iSAX: Indexing and Mining Terabyte Sized Time Series

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INTRODUCTION

Time Series:

- Increasing large
- Existing indexing techniques do not scale efficientely

iSAX:

- Modifies SAX to support extensible hashing, allowing efficient indexing.
- Enables fast exact search and ultra-fast approximate search

BACKGROUND

Dynamic Time Warping:

- Superior to Euclidean Distance
- Degenerates to simple ED when the dataset is too large

SAX:

- Reduces efficiently the dimensionality
- Suitable for indexing as it provides a lower bound for distance calculations
- Allows quick search and retrieval of similar time series patterns
- Fixed Resolution, meaning it’s not scalable

ISAX

- iSAX extends SAX by introducing **multi-resolution representations**
- Properties:
  - **Binary encoding** instead of integer symbols for SAX words, meaning they become **hierarchical**
  - **On-the-fly resolution adjustment**
  - **Indexing without overlap** at leaf nodes

COMPONENTS

- **PAA**
  - Reduces dimensionality by averaging segments
- **SAX Encoding**
  - Converts PAA representation into symbolic words, based on breakpoints derived from a Gaussian distribution
- **iSAX indexing tree**
  - Hierarchical structure of nodes that represent different resolutions
  - Dynamic splitting

EXPERIMENTS

- **Tightness of Lower Bounds:**
  - Measures preservation of distances
  - iSAX outperforms traditional methods
- **Indexing Performance**
  - Evaluated in various datasets of various sizes
  - iSAX indexed them more efficiently
- **Approximate vs Exact Search**
  - Approximate search led to relevant results 91.5% of the time
  - Exact search 20x times faster than brute-force sequential search

EXPERIMENTS

Real-World Applications:

- **EGC Anomaly Detection:** 44x speedup over brute force
- **DNA Sequence Matching:** Reduced efficiently the search time from 13.54 hours to 21.8 minutes

Pros of iSAX

- **Scalability:** Tested with terabyte-sized datasets efficiently, with 100 million time series
- **Fast Search:** Tested the speed of the searching methods of iSAX
- **Multi-Resolution proof:** Showed how the model adapts dynamically to different levels of granularity, without unnecessary storage of data needed
- **Compatibility:** Addressed if it works with standard file systems
- **Real World Applications:** Successfully applied iSAX to ECG anomaly detection and DNA sequence matching

Cons of iSAX

- **Incomplete comparison:** Prior techniques of tree-based indexing methods, such as **VP-Trees** or **R-Trees** not explored
- **Limited Benchmark Diversity:** A big number of synthetic Datasets tested than real world datasets.
- **Dependence on Euclidean Distance:** Earlier methods emphasized compatibility with DTW, while iSAX remains heavily dependent on Euclidean distance, even though Keogh's paper on PAA (2001) indexing emphasized compatibility with DTW
- **Lack of theoretical guarantees:** Effectiveness is portrayed empirically rather than theoretical guarantees.
- **Storage Overhead:** Claims of scalability while storing multiple levels of resolution compared to classic SAX

Code Replication

Code replicated:

- https://github.com/Alexkv99/ISAX_revision

Performed:

- Benchmarked on random synthetic data & real-world datasets
- Performed Exact and Approximated Search on data
- Graphic Representation of the results

DATASETS

Mallat:

- Waveform Time Series consisting of simulated and real wave forms
- Objective is to classify the wave pattern
- Univariate time series

Non-Invasive Fetal ECG Thorax:

- Biomedical Time series, with extracted thoracic recordings of pregnant women.
- Objective is to separate maternal and fetal heart signals
- Multivariate time series

*Dataset Mallat **Dataset ECG

Algorithms

Algorithm 1 SAX Transformation

```
Input: PAA representation of time series
Output: SAX symbolic representation
Compute breakpoints from Gaussian distribution
for each PAA value do
    Compare value with breakpoints
    Assign corresponding symbol
end for
return SAX symbols
```

Algorithm 2 iSAX Tree Insertion

```
Input: Time series
Convert time series to PAA
Transform PAA into SAX word
if root node is empty then
    Create root node with SAX word
else
    Insert SAX word into appropriate node
    if node exceeds max size then
        Split node and refine resolution
    end if
end if
```

Algorithm 3 Splitting an iSAX Node

```
Input: Overfilled node
Identify the SAX dimension with the highest variance
Increase resolution in that dimension
for each time series in node do
    Assign to appropriate child node
end for
Update tree structure
```

Algorithms

Algorithm 4 Approximate Search in iSAX

```
Input: Query time series
Convert query to SAX word
Traverse tree following closest match
if leaf node reached then
    Retrieve stored time series
end if
return Best approximate match
```

Time Complexity: O(logn)
Space complexity: O(1)

Algorithm 5 Exact Nearest Neighbor Search

```
Input: Query time series
Perform approximate search to get initial candidate
Initialize priority queue with root node
while queue is not empty do
    Extract node with smallest distance
    if node is a leaf then
        Compute exact distance to all stored time series
        Update best-so-far match
    else
        Add child nodes to priority queue
    end if
end while
return Exact nearest neighbor
```

Time Complexity: O(klogn)
Space complexity: O(k)
k: nodes fully explored before going to nearest neighbor

BENCHMARKING

Dataset	Insertion Time
Random	1.82s
ECG	0.47s
Mallat	0.66s

- **iSAX indexing** drastically outperforms
- **ECG dataset** had lower insertion time than Mallat, indicating that it has a more **compact structure**
- **Random data exhibited the highest speedup factor**, likely due to **greater variance** in patterns
- **Mallat dataset had a more complex structure**, leading to higher search times

Random Data	
Approx Search	0.0184s
Brute Search	6.03s
Speedup	328.45x

ECG	
Approx Search	0.0273s
Brute Search	2.27s
Speedup	83.19x

Mallat	
Approx Search	0.0389s
Brute Search	4.54s
Speedup	116.89x

SEARCH RESULTS

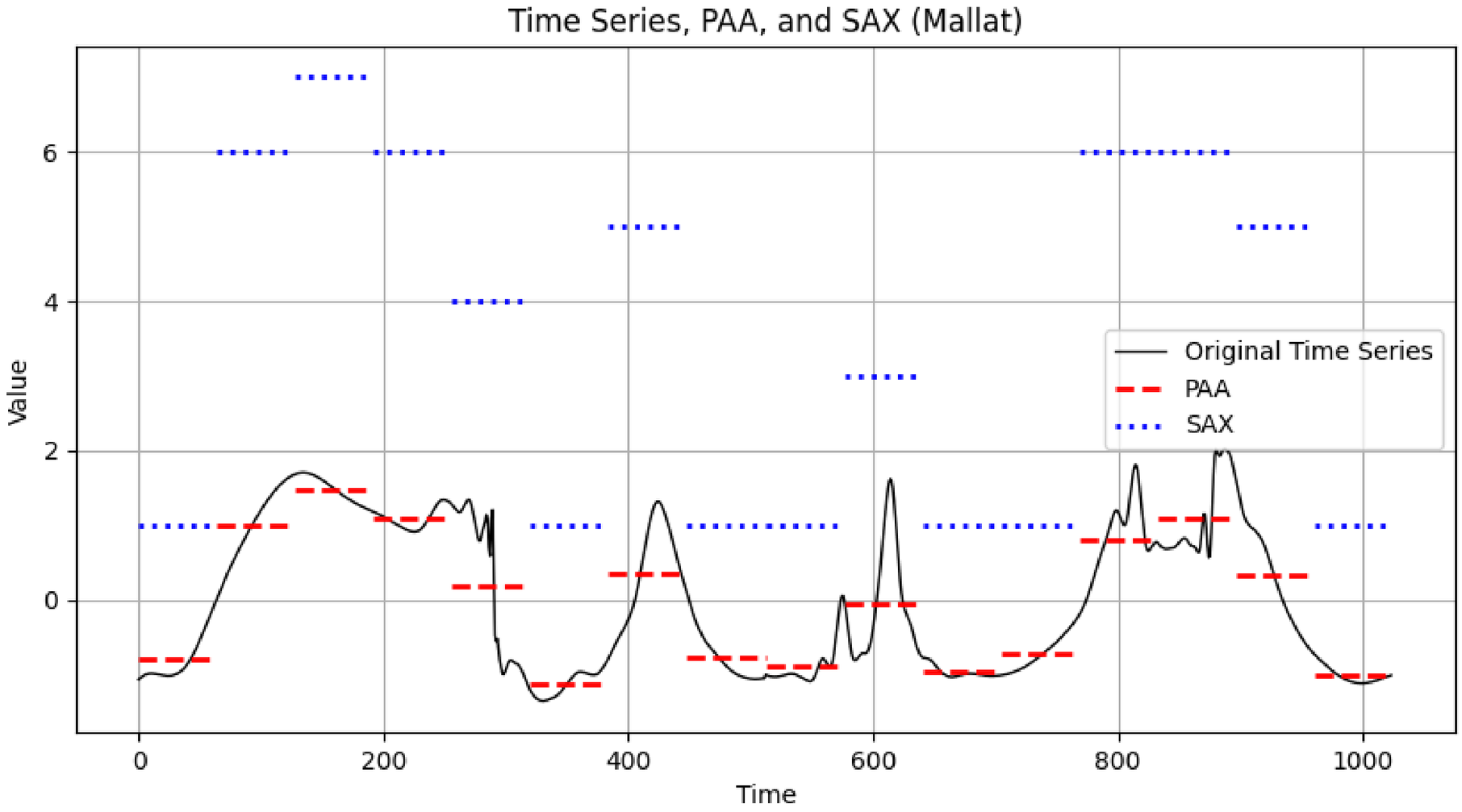
Mallat Dataset

- Query 1:
  - Approximate Match: **[-1.0905, -1.0999, -1.1090, -1.1180, -1.1265]**
  - Exact Match: **[-1.0691, -1.0550, -1.0418, -1.0296, -1.0187]**
- Query 2:
  - Approximate Match: **[-0.9632, -0.9645, -0.9662, -0.9682, -0.9705]**
  - Exact Match: **[-1.2180, -1.2118, -1.2054, -1.1989, -1.1921]**
- Average Distance Error: **4.4544**

ECG Dataset

- Query 1:
  - Approximate Match: **[3.1544, 3.1264, 3.0727, 2.9856, 2.8435]**
  - Exact Match: **[3.3224, 3.3224, 3.2787, 3.1752, 3.0400]**
- Query 2:
  - Approximate Match: **[3.2588, 3.2499, 3.1934, 3.1236, 3.0286]**
  - Exact Match: **[3.2874, 3.2874, 3.2473, 3.1464, 2.9462]**
- Average Distance Error: **2.0560**

GRAPH REPRESENTATION



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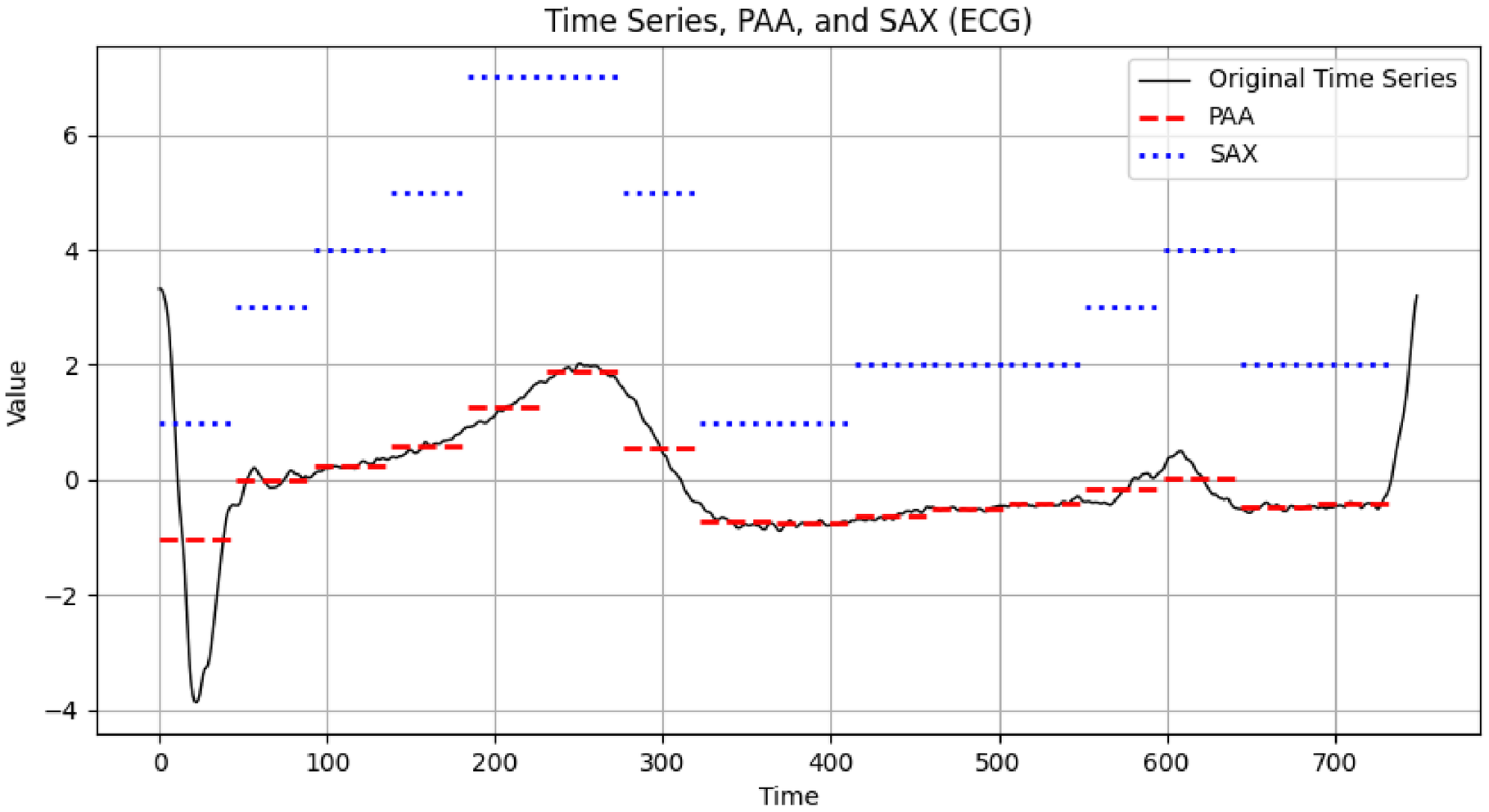

CONCLUSIONS

- The methodology of the paper is correctly replicated
- Even though there are some limitations of the paper, the pros outweigh the cons
- The method proves robust in two different datasets
- The code was successfully reproduced and the results were evaluated.

THANK YOU FOR YOUR ATTENTION

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