

Wavelet-based ECG delineation for SVT

Workflow

Supraventricular Tachycardia Explanation

General description,
highlighting signal
morphology
characteristics

Dataset Descriptions

Pros, cons, selected
samples presentation,
label explanations and
brief dataset inspection

Algorithm Implementation

Based on "A wavelet-
based ECG delineation
algorithm for 32-bit
integer online
processing" Luigi Y Di
Marco and Lorenzo
Chiari

Performance Quantification on Fully Annotated Data

Global precision, recall,
F1, mean MSE; individual
signals plots analysis

Performance Quantification on Partially Annotated Data

Signal extraction from
image, rhythm
classification using
Random Forest, TSNE

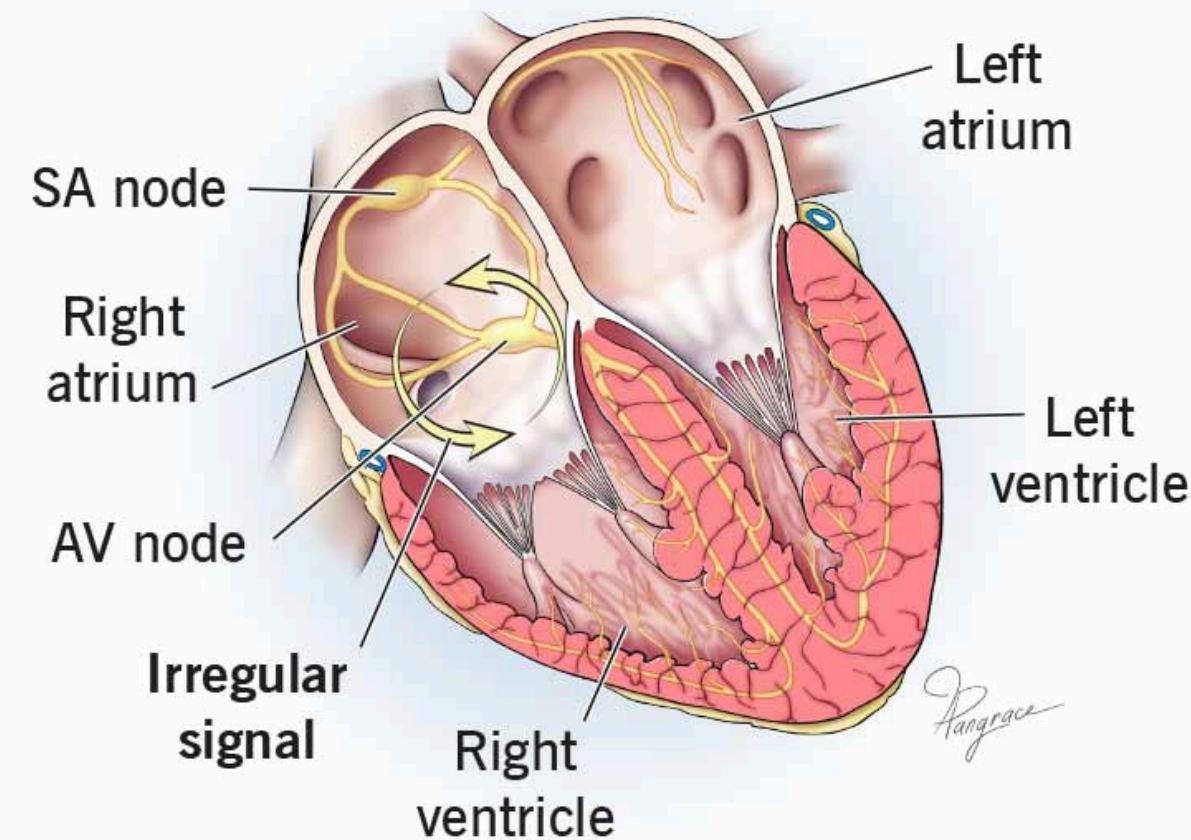
Supraventricular Tachycardia explained

Supraventricular tachycardia (SVT) is a group of rapid heart rhythms originating above the ventricles, typically from the atria or the atrioventricular (AV) node.

SVT can cause symptoms such as palpitations, dizziness, syncope, or chest discomfort. Its identification relies on correlating clinical presentation with characteristic ECG findings.

The onset and duration of SVT episodes vary, with some forms exhibiting abrupt episodes and others being more persistent.

ELECTROCARDIOGRAPHIC FEATURES



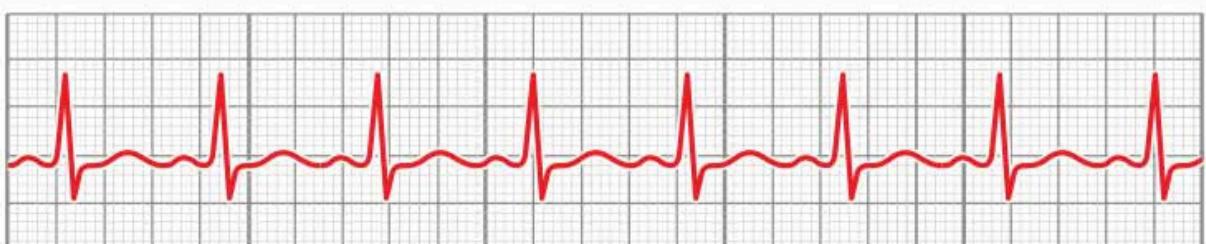
Normal sinus rhythm

60-100 bpm



Tachycardia

> 100 bpm



1.

**HEARTBEAT
>100 bpm**

2.

**NARROW
<120ms QRS
COMPLEXES**

3.

**HIDDEN OR
ABNORMAL
P-WAVES**

4.

**USUALLY
REGULAR RR
INTERVALS**

PROs:

- **12-lead** ECG dataset, each lead fully annotated.
- Manual annotations of P, QRS and T boundaries and peaks, done independently per lead by cardiologists.
- Clear metadata covering diagnostic, **rhythm** and **form** statements.
- Includes co-occurring pathologies.
- Recent: published in 2021.
- Mostly clean, high resolution recordings: 500 Hz.

CONs:

- High resolution → the algorithm is designed for 32-bit integers, but only to avoid overflow inside the filter bank → math, thresholds or delineation are unaffected.
- Very few data: 200 ECG recordings.
- Lacks samples on some SVT-related pathologies and has very few healthy control samples.
- Short duration: **10s recordings** → can affect learning times.

Selected SVT-related samples

Rhythm-related: **20**

AFIB: 13, STACH: 4, AFLT: 3, PSVT: 0

Form-related: **7**

PAC: 7 (some are overlapping)

Control group: **23**

Sinus Rythm: 23

dataset 1 LUDB

Kalyakulina, A., Yusipov, I., Moskalenko, V., Nikolskiy, A., Kosonogov, K., Zolotykh, N., & Ivanchenko, M. (2021). Lobachevsky University Electrocardiography Database (version 1.0.1). PhysioNet. RRID:SCR_007345.

<https://www.physionet.org/content/lfdb/1.0.1/>

Extrasystoles

Atrial extrasystole, undetermined

Atrial extrasystole, low atrial

Atrial extrasystole, left atrial

Atrial extrasystole, SA-nodal extrasystole

Atrial extrasystole, type: single PAC

Atrial extrasystole, type: bigemini

Atrial extrasystole, type: quadrigemini

Atrial extrasystole, type: allorhythmic pattern

PROs:

- Large **12-lead ECG** dataset: 21799 ECGs, 18869 patients
- Clear and standardized annotations, validated by cardiologists, covering diagnostic, **rhythm** and **form** statements.
- Includes both co-occurring pathologies and healthy control samples.
- Recent: published in 2022.
- Has many SVT recordings (which is rare) → they're characterized by transient-dominant features, making them perfect for wavelet-based delineations.
- Mostly clean, high resolution recordings: 500 Hz.

CONs:

- High resolution.
- Short duration: **10s recordings**.
- No specific annotations on exact QRS times → makes validation less straightforward.

Selected SVT-related samples

Rhythm-related: **132**

AFLT: 56, AFIB: 48, PSVT: 24, STACH:4

Form-related: **37**

PAC: 37

Control group: **169**

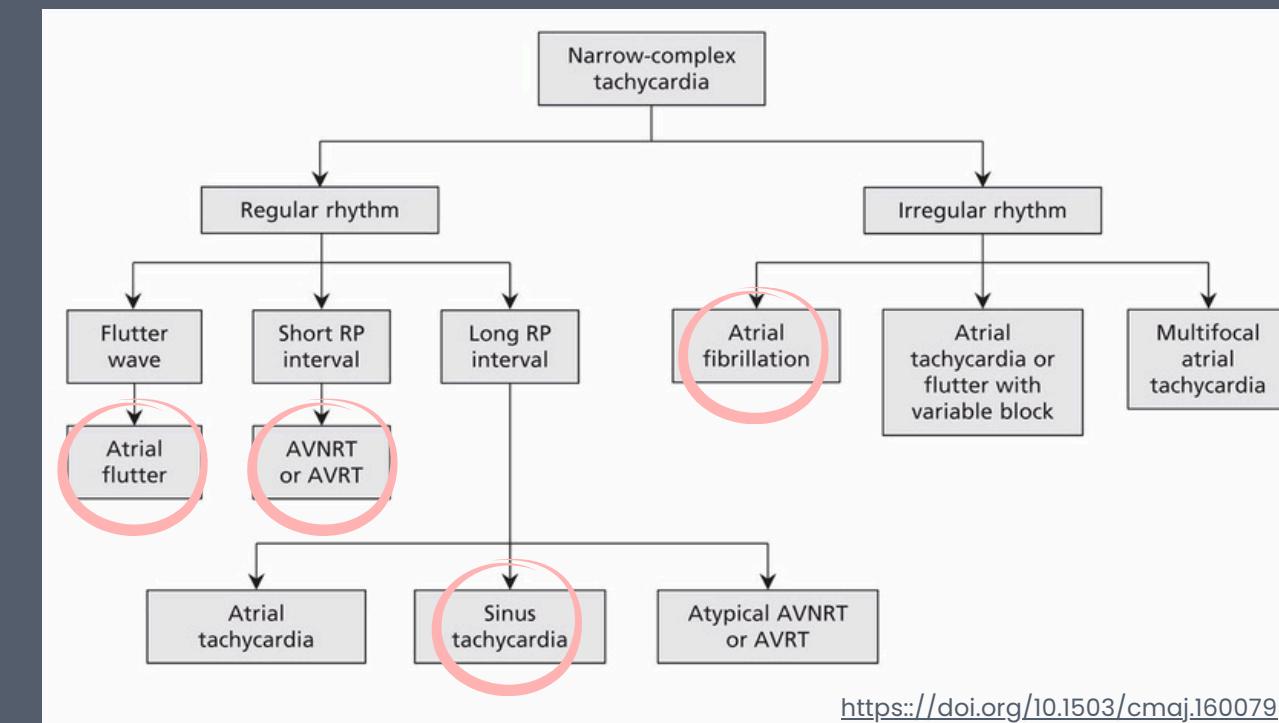
NORM: 169

dataset 2 PTB-XL

Wagner, Patrick, et al. "PTB-XL, a large publicly available electrocardiography dataset" (version 1.0.3). PhysioNet (2022).

RRID:SCR_007345

<https://physionet.org/content/ptb-xl/1.0.3/>

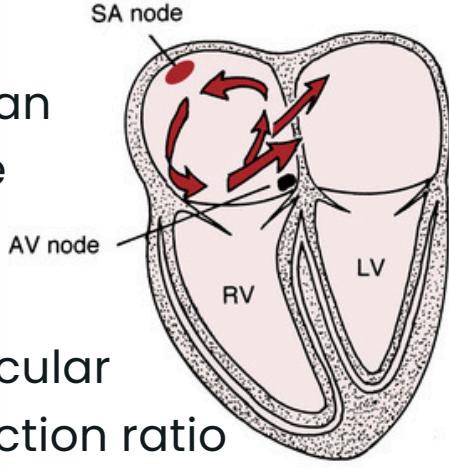


<https://doi.org/10.1503/cmaj.160079>



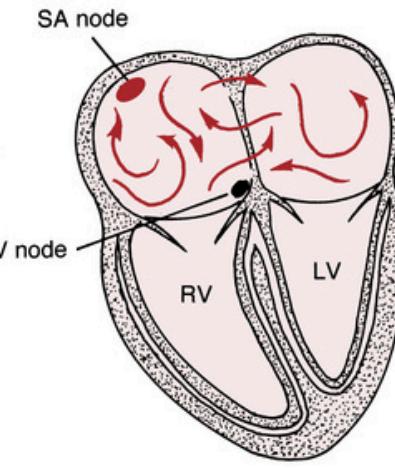
1. [AFLT] ATRIAL FLUTTER

- A macroreentrant circuit within an atrium causes impulses to cycle
→ produces characteristic sawtooth pattern (F waves)
- Regular atrial activity, but ventricular response depends on AV conduction ratio



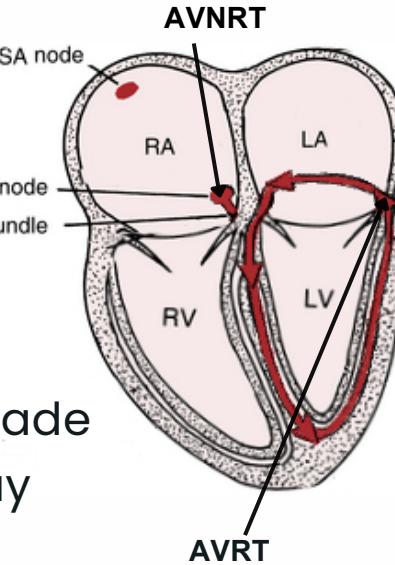
2. [AFIB] ATRIAL FIBRILLATION

Multiple electrical impulses arise simultaneously from various areas in the atria, creating chaotic, disorganized atrial activation
→ no distinct P waves and irregular RR intervals



3. [PSVT] PAROXYSMAL SUPRAVENTRICULAR TACHYCARDIA

- A reentrant circuit within the AV node (AVNRT) or through an accessory pathway (AVRT) causes impulses to loop repeatedly between atria and ventricles
→ P waves are either hidden, retrograde or altered depending on the pathway
- Highly regular



4. [STACH] SINUS TACHYCARDIA

Common tachycardia

SVT *rhythms* 6

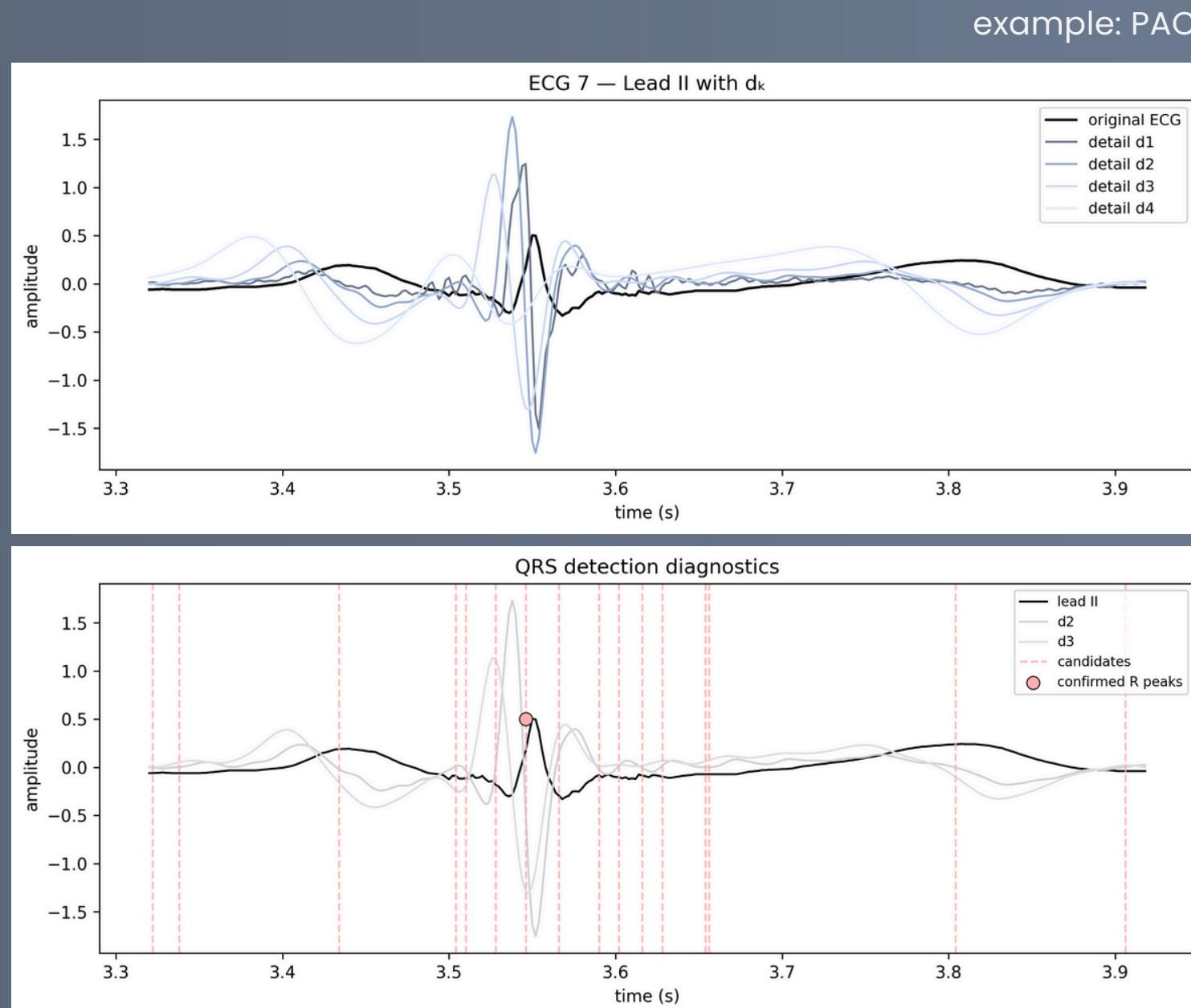
Algorithm Pipeline

by Luigi Y Di Marco and Lorenzo Chiari

Wavelet Transform

- The ECG is decomposed using an undecimated spline-8 wavelet transform in the frequency domain.
- The low-pass and high-pass filters are defined directly by their analytic frequency responses [1] and [2].
- Dyadic-scale filters are built by cascading H and applying G .
- Wavelet coefficients at each scale are obtained by frequency-domain multiplication and inverse FFT of the filtered signal.
- No explicit group-delay correction is applied, since the phase is already included by definition.

**Multi-scale detail
OUTPUT coefficients (4-scale d_k)
for leads II and V1**



$$[1] \quad H(e^{j\omega}) = e^{\frac{j\omega}{2}} \left(\cos \frac{\omega}{2} \right)^7$$

$$[2] \quad G(e^{j\omega}) = 4je^{\frac{j\omega}{2}} \sin \left(\frac{\omega}{2} \right)$$

QRS Detection

- The code processed the coefficients sample-by-sample in an online fashion, with an initial learning period to adjust adaptive thresholds, which was shortened from 8 to 0.5s to accomodate the length of the dataset's samples.
- For each **zero-crossing** in d_2 , the adjacent **modulus maxima** pair was found and the amplitude computed.
- A 250 ms window was maintained where only the strongest zero-crossing survived and became the QRS candidate.
- When the window closed, the candidate was evaluated by looking at the highest and lowest coefficient values inside a short 100ms window at d_2 and d_3 . These values were finally compared to adaptive thresholds: if both were exceeded, the candidate was accepted.

OUTPUT

R peaks list (lead II)

Algorithm Pipeline

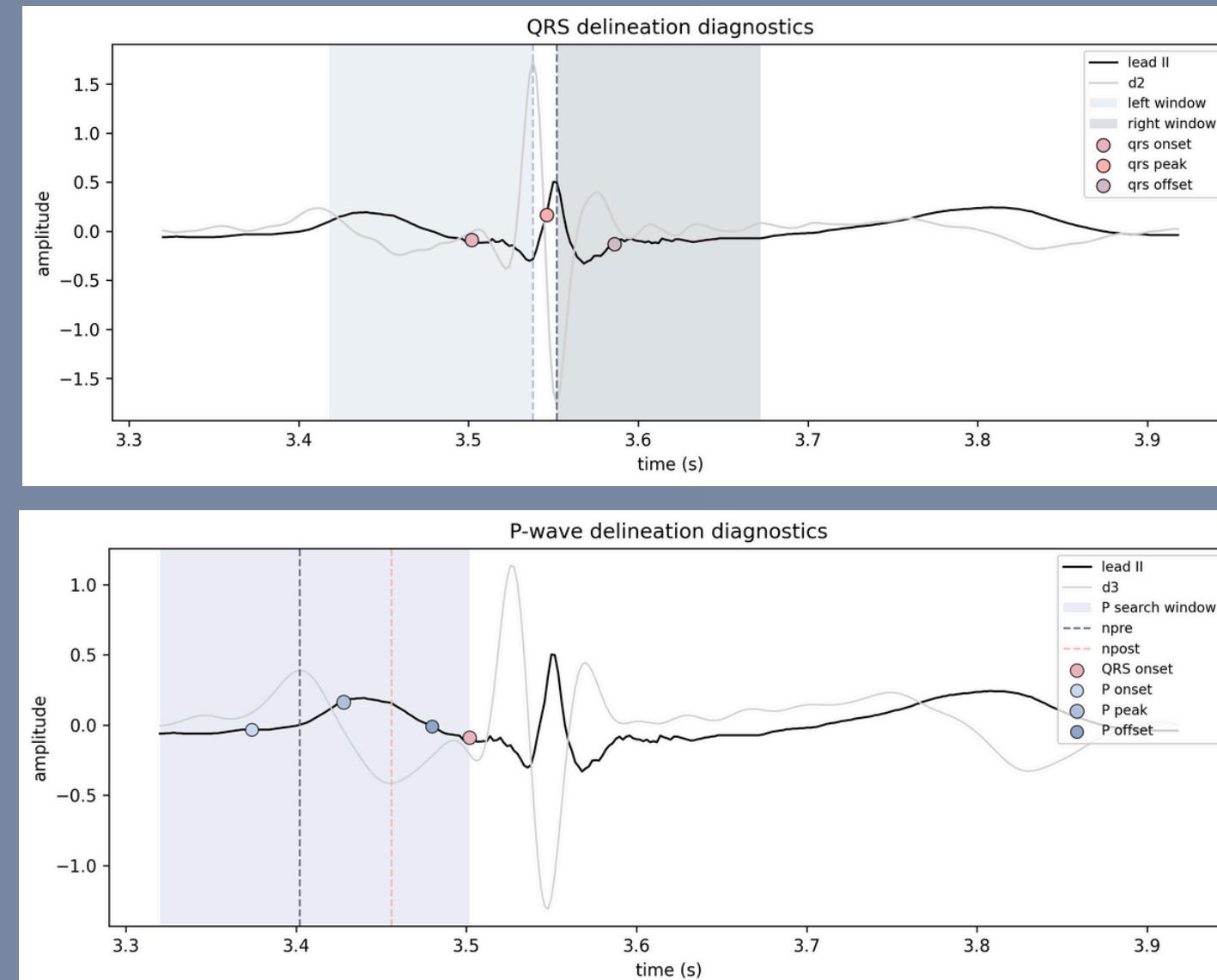
by Luigi Y Di Marco and Lorenzo Chiari

QRS Delineation

- First, the modulus maxima immediately before and after each peak were computed in d_2 .
- To determine the **onset**, the algorithm began from the modulus maximum preceding the peak and searched backward over a fixed 120ms window.
- The **offset** was computed symmetrically by searching forward from the modulus maximum after the peak.
- Progressively stronger thresholds were used: onset and offset were assigned at the first point where the coefficients decayed beyond them.

OUTPUT

**R peaks, Q onsets,
S offsets (lead II)**



P-Wave Delineation

- The algorithm searched backward in d_3 , from the QRS onset within a window defined by the shorter of 300 ms or half the previous RR interval.
- It identified zero-crossings, found the nearest left and right modulus maxima for each, and selected the dominant zero-crossing based on amplitude balance.
- Nearby crossings within ± 100 ms are checked to detect **biphasic** P-waves and adjusted accordingly.
- The P **onset** and **offset** are then determined by searching backward and forward from the selected maxima until the signal falls below the respective thresholds.

OUTPUT

**R peaks, P onsets, P offsets
(lead II and V1)**

Algorithm Pipeline

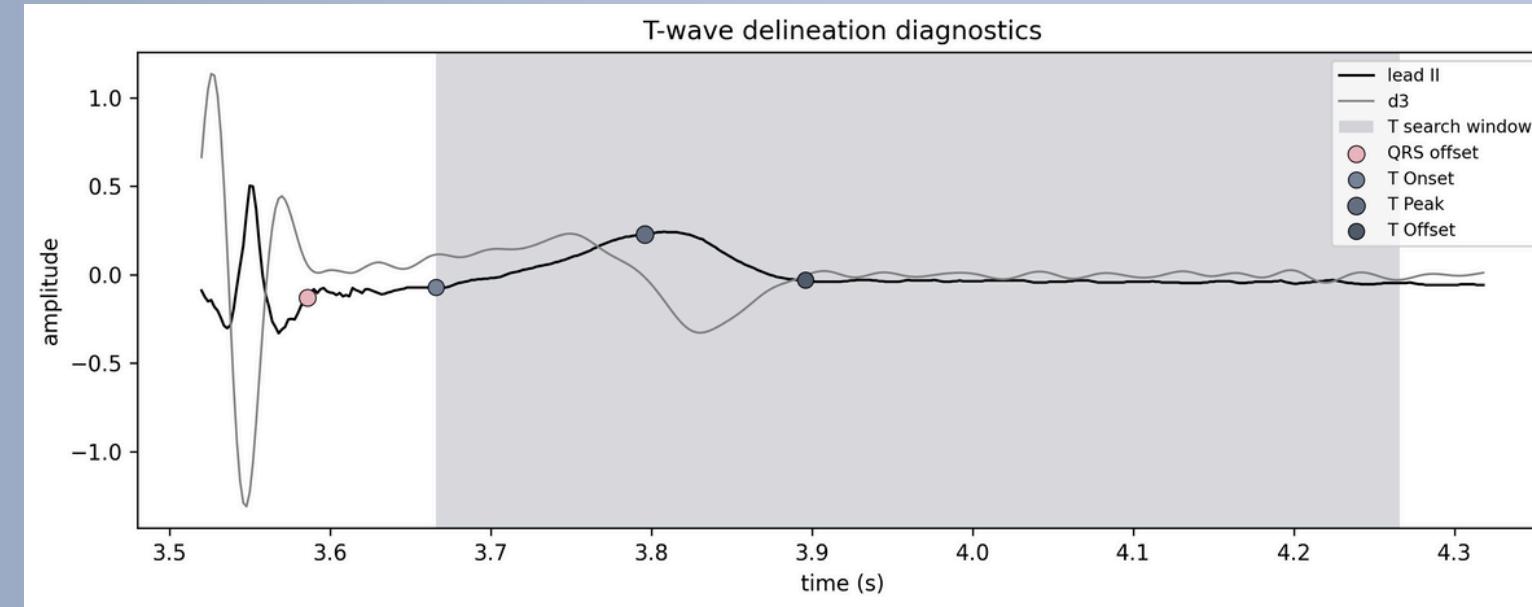
by Luigi Y Di Marco and Lorenzo Chiari

T-Wave Delineation

- Analysis windows were defined based on previous QRS offsets and RR intervals.
- Zero-crossings in d_3 were found to locate candidate peaks and modulus-maxima pairs were computed to select the dominant T peak.
- Checked for biphasic T-waves and adjusted peak and end accordingly
- Searched for T offset and end using threshold relative to post-peak amplitude.

OUTPUT
**T peaks, T onsets*,
T offsets (lead II)**

* No information was provided in the paper on how to compute T onset, so it was simply set as the search window's left extremum



RR_mean	RR_std	RR_CV	RMSSD	PR_mean	PR_std	PR_CV
0.974	0.143595	0.147428	0.251373	-0.838889	0.138317	None
P_presence_ratio	QRS_duration_mean	QRS_duration_std	QT_mean	QTc_mean		
1.0	0.085	0.004669	0.414889	0.42039		
SVT_score	Fwave_mean	BaselineNoise_mean	HR_mean	HR_std	P_axis	
0.0	0.081234	0.077592	63.612511	13.786228	0.111269	
QRS_axis	T_axis	ecg_id	rhythm_type			
0.198722	0.184028	7	PAC			

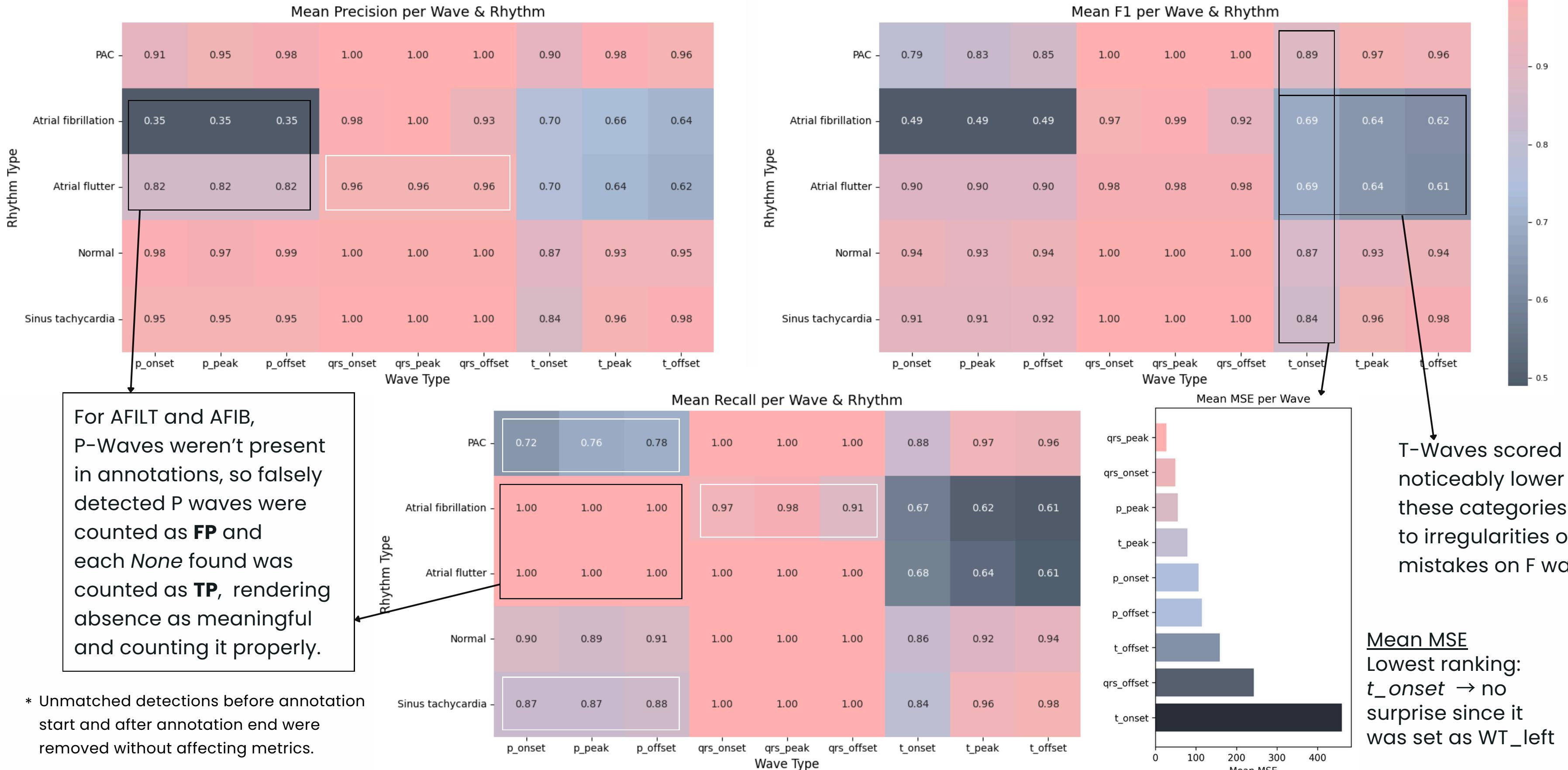
Metrics Calculation

- RR_mean / RR_std / RR_CV** → average, variability, and coefficient of variation of RR intervals lar
- RMSSD** → root-mean-square of successive RR differences
- PR_mean / PR_std / PR_CV** → timing between P onset and QRS onset
- P_presence_ratio** → fraction of beats where P-wave is detected
- QRS_duration_mean / QRS_duration_std** → width of QRS complex
- QT_mean / QTc_mean** → total ventricular depolarization + repolarization
- SVT_score** → combines P-wave presence and RR variability
- F-wave / BaselineNoise** → standard deviation in PR segment (F-waves) & pre-QRS baseline noise
- HR_mean / HR_std** → heart rate metrics from RR intervals
- P_axis / QRS_axis / T_axis** → mean amplitude-based axes in lead II

global ANALYSIS

LUDB LEAD II ONLY

Each detected fiducial point was matched to the nearest annotation within 150 ms (ANSI/AAMI-EC57:1998) and removed. Matches within the window are true positives (**TP**), unmatched annotations are false negatives (**FN**), and unmatched detections are false positives (**FP**)*.

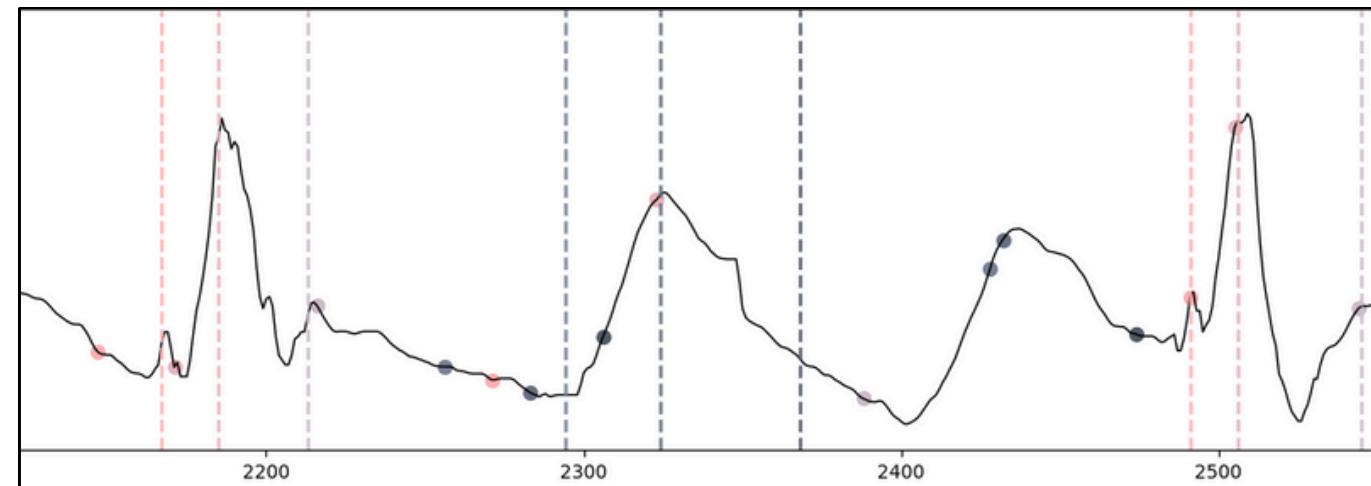


worst-case ANALYSIS

■ = annotated values
● = detected values

p_onset	qrs_onset	t_onset
p_peak	qrs_peak	t_peak
p_offset	qrs_offset	t_offset

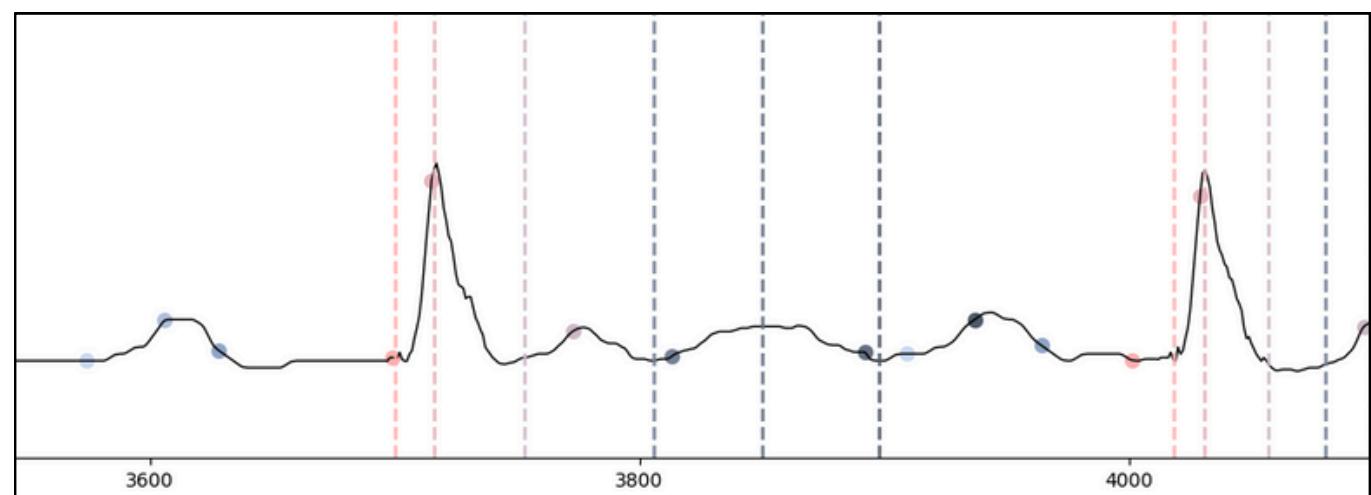
1. ATRIAL FLUTTER → lowest QRS precision, T-Wave f1



WORST CASE
Misidentified F-waves
as QRS complexes
and T-wave.

2. ATRIAL FIBRILLATION

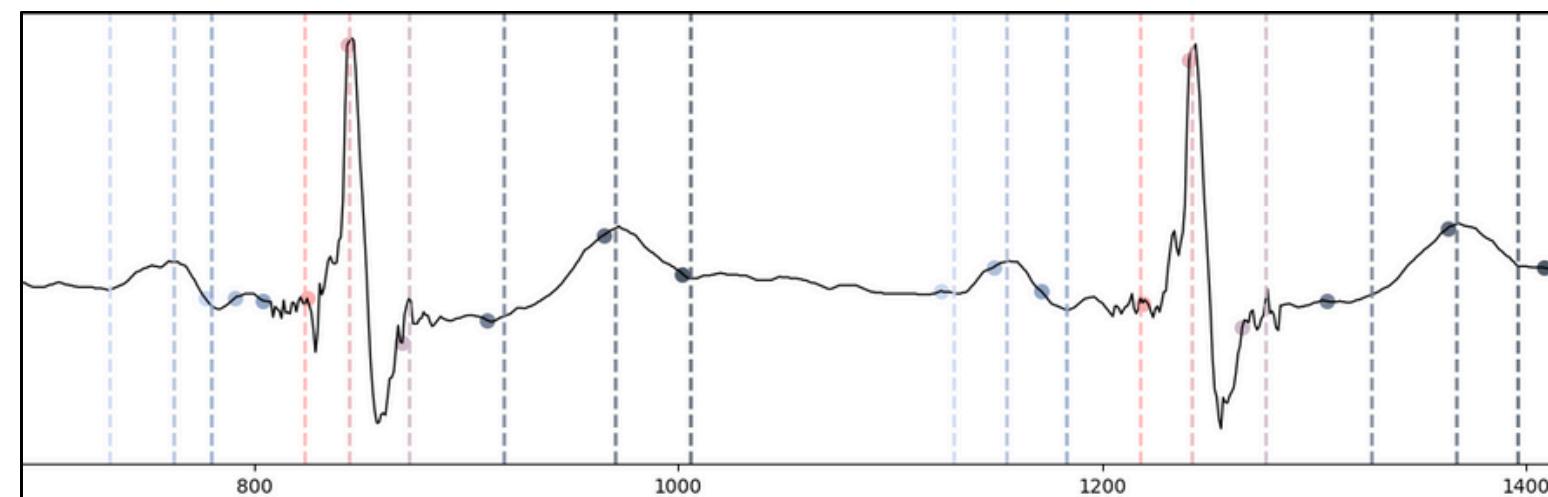
→ lowest QRS detection recall, P-Wave
precision, T-Wave f1



WORST CASE
Wrongly identified P-
waves; QRS offset
moved T-wave too
forward due to
irregular beats and
waveforms.

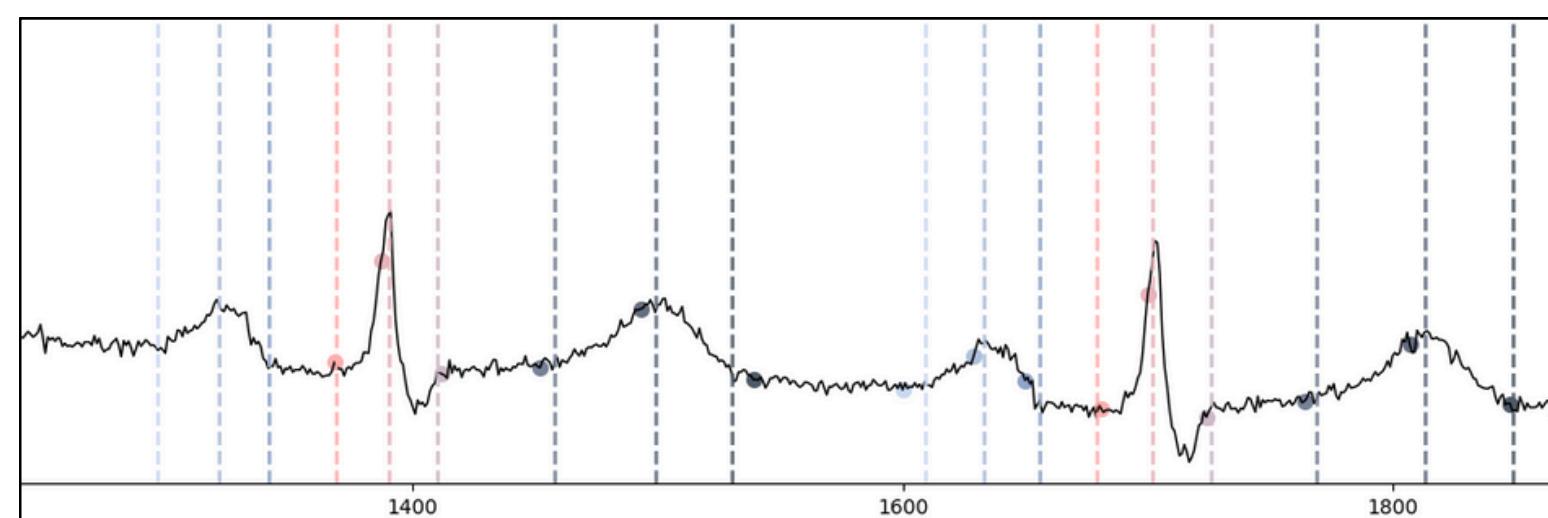
→ lowest recall in P-Wave detection

3. SINUS TACHYCARDIA



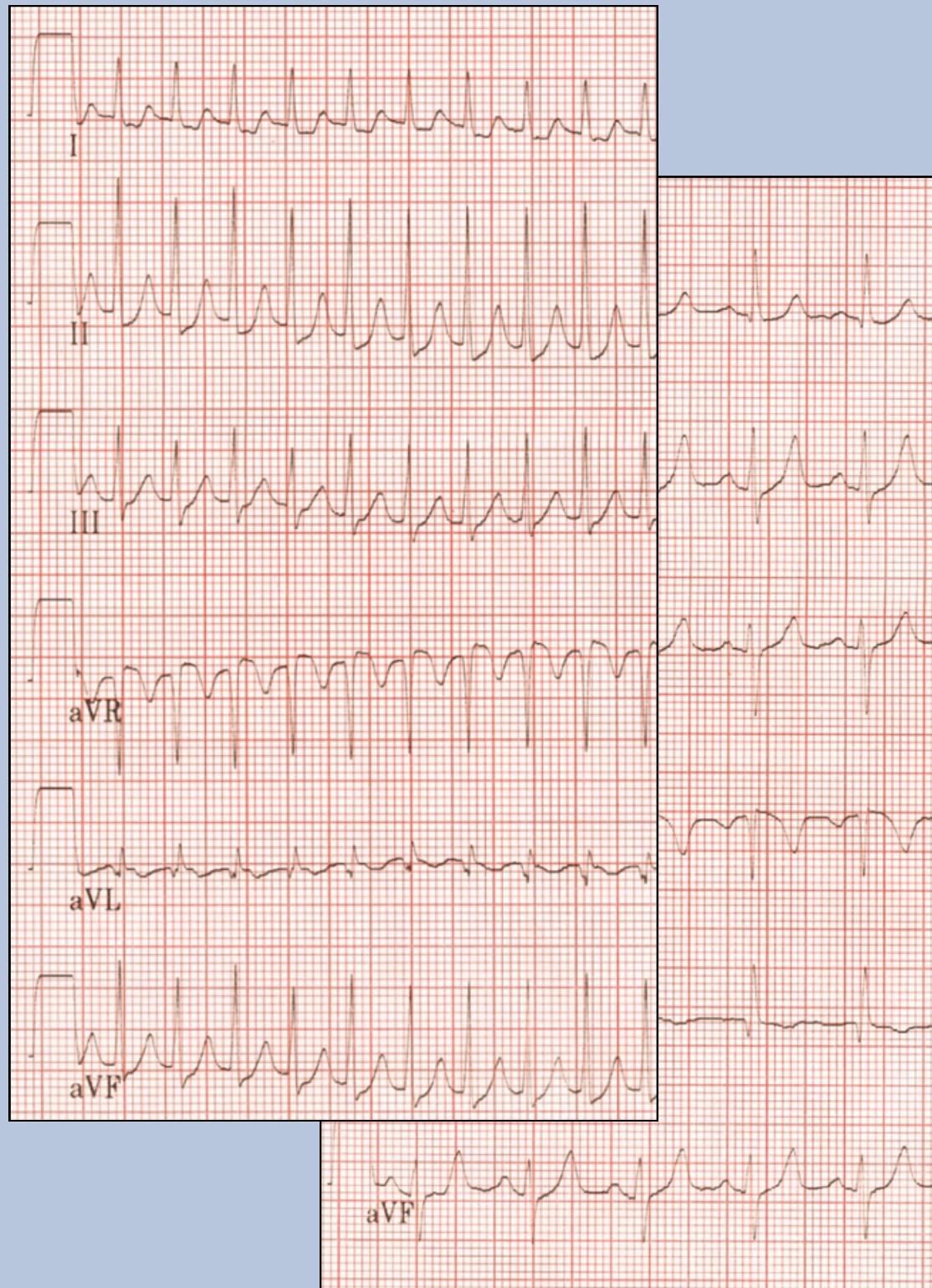
Misidentified P-wave: when the heart rate is fast, because the PR interval shortens, the T-wave of the previous beat may still be decaying, and the next P-wave starts early → this can cause a small positive deflection between the P-wave and QRS.

4. PREMATURE ATRIAL COMPLEX



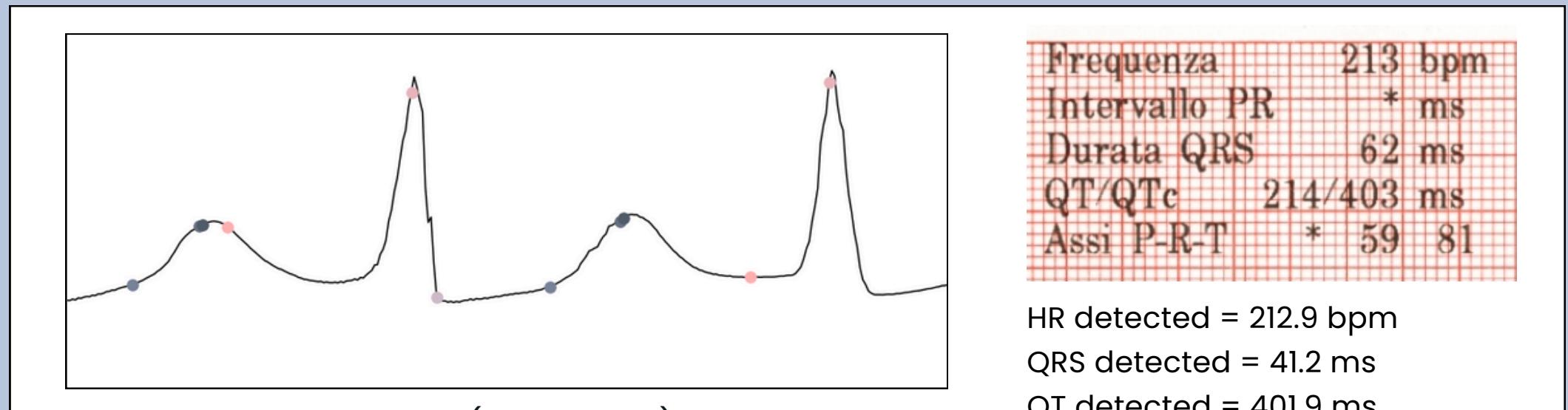
Just missed this one for some reason
(probably due to noisy ECG)

PSVT ANALYSIS



Using a background removal application, I was able to convert the image to a transparent png. After that, lead II was cropped and the alpha channel isolated to identify the visible ECG trace.

Using the known chart duration, chart speed (mm/s), and amplitude scaling (mm/mV) from the metadata, the pixel-to-millimeter ratio was reverse-engineered to calibrate both the amplitude and the time axis. The signal was resampled to a higher sampling rate.

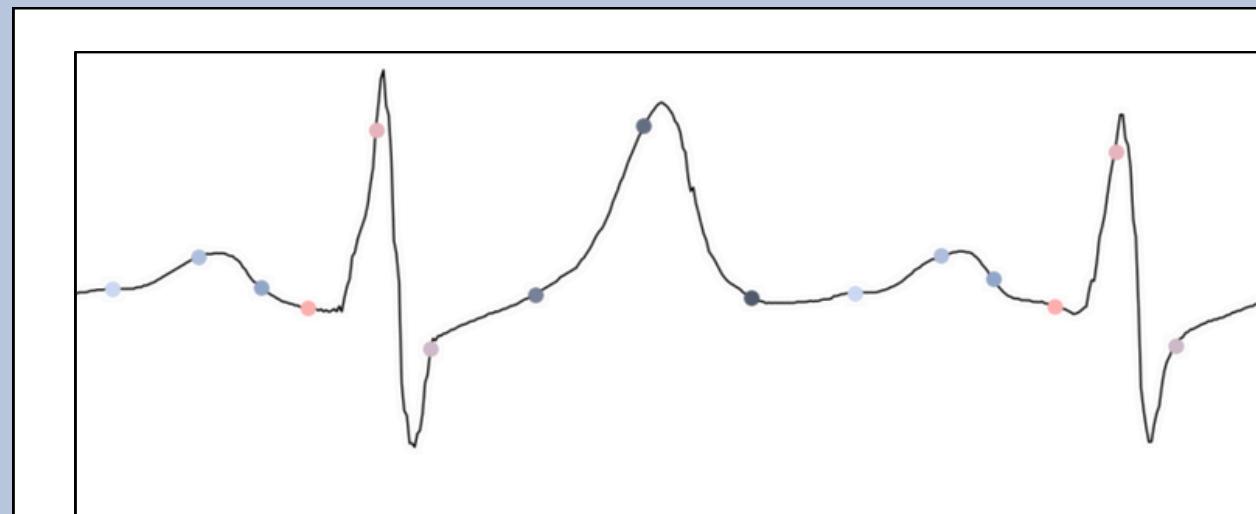


Due to hidden P-wave (AVRT case) the QRS onset and T-wave offset were found too prematurely.

Frequenza	213 bpm
Intervallo PR	* ms
Durata QRS	62 ms
QT/QTc	214/403 ms
Assi P-R-T	* 59 81

HR detected = 212.9 bpm
QRS detected = 41.2 ms
QT detected = 401.9 ms
QTc detected = 756.9 ms

PSVT



The accuracy of the detection was not as bad for the normal case.

Frequenza	100 bpm
Intervallo PR	142 ms
Durata QRS	72 ms
QT/QTc	326/420 ms
Assi P-R-T	66 -8 67

HR detected = 104.1 bpm
QRS detected = 25.3 ms
QT detected = 374.3 ms
QTc detected = 493.1 ms

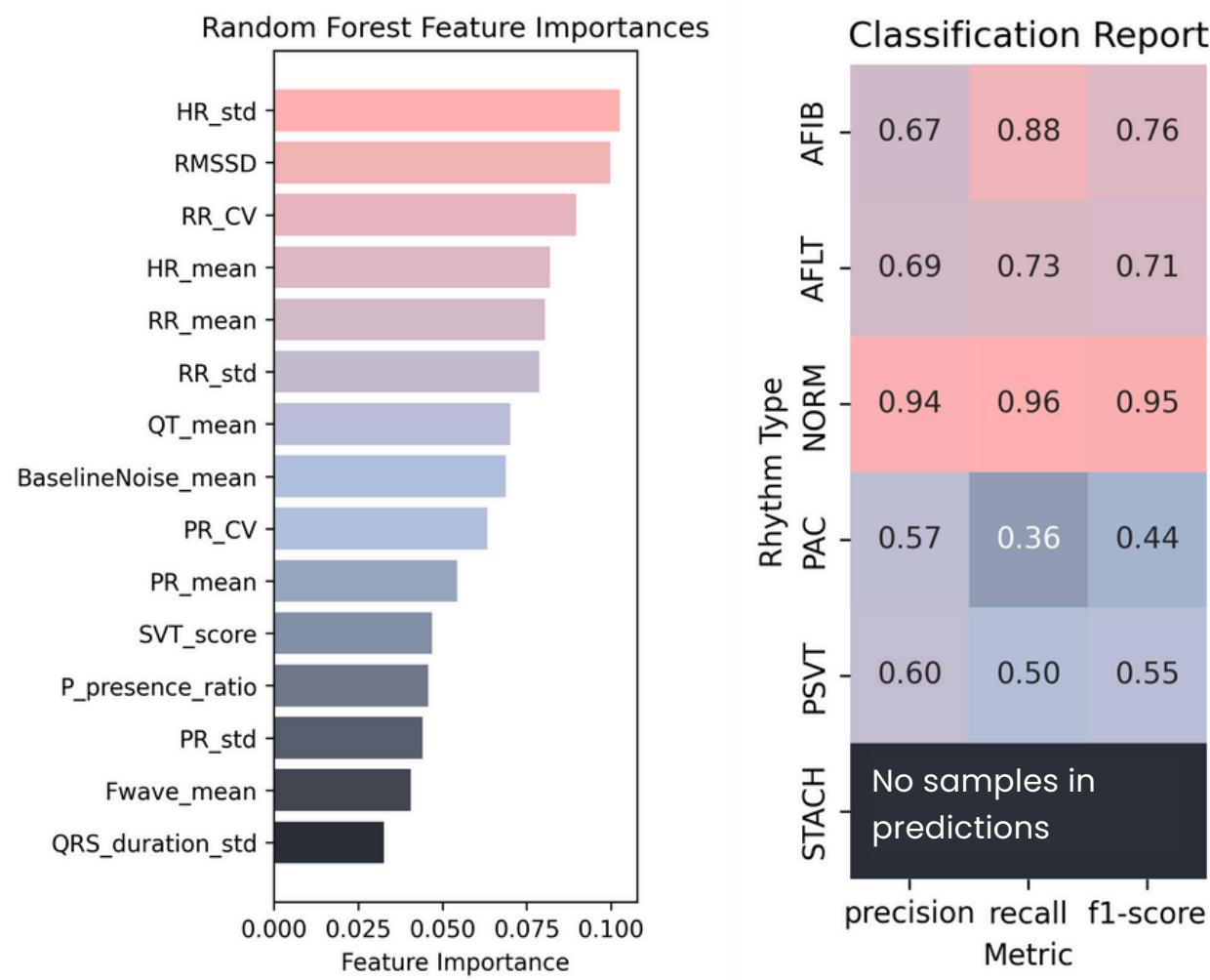
NORM/STACH

Unfortunately, the algorithm didn't perform well on the PSVT sample, though it correctly identified no P-waves and a good approximate of HR. Nonetheless, the normal case detection wasn't perfect either, so there's likely an issue in artifacting.

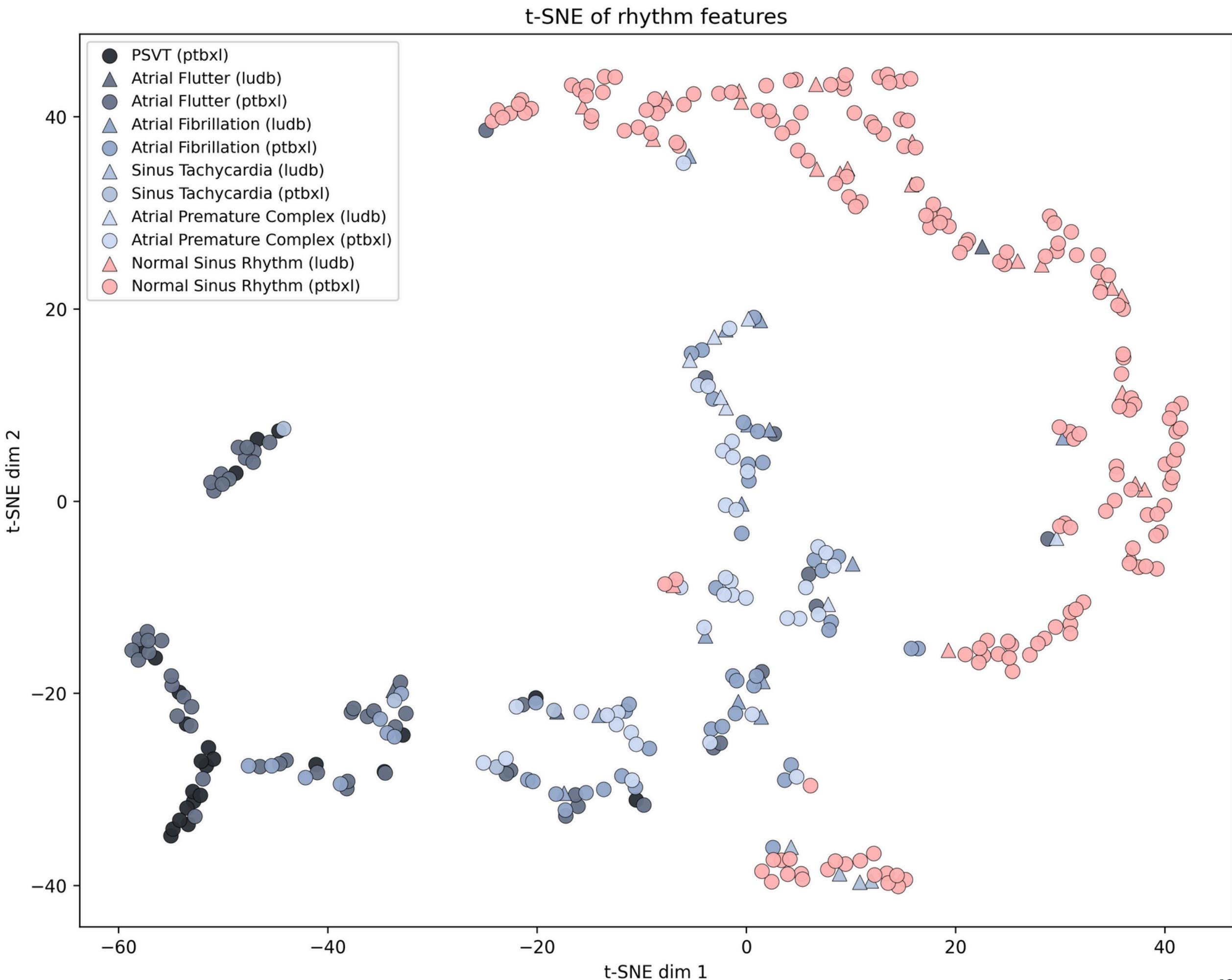
ML ANALYSIS

Given the lack of annotations in PTB-XL, to asses the performance on both datasets, an unsupervised ml pipeline was implemented with the task of rhythm classification, on the metrics calculated from the algorithm's results from the two datasets merged.

Random Forest overall accuracy: 0.79



Both Random Forest and T-SNE show accurate classifications for normal samples and a worse performance when distinguishing SVT cases.





Thank you!