

A Comparison of Methodologies for Pulmonary Veins Segmentation in High Definition Voltage Maps of Patients with Atrial Fibrillation

Leire Moriones¹, Iker González¹, Blas Echebarria², Susana Ravassa³,
Javier Ibero⁴, Ignacio García-Bolao⁴ & Jean Bragard¹

¹ School of Sciences, Universidad de Navarra, Pamplona, Spain

² Universitat Politècnica de Catalunya, Barcelona, Spain

³ CIMIA, Universidad de Navarra, Pamplona, Spain

⁴ CUN, Universidad de Navarra, Pamplona, Spain.

Abstract

The aim of this paper is to present three methodologies that have been used during the segmentation of images extracted from atria of patients with atrial fibrillation (AF). We collected voltage maps of the left atrium of 120 patients, prior of being treated for AF with tissue ablation. The high definition voltage maps (HDVM) were extracted with the Rhythmia software system from Boston Scientific and subsequently analyzed offline in the MATLAB environment.

The present study compares three different methodologies that have been used in the image analysis. During the analysis, one to segment the atrium in three main structures: body, pulmonary veins (PVs) and mitral valve (MV).

Method I is essentially based on a manual elimination of the PV by the operator. Method II uses a semi-automatic method based on geometric considerations, coupled with a threshold for voltage value. Method III also uses geometric features, i.e. the geometric curvature, in order to eliminate the PVs of the maps.

In this paper, we quantitatively compare the efficiency and the easiness of use of the two first methods. In particular, the values of two electrical biomarkers associated with the maps are computed before and after the PV's elimination process. This allows to classify them according to their sensitivity with respect to the cleaning of the PVs.

We discuss which methodology is more adequate to perform the PVs and MV segmentation in light of improving the precision of the resulting maps.

1. Introduction

The field of medical technology is experiencing a revolution towards the objective of “personalized medicine”. Cardiovascular diseases are the leading cause of death and are a medical research priority in the European Union

(EU). Despite the number of existing satisfactory treatments, researchers are looking for more advanced technological development in order to refine the current's procedures [1].

Atrial Fibrillation (AF) has become a recurrent pathology during the last decades. It is the most common arrhythmia related with the aging population and entails a high risk of mortality and morbidity. From the electrophysiological point of view, AF is produced in the left atria (LA) associated to failures in action potential propagation. Ablation therapy is successful in 70% of the cases. Additional approaches for diagnosis and therapies are needed to improve these figures.

In the clinical practice, it is important to distinguish between the atrium main structures: body, pulmonary veins (PVs) and mitral valve(MV). It is important to distinguish the last two, due to the segmentation methodology used. This is known as “image segmentation” and it has been studied for years. Several methods have been proposed [2]. An adequate segmentation of the atrium leads to a better understanding of what actually occurs inside the atrium.

To investigate further the process of segmentation we provide a comparative analysis of three methods. We have access to a cohort of 120 patients who are treated for AF. Before undergoing ablation therapy, a HDVM was acquired for each patient (as shown in Fig.(1)). These atria's images are used for the segmentation of the PVs and MV. As shown on the maps, the PVs and MV have low voltage values, so they are not as electrically (and mechanically) active as the rest of the body of the atrium.

In this paper, we compare two methodologies to improve the accuracy of the voltage calculations in AF patients.

2. Methods

In this study, we included 120 patients with paroxysmal or persistent AF prior to pulmonary vein isolation (PVI).

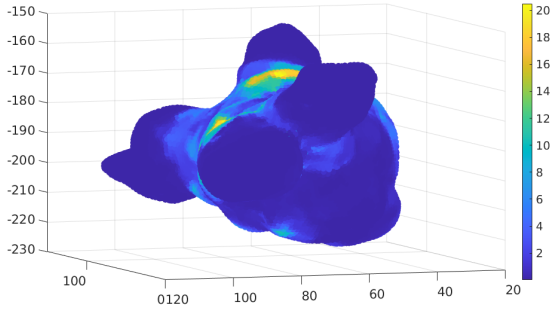


Figure 1. Atrial bipolar voltage map. Color scale for voltage expressed in mV units and the axes indicate position in mm. PVs and MV have been removed, as indicated in the text.

The left atrium images are acquired using an ultra-high definition voltage mapping (uHDM) system. The study was conducted following the ethical principles of the Declaration of Helsinki. All patients gave their informed consent.

2.1. Data acquisition

Mapping of the LA was conducted with a HDMV system (Rhythmia; Boston Scientific Corporation, Marlborough, MA) and a 64–electrode basket–type catheter (IntellaMap Orion, Boston Scientific Corporation) during paced atrial rhythm. Bipolar electrogram recordings were filtered between 40 to 400Hz and were saved in a file format suitable for further analysis in the MATLAB environment. Only points located within 2 mm of the external surface of the map were considered for analysis. After mapping, PVIs and MV segmentation was performed following the three methodologies described below.

2.2. Data analysis

All the 120 HDVMs maps were analyzed to compute several electrical indicators associated with the electrical state of the atrium. All the data analysis is done using the commercial mathematical software *MATLAB* [MATLAB and Statistics Toolbox Release R2022b, The MathWorks Inc., Natick, Massachusetts, United States] in several stages:

Preprocessing of the signal

Bipolar electrogram recordings were filtered between 40 to 400Hz and were saved in MATLAB file format.

Segmentation methodologies

For the segmentation of PVs and MV, three algorithms were used and the following parameters are calculated (be-

fore and after the segmentation process): (a) The number of points in the map; (b) The spatial average value of the bipolar potentials on the map surface (Vm); (c) The slope of the voltage histogram in logarithmic scale (Vs).

Method I is based on the manual elimination by the operator. The map is shown on the display and the PVs and the MV were selected and deleted from the map. The resulting map is then saved in a new file and kept for subsequent analysis. This algorithm is obviously highly dependent of the operator.

Method II [3] used the atria geometry to perform the segmentation. Four seeds indicating four points on the extremity of the PVs are set by the operator. The method determines a centerline of the inside of each PVs. The distance and curvature of the surrounding tissue of the map indicate if the centerline is still in the PVs or either reaching the main part of the atrium. This allows to determine the border between the PVs and the atria body. This is a semi-automatic methodology and it works as long as the geometry is not too complex. When the structure of the PVs is more complex (i.e., branching of the PVs), the process sometimes fails and manual adjustments are in order.

Method III [4] also used geometrical considerations. Method III fits a portion of ellipsoid for each of the PVs. The fitting of the portion of the ellipsoid is performed through an optimization process based on Eq. 1.

$$A_T v_\lambda = \lambda v_\lambda \quad (1)$$

After the determination of the ellipsoid, the border between the PVs and the atrium body is determined with two constraints. One is based on the voltage gradient calculated on the ellipsoid and the second is based on curvature considerations. This methods lays on the consideration that the voltage in the PVs and the MV is substantially lower than in the atria body and also that the curvature of the main atrium is substantially lower than the curvature of the PVs. This methodology is automatic in the sense that no intervention from the operator is required.

Determination of the two main parameters: Vm, Vs

In order to compare the segmentation process we evaluate two indicators related with the maps. The mean voltage (Vm) and the slope of the voltage histogram (Vs).

Since the spatial voltage distribution typically follows an exponential distribution on the map, we compute the slope of the histograms (in log-linear scales) as the simplest way to characterize it [5]. In each case, we verified that the corresponding adjusted R^2 was appropriate and that the 95% confidence interval for the slope estimation was sufficiently narrow. We used the MATLAB command “hist(y,M)” for the binning method, with M number of bins set to 50 for all the analyzed data sets. We used linear interpolation to calculate the slope and the corresponding stan-

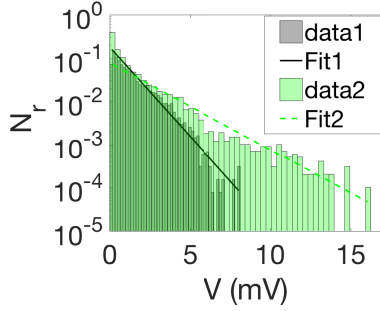


Figure 2. Illustration of two individual spatial bipolar voltage distributions with their corresponding best fits in log-linear scale.

standard error. By measuring the histogram slope, we obtained a characteristic voltage decay for each patient (expressed in mV^{-1}) (see details in Fig. 2).

The modification of the indicators induced by the segmentation are gathered in Table 2.

Statistical analysis comparing segmentation with Method I versus Method II

Six statistical tests are performed to compare Method I and Method II. For the mean voltage we compare the computed mean voltage after and before the segmentation process through a standard paired t-test for the 120 patient cohort. We also compare through a paired t-test the results after the segmentation between the two methods. We repeat the same with the voltage slope. This amounts to a total of six statistical test. The null hypothesis for all the test being that there is no difference between the two conditions (either after and before or Method I and Method II). The p-values for each of the tests are gathered in Table 3 and a significance level of $\alpha = 0.05$ is considered.

3. Results and discussions

We discuss the quantitative aspects that were defined in the Method section.

Summary of the three methodologies

Table 1. Summary of Segmentation Method' characteristics.

Method	Based on	Procedure	Type
I	Operator	Select & Delete	Manual
II	Distance	Seed to atria body	Semi-automatic
III	Elipsoid	PVs and MV	Automatic

Table 1 summarizes the characteristics of the three methodologies described above. The importance of the operator is highlighted in each method. The intended result

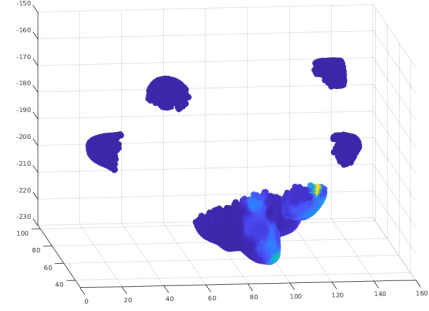


Figure 3. Illustration of the eliminated portions of the PVs and MV after segmentation with Method II.

of the segmentation is illustrated in Fig 3.

Results for different methodologies

We computed the relative distribution of three parameters (N_{vert} , V_m and V_s) after and before the process of segmentation. The results are shown (for all 120 patients) in Figs. 4 and 5 and summarized in Table 2. Quantitatively, we found that the mean voltage was: 0.8814 ± 0.5379 mV, 1.1182 ± 0.6940 mV and 1.0510 ± 0.6656 mV, before segmentation and after method I and Method II, respectively.

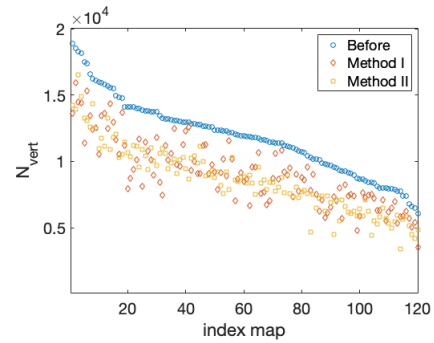


Figure 4. Differences in the elimination of vertices N_{vert} with Method I and II segmentation.

Table 2. Values for the parameters' differences (in relative percentage values).

Parameter	Method	Distribution (%)	StdDev (%)
NumVert	I	-22.8400	10.1300
	II	-27.3100	7.4200
Voltage	I	27.2900	0.1501
	II	18.1600	0.1029
Slope	I	0.1191	0.1729
	II	0.9550	0.2182

Results for the segmentation comparison

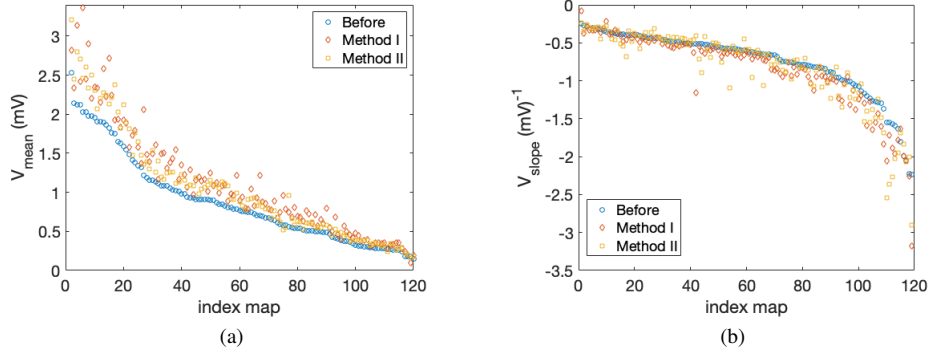


Figure 5. Change of mean voltage (panel a) and voltage slope (panel b) according to Method I and II for segmentation.

Table 3 collects the results of the paired t-tests comparing Method I and Method II. Individually, each method shows that the process of segmentation modifies significantly the values of mean voltage and the voltage slope. However, the p-values associated with the voltage slope are order of magnitude larger than the p-values associated with the mean voltage. The latter meaning that the voltage slope seems to be a more robust biomarker with respect to the process of segmentation.

To further illustrate this idea we have performed two additional paired t-tests comparing directly the values after segmentation for the two methods. The comparison between the mean voltage between Method I and Method II is statistically significant as we get a p-value of approximately $1.8 \cdot 10^{-4}$. However, the comparison for the voltage slope is not significant between the two methods (p-value of 0.29). Recall that the null hypothesis used here says that there is no statistical difference between the values after and prior to the treatment.

As a conclusion we have shown that in general segmentation affects greatly the computation of biomarkers from the voltage maps. However, some biomarkers, as the voltage slope from the histogram, are more robust and therefore should be preferred in order to avoid results dependent of the operators.

Table 3. Values for the V_m and V_S paired samples t-test analysis (see text for details).

Parameter	Method	p-value
Voltage	I	$5.9253 \cdot 10^{-22}$
	II	$1.6721 \cdot 10^{-22}$
	II vs I	$1.8396 \cdot 10^{-4}$
Slope	I	$1.2210 \cdot 10^{-11}$
	II	$5.1675 \cdot 10^{-06}$
	II vs I	0.2916

Based on the hypothesis described, the operator has a

large influence during the segmentation process. In addition, the complex geometry of the patients' high-definition voltage maps does not facilitate the process of elimination of the PVs and MV from the body of the atrium. Further methodologies are under study in order to improve the automatization and accuracy of the segmentation procedure.

Acknowledgements

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Address for correspondence:

Jean Bragard
 c/ Irunlarrea, 1
 Universidad de Navarra,
 31008 Pamplona
 Email: jbragard@unav.es