Detecting Variable Length Anomaly Patterns in Time Series Data

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Introduction

- A time series is a sequence of data points made over a continuous time interval
- Anomaly Patterns are subsequences that do not conform to a well defined notion of normal behavior
- Application areas that explore such time series anomalies include fault diagnostics, intrusion detection, fraud detection, auditing and data cleansing

Introduction

ECG qtdb/sel102 (excerpt)
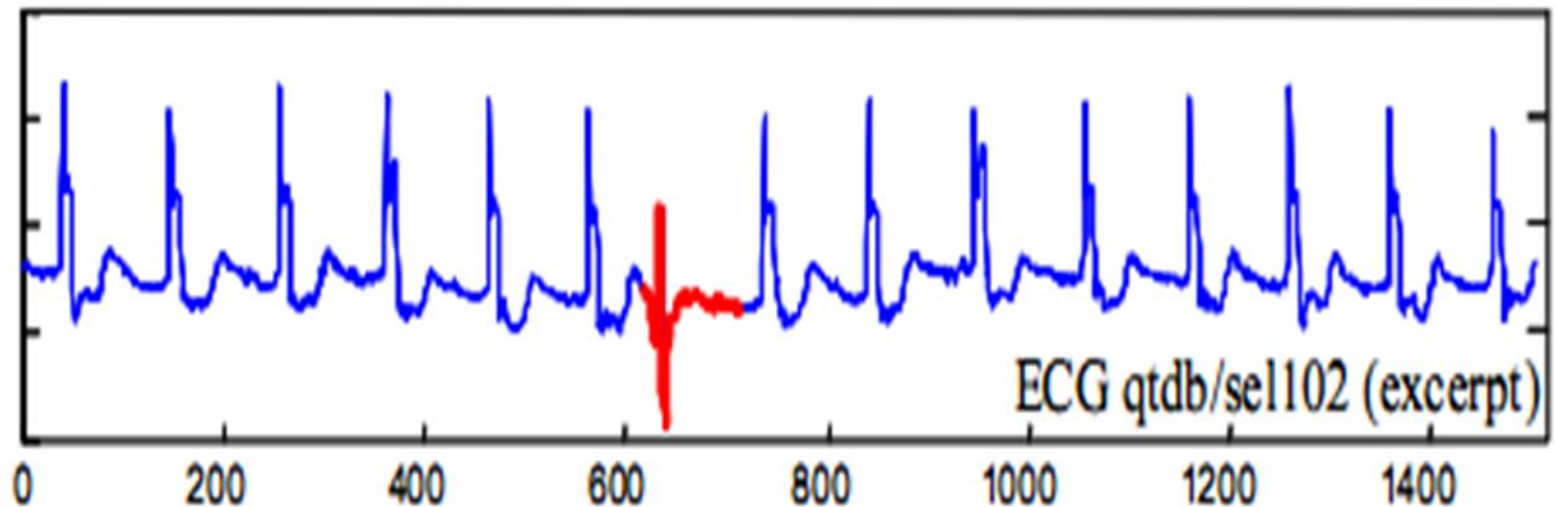
unusual subsequence in time series data

Introduction

- Anomalous subsequences detection is a challenging topic

- The exact lengths of the unusual subsequence are vary and are often unknown.

- Best similarity/distance measures which can be used for different types of time series is not easy to determine.

- Time series in real applications are usually long and as the length increases the computational complexity also increases.

Some Definitions

- *Time Series*: A time series $T = t_1, t_2, ..., t_m$ is an ordered set of m real values measured at equal intervals.

- *Subsequence*: 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., $C = t_p, t_{p+1}, ..., t_{p+n-1}$, 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 $e_{p+n-1} = t_{p+n-1}$.

Some Definitions

- *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

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

        i) For at least *k* patterns *Q′* ∈ *D* it holds that *Dist*(*D, Q′*) ≤ *Dist*(*D, Q*).

        ii) For at most *k-1* patterns *Q′* ∈ *D* \{*Q*} it holds that *Dist*(*D, Q′*) < *Dist*(*D, Q*).

Some Definitions

- *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)* ≥ *e* or *|p - q|* ≥ *n*, where *e* is a given value of distance threshold.

- *Anomaly factor*: For any pattern set *D* and a pattern *P* ∈ *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*)).

- *Anomaly Pattern*: Given any pattern set *D*, a pattern *P*∈ *D*, *P* is anomaly only if its anomaly factor is larger than *a*, where *a* is the threshold of anomaly pattern

Related Works

- Hot Sax (E. Keogh et al. 2005).
- WAT (Y. Bu et al. 2007).
- Method based on PAA bit representation and clustering (Li et al. 2013)
- Method based on Segmentation and Anomaly Factors (M.Leng et al. 2008)

HOT SAX

- Find discord of length $n.$
- A discord is a subsequence which have largest nearest neighbor distance.
- Use heuristic to improve brute-force.
- Distance function: Euclid distance.

HOT SAX

Function *[dist, loc]= Heuristic_Search(T, n, Outer, Inner)*
best_so_far_dist = 0
best_so_far_loc = NaN
For *Each p in T ordered by heuristic Outer* // *Begin Outer Loop*
   nearest_neighbor_dist = infinity
  For *Each q in T ordered by heuristic Inner* // *Begin Inner Loop*
    IF $|\, p - q\, | \geq n$ // *non-self match?*
      IF *Dist* $((t_p, ..., t_{p+n-1}), (t_q, ..., t_{q+n-1}))$ < *best_so_far_dist*
        Break   // *Break out of Inner Loop*
      End
      IF *Dist* $((t_p, ..., t_{p+n-1}), (t_q, ..., t_{q+n-1}))$ < *nearest_neighbor_dist*
        nearest_neighbor_dist = Dist $((t_p, ..., t_{p+n-1}), (t_q, ..., t_{q+n-1}))$
      End
    End   // *End non-self match test*
  End   // *End Inner Loop*
  IF *nearest_neighbor_dist > best_so_far_dist*
    best_so_far_dist = nearest_neighbor_dist
    best_so_far_loc = p
  End
End   // *End Outer Loop*
Return*[best_so_far_dist, best_so_far_loc]*
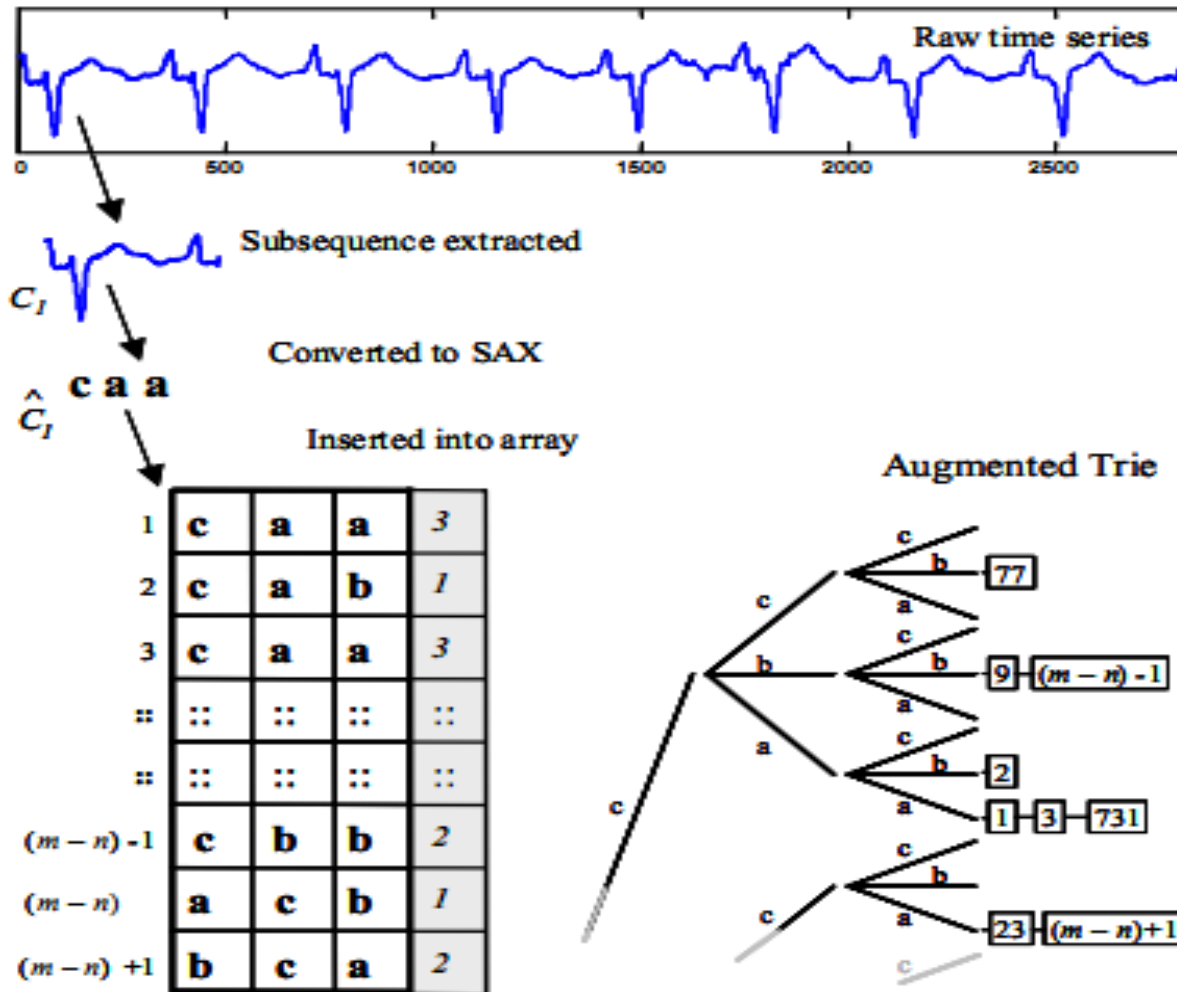
HOT SAX

- Present subsequences of length n to SAX words.

  - Use PAA for Dimensionality reduction

- Use an array and an augmented trie to embed all the SAX words

HOT SAX
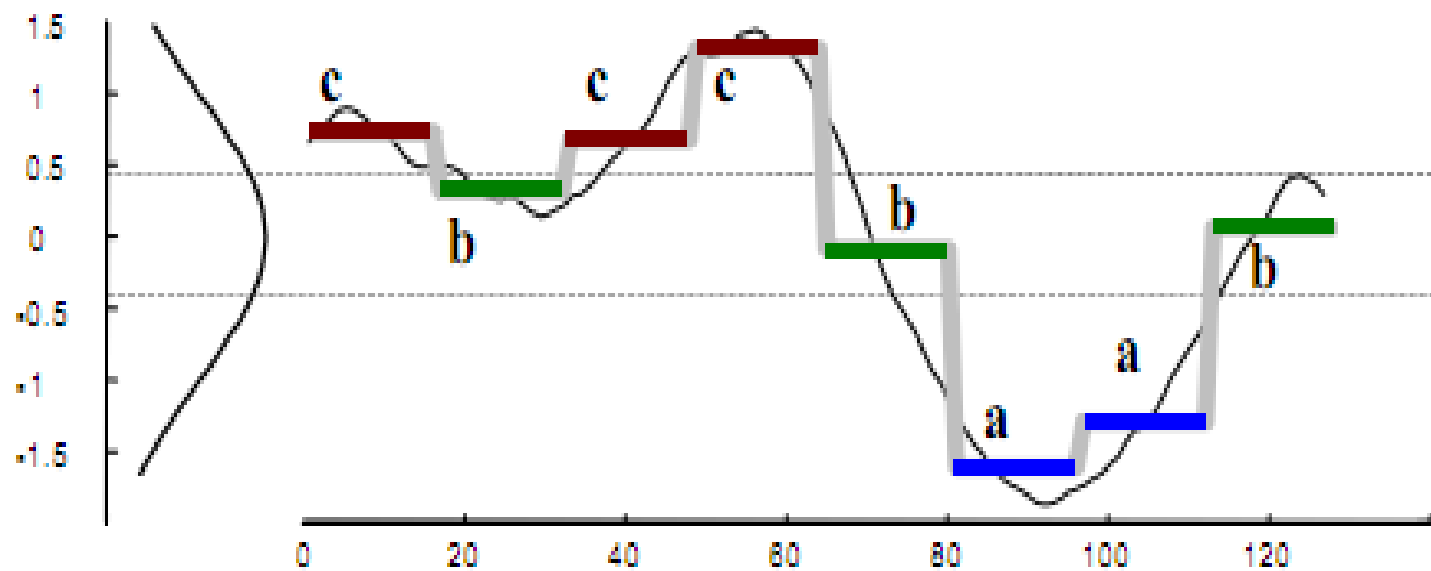
HOT SAX

HOT SAX

- In outer loop, subsequences presented by words which have smallest appearing frequency in the array are checked first

- In inner loop, subsequences belong to the same left node in the augmented trie with the subsequence chosen at outer loop are checked first.

WAT

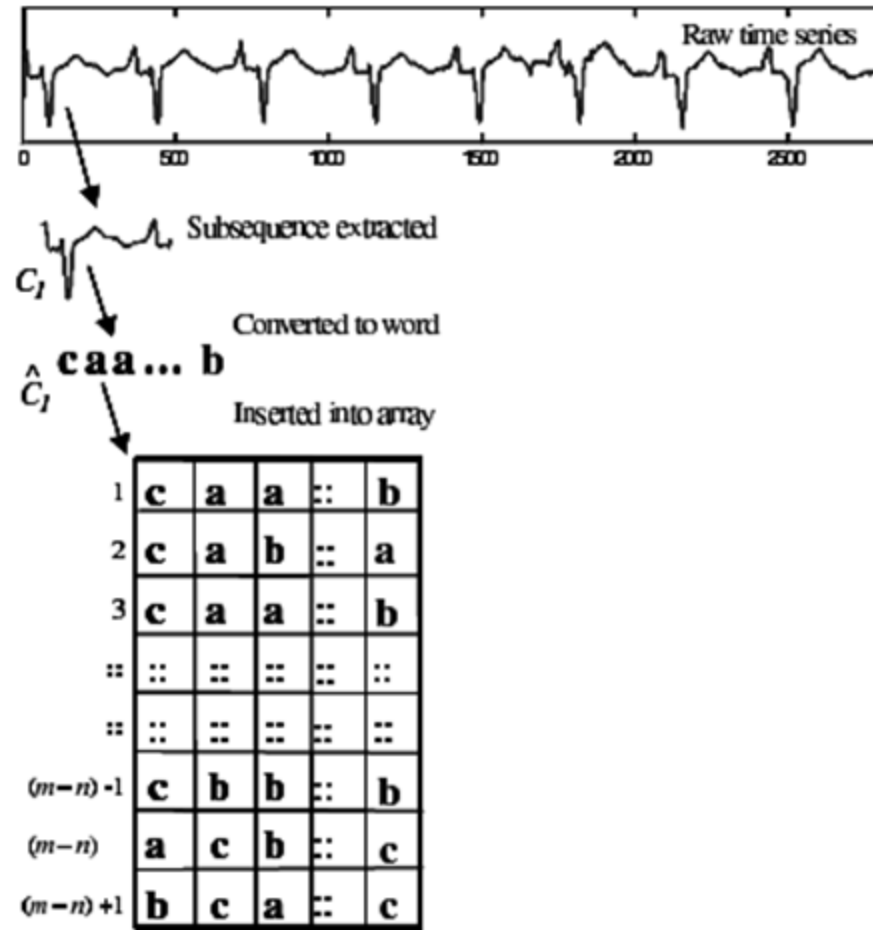- Same HOT SAX but use Haar wavelet instead of PAA.

WAT

- Haar wavelet can be seen as a series of averaging and differencing operations
- Ex: *f(x)* = (9, 7, 3, 5) -> (6, 2, 1, -1)
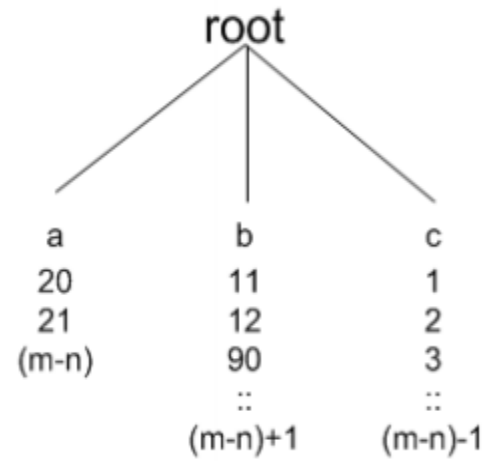
Resolution	Averages	Coefficients
4	(9 7 3 5)	
2	(8 4)	(1 -1)
1	(6)	(2)

WAT

WAT

WAT

WAT

- In outer loop, subsequences presented by words which have smallest appearing frequency in the array are checked first

- In inner loop, subsequences belong to the same left node in the tree with the subsequence chosen at outer loop are checked first.

Method based on PAA bit representation and clustering

- PAA Bit representation of a series
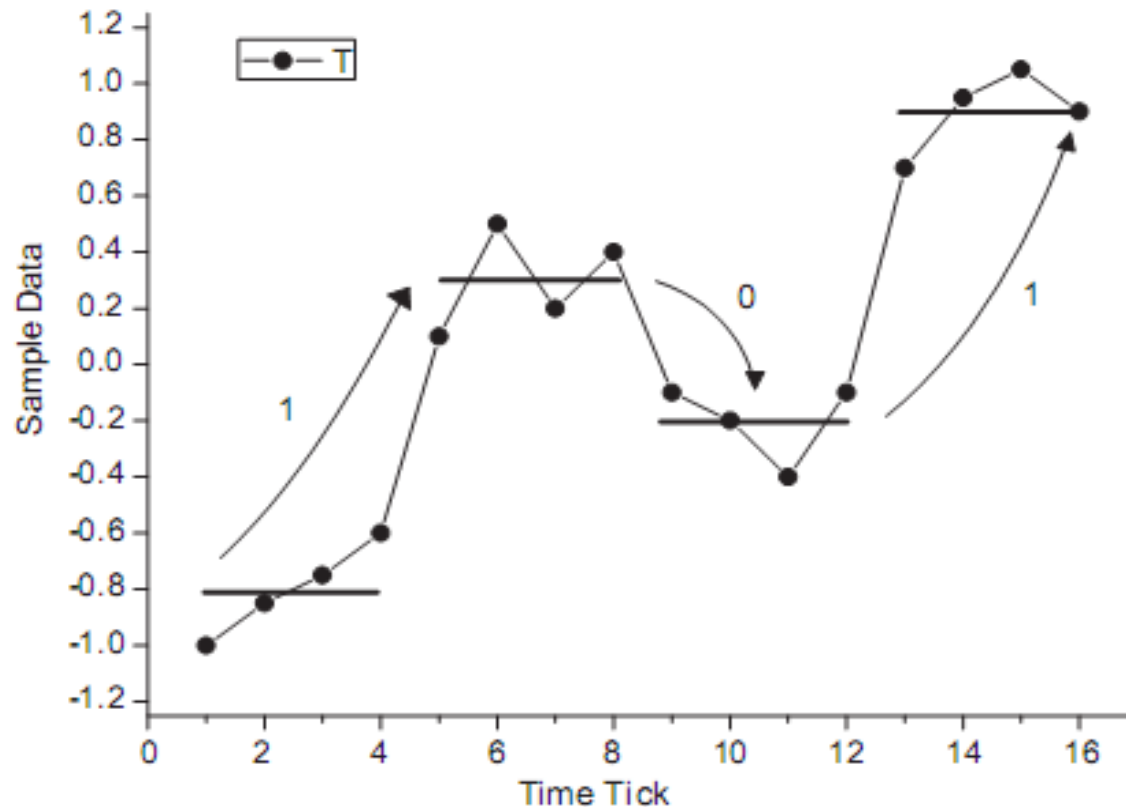
Method based on PAA bit representation and clustering

- Bit distance between of two PAA bit representation $s = \{s_1, s_2, ..., s_{w-1}\}$ and $t = \{t_1, t_2, ..., t_{w-1}\}$

- $BitSeries\_Dist(s, t) =$
$$\frac{1}{w-1} \sum_{1}^{w-1} BDist(s_i, t_i)$$

- Here, $BDist(s_i, t_i) = \begin{cases} 1 & if\ s_i \neq t_i \\ 0 & otherwise \end{cases}$

Method based on PAA bit representation and clustering

- k bit representations are randomly chosen as k cluster centres

- A bit representation is assigned to the nearest cluster.

- In outer loop, subsequences which have bit representations belong to the smallest cluster (cluster has the fewest elements) is checked first

- In inner loop, subsequences belong to the same cluster with the subsequence chosen at outer loop are checked first.

Method based on PAA bit representation and clustering

- 3 above algorithms need to know the length of anomaly subsequence in advance.

Method based on Segmentation and Anomaly Factors

- Proposed by Leng et al. in 2008
- The method includes 2 phase
- Phase 1: use quadratic regression model to segment time series. Regression function is defined as $f(t) = \beta_0 + \beta_1 t + \beta_2 t^2$,
- Phase 2: Calculate anomaly factors for the subsequences and show abnormal patterns.

1. Let $s_1 = 1$ denote the start position of the first segment, l denote the initial length of each segment, $m = s_1$ 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 $SSE < \varepsilon_1$ let $l = l + 1$, go to step 1, else go to step 3.

3. Let (s_1, e_1) denote this segment, e_1 denotes the end position of this segment and $e_1 = l - 1$.

4. Let $i = 1$, if $Dist((s_1, e_1), (s_1 + i, e_1 + i)) \leq \varepsilon_2$, increment i by 1, calculate it, repeat this procedure until $Dist((s_1, e_1), (s_1 + i, e_1 + i)) > \varepsilon_2$ or $i > (e_1 - s_1)$, let $s_2 = e_1 + i$, 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.

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 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.

Method based on Segmentation and Anomaly Factors

- Don't need to know the length of anomaly patterns in advance

- Use DTW to calculate distance between two subsequences of different length

- Time consuming

Proposed Algorithms

- Use Homothetic Transformation + Modified Euclidean Distance instead of DTW

- Reduce the number of distance calculating in building distance matrix.

- Proposed a segmentation method based on important extreme points as alternative segmentation method

New distance function

- A Homothetic Transformation with center *O* and ratio *k* transforms the point *M* to the point *M'* such that

$$\overrightarrow{OM'} = k \times \overrightarrow{OM}.$$

New distance function

- Apply to time series, a homothety transforms a time series T of length n ($T = \{y1, y2, ..., yn\}$) to time series T' of length n' by performing the following steps.

- First, compute $Y\_MAX = MAX(y1, ..., yn)$, $Y\_MIN = MIN(y1, ...,yn)$.

- 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

New distance function

$$\textbf{Function } Dist(X, Y)$$
$$\textbf{if } (X.length == Y.length) \textbf{ return } Euclid(X, Y)$$
$$\textbf{else}$$
$$MEAN = |(Y.length + X.length)| / 2$$
$$Y' = Homothety(Y, MEAN)$$
$$X' = Homothety(X, MEAN)$$
$$\textbf{return } Euclid(X', Y')$$

New distance function

- Minimum Euclidean Distance between

$T' = \{T'_1, T'_2, ..., T'_{N'}\}$ and $Q' = \{Q'_1, Q'_2, ..., Q'_{N'}\}$

$$D(T',Q') = Min\left\{\sum_{i=1}^{N'}(T'_i - Q'_i - b)^2\right\}$$

$$b = \frac{1}{N'}\sum_{i=1}^{N'}(Q'_i - T'_i)$$

Time Complexity of new distance function: O(n)

Reduce the number of distance calculating

- Propose parameter *r*
- Replace formula (1) to

$$d_{ij} = \min_{l_{lower} \le l \le l_{upper}} Dist((s_i, e_i), (s_j, s_j + l)) \quad (1')$$

Where

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

l_{avg} is mean length of the subsequences.

Alternative segmentation method

- Based on the concepts of Important Extreme Points, proposed by Pratt and Fink in 2002

- Extract all important extreme points of the time series T. The result of this step is a sequence of extreme points $EP = (ep_1, ep_2, ..., ep_l)$

- Compute all the candidate patterns iteratively. A candidate pattern $CP_i(T)$, $i = 1, 2,..., l$ -2 is the subsequence of T that is bounded by extreme points ep_i and ep_{i+2}.

Alternative segmentation method

- **Parameter:**

- Compression rate: $R > 1$

- Lower bound for the distance two extracted extreme points: *min_length.* So the minimum length of a subsequence is 2*min_length*
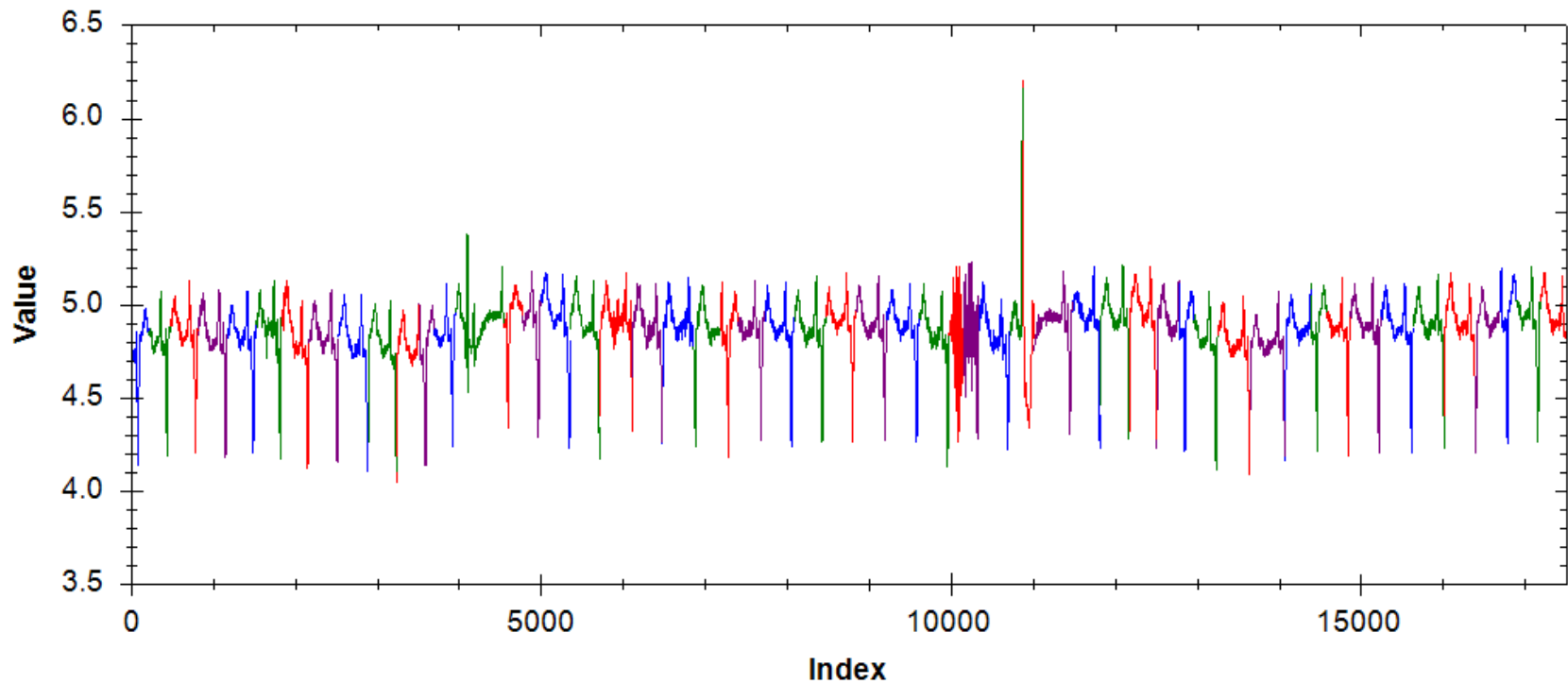
Segmentation based on quadratic regression
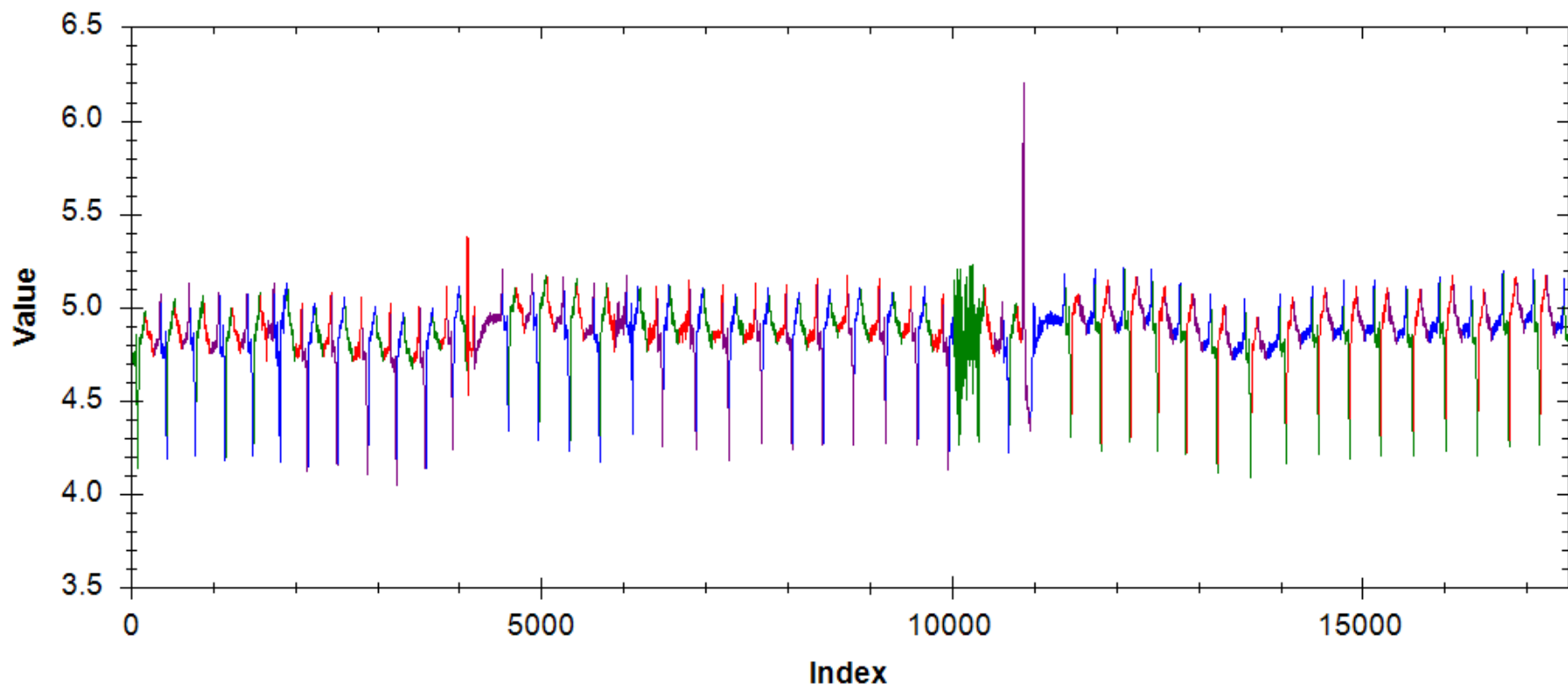
Segmentation based on important extreme points

Experimental Evaluation

- VL_QR| HT: The proposed algorithm with quadratic regression

- VL_EP| HT: The proposed algorithm with important extreme points.

- Compare results and running time among VL_QR| HT, VL_EP| HT and HOT SAX

- Compare running time between VL_QR| HT with the original algorithm proposed by Leng et al.

Experimental Evaluation

- Experiments environment : Intel® Core™ 2 Duo 2.0GHz, Ram 3072MB PC

- All algorithms are implemented in Microsoft Visual C# programing language

Compare VL_QR| HT, VL_EP| HT and HOT SAX

- Use 8 time series in diverse domains:

ECG 108, ECG 308, ERP, Memory, Power Demand In Italy, Dutch Power Demand, Stock20 and TEK16

- To compute location difference of anomaly subsequences use:

$$d = |p - q|/l \times 100$$

where p is the start position of the anomaly pattern found by proposed algorithm and q is the start position of the anomaly pattern found by HOT SAX and l is it's length

Parameter values in the three algorithms for each series

Datasets	VL_QR| HT	VL_EP| HT	HOT SAX
ECG108 (17500 points)	$\varepsilon_1 = 5.0$, $\varepsilon_2 = 0.3$, $a = 3.5$, $r = 0.1$	$R = 1.04$, $min\_length = 50$, $a = 4$, $r = 0.1$	$n = 600$, $PAA\_size = 60$
ECG308 (1300 points)	$\varepsilon_1 = 51000$, $\varepsilon_2 = 50$, $a = 2.2$, $r = 0.1$	$R = 1.03$, $min\_length = 10$, $a = 2.5$, $r = 0.23$	$n = 60$, $PAA\_size = 6$
ERP (5000 points)	$\varepsilon_1 = 3.0$, $\varepsilon_2 = 1.0$, $a = 3.0$, $r = 0.15$	$R = 1.42$, $min\_length = 10$, $a = 3.5$, $r = 0.1$	$n = 100$, $PAA\_size = 10$
Memory (6875 points)	$\varepsilon_1 = 8.0$, $\varepsilon_2 = 0.1$, $a = 2.2$, $r = 0.1$	$R = 1.1$, $min\_length = 40$, $a = 1.6$, $r = 0.1$	$n = 100$, $PAA\_size = 20$
Power Demand Italy (7000 points)	$\varepsilon_1 = 100000$, $\varepsilon_2 = 100$, $a = 2.5$, $r = 0.1$	$R = 1.8$, $min\_length = 20$, $a = 3.0$, $r = 0.1$	$n = 300$, $PAA\_size = 30$
Dutch Power Demand (9000 points)	$\varepsilon_1 = 31000000$, $\varepsilon_2 = 500$, $a = 1.6$, $r = 0.2$	$R = 1.7$, $min\_length = 180$, $a = 1.33$, $r = 0.25$	$n = 1200$, $PAA\_size = 120$
Stock20 (5000 points)	$\varepsilon_1 = 2.0$, $\varepsilon_2 = 0.1$, $a = 3.5$, $r = 0.1$	$R = 1.01$, $min\_length = 200$, $a = 1.5$, $r = 0.1$	$n = 700$, $PAA\_size = 70$
TEK1 (5000 points)	$\varepsilon_1 = 14.5$, $\varepsilon_2 = 0.1$, $a = 2.0$, $r = 0.1$	$R = 1.02$, $min\_length = 50$, $a = 1.5$, $r = 0.1$	$n = 128$, $PAA\_size = 8$

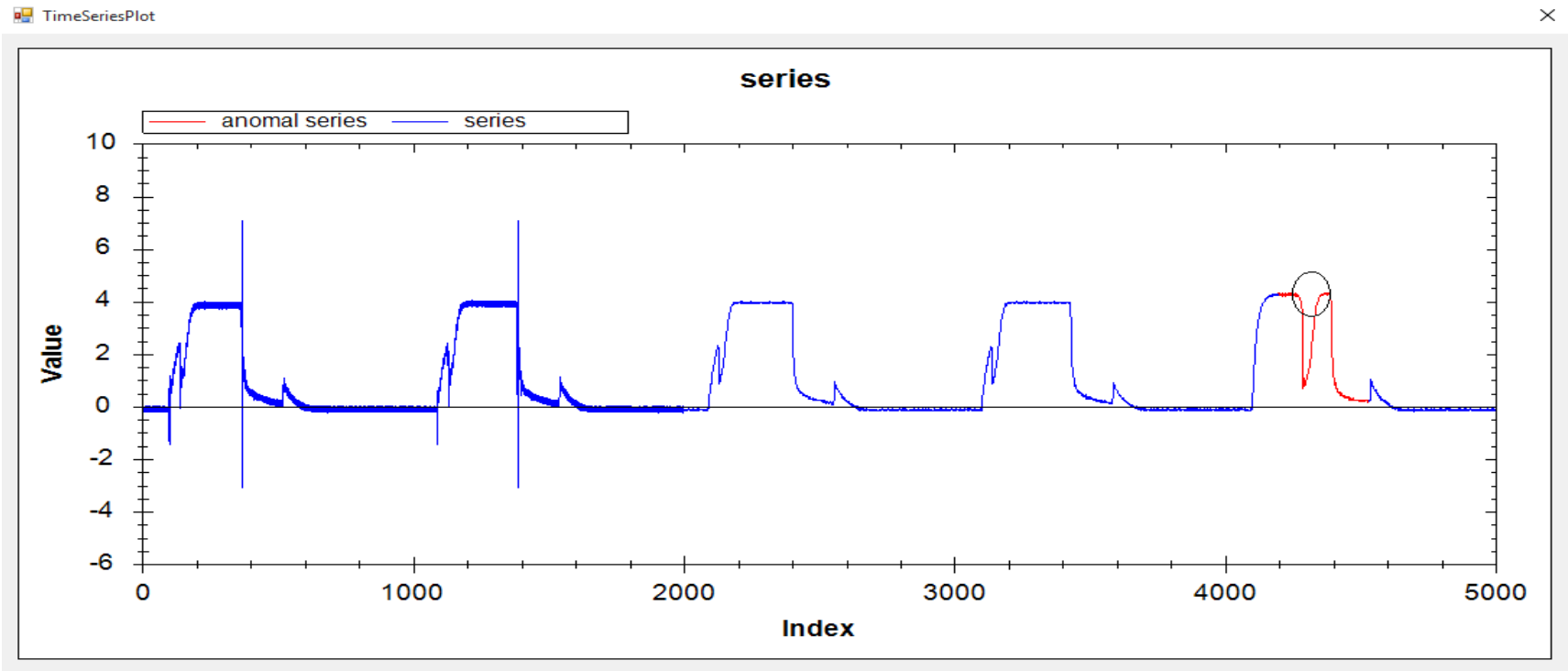# Positions of anomaly patterns detected by VL_QR|HT and VL_EP|HT and HOT SAX

Dataset	VL_QR|HT		VL_EP|HT		HOT SAX
	Start position	Location difference (d)	Start position	Location difference (d)	Start position
ECG 108	10875	1.5%	10792	12.3%	10866
ECG 308	656	33%	673	5%	676
ERP	2617	32%	2602	17%	2585
Memory	2425	2%	2399	11%	2421
Power Demand Italy	5311	4%	5383	13.33%	5343
Dutch Power Demand	6424	1.3%	6277	11%	6466
Stock20	2961	1.7%	2960	1.6%	2949
TEK16	4262	24%	4197	27%	4231

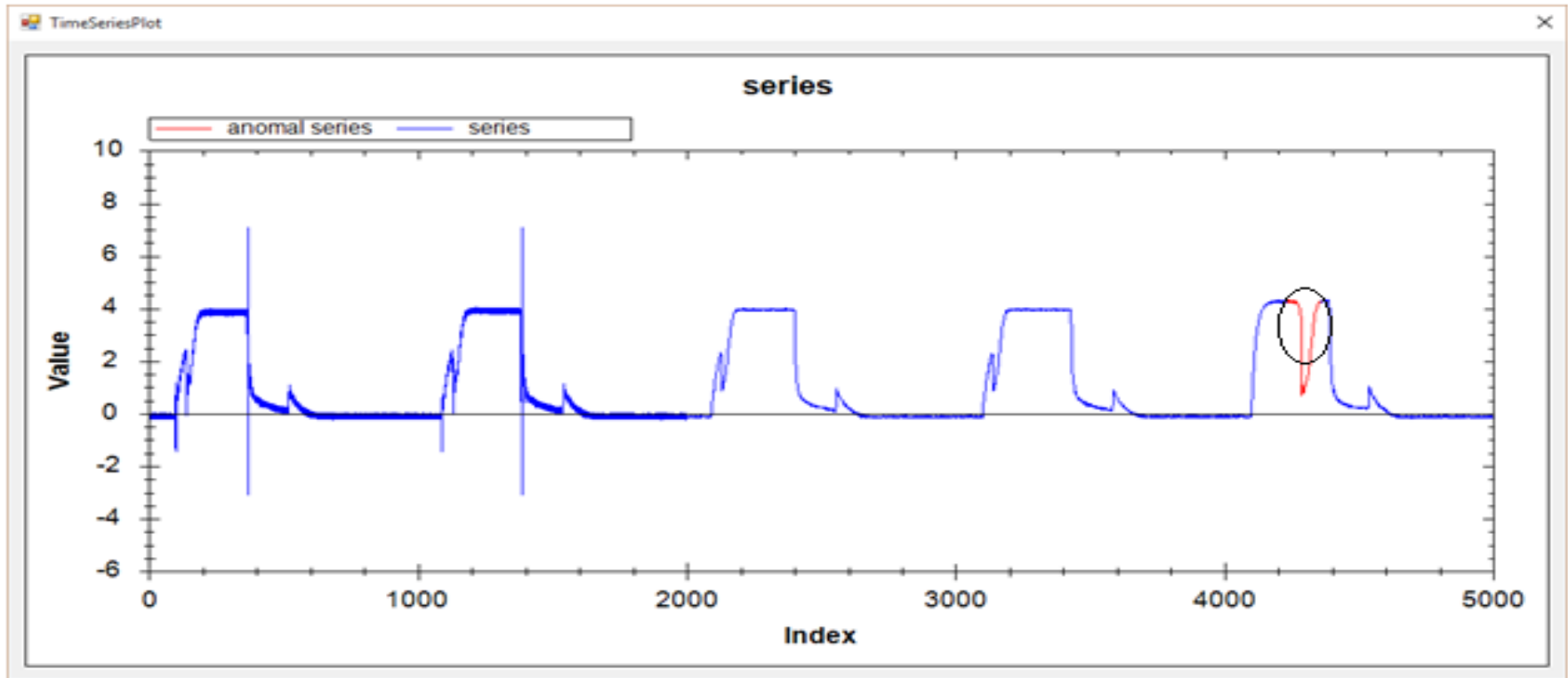# Positions of anomaly patterns detected by VL_QR|HT and VL_EP|HT and HOT SAX
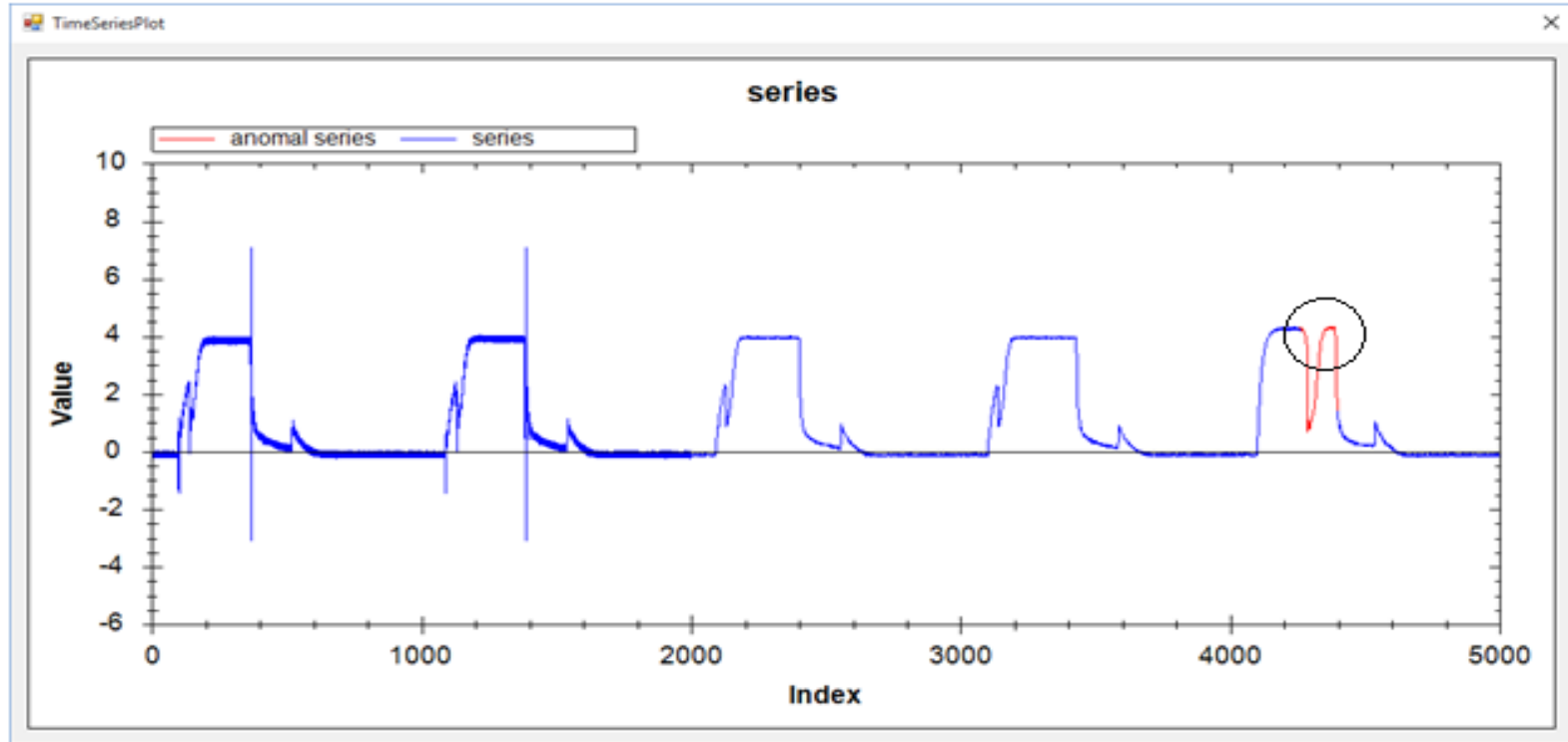
- Result of VL_QR | HT with series TEK16

Positions of anomaly patterns detected by VL_QR|HT and VL_EP|HT and HOT SAX

- Result of VL_EP | HT with series TEK16

Positions of anomaly patterns detected by VL_QR|HT and VL_EP|HT and HOT SAX

- Result of HOT SAX with series TEK16

Running time among VL_QR|HT, VL_EP|HT and HOT SAX (s)

Dataset	VL_QR| HT	VL_EP| HT	HOT SAX
ECG 108	10	47	458
ECG 308	0.31	2	13
ERP	7	14	60
Memory	4	6	79
Power Demand Italy	9	11	102
Dutch Power Demand	1	9	302
Stock20	1	1	94
TEK16	1	1	52

Running time between VL_QR| HT with the original algorithm (s)

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 Demand In Italy (3000 points)	6	200
Dutch Power Demand (3000 points)	1	24
Stock20 (3000 points)	2	194
TEK16 (2000 points)	1	81

Conclusion

- VL_QR|HT and VL_EP|HT bring out a remarkable improvement for the original algorithm in time efficiency without compromising anomaly detection accuracy.

- Experimental results on eight datasets demonstrate these algorithms outperform the VL_QR|DTW in time efficiency.

- Not easy to estimate the regression error threshold ε_1 and the non-self match threshold ε_2 in the segmentation phase of VL_QR|HT.

- Not easy to find the R in VL_EP|HT.

- Future work: apply some more advanced method of time series segmentation.

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Q & A

Thank you!