

# Multivariate Symbolic Aggregate Approximation for ECG Analysis

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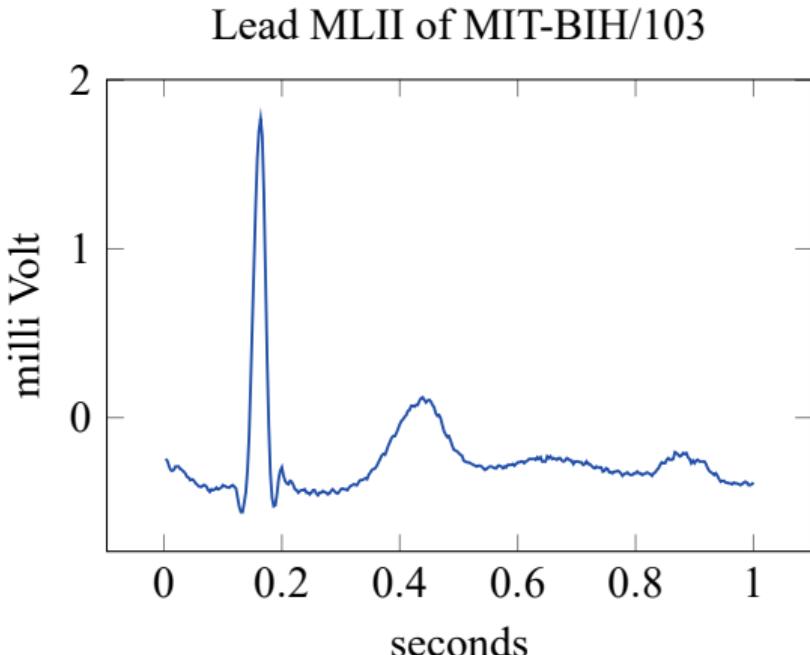
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# Introduction

- ischemic heart disease (IHD) makes up 16% of global deaths but can be diagnosed using an electrocardiogram (ECG or EKG)
- manual ECG analysis is slow and error-prone, computers can help
- long ECGs are problematic even for computers → simplification through representation
- such representations should be simpler, but still correspond to the original data

# What is an ECG?



- records the heart's electrical activity
- contains up to 12 leads (simultaneous measurements)

Figure 1: ECG of one heartbeat.

# Representation and Classification

- for simplification, time series can be represented, e.g. as SAX or MSAX
- then, the representation can be analyzed instead of the raw data
- HOT SAX can be used to classify ECG segments into discord and non-discord
- this work uses HOT MSAX to combine MSAX and HOT SAX
- effectiveness of the methods will be judged by recall and precision

# Research Questions & Hypothesis

- Using the MIT-BIH ECG database, what parameters maximize HOT SAX and HOT MSAX recall?
- Which is better: optimal HOT SAX or optimal HOT MSAX?

HOT MSAX should have higher recall than HOT SAX if both use their best parameters

# Novel Contributions

- application of MSAX to ECG discord discovery and medical data in general
- the HOT MSAX algorithm, a modification of HOT SAX that uses MSAX
- the expansion of HOT SAX to multivariate time series through HOT MSAX

# Method Background

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

# SAX and MSAX – Overview

SAX		MSAX
Application		
univariate time series, e.g. a single ECG lead		multivariate time series, e.g. multiple ECG leads (whole ECG)
Steps		
(1) univariate z-normalization (2) PAA dimension reduction ( $w$ ) (3) SAX discretization ( $a$ )		(1) multivariate z-normalization (2) PAA dimension reduction ( $w$ ) (3) SAX discretization ( $a$ )

# SAX and MSAX – Step (2)

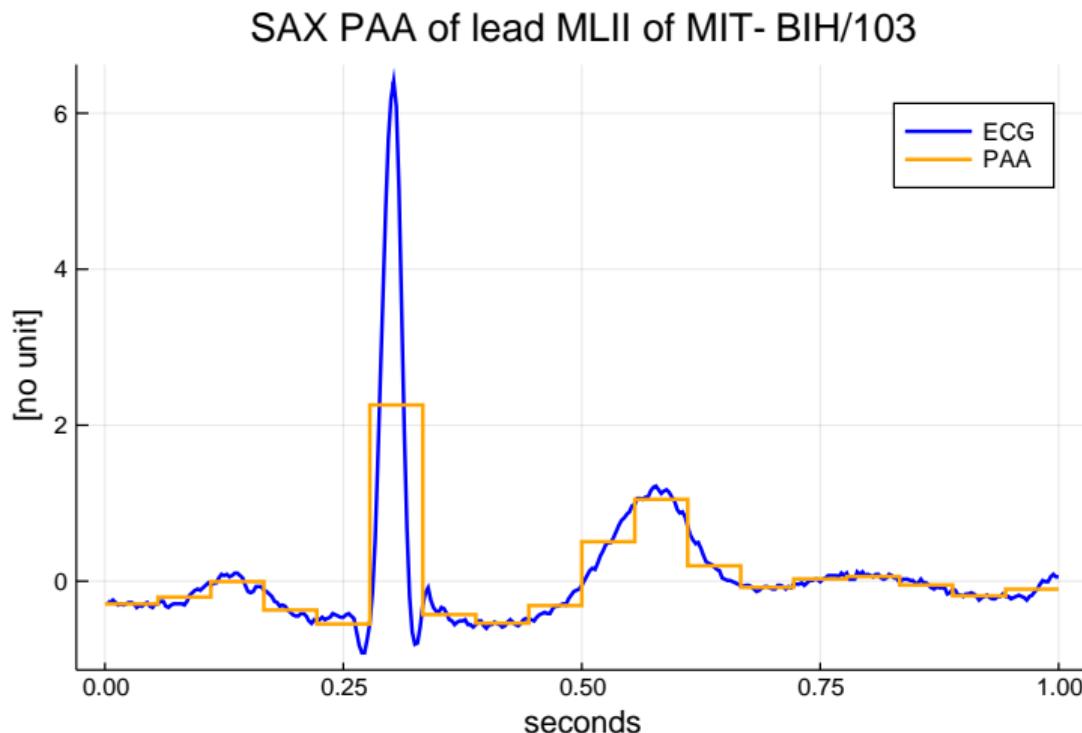


Figure 2:  
ECG with  
PAA,  $w = 18$

## SAX – Step (3)

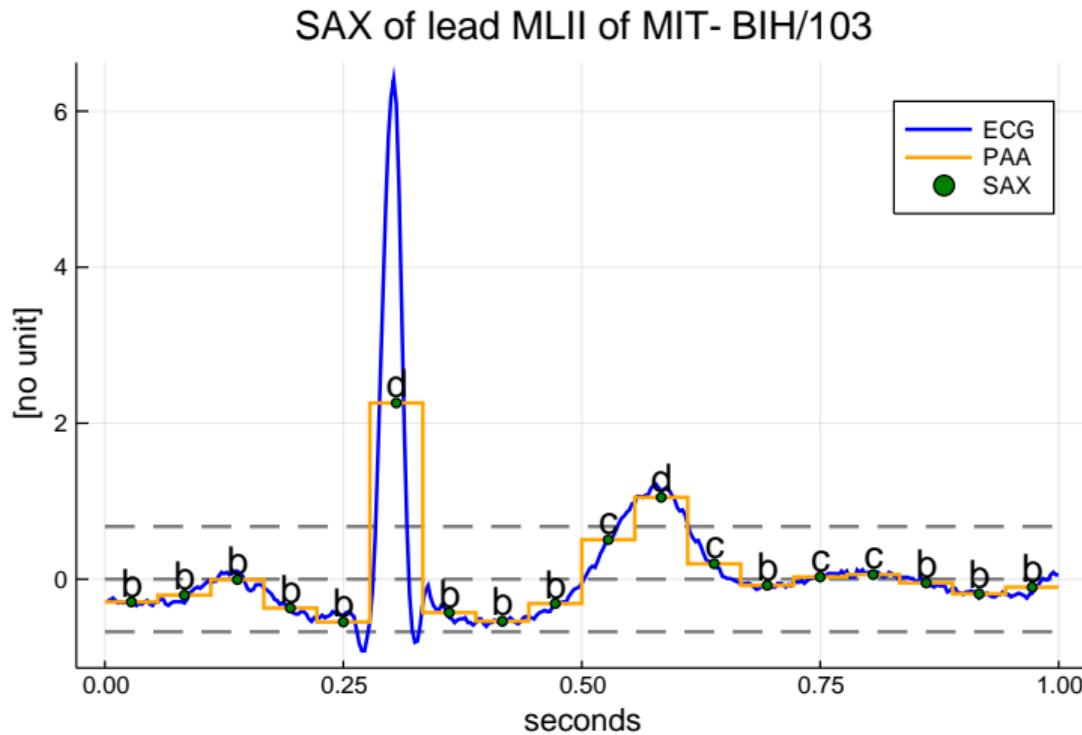
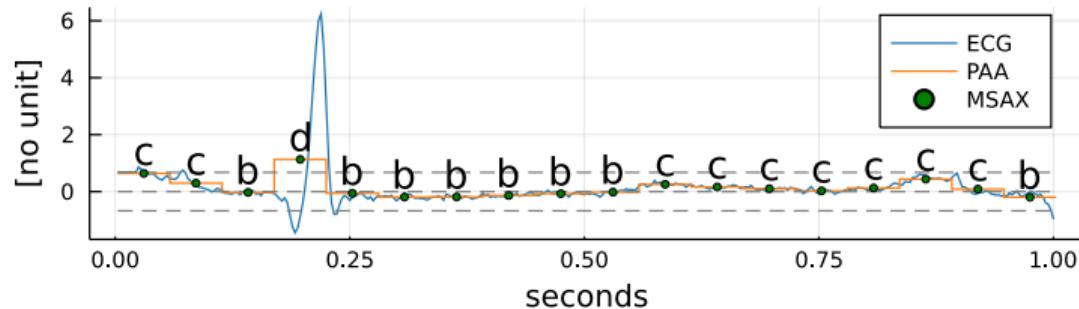


Figure 3:  
ECG with  
SAX,  $w = 18$ ,  
 $a = 4$

# MSAX – Step (3)

MSAX of lead MLII of MIT-BIH Database/100



MSAX of lead V5 of MIT-BIH Database/100

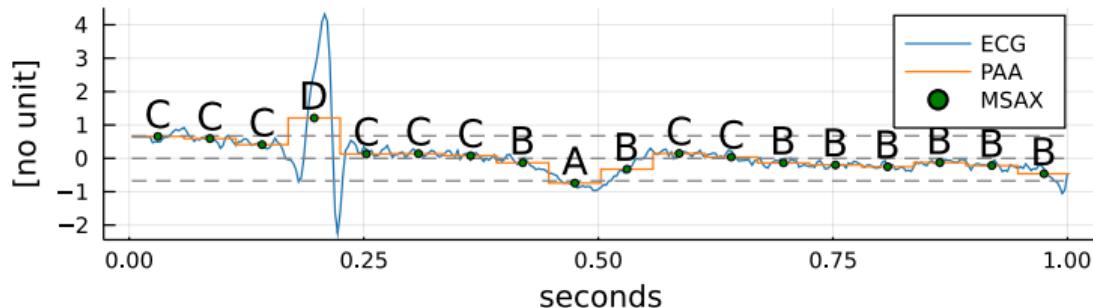


Figure 4:  
ECG with  
MSAX,  
 $w = 18$ ,  
 $a = 4$

# SAX and MSAX – Distance Measure

- needed to compare two SAX/MSAX segments
- sum of distances between symbols
- symbol distance is based on difference of breakpoints
- lower-bounds Euclidean Distance, i.e. corresponds to “real” distance

# HOT SAX and HOT MSAX – Overview

- HOT SAX: find discords in SAX-represented time series
- classifies time series segments into “discord” and “non-discord”
- HOT MSAX: uses MSAX instead of SAX
- HOT MSAX can work with multivariate time series

# HOT SAX and HOT MSAX – Heuristic

- two parameters:  $m$  and  $k$
- two assumptions:
  - time series discords are rare
  - segments similar to discords may also be discords
- speed up discord discovery:
  - consider rarest segments first
  - consider similar segments together

# Analysis Process

- (1) perform HOT SAX and HOT MSAX for many parameter combinations for all ECGs in the MIT-BIH database
- (2) find recall, precision for each combination
- (3) set recall threshold of 95%, then sort by precision
- (4) choose top 10 of those parameters for each method
- (5) choose best parameters for each method using box plot, interquartile range, outliers

# Three Datasets

- (1) S-SAX: data for HOT SAX algorithm, considering each lead separately
- (2) D-SAX: data for HOT SAX, considering both leads combined
- (3) MSAX: data for the HOT MSAX algorithm

# Overview of Results

**Table 1:** Coarse Overview of Results. Shown are sets of parameters for each method that satisfy the recall threshold of 95%.

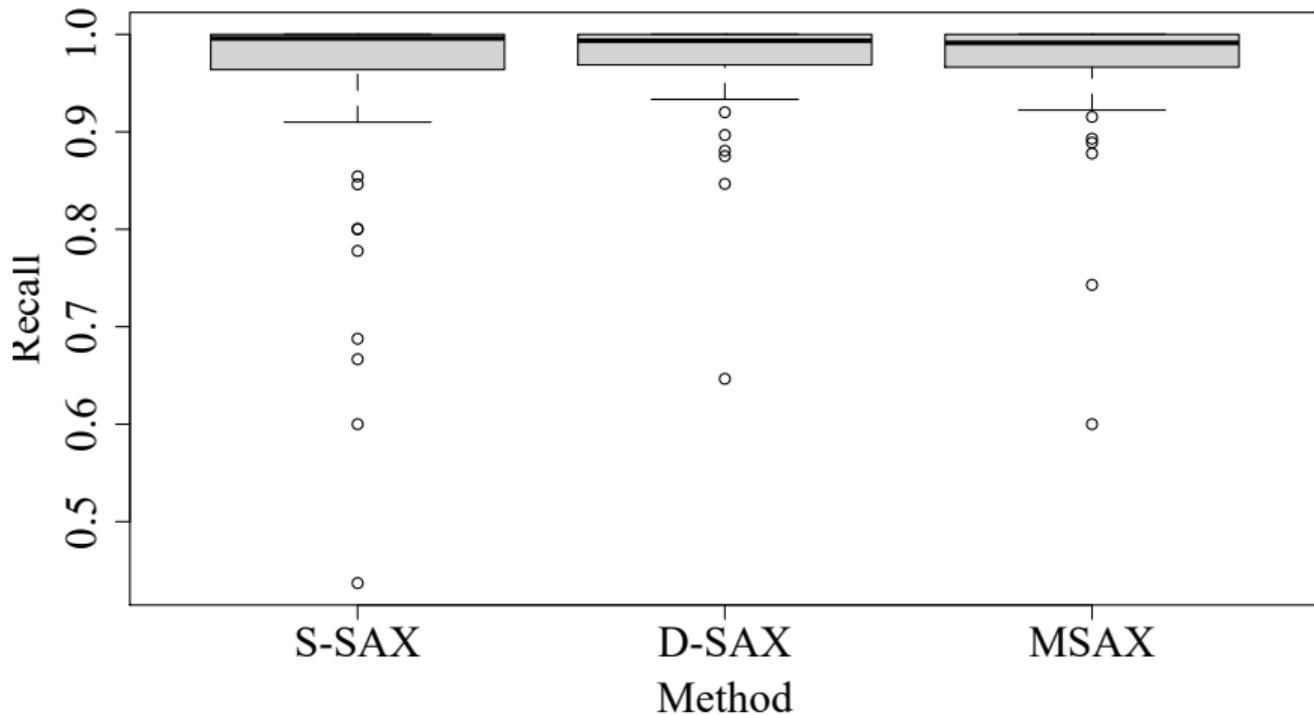
Method	Total Sets	Sets Satisfying recall $\geq 95\%$
S-SAX		99 (1.2%)
D-SAX	4,968	192 (3.9%)
MSAX		255 (5.1%)

# Best Parameter Sets by Method

**Table 2:** Best Parameter sets for each of the methods. Best overall parameters highlighted in bold.

Method \ Parameter	$k$	$w, m$	$a$
S-SAX	-1	36	21
D-SAX	-1	<b>12</b>	24
MSAX	-1	<b>12</b>	<b>17</b>

## Boxplot of Recall by Method for Optimal Parameters



# Comparing Best Parameter Sets – Recall

**Table 3:** Statistical measures for recall of optimal parameter sets. Best overall values highlighted in bold.

Method \ Measure	IQR	Median	Outliers
S-SAX	0.035	<b>99.60%</b>	11
D-SAX	<b>0.030</b>	99.35%	<b>6</b>
MSAX	0.033	99.13%	<b>6</b>

## Discussion

- no statistically significant difference in recall for the methods
  - hypothesis cannot be supported
- MSAX has both the smallest alphabet size and highest dimension reduction
  - this points to MSAX being more efficient in achieving the same results
- Anacleto, Vinga, and Carvalho [5] showed similar performance for ECG classification, supports this work's conclusion

# Conclusion

- could not demonstrate superiority of HOT MSAX for best parameters
- contributed the HOT MSAX method to literature
- showed viability of a discord classifier for ECG analysis
- in future research: different ECG data, different detection criteria

# References I

- [1] *The top 10 causes of death*, 2020. [Online]. Available: <https://www.who.int/news-room/fact-sheets/detail/the-top-10-causes-of-death> (visited on 05/25/2021).
- [2] J. Lin, E. Keogh, S. Lonardi, and B. Chiu, “A symbolic representation of time series, with implications for streaming algorithms,” in *Proceedings of the 8th ACM SIGMOD Workshop on Research Issues in Data Mining and Knowledge Discovery - DMKD '03*, San Diego, California: ACM Press, 2003, pp. 2–11. doi: 10.1145/882082.882086.
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## References II

- [5] M. Anacleto, S. Vinga, and A. M. Carvalho, “MSAX: Multivariate Symbolic Aggregate Approximation for Time Series Classification,” in *Computational Intelligence Methods for Bioinformatics and Biostatistics*, P. Cazzaniga, D. Besozzi, I. Merelli, and L. Manzoni, Eds., ser. Lecture Notes in Computer Science, Cham: Springer International Publishing, 2020, pp. 90–97. doi: [10.1007/978-3-030-63061-4\\_9](https://doi.org/10.1007/978-3-030-63061-4_9).

Thank You!