

Multivariate Symbolic Aggregate Approximation for ECG Analysis

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Outline

1 Introduction

2 Methods

3 Preliminary Results

Introduction

What is an ECG?

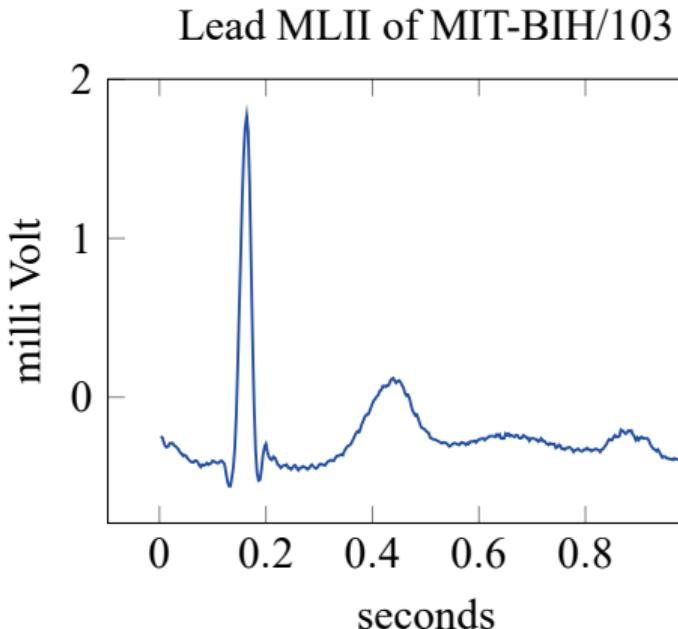


Figure 1: ECG of one heartbeat

- electrocardiogram (ECG or EKG) records the heart's electrical activity
- contains up to 12 simultaneous measurements—the leads
- common medical diagnostic tool

Lead MLII of MIT-BIH/103

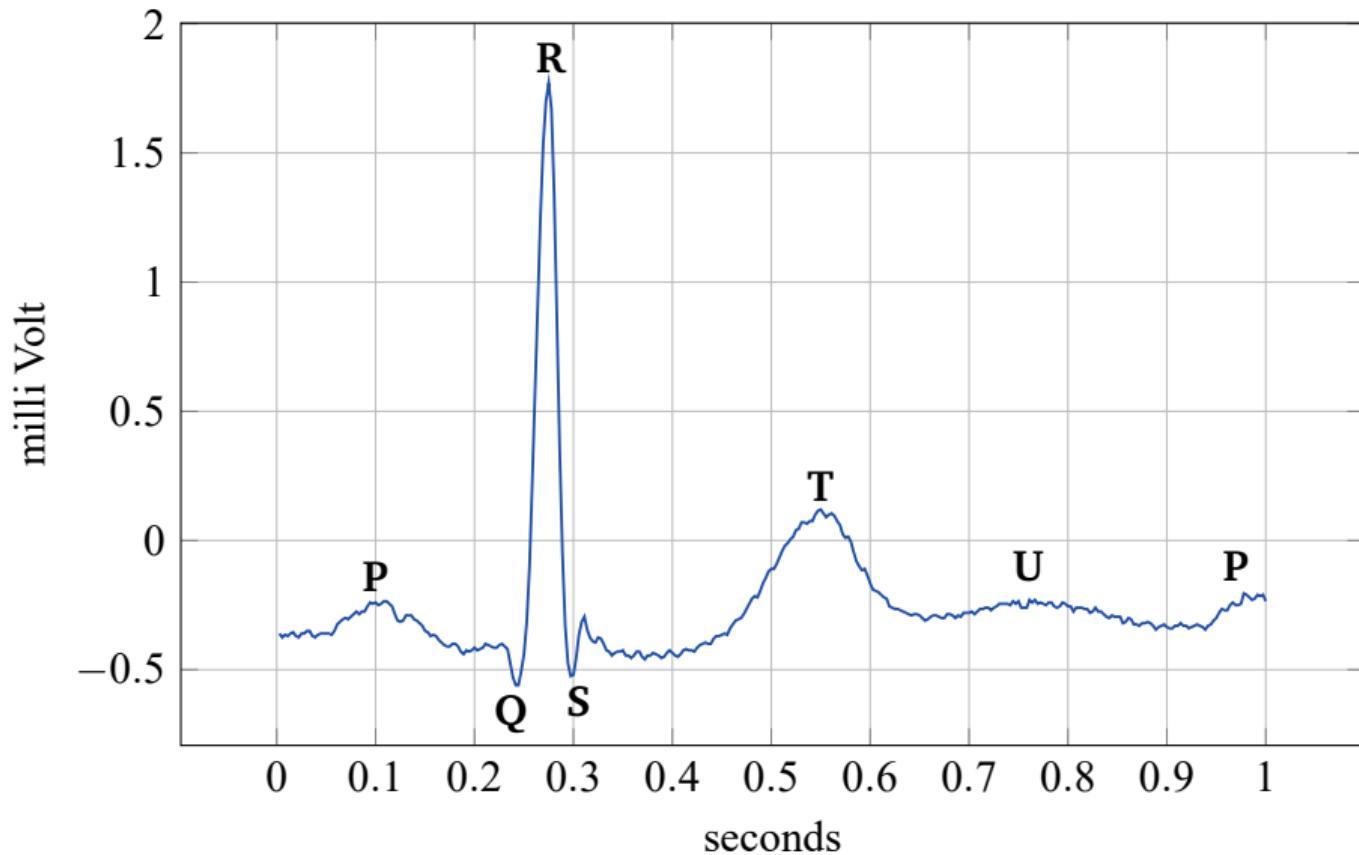


Figure 2: Annotated ECG of one heartbeat

ECGs as Time Series

Definition

A discrete time series is an ordered sequence that, at discrete points in time, has n values each. If $n = 1$, the series is univariate and if $n > 1$, it is multivariate.

- digital ECGs are discrete multivariate time series:
 - have > 1 value at each point, often $n = 12$
 - recorded at discrete, evenly spaced time points
- time series analysis methods can be applied to ECGs

ECG Analysis

- standard method: manual analysis by cardiologist
- recently: automated or computer-assisted ECG analysis
- multiple stages:(1) signal acquisition; (2) data transformation, processing, filtering; (3) waveform recognition, feature extraction; (4) classification
- current research focus: artificial neural networks
- relatively new methods are SAX, MSAX, and HOT SAX

SAX, MSAX, and HOT SAX

- Lin *et al.* (2003): Symbolic Aggregate Approximation (SAX)—simplified, symbolic representation
- Anacleto *et al.* (2020): Multivariate SAX (MSAX)—expands SAX to multivariate time series
- Keogh *et al.* (2005): Heuristically Ordered Time series using Symbolic Aggregate Approximation (HOT SAX)—discord discovery algorithm for SAX

Time Series Discords

Definition

A time series discord is the subsequence of a time series that is most different from all other subsequences.

k time series discords are the k most different subsequences.

- discords represent anomalies in an ECG
- can be found by comparing all subsequences to all other subsequences; does not scale well
- HOT SAX makes this process faster

Hypothesis

HOTSAX with MSAX will increase the number of relevant discords detected compared to HOTSAX with SAX.

Accuracy can be judged with the help of annotated ECGs from online databases.

Methods

Step 1: Z-Normalization

Assumption

The time series values are normally distributed.

SAX

- normalize univariate time series
- uses scalar mean and variance

MSAX

- normalize multivariate time series
- uses vector mean and covariance matrix

Step 2: Dimensionality Reduction

PAA

Piecewise Aggregate Approximation (PAA) takes T time series points, splits it into w ($w < T$) segments, and averages each of them.

SAX

- apply PAA to time series

MSAX

- apply PAA to each of the time series individually

SAX PAA of lead MLII of MIT- BIH/103

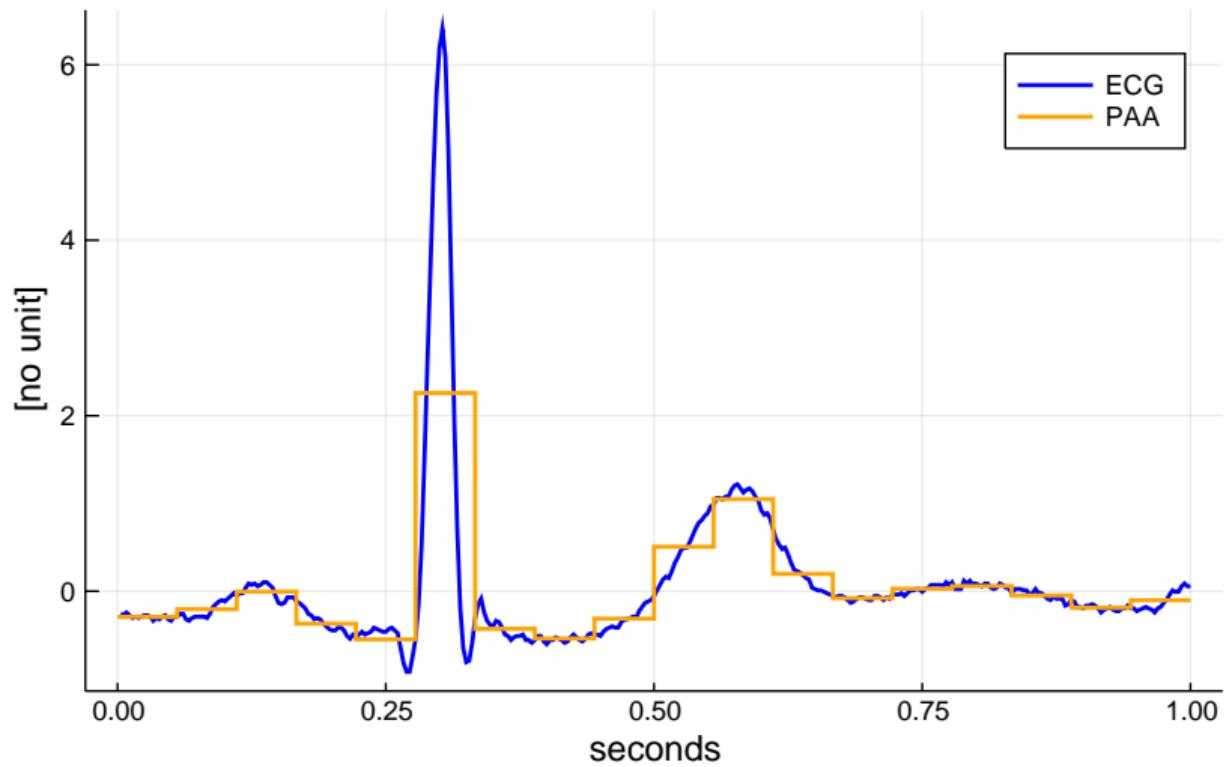


Figure 3: ECG with PAA (MITBIH/100, $w = 18$, $T = 360$)

Step 3: Discretization

SAX Discretization

Find breakpoints splitting $\mathcal{N}(0, 1)$ into B equiprobable segments.

Assign a letter to each area: a to most-negative, b to the next biggest...

PAA segments get letters based on which area they are in.

SAX

- discretize the time series
- results in one word

MSAX

- discretize each time series individually
- results in one word, one letter per time series

SAX of lead MLII of MIT- BIH/103

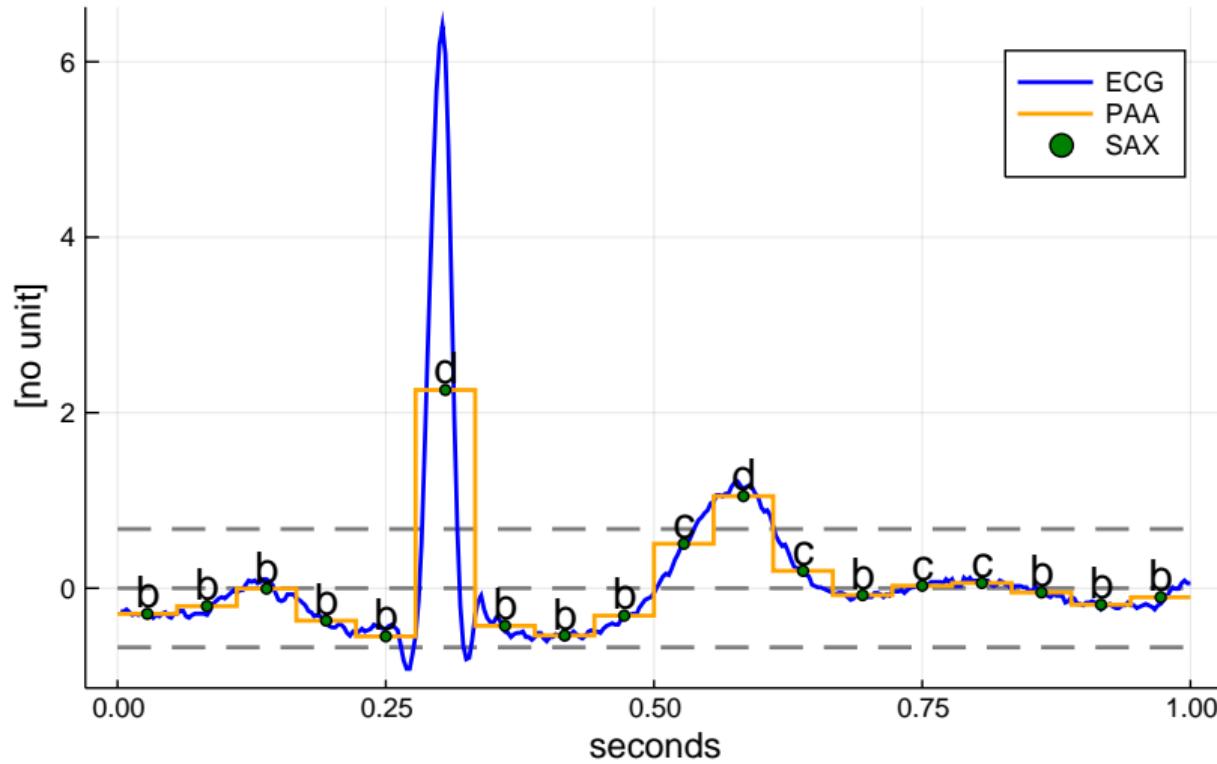


Figure 4: SAX (MITBIH/100, $w = 18$, $T = 360$, $B = 4$)

Step 4: Distance Measure

MINDIST

A distance measure is defined to compare two SAX words. Distance is defined for a pair of letters: 0 if they are neighbors; absolute difference of breakpoint values otherwise.

SAX

$$\sqrt{\frac{T}{w}} \sqrt{\sum_{i=1}^w (\text{dist}(\hat{q}[i], \hat{c}[i]))^2}$$

MSAX

$$\sqrt{\frac{T}{w}} \sqrt{\sum_{i=1}^w \left(\sum_{j=1}^n (\text{dist}(\hat{q}_j[i], \hat{c}_j[i]))^2 \right)}$$

Difference Matrix

Table 1: Difference matrix for $B = 4$

	a	b	c	d
a	0	0	0.67449	1.34898
b	0	0	0	0.67449
c	0.67449	0	0	0
d	1.34898	0.67449	0	0

HOTSAX

- “brute-force” discord discovery is slow, needs T^2 operations
- HOTSAX speeds up discord discovery by considering that
 - discords are rare, start with rarest segment
 - similar segments have similar distances, consider together
- HOTSAX detects anomalies, it is not a classifier
- it uses SAX and MSAX for dimensionality reduction

Results

Implementation

- SAX, MSAX, HOT SAX implemented in Julia, a scientific programming language
- used annotated digital ECGs from the MIT-BIH arrhythmia database
- HOT SAX performed for different w, B , subsequence lengths
- results exported to CSV file and analyzed using the R programming language

Preliminary Results

- focus on comparing SAX and MSAX with the top $k = 80$ discords
- to analyze the relevance of results, recall (sensitivity) is used
- analyzed total of 816 results for different parameters (SAX and MSAX for each)
- recall for MSAX is higher compared to SAX
- if SAX is applied to 2 leads and the results combined, it slightly outperforms MSAX

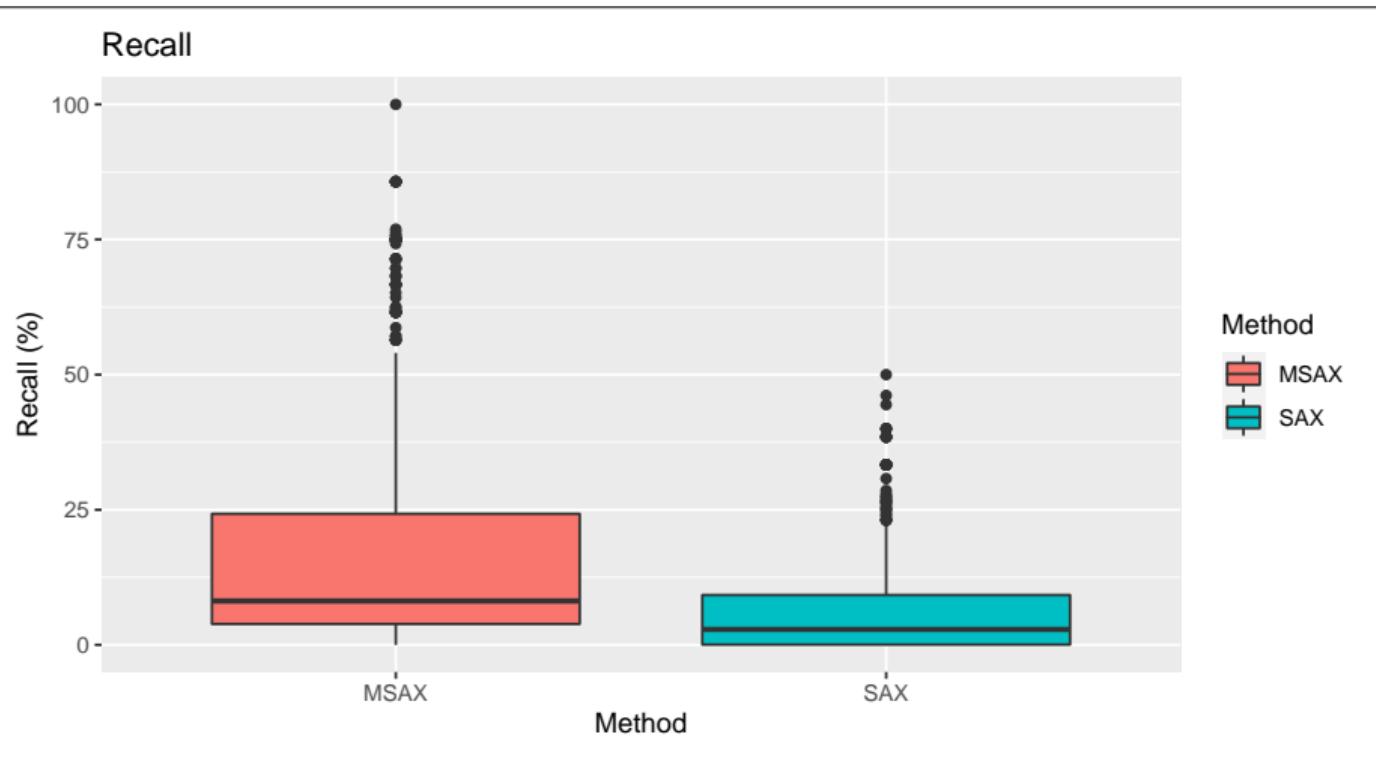


Figure 5: Boxplot comparing Recall for MSAX and single-lead SAX

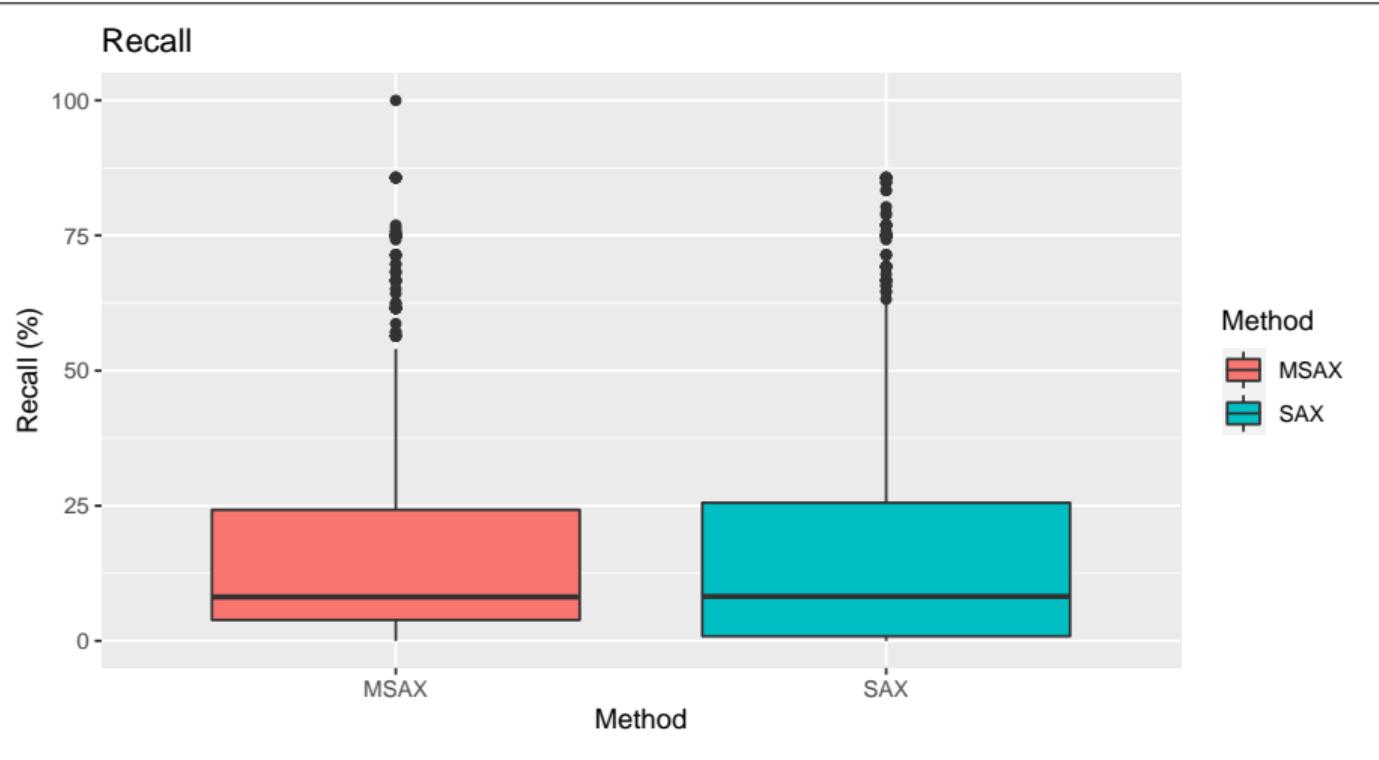


Figure 6: Boxplot comparing Recall for MSAX and dual-lead SAX

Outlook

- perform statistical tests for significance of the result
- analyze the outliers visible in the boxplots
- more tests with different sets of parameters
- explore the influence of parameters on the result
- use the 12-lead INCART ECG database to investigate the influence of larger numbers of leads

Thank You!

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