

Multivariate Symbolic Aggregate Approximation for ECG Analysis

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ECG Basics

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- record electrical impulses of the heart
- modern ECGs have 12 leads, online datasets contain 2 or more
- ECGs are multivariate data (multiple data points at each sample point)

$$\mathbf{x}^i[t] = (x_1^i[t], \dots, x_n^i[t])$$

- ECGs are very common diagnostic tools

ECG waveform

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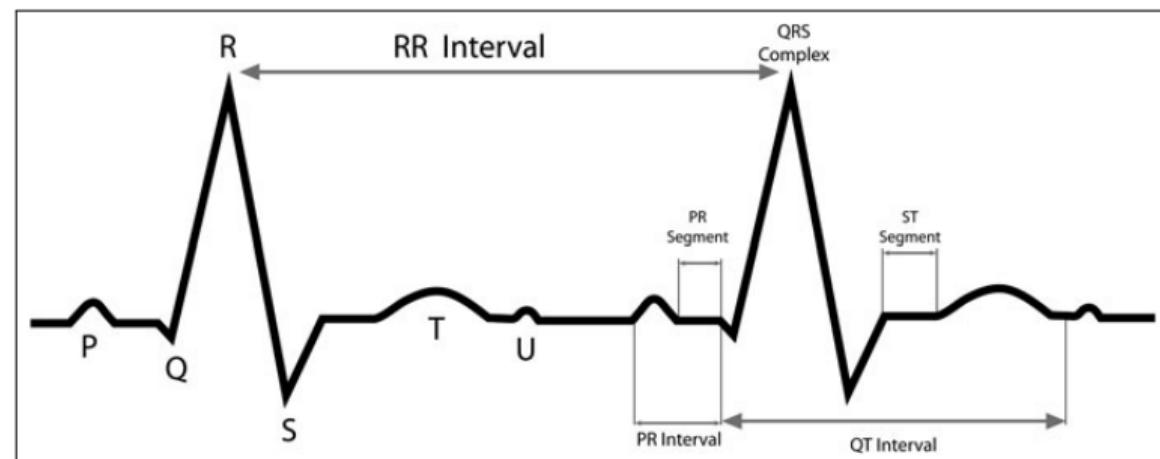


Figure 1.1: A standard ECG waveform with annotations

Automated ECG Analysis

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- ECGs represent large amounts of data, thorough analysis is required
- 5 stages: (1) signal acquisition, filtering; (2) data transformation, processing; (3) waveform recognition; (4) feature extraction; (5) classification
- some methods include FFT, DWT, ANN, kNN, filters
- balance between accuracy and complexity needed

SAX and MSAX

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- Symbolic Aggregate Approximation (SAX) creates a simplified, symbolic representation
 - is guaranteed to behave like the original data
 - works on univariate time series, has been used on ECGs
 - Multivariate SAX (MSAX) expands SAX to multivariate time series
- using MSAX on ECGs should increase the accuracy of discord detection compared to SAX

MSAX for ECG Analysis

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- assumption: data is approximately normally distributed
- to analyze time series, they are first normalized so that $\mu = 0$ and $\sigma = 1$

$$x^i[t] = \frac{X^i[t] - \mu}{\sigma}$$

- enables comparison between different time series

PAA

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- piecewise aggregate approximation (PAA) reduces dimensionality (through averaging of segments)

- simplifies the time series

- results in $\bar{C} = \bar{c}_1, \dots, \bar{c}_w$

- getting element i of \bar{C} (time series x has length n)

$$\bar{c}_i = \frac{w}{n} \sum_{j=\frac{n}{w}(i-1)+1}^{\frac{n}{w}i} x_j$$

PAA Graph

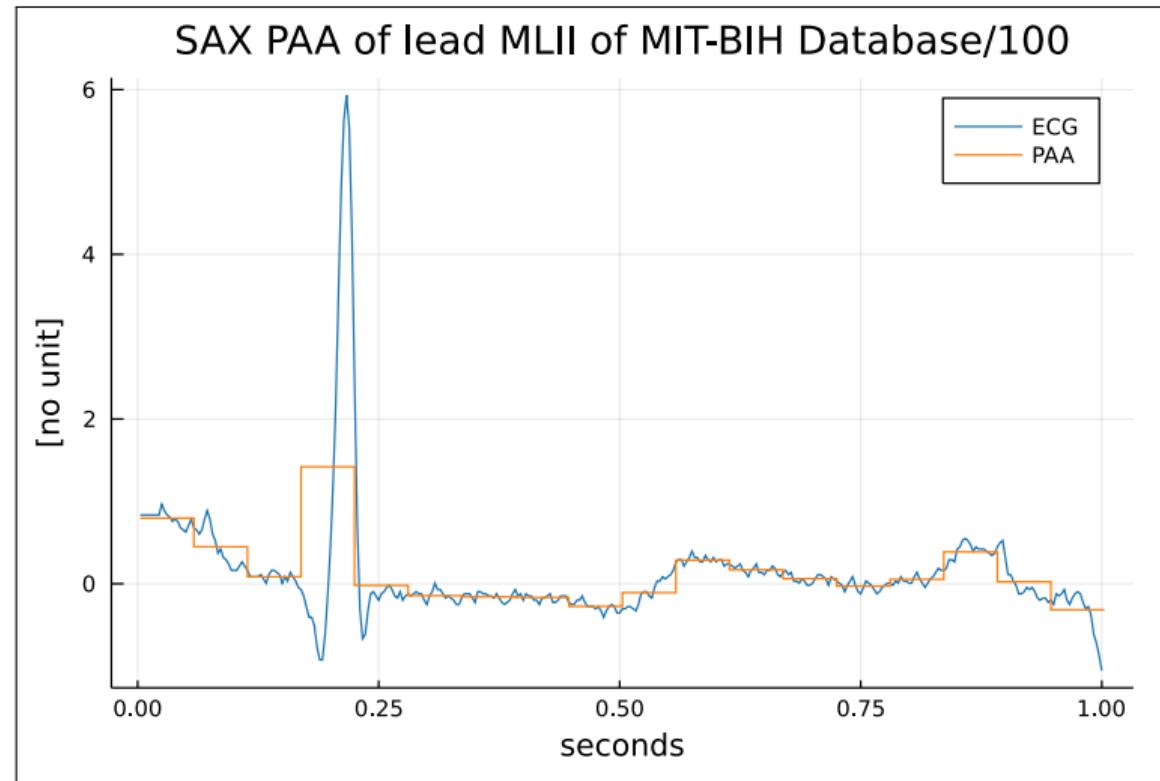


Figure 2.1: ECG with PAA (MITBIH/100, $w = 18$, $n = 360$)

Discretization

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- assign letters to PAA segments
- breakpoints are created that divide a Gaussian curve into equal parts
- number of breakpoints dependent on size of alphabet
- all PAA below lowest breakpoint are a , the ones above it $b\dots$

Discretization Graph

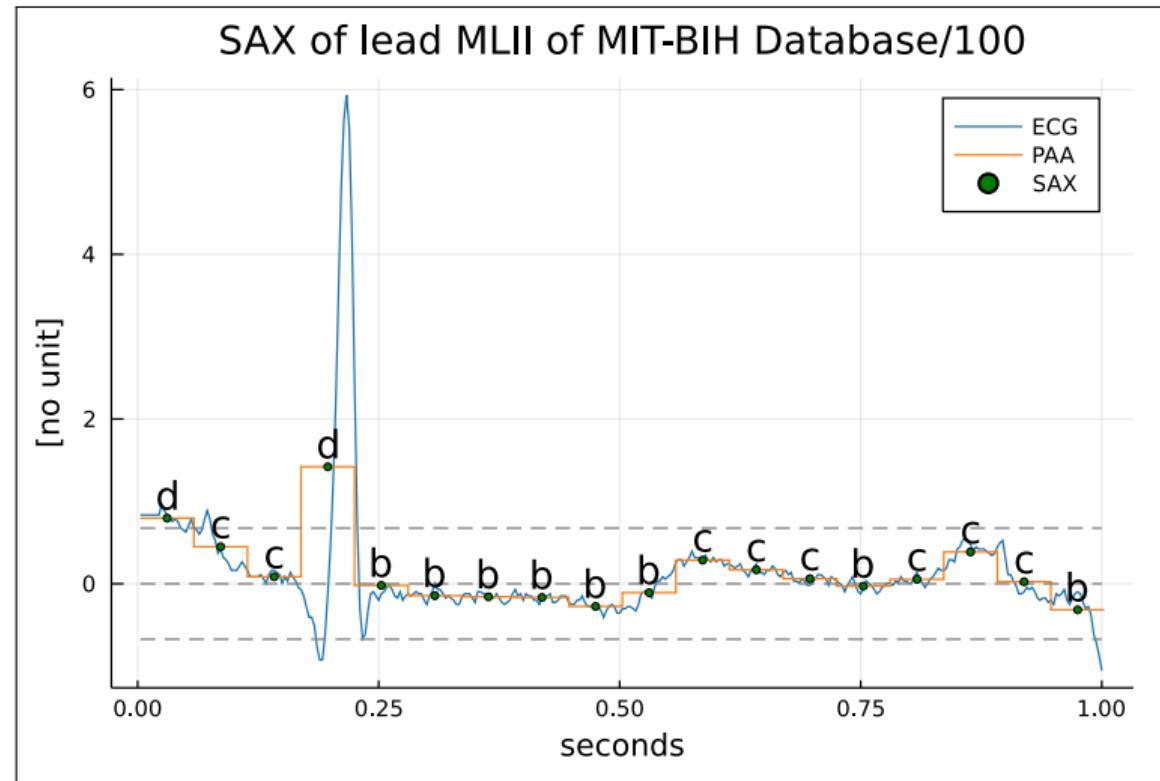


Figure 2.2: SAX (MITBIH/100, $w = 18$, $n = 360$, alphabet size 3)

Distance Measure

- SAX lower bounds the Euclidean distance, i.e. SAX distances correspond to Euclidean distances
- Euclidean distance between 2 time series Q, C

$$D(Q, C) \equiv \sqrt{\sum_{i=1}^n (q_i - c_1)^2}$$

- SAX distance

$$MINDIST(\hat{Q}, \hat{C}) \equiv \sqrt{\frac{n}{w}} \sqrt{\sum_{i=1}^w (dist(\hat{q}_i, \hat{c}_i))^2}$$

- $dist(\hat{q}_i, \hat{c}_i)$ is the difference between the breakpoints of \hat{q}_i, \hat{c}_i

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- perform multivariate normalization
- mean vector μ as vector of the means for each time series
- covariance matrix Σ for variances and covariances between the different time series

$$\mathbf{x}[t] = \Sigma^{-1/2}(\mathbf{X}[t] - \boldsymbol{\mu})$$

- this uses mean and covariance structure of the multivariate data

PAA and Discretization

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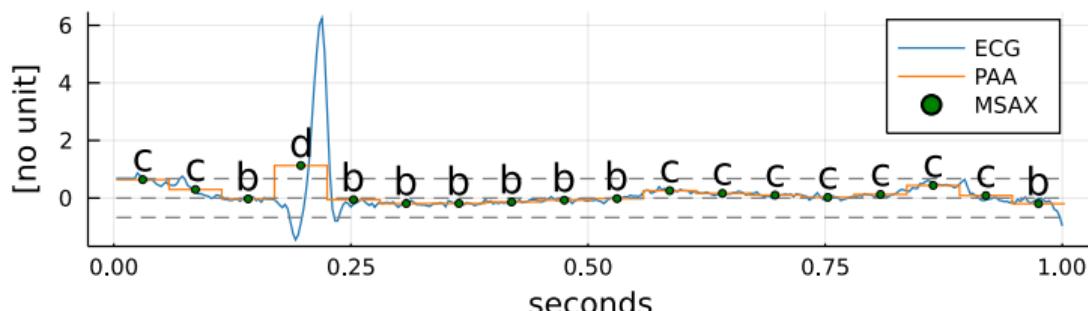
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- PAA is used here like in SAX, each time series is handled separately
- the discretization process works the same way too
- each time series component is discretized separately
- to differentiate them, one alphabet can for example be uppercase

Discretization Graph

MSAX of lead MLII of MIT-BIH Database/100



MSAX of lead V5 of MIT-BIH Database/100

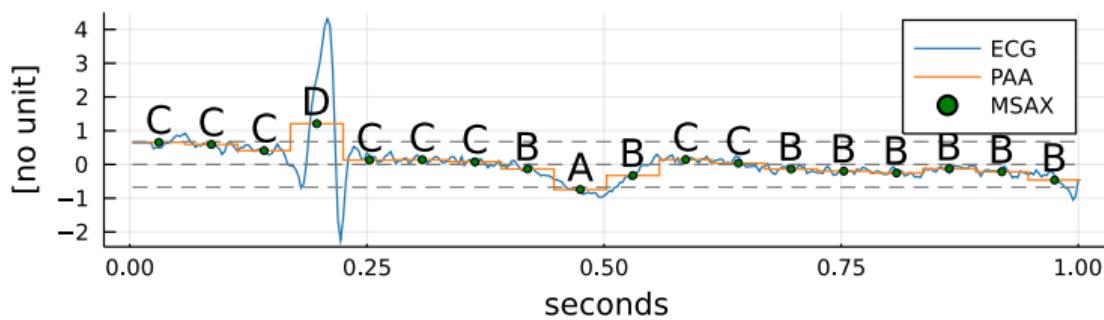


Figure 3.1: MSAX (MITBIH/100, $w = 18$, $n = 360$, alphabet size 3)

Distance Measure

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- this distance measure is based on *MINDIST*
- it is also lower bounding the Euclidean distance
- it adds an extra step of adding the *dist* values for the time series components

$$MINDIST_MSAX(Q, C) = \sqrt{\frac{n}{w}} \sqrt{\sum_{i=0}^w \left(\sum_{i=0}^n dist(q[i], c[i])^2 \right)}$$

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HOT SAX

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- time series discords are sections of a time series that are most different from all other segments of the time series (e.g. diseases in an ECG)
 - can be found by comparing all segments to all other segments
 - Heuristically Ordered Time series using Symbolic Aggregate Approximation is better
 - discords are generally rare, start with the rarest segment
 - similar segments are likely to have similar distances, consider them together
- applying HOT SAX with MSAX to ECGs should discover more discords than HOT SAX with SAX

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- used the MIT-BIH ECG database
- database has 48 recordings, every heart beat has been annotated by experts
- use HOTSAX with SAX, MSAX to find discords
- use the annotations to check if the discovered discord is a normal heart beat or not
- in ECG 108, HOTSAX with SAX found 16 discords, HOTSAX with MSAX found 21

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- perform more sophisticated analysis of results
- apply the process to all ECGs in the MIT-BIH database
- experiment with different parameters for SAX/MSAX
- use the method on a different ECG database

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