. In those cases, and if the distance function is the Euclidean one, it is possible to take advantage of the low complexity of the $MINDIST$ and discard calculations on the original time series whenever $MINDIST(\hat{S_q}, \hat{S_i}) >$

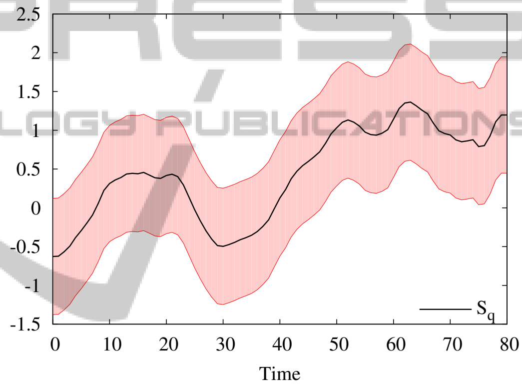


Figure 7: Subsequences S_i that satisfy $D(S_q, S_i) \leq R$ are possibly in the highlighted area.

R, since the $MINDIST$ is a lower bound to the Euclidean distance.

4 SYNTHETIC DATA ANALYSIS

To validate our method, we performed tests on a synthetic time series generated by random walk of size $m = 1,000$. We also embedded a motif of size 100 in four different positions of the time series. Figure 8 shows the embedded motif and its variants. The motifs were planted on positions 32, 287, 568 and 875, as shown in Figure 9. We ran the TrieMotif using the bin discretization method with $n = 100$, $R = 2.5$, $w = 16$, $a = 4$ and $\delta = 1$. As expected, the TrieMotif was able to successfully find the motif on the planted positions.

Knowing that our method is able to find the embedded motifs, we made a series of experiments varying the length of the time series to evaluate the method efficiency. We compared our method with the

Algorithm 1 : K-TrieMotif Algorithm.

Input: T, n, R, w, a, δ, K
Output: List of the top K-Motif

$ListOfMotif \leftarrow \emptyset$
for all Subsequence S_i with size n of T **do**
  $\hat{S}_i \leftarrow$ ConvertIntoSymbol(S_i, w, a)
  Insert $\hat{S}_i$ in the Trie index
end for
for all Subsequence $\hat{S}_i$ of T **do**
  $C \leftarrow$ GetCandidatesFromTrie($\hat{S}_i$, δ)
  $MotifS \leftarrow \emptyset$
  for all $C_j \in C$ **do**
    if $NonTrivialMatch(S_i, C_j, R)$ **then**
      Add C_j to $MotifS$
    end if
  end for
  Insert $MotifS$ in the $ListOfMotif$
end for
Sort $ListOfMotif$ by size in decreasing order
$TopKMotifs \leftarrow \emptyset$
$k \leftarrow 0$
for all $(F^{\{i\}} \in ListOfMotif)$ **and** $(k < K)$ **do**
  if $(Distance(F^{\{i\}}, F^{\{l\}}) \leq 2R)$, $\forall F^{\{l\}} \in TopKMotif$ **then**
    Discard $F^{\{i\}}$
  else
    Insert $F^{\{i\}}$ in $TopKMotif$
    k++
  end if
end for
return $TopKMotif$

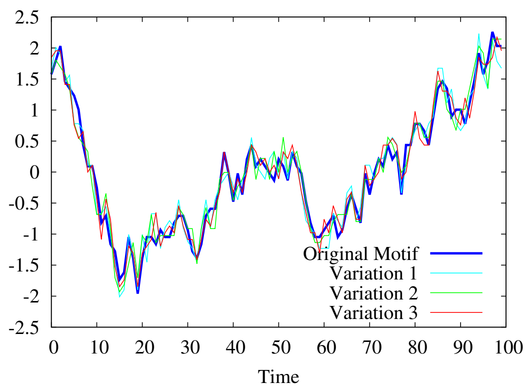


Figure 8: Planted motif and its variants into a longer dataset for evaluation tests.

brute force algorithm and with a Random Projection method, since it used extensively and is the basis of others algorithms in the literature. We searched for motifs of size $n = 100$ and used the Euclidian distance. For both Random Projection and TrieMotif we

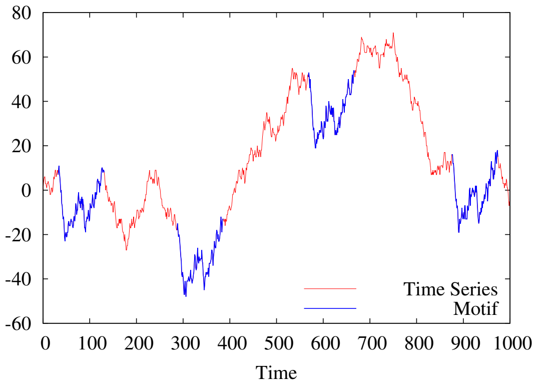


Figure 9: A random walk time series with the implanted motif (blue).

used the same parameters for the discretization, $a = 4$ and $w = 16$. We ran the Random Projection with 100 iterations. For the TrieMotif, we used both bin and SAX representations with $\delta = 1$. We varied the time series length from 1,000 to 100,000. Each set of parameters were tested using 5 different seeds for the random walk. All tests were performed 5 times, totalizing 25 executions. The wall clock time and memory usage measurements were taken from these 25 runs of the algorithm. The presented values correspond to the average of the 25 executions. Due to time limitations, the brute-force algorithm was not executed for time series with lengths above 40,000. The experiments were performed in an HP server with 2 Intel Xeon 5600 processors with 96 GB of main memory, under CentOS Linux 6.2. All methods (TrieMotif, Random Projection and Brute-force) were implemented using the C++ programming language. The efficiency comparison is shown in Figure 10 and the memory usage is shown on Figure 11.

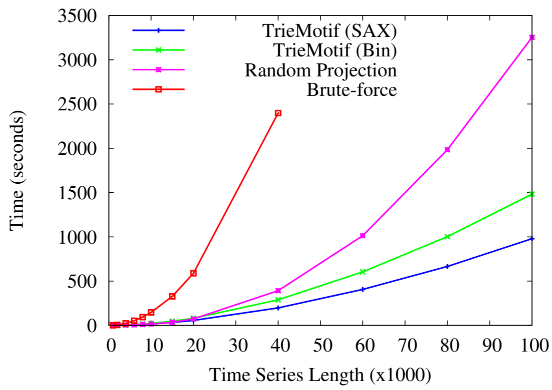


Figure 10: Efficiency comparison of the TrieMotif with brute force and Random Projection.

As expected, both Random Projection and TrieMotif performed better than the brute-force approach. For time series of length below $10,000$, both Random Projection and the TrieMotif had a similar performance. However, as the time series length grows, the TrieMotif presented a better performance. This result is due to the fact that TrieMotif selects only the candidates that are probably a match of a motif, reducing the number of unnecessary distance calculations. It is also possible to notice a better performance of the TrieMotif using the SAX representation. The TrieMotif also consumes less memory than the Random Projection, since the Random Projection algorithm needs at least m^2 memory for the collision matrix. From Figure 11, we can see that the memory requirements of our method is significantly less demanding than Random Projection, requiring 10 times less memory than the state of the art (the Random Projection approach).

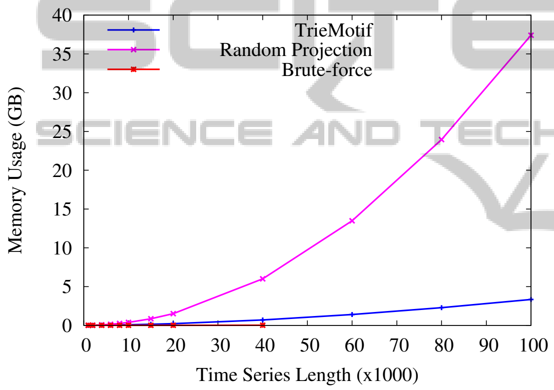


Figure 11: Comparison of maximum memory usage of the TrieMotif and Random Projection.

5 REAL DATA EXPERIMENTS

We also performed experiments using data from real applications. For this evaluation, we extracted data from time series of remote sensing images gathered by AVHRR/ NOAA satellite (Advanced Very High Resolution Radiometer/National Oceanic and Atmospheric Administration). These images correspond to monthly measures of the Normalized Difference Vegetation Index (NDVI), which indicates the soil vegetative vigor represented in the pixels of the images and is strongly correlated with biomass. We used images of the São Paulo state, Brazil (Figure 12), corresponding to the period between April 2001 and March 2010. From these images, we extracted 174,034 time series of size 108. Each time series corresponds to a pair of latitude and longitude of the São Paulo state, excluding the coastal region. In order to find the motifs in a time series database, we created a longer time series by concatenating all time series. The TrieMotif algorithm was created using this longer time series. It is important to highlight that in the subsequence extraction, on the first stage, we avoided creating subsequences containing parts of two distinct time series, that is, the end of a time series concatenated to the beginning of the next one.

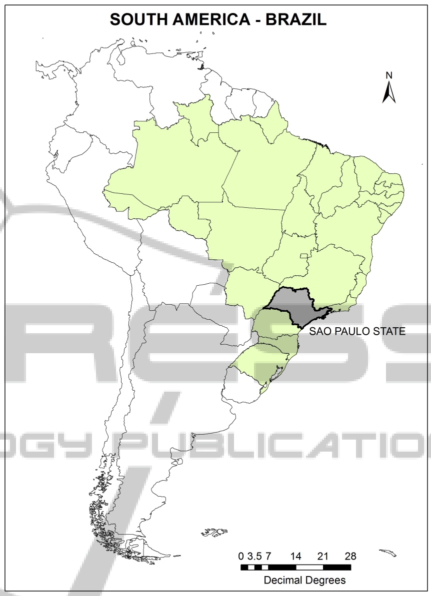


Figure 12: State of São Paulo, Brazil.

The São Paulo state was divided into 5 regions of interest (Figure 13). The regions were obtained through a clustering algorithm and the results were analyzed by specialists in the agrometeorology and remote sensing fields. According to them, region 1 corresponds to water and urban areas, regions 2 and 3 correspond to a mixture of crops (excluding sugarcane) and grassland, region 4 corresponds to sugarcane crops and region 5 to forest. Figure 14 shows a summary of each region of interest and the number of time series in each region. The São Paulo state is one of the greatest producers of sugarcane in Brazil. In this work, we consider complete sugarcane cycles of approximately one year, each of which starting in April and ending in March, thus, we looked for the top 4-Motifs of size $n = 12$ (annual measures). We ran the TrieMotif algorithm using the bin discretization with $R = 1.5$, $w = 4$, $a = 4$ and $\delta = 1$. The experiments were performed using the same computational infrastructure of the synthetic data.

Figures 15, 16, 17, 18 and 19 show the top 4-Motif for each region of interest. The plots are not normalized due to the specialists restrictions for analyzing them. The 1-Motif found on region 1 (Figure 15(a)) has a pattern with low values and variation, which ex-

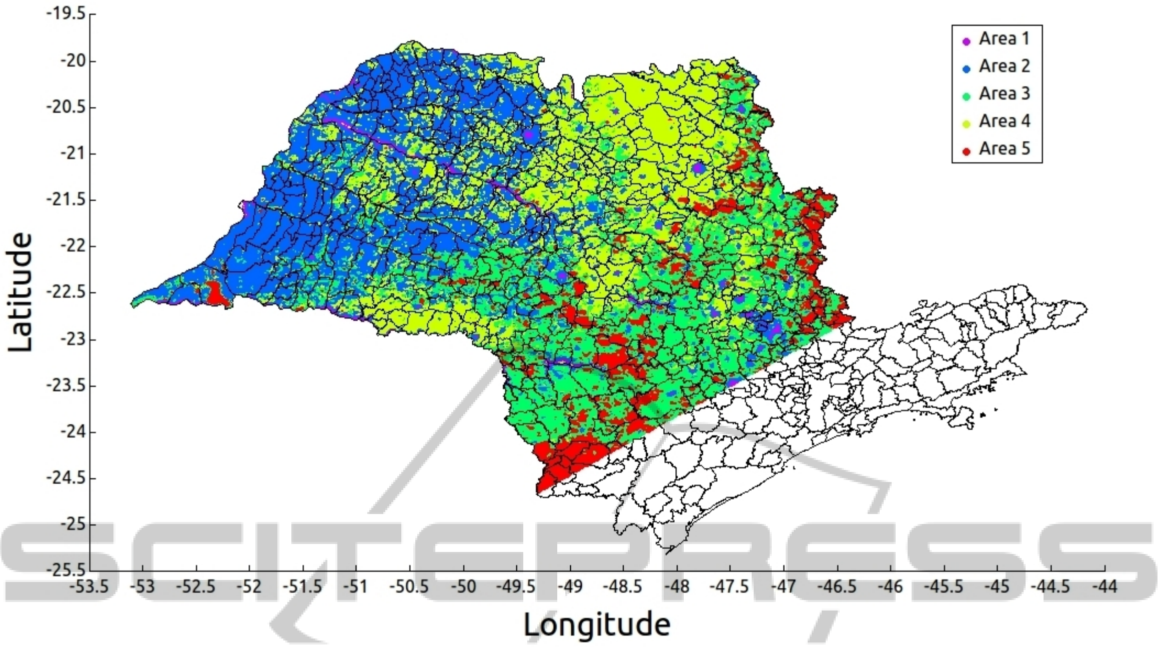
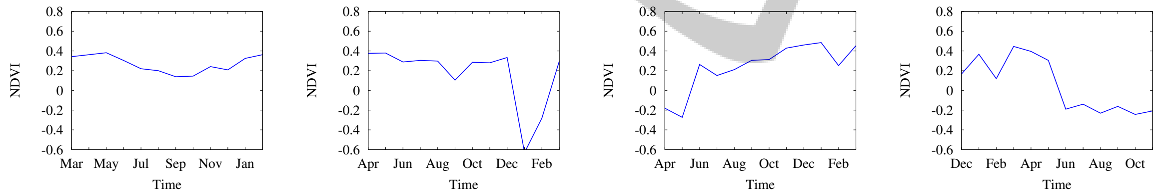


Figure 13: The São Paulo state was divided into 5 regions of interest. Region 1 (purple) corresponds to water/cities, Region 2 and 3 (blue and green respectively) to a mixture of crops and grassland, Region 4 (yellow) is sugarcane crop and Region 5 (red) corresponds to forest. The black lines represent the political counties of the state. The south of the state is a forest nature federal reserve.



(a) 1-Motif (b) 2-Motif (c) 3-Motif (d) 4-Motif

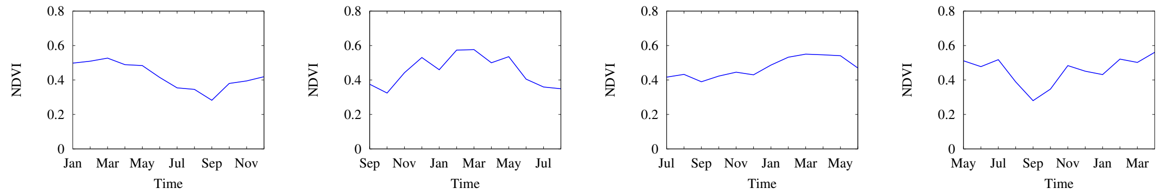
Figure 15: Top 4-Motif for Region of interest 1.

Region	Color	# of Series	Represents
1	Purple	2,804	Water and Cities
2	Blue	55,815	Grassland and Mixture of Crops
3	Green	50,785	
4	Yellow	48,301	Sugarcane crops
5	Red	16,329	Forest

Figure 14: Number of time series in each region of interest.

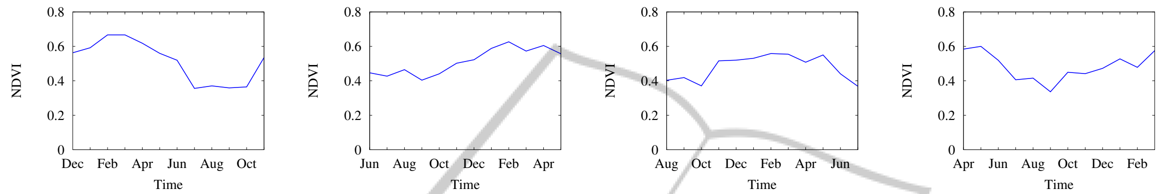
perts say correspond to urban regions. The other Motifs found in region 1 (Figures 15(b), 15(c) and 15(d)) have a pattern that corresponds to water regions. Figures 16 and 17 show patterns with a higher value of NDVI and with a high variation, which specialists attribute to agricultural areas.The top 3-Motifs found on region 4 (see Figures 18(a), 18(b) and 18(c)) is clearly recognized by agrometeorologists as a sugarcane cycle, with its high values of NDVI on April and low values on October. Since sugarcane harvesting begins in April, the NDVI slowly starts to decrease in this period. On October, the harvest finishes and the soil remains exposed, thereafter the NDVI has the lowest value. From October to March, the sugarcane grows and the NDVI increases again. Figure 19 shows a pattern with high values of NDVI and low variations, corresponding to the expected forest behavior, where the NDVI follows the local temperature variation.

The TrieMotif algorithm obtained interesting results, finding patterns that were not expected by the specialists. According to them, for some regions, the 4-Motifs found do not resemble with the expected patterns. The 4-Motifs found on both regions 2 and 3 (Figures 16(d) and 17(d) respectively) indicates the presence of sugarcane and the 4-Motif found on region 4 (Figure 18(d)) does not resemble a sugarcane cycle. This result indicates the need for a further inspection in the areas where these patterns occur.



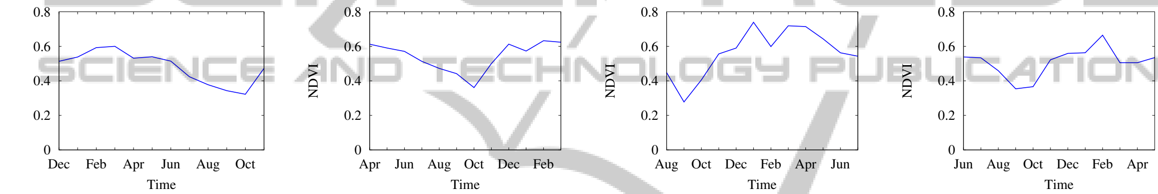
(a) 1-Motif (b) 2-Motif (c) 3-Motif (d) 4-Motif

Figure 16: Top 4-Motif for Region of interest 2.



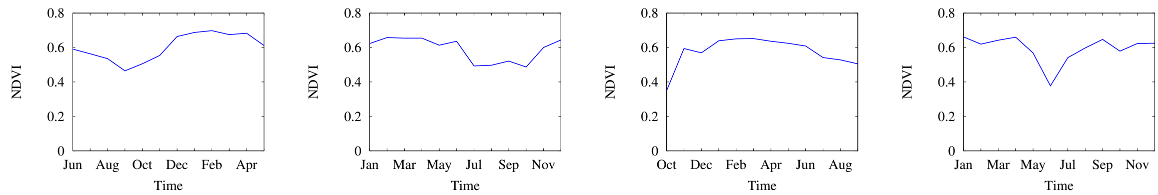
(a) 1-Motif (b) 2-Motif (c) 3-Motif (d) 4-Motif

Figure 17: Top 4-Motif for Region of interest 3.



(a) 1-Motif (b) 2-Motif (c) 3-Motif (d) 4-Motif

Figure 18: Top 4-Motif for Region of interest 4.



(a) 1-Motif (b) 2-Motif (c) 3-Motif (d) 4-Motif

Figure 19: Top 4-Motif for Region of interest 5.

6 CONCLUSIONS

Finding patterns in time series is highly relevant for applications where both the antecedent and the consequent events are recorded as time series. This is the case of climate and agrometeorological data, where it is known that the next state of the atmosphere depends in large amount of its previous state. Today, a large network of sensing devices, such as satellites recording both earth and solar activities, as well as ground-based whether monitoring stations keep track of climate evolution. However, the large amount of data and their diversity makes it hard to discover complex patterns able to support more robust analyzes. In this scenario, is is very important to have powerful and fast algorithms to help analyzing the that data.

In this paper we proposed TrieMotif, a novel technique that provides, in an integrated framework, an automated technique to extract frequent patterns in time series as K-Motifs. It reduces the resolution of the data, speeding up the sub-sequence comparison operations, indexes them in a trie structure and adopts heuristics commonly employed by the meteorologists to prune from the similarity search operations those branches that do not represent interesting answers. In this way, our technique is able to select only candidate subsequences that have high probability to match a motif, thus, reducing the number of comparisons performed.

Experiments performed over data from both synthetic and real applications showed that our technique indeed perform in average 3 times faster them the state of the art approach (Random Projection), including the best methods previously available. It also requires less memory, and the experiments revealed that it requires up to 10 times less memory than the competitor methods. We presented the results to specialists in the field (meteorologists), that confirmed that the results are indeed correct and useful for their day-to-day activities to process climate data. For future works, we intend to explore data from larger regions, as the whole Brazil and South America. We also intend to explore data from different sensors in order to evaluate improvements that may be needed.

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