A Machine Learning Based Approach for Localization of Atrial Tachycardia Origin

Celine Hajjar[1], Thomas Boudou[2], Jérôme Kalifa[2], Julien Seitz[2,3], Clément Bars[2,3]

[1] École Polytechnique, Palaiseau, France
[2] Volta Medical, Marseille, France
[3] Saint-Joseph Hospital, Marseille, France

Abstract

Ablation procedures targeting Atrial Tachycardia (AT) can be drastically facilitated if the origin of the abnormality is located in advance using electrocardiogram (ECG) signals. The ECG recordings contain so called P waves, which represent overall summary waves generated by the atrial depolarization. Previous work has shown the possibility to predict the origin of localized AT (excluding flutters) based on P wave morphology segmented from the ECG. The present study aims to develop a machine learning algorithm that detects the likely origin of localized AT based both on P wave characteristics extracted from ECG and signals recorded in the Coronary Sinus (CS).

1. Introduction

Atrial tachycardia (AT) is a type of supraventricular arrhythmia that affects the atria and accelerates the natural rhythm of the heart in an organized and regular fashion. They are known to arise either from re-entry mechanisms or focal origins located within both left (LA) and right atria (RA). Localized AT is characterized by efferent circumferential potential propagation originated from a single location. A widely spread treatment of this type of AT is catheter ablation procedure, which requires long and meticulous high-density mapping of both atria in order to reconstruct electrical activation maps [1]. Any prior knowledge about the localization of ongoing AT focus is essential for the guidance of the ablation procedure, reducing operating time and limiting the anatomical region coverage during the mapping phase.

Most of the research providing insights into ATs localization are based on the analysis of P waves, as it is generally known that features visually extracted from the ECG leads help electrophysiologists to conjecture the area of ongoing AT foci. In 1995, Tang et al. [2] analyzed the polarity of P waves in surface electrodes to predict which atrium (right or left) is the main source of pathological circumstances (like abnormal focus or heterogeneous tissue). The aVL and V1 leads were found to be the most useful in distinguishing right from left foci: a positive P wave in the aVL lead predicts a right focus with a sensitivity of 88% and a specificity of 79%. The sensitivity and specificity of a positive P wave in the V1 lead predicting a left focus were 93% and 88%, respectively. Since then, several studies have extended the analysis of P wave polarity to predict focus location with higher precision. Kistler et al. [3,4] studied 130 recordings of focal ATs to construct a decision tree to find the origin among 10 possible regions, where nodes are split following the polarity of the P waves in the different ECG leads (see figure 1). The algorithm managed to correctly classify the origin in 93% of 30 ATs unseen during the training.

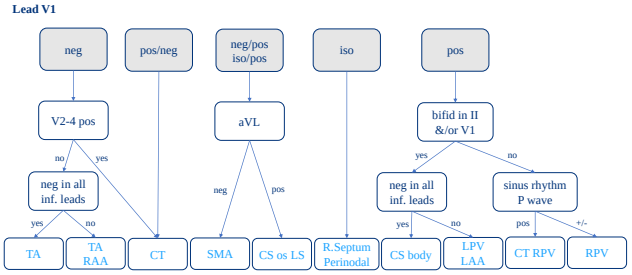

Figure 1. The decision tree presented by Kistler et al. Abbreviations: CT - crista terminalis, TA - tricuspid annulus, LAA (RAA) - left (right) atrial appendage, LPV (RPV)- left (right) pulmonary vein, MA - mitral annulus

Similar work has been done by Qian et al, who found that the combination of information from multiple leads and regrouping of sites of origin improve the predictive value for the prediction of the origin [5].

In this work we designed a classification model that predicts the region containing the electrical abnormalities perpetuating the AT. We developed an automatic machine

learning algorithm that analyzes ECG recordings captured by 9 electrodes of the standard 12 electrodes (as aVL, aVF, aVR are linear combinations of I, II and III) placed on the patient's torso and signals captured by a probe that remains in the CS throughout the catheter ablation procedure. Inspired by previous work, a set of features was designed, including different characteristics of P waves morphology and features extracted from CS catheter. This implementation is intended to process operating room signals in real time.

2. Material and Methods

2.1. Dataset description and annotations

Signals used to train and test the present algorithm were extracted from a General Electric Cardiolab recording system from Saint-Joseph Hospital, Marseille, France, with a sampling frequency of 977 Hz. A total of 236 10-seconds rhythms recorded during ablation procedures were included in the train set, 40 in the test set. Each segment contains synchronized signals from 9 ECG and 5 CS leads. The rhythm was annotated with the region where the ongoing AT was terminated. The regions are defined as follows: Left, Right, Septal and Left Lateral. The distribution of the train and test dataset can be seen in 2.

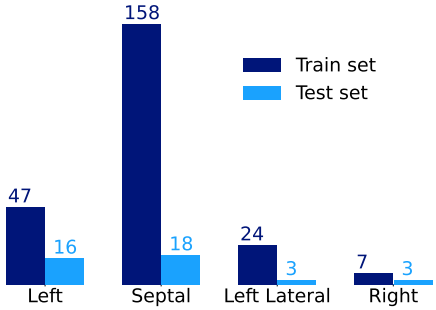

Figure 2. Distribution of our dataset.

2.2. Feature extraction

A large set of features targeting properties of the signal that are relevant for the localization of AT focus, was designed and extracted from ECG and CS signals.

P waves were detected and segmented from ECG leads using a deep learning model based on the U-net architecture [6]. Three groups of features were subsequently gathered from the P wave segments: wave polarity, peaks features, wave integral.

On a given lead, the polarity of each P wave is determined using signal template-matching. For this purpose, a template atlas including positive, negative, biphasic and isoelectric waves was created by averaging manually labeled P wave segments. The difference between each P wave and all 4 templates is computed using Dynamic Time Warping [7]. This method calculates the euclidean distance between aligned (i.e. re-sampled) versions of the input time series. The template that minimizes the distance is retained as P wave's polarity. The polarity of a lead segment is then defined as the most frequently predicted polarity over all its P waves.

In order to avoid potential bias caused by restriction of P waves morphology into four groups, we decided to broaden the feature set of morphology characteristics by adding peak properties of P waves, without predetermining their polarity. To do so, positive and negative peaks were detected within each P wave segment and their number and maximal prominences (the vertical distance between the peak and its lowest contour line) were computed. The mean of these features over the lead segment is retained.

The area under the curve formed by the P wave signal can also provide some information about the intensity and overall polarity of the wave. The integral is computed using the composite trapezoidal rule for each P wave and its mean value over the lead is added to the set of P wave features.

During the procedure, the CS probe stays still and can record up to five different leads depending on the catheter used. The relative positions of the same beat's activation onsets through leads form a so called CS sequence and can be an indicator of whether the focus lies in the left or the in right atrium (see Figure 3). Therefore, the activation delays of the four subsequent CS leads relative to the first were also included in the set of features.

Figure 5 illustrates the steps of the proposed method.

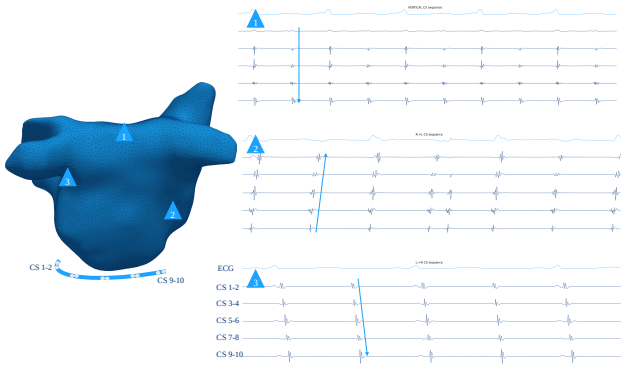

Figure 3. CS sequence can be an indicator of the site of origin

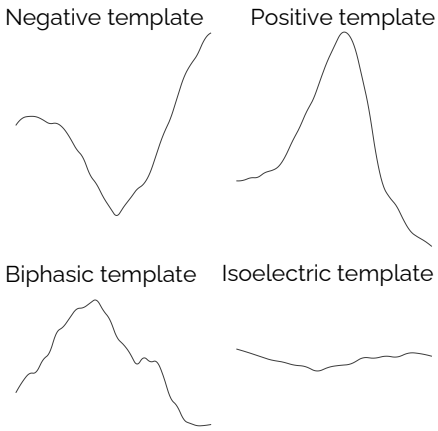

Figure 4. The four P wave polarity templates.

2.3. Model and feature selection

We tackled the localization of the AT site of origin with a classification model.

Every rhythm was cropped by a window size of 10000 frames then downsampled by a factor of 4. Given that a 10-second signal corresponds, in average, to 10 heartbeats, several P waves are detected in every window. The P wave features presented above are calculated for every P wave, then the voted majority (or mean for numerical features) is kept as the final value. Likewise, CS signals present several activation sequences in one rhythm, so the average is used as the final feature. A sequence is represented by the 4 relative delays of CS electrodes (delay between 3-4 and 1-2, between 4-5 and 3-4, etc).

Feature selection techniques were used to decrease the complexity of the model and increase its interpretability. We combined two methods, one that evaluates each feature independently and one that evaluates subsets of features to have the best of the two. That led us to consider the union of the 10 features that had the best ANOVA (Analysis of Variance) F-statistic, and the subset of 10 features that led to the best overall results with a Random Forest classifier over the entire training set.

Given the relatively small dataset, and inspired by previous work, we considered tree ensemble method algorithms [8], although we tested multiples machine learning classification models, settling on a Random Forest model as it produced the best overall results.

To fine tune the hyperparameters of our model, we used a 5-fold cross validation with a Bayesian optimization method (namely, the tree-structured Parzen estimator [9]).

3. Results and discussion

Our model was trained on the 236 rhythms and tested on a separate dataset of 40 rhythms. The 40 rhythms included in the test set came from different procedures in order to avoid data leakage. Our model achieves a Cohen Kappa Score [10] of 0.55 and an overall accuracy of 74% (see table 1 for detailed results).

The main limitation of the study was to obtain accurate results from our dataset. Its imbalance and the underwhelming amount of examples, particularly for observations of right and left lateral regions, were indeed major limitations and resulted in low performances for accurately identifying those regions as origins of AT. Still, we deem our current results promising and we believe that alleviating these limitations would lead to more satisfactory results.

division	# of examples	precision	recall
Left	15	0.92	0.80
Right	3	0	0
Septal	18	0.68	0.94
Left Lateral	3	0	0

Table 1. Detailed results summary

Noteworthy, to go beyond the four region partition, we could have used a finer grained tessellation of the atria, annotated our dataset consequently, and could have tackled this problem as a regression over the atrial surface. Regression models offer the benefit that predicted regions adjacent to the annotated site of origin would yield a better score than remote ones. That approach would however require a more substantial dataset and would fare poorly with ours. Moreover, we believe the localization of AT for a four region partition to already be of high interest.

Finally, we would like to emphasize the difficulty of the problem: different heart morphologies, previous ablation or structural arrangements may entail various conduction anomalies; different electrode placements that lead to an ill-posed localization problem, along with the inherent imperfection of the segmentation of the ECG and CS. To go beyond, the localization of the AT site of origin would benefit from more train and test data and consequently the use of state-of-the-art deep learning models.

4. Conclusion

This work lays the foundation for future endeavors in the field of machine learning applied to cardiology. The suggested algorithm, that analyzes ECG and CS signals, has shown its potential in determining the origin of localized AT. Such predictive models could be deployed in the operating room and be a useful tool to assist physicians.

Acknowledgments

We would like to express our gratitude to all members of the Data Science Team of Volta Medical (T. Demarcy,

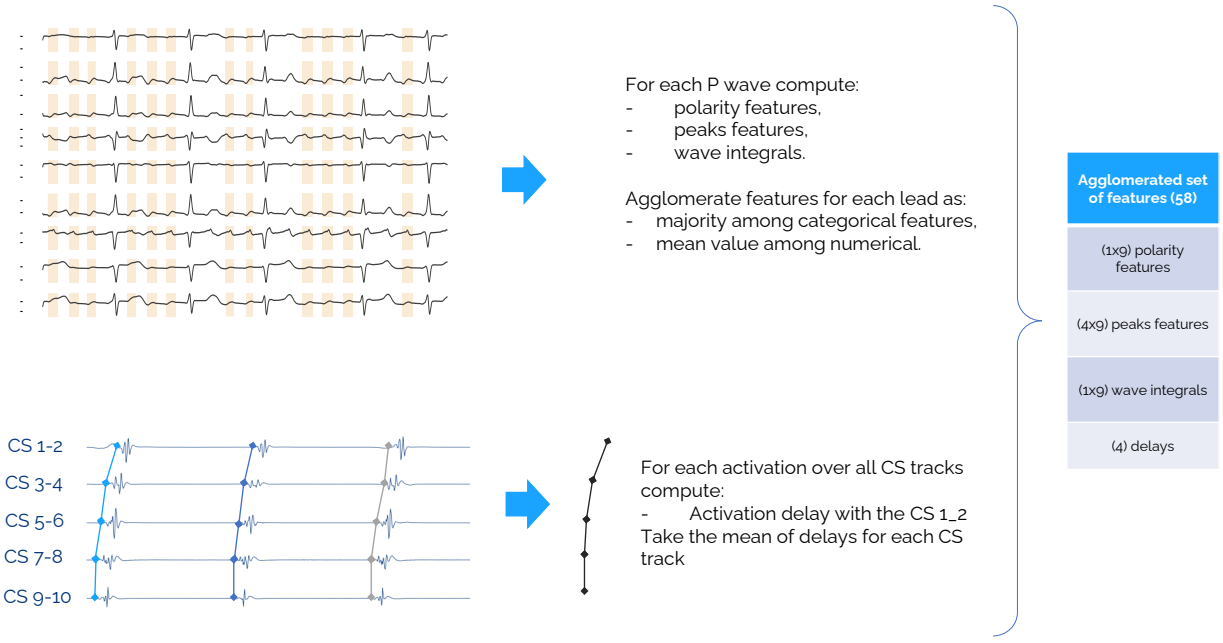

Figure 5. The feature extraction process. Orange bars represent segments of detected P waves.

M. Fedotenkova, L. Genin, El. Voundy, D. Veshchezerova) for their precious help in writing this paper.

References

[1] Y. Hung, S. Chen, S. Chang, W. Lin, and W. Lin. "Atrial Tachycardias After Atrial Fibrillation Ablation: How to Manage?" *Arrhythmia and Electrophysiology Review*, 9(2):54–60, August 2020.

[2] C. Tang, M. Scheinman, G. Van Hare, L. Epstein, A. Fitzpatrick, R. Lee, and M. Lesh. "Use of P-Wave Configuration During Atrial Tachycardia to Predict Site of Origin". *Journal of the American College of Cardiology*, 26(5) 1315–1324, November 1995.

[3] P. Kistler, D. Chieng, I. Tonchev, H. Sugumar, A. Voskoboinik, L. Schwartz, A. McLellan, D. Prabhu, L. Ling, A. Al-Kaisey, R. Parameswaran, R. Anderson, G. Lee, J. Kalman, "P-Wave Morphology in Focal Atrial Tachycardia: An Updated Algorithm to Predict Site of Origin", *JACC: Clinical Electrophysiology*.

[4] P. Kistler, K. Roberts-Thomson, H. Haqqani, S. Fynn, S. Singarayar, J. Vohra, J. Morton, P. Sparks, and J. Kalman. "P-Wave Morphology in Focal Atrial Tachycardia: Development of an Algorithm to Predict the Anatomic Site of Origin". 48:1010–1017, September 2006.

[5] Z. Qian, Xiao-Feng Hou, D. Xu, B. Yang, M. Chen, C. Chen, F. Zhang, Q. Shan, K. Cao, and J. Zou. "An Algorithm to Predict the Site of Origin of Focal Atrial Tachycardia". *Pacing Clin Electrophysiol*, 34(4) 414–421, April 2011.

[6] O. Ronneberger, Ph. Fischer, T. Brox. "U-Net: Convolutional Networks for Biomedical Image Segmentation", *Navab, N., Hornegger, J., Wells, W., Frangi, A. (eds) Medical Image Computing and Computer-Assisted Intervention – MICCAI 2015. MICCAI 2015 Lecture Notes in Computer Science*, vol. 9351, 2015.

[7] H. Sakoe and S. Chiba. "Dynamic Programming Algorithm Optimization for Spoken Word Recognition". *IEEE Transactions on Acoustics, Speech, and Signal Processing*, 26(1):43–49, 1978.

[8] Trevor Hastie, Robert Tibshirani, and Jerome Friedman. "The Elements of Statistical Learning". *Springer Series in Statistics*. Springer New York Inc., New York, NY, USA, 2001.

[9] R. Turner, D. Eriksson, M. McCourt, J. Kiili, E. Laaksonen, Z. Xu, and I. Guyon. "Bayesian Optimization is Superior to Random Search for Machine Learning Hyperparameter Tuning: Analysis of the Black-Box Optimization Challenge 2020", 2021.

[10] M. McHugh. "Interrater Reliability: The Kappa Statistic". *Biochem Med (Zagreb)*, 22:276–282, October 2012.

Address for correspondence:

Thomas Boudou
Volta Medical, 65 avenue Jules Cantini, Marseille, 13006, France
thomas.boudou@volta-medical.com