Non-uniform Interpolation of Cardiac Navigation Maps Using Support Vector Machines with Autocorrelation Kernel

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Abstract

A new method for non-uniform interpolation of electro-anatomical cardiac maps from Cardiac Navigation Systems (CNS) is here proposed and benchmarked. We adapted the equations of support vector machines for estimation problems in terms of the two angular dimensions azimuth and elevation and used an autocorrelation kernel. Moreover, the influence of the number of spatial locations, its minimum number to obtain a map that precisely replicates the original or gold-standard and the effect of working in 2D from 3D were also studied. Two basic simulation scenarios were used: (a) a prolate semi-ellipsoid, yielding a geometry similar to the ventricular chamber, with different width pulse and Gaussian activations; and (b) detailed simulated models of cardiac activity in the atria. Results were compared with those obtained with other interpolation methods. In the Gaussian and pulse-like activations the largest decrease in mean absolute error (MAE) for the test set was achieved by using 150 spatial locations (MAE from 0.007 to 0.117). In the simulation models the error stabilized at 500 spatial locations (MAE from 0,002 to 0.014). The proposed method can provide improved quality for electro-anatomical maps interpolation.

1. Introduction

Arrhythmias are alterations of normal cardiac rhythm, which cause the heart to abnormally beat too fast, too slow, or with an irregular rhythm [1]. Cardiac Navigation Systems (CNS) allow replicating the patient cardiac anatomy in a computer system, addressing catheters precisely within the heart, and registering the cardiac electrical activity. The integration of both anatomical and electric data compounds electro-anatomical maps of the cardiac chamber, in which a compromise between map quality and its acquisition time is required. Given that the electrical feature is measured only in a few spatial locations, an interpolation algorithm is needed to estimate the feature value at points with no measure and build the map from those samples. Precision in the diagnosis and treatment of arrhythmias using CNS is directly related to the quality of the map, and hence to the interpolation method to be considered [2].

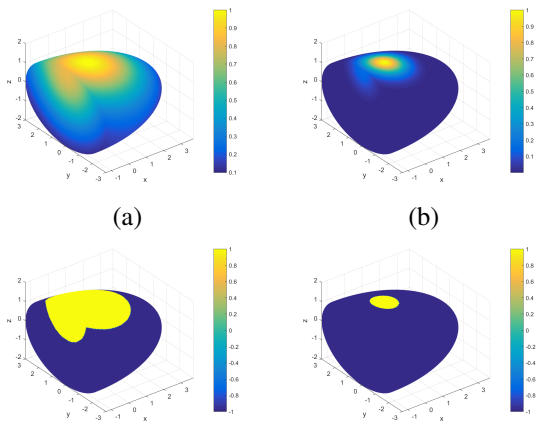
In this work, a Support Vector Machine (SVM) algorithm with autocorrelation (AC) kernel has been chosen as interpolation method because of its promising results versus other interpolation methods in the presence of non-uniform data [2]. The effect of working in 2D is also studied, and compared to 3D Cartesian coordinates of the spatial locations, so that the corresponding values of an electrical feature measured on those 3D spatial locations were transformed to spherical coordinates and then the radius coordinate was discarded.

The data used to evaluate the algorithm under study are a set of four simple features over the surface of a prolate semiellipsoid and some activation time maps obtained from two simulations which replicate the structure of maps generated by a CNS.

The paper is organized as follows. Section 2 contains the details of the SVM interpolation algorithm considered. In Section 3, the materials and methods used are detailed. In Section 4, the performed experiments are described and their results are shown. In Section 5, the conclusions reached from results are shared.

2. Non-uniform interpolation with SVM

Several previous works studied the influence of the interpolation methods in the quality of cardiac electro-anatomical maps [2, 3]. In [2], Triangulated Irregular Network (TIN), Thin Plate Spline (TPS), and SVM with Radial Basis Function (RBF) kernel were studied for anatomical and electro-anatomical maps interpolation. That work concluded that TPS, followed by SVM with RBF kernel, yielded the best results in terms of precision and computational cost. In order to improve the results of that work, we



(a) (b) (c) (d)

Figure 1. Geometry and activations of synthetic data, for (a) Wide Gaussian, (b) Narrow Gaussian, (c) Wide Pulse, and (d) Narrow Pulse.

propose here to use an SVM algorithm with an AC kernel that has stood out on the RBF kernel with both uniform and non-uniform sampling in other applications [4].

The SVM model for electro-anatomical cardiac maps estimation uses the following nonlinear regression model:

$$\hat{y} = f(\boldsymbol{x}) = \langle \boldsymbol{w}, \varphi(\boldsymbol{x}) \rangle + b \tag{1}$$

Considering a dataset $D = \{\boldsymbol{x}_1, y_1\}, \ldots, \{\boldsymbol{x}_N, y_N\}$, $\boldsymbol{x} \in \mathbb{R}^d$, $y \in \mathbb{R}$, where d is the dimension of the input data, N is the number of samples, and the ν-SVR algorithm functional to be minimized is the following:

$$\frac{1}{2}||\boldsymbol{w}||^2 + C\left(\nu\varepsilon + \frac{1}{N}\sum_{i=1}^{N}(\xi_i^{'} + \xi_i)\right) \tag{2}$$

where the first term is an L2 regularization and the second term is the ε-insensitive loss function, with ε being the insensitiveness parameter; C is a pre-established parameter that allows us to adjust the compromise between the error tolerance and the softness of the regression; $\xi_i^{'}$ and ξ_i are the slack variables, which represent the excess of error for each sample (x_i, y_i), according to the loss function used; and ν is the parameter used to control the variable ε, which is the maximum deviation from the real value allowed at each point. Taking into account the following constrains,

$$\xi_i, \xi_i^{'} \geq 0, \forall i = 1, 2, 3 \ldots N \tag{3a}$$

$$y_i - (\langle \boldsymbol{w}, \boldsymbol{\varphi}(\boldsymbol{x}) \rangle + b) \leq \xi_i + \varepsilon \tag{3b}$$

$$(\langle \boldsymbol{w}, \boldsymbol{\varphi}\,(\boldsymbol{x}) \rangle + b) - y_i \leq \xi_i^{'} + \varepsilon \tag{3c}$$

and using a Lagrangian functional, the solution to the nonlinear SVR is

$$\boldsymbol{w} = \sum_{i=1}^{N} \eta_i \boldsymbol{\varphi}(\boldsymbol{x}_i) \tag{4}$$

where $\eta_i, i = 1, 2, \ldots N$ are scalars, and samples $\boldsymbol{x}_i$ for which $\eta_i \neq 0$ are the so named support vectors. Thus,

$$y = f(\boldsymbol{x}) = \langle \boldsymbol{w}, \boldsymbol{\varphi}(\boldsymbol{x}) \rangle + b = \sum_{i=1}^{N} \eta_i \langle \boldsymbol{\varphi}(\boldsymbol{x}_i), \boldsymbol{\varphi}(\boldsymbol{x}) \rangle + b \tag{5}$$

which is the same as:

$$\hat{y} = f(\boldsymbol{x}) = \sum_{i=1}^{N} \eta_i \boldsymbol{K}(\boldsymbol{x}_i, \boldsymbol{x}) + b \tag{6}$$

That is, the solution can be linearly expressed in terms of the kernel function. Among the most common Mercer kernels, we find the *linear* and the *Gaussian* ones. Here, we propose to use the AC kernel, able to get a better adaptation to this type of data, following the ideas in [4] for interpolating one-dimensional signals. Thus,

$$\boldsymbol{K}(\boldsymbol{x}_i, \boldsymbol{x}) = \boldsymbol{R}_y(\boldsymbol{x}_i - \boldsymbol{x}) \tag{7}$$

where $\boldsymbol{R_y}$ is the spatial correlation of the feature y to be interpolated. This kernel is able to adapt spectrally to both low-pass and band-pass signals.

3. Materials and methods

Two datasets, which simulate electro-anatomical cardiac maps, were used to evaluate the proposed algorithm. Firstly, some synthetic data produced ad-hoc to ensure the suitability of the implementation of the algorithm. These data consist of four simple features over the surface of a prolate semiellipsoid having its longest radius along its body and with a flat elliptical lid. The highest radius is 150% higher than the lowest radius r_0 on the lid ellipse, and the other lid radius is 50% higher than the lowest one. With this geometry, we intended to emulate a left ventricle, as seen in Fig. 1. The features synthesized are a couple of Gaussian and a couple of uniform or pulse-like features.

The widest Gaussian feature was designed so that most of its variation is spread across the upper half of the semiellipsoid, occupying part of its lid, whereas the narrowest gaussian feature was designed so that variation is fully located entirely on the curved area, without occupying the lid at all. The pulses allow us to observe how the algorithm responds to scarce yet abrupt variations. The widest one provides a way to evaluate how the algorithm could respond to feature discontinuities between values more or less with the same frequency, while the narrowest one is useful to evaluate how the algorithm could respond to the presence of outliers.

Secondly, we used simulated data generated with a detailed computer model [5]. They comprise four activation

Table 1. Results (MAE and execution time) on synthetic features for different interpolation and validation methods.

Feature	Property	NN&HOV	LI&HOV	LI&CV
WG	MAE	0.0125	0.0081	0.0045
	Time (s)	90.28	95.85	422.16
NG	MAE	0.0071	0.0034	0.0017
	Time (s)	79.35	75.76	421.96
WP	MAE	0.0751	0.0674	0.0543
	Time (s)	81.64	76.75	449.01
NP	MAE	0.0297	0.0178	0.0129
	Time (s)	80.32	76.69	504.19

Table 2. MAE of different interpolators for simulation data with 1200 training spatial locations.

Rhythm	2D AC SVM	3D AC SVM	RBF SVM	TPS
RA SR	0.0017	0.0018	0.0022	0.0010
LA SR	0.0037	0.0035	0.0021	0.0014
RA FL	0.0156	0.0126	0.0179	0.0073
LA FL	0.0117	0.0029	0.0023	0.0023

time maps obtained from two simulations that correspond to a flutter (FL) and to a sinus rhythm (SR) in the right atrium (RA) and in the left atrium (LA).

The maps data consisted of the Cartesian coordinates (x, y, z) of every vertex on the map and their corresponding feature (activation time, voltage, latency...) values.

Although the electro-anatomical maps of CNS are defined in 3D, we also explored a 2D-SVM interpolation from these data and compared the results with those of a 3D-SVM. Thus, for 2D-SVM, a coordinates conversion from Cartesian to spherical system was performed previous to the SVM processing, being the radial coordinate discarded and preserving only the angular coordinates, elevation and azimuth.

The proposed algorithm implies the estimation of the AC of the differences between every sample pair in the training dataset. To make this possible, the training samples had to be converted first into a uniform sampled dataset. Hence, a uniform resampling of the electrical feature training samples was performed interpolating them onto a uniform grid. Searching accuracy in the result, the grid was built for the 2D-SVM with as many positions in each dimension as the size of the training dataset. In order to avoid too heavy computational burden in 3D-SVM, this design was adapted with a number of grid positions in each dimension of only the ceiling of the cubic root of the size of the training dataset. Two different interpolation methods were considered, namely, nearest neighbors (NN) and linear interpolation (LI).

Both hold-out validation (HOV) and cross-validation (CV) were tried and compared. CV was implemented as a k-fold validation with $k = 5$. This number of folds allowed not too long tests with a suitable quality.

For synthetic and simulated data, the subsets used in training, validation, and test were randomly picked from the full dataset. Results evaluation was conducted taking the Mean Absolute Error (MAE) as the reference error measure in both plane and 3D representations.

4. Results

A balance between quality and processing time can be achieved by exploring 20 values of C (from 0.5 to 10) and ν (from 0.05 to 1). This tuning strategy was applied to the whole work.

Synthetic Data Experiments. In these experiments, we consider NN and LI as interpolation methods, and HOV and 5-fold CV as validation methods. Table 1 summarizes the test results for 500 training points and 700 validation points in HOV and 1200 training-validation points in CV. It shows the MAE and the algorithm execution time for the selected algorithm parameters after tuning. LI reduces the MAE 35% for the WG, 52% for the NG, 10% for the WP, and 40% for the NP. However, the interpolation method do not seem to influence the algorithm execution time. The better the quality is (the lowest MAE) with LI in relative terms. On the other hand, it is observed a MAE reduction with CV over HOV of 45% for the WG, 49% for the NG, 19% for the WP, and 27% for the NP. These results made clear the need of using LI and CV.

Figure 2 compares the absolute error results of the 2D and the 3D versions with 1200 spatial locations. It also includes a 3D representation over the semiellipsoid surface for each algorithm version, that allows us to evaluate the results also visually. The 3D error peaks are lower than the 2D peaks for the WG and look in general lower for the WP too (though the relative difference is lower in this case), but the 3D peaks are higher than the 2D peaks for both narrow features. Visually, only the WG presents better results in 3D. Thus, it is worth to work in 2D version.

Simulation Data Experiments. These experiments used the two SR and the two FL simulation latency maps data described in the previous section. Table 2 gathers the validation MAE for the 2D and the 3D versions of the AC SVM algorithm obtained from this work and for the RBF SVM algorithm and the TPS algorithm of the previous work [2] with their respective widest training datasets. Note that 1200 spatial locations use the AC SVM algorithm and 500 spatial locations use the RBF SVM and TPS algorithms. Only validation results can be compared with those of the previous work [2] for the RBF SVM and TPS algorithms, since there are no test results in that study. It must be taken into account that the present work training dataset might not have any spatial locations in common with the one of the previous work. The SVM algorithm with AC kernel overcomes the SVM with RBF kernel for

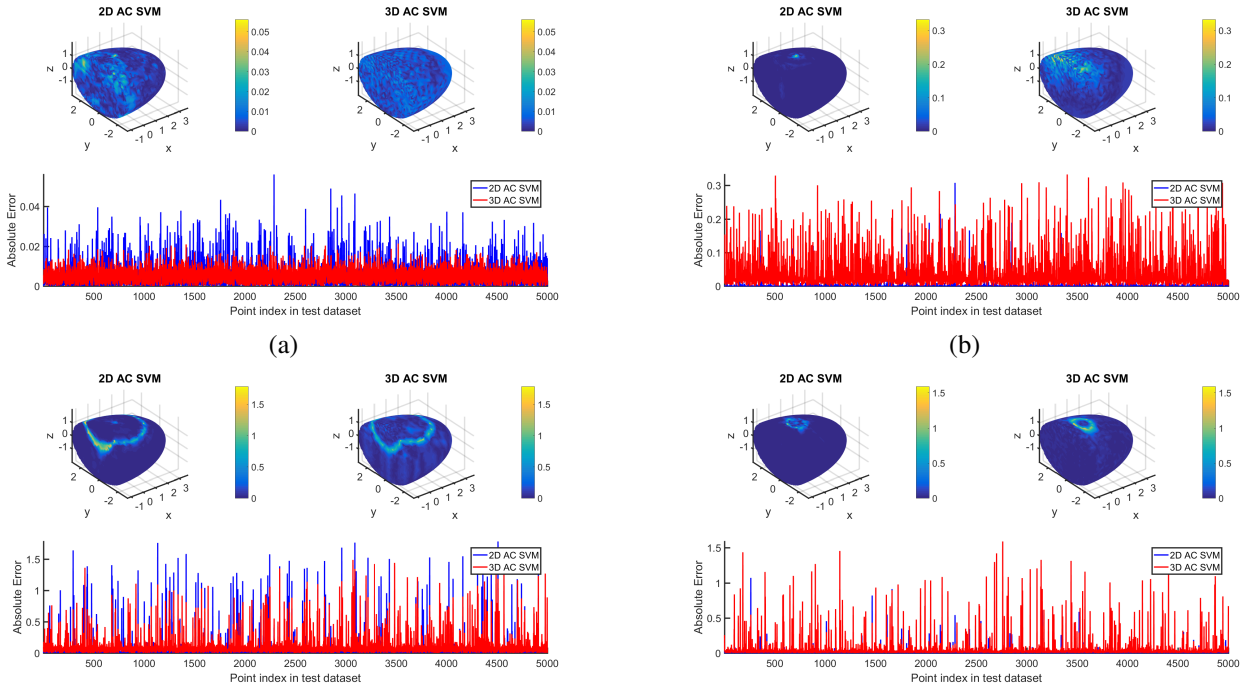


Figure 2. Absolute Errors of the synthetic test data and 2D and 3D interpolations of the synthetic features with 1200 training spatial locations, for (a) Wide Gaussian, (b) Narrow Gaussian, (c) Wide Pulse, and (d) Narrow Pulse.

the RA rhythms (either SR or FL). The 2D AC SVM gets slightly better results than the 3D AC SVM algorithm for the RA SR. For the rest of the simulation rhythms latency maps, the 3D version of the AC SVM algorithm provides better results in terms of MAE than the 2D version. Thus, the 2D SVM-based interpolation with AC kernel can be an alternative to other traditional interpolation methods for CNS data.

5. Conclusions

A SVM algorithm with AC kernel has been studied as non-uniform interpolator of electro-anatomical cardiac maps from CNS. Moreover, the influence of the number of spatial locations and its minimum number to obtain a map that precisely replicates the original or gold-standard have also been studied. Finally, the effect of working in 2D was studied and compared with 3D algorithms. The results with synthetic and simulation data shown that a SVM algorithm with AC kernel can be an alternative to other traditional non-uniforms interpolators for CNS data, both 2D and 3D versions. Oncoming work is devoted to extend this work to real scenario comprising some CNS real data of different cardiac chambers.

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References

[1] Mann D, Zipes D, Libby P, Bonow R. Braunwald's Heart Disease: A Textbook of Cardiovascular Medicine. 10th edition. Elsevier, 2014.

[2] Sanromán-Junquera M, Díaz-Valencia R, García-Alberola A, Rojo-Álvarez J, Mora-Jiménez I. Effect of interpolation on electroanatomical mapping. In 2015 Computing in Cardiology Conference (CinC). IEEE, 2015; 361–364.

[3] Gao G, Chinchapatnam P, Wright M, Arujuna A, Ginks M, Rinaldi A, Rhode K. An MRI/CT-based cardiac electroanatomical mapping system with scattered data interpolation algorithm. 2010 IEEE International Symposium on Biomedical Imaging From Nano to Macro 2010;.

[4] Figueras C, Barquero-Pérez O, Rojo-Álvarez JL, Martínez-Ramón M, Guerrero-Curieses A, Caamaño A. Spectrally adapted Mercer kernels for support vector nonuniform interpolation. Signal Processing 2014;94:421–433.

[5] Tobón C, Ruiz-Villa C, Heidenreich E, Romero L, Hornero F, Saiz J. A three-dimensional human atrial model with fiber orientation. electrograms and arrhythmic activation patterns relationship. PloS one 2013;8(2):e50883.