Noninvasive Estimation of Maximum Elastance from Color-Doppler M-Mode Echocardiograms Using Support Vector Machines

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Abstract

Peak systolic elastance (E_{max}) has been established as a quantitative measurement of left ventricular (LV) global systolic chamber function. However, a measurement of E_{max} is not possible in everyday clinical practice, due to the need of sophisticated catheterization procedures. Given that color-Doppler M-mode (CDMM)echocardiogram image represents the blood velocity, and given that fundamental hemodynamic magnitudes are related by complex physical laws, we hypothesize that E_{max} can be estimated noninvasively by adequate post-processing of CDMM. We propose to use Support Vector Machines (SVM) for building a model based on CDMM velocity image. In an animal model (9 healthy pigs), several interventions were performed to obtain a range in E_{max} wider than basal values. CDMM images were acquired, together with E_{max} from catheters. Intraclass correlation coefficient for the combined independent test sets was 0.81 with the linear kernel and, surprisingly, lower (0.67) with the Gaussian kernel. In conclusion, the noninvasive estimation of E_{max} can be successfully addressed by using SVM regression on CDMM images.

1. Introduction

Ventricular function in the patient with heart disease is often evaluated by means of a wide number of catheter-provided hemodynamic indices, which are extremely informative for the clinician. At the left ventricular (LV) chamber integration level, mathematical and physical basis have been well established for using peak systolic elastance (E_{max}) as quantitative measurement of LV global systolic chamber function [1] . However, a direct measurement of E_{max} is not possible in everyday clinical practice, due to the need of sophisticated catheterization procedures. Also, because it is fully noninvasive, portable, and relatively inexpensive, Doppler echocardiography is the most generalized technique used in patients to assess cardiovascular function. Nevertheless, many aspects of LV physiology can not be directly measured using this technique, and a number of aspects of ventricular physiology are approximated indirectly from measurements of flow velocities with Doppler.

The present study proposes a different approach. Given that color Doppler M-mode (CDMM) echocardiogram image represents the blood velocity, and given that fundamental hemodynamic magnitudes (flow, pressure, volume) are related by (complex) physical laws, we hypothesize that E_{max} can be estimated noninvasively by adequate, possibly nonlinear, post-processing of CDMM images.

The emerging use of Support Vector Machines (SVM) in learning from samples applications [2] is a promising tool for this purpose, due to several well-proven properties. SVM work well for high-dimensional input spaces (as those given by raw images or gene expression); they have a single minimum; large scale algorithms are continuously being developed; and they exhibit excellent generalization performance. We propose to use a regression version of SVM algorithm. According to the incomplete knowledge about the underlying noise distribution, the ε-Huber cost is considered here, as described in [3], for providing with a robust estimation approach.

The outline of the paper is as follows. First, the SVM regressor is briefly reviewed. Then, the animal model is described and the experiments with simultaneously acquired hemodynamical measurements of E_{max} and CDMM velocity images are presented. Finally, conclusions and future research are drawn.

2. SVM regression

We propose to use SVM regression [2] for exploring the possibility of modeling the functional relationship between the velocity field, as recorded noninvasively in the CDMM image, and the value of the simultaneously in-

vasively measured hemodynamical index E_{max}. Let $\mathbf{x}^v$ denote a V-dimensional vector containing a CDMM image. Assume that there exists a possibly nonlinear transformation of the velocity vector into a higher dimensionality space, $\varphi(\mathbf{x}^v) : \mathbb{R}^{\mathbb{V}} \to \mathfrak{F}_{\mathfrak{v}}$, where $\mathfrak{F}_{\mathfrak{v}}$ is known as *feature space*. A linear regression operator can be found there, given by $\mathbf{w} \in \mathfrak{F}_{\mathfrak{v}}$. Assume that a set of measured observations $\{y_i, \mathbf{x}_i^v\}$, with $i = 1, \ldots, N$, is available. Under these assumptions, the regression model is

$$y_i = < \mathbf{w}, \varphi(\mathbf{x}_i^v) > + b_r + e_i \qquad (1)$$

where b_r is the intercept, and e_i represent the model errors or residuals.

The SVM methodology [2] allows us to use different cost functions of the residuals. A suitable robust cost function, that has been proposed for time series and regression-like problems, is the ε-*Huber cost* [3], given by

$$L^P(e_i) = \begin{cases} 0, & |e_i| \leq \varepsilon \\ \frac{1}{2\gamma}(|e_i| - \varepsilon)^2, & \varepsilon \leq |e_i| \leq e_C \\ C(|e_i| - \varepsilon) - \frac{1}{2}\gamma C^2, & |e_i| \geq e_C \end{cases} \qquad (2)$$

where $e_c = \varepsilon + \gamma C$. This cost function has been shown to be useful in the presence of non-Gaussian perturbations, and it can be adapted to different kinds of noise. The SVM algorithm consists of minimizing the ε-Huber cost when it is regularized with the L_2 norm of the regression vector, this is, we minimize

$$\frac{1}{2}\|\mathbf{w}\|^2 + \frac{1}{2\gamma} \sum_{i \in I_1} \left(\xi_i^2 + \xi_i^{*2} \right) + C \sum_{i \in I_2} \left(\xi_i + \xi_i^* \right) - \sum_{i \in I_2} \frac{\gamma C^2}{2}$$

constrained to

$$y_i - < \mathbf{w}, \varphi(\mathbf{x}_i^v) > -b_r \quad \leq \quad \varepsilon + \xi_i \qquad (3)$$

$$-y_i + < \mathbf{w}, \varphi(\mathbf{x}_i^v) > +b_r \quad \leq \quad \varepsilon + \xi_i^* \qquad (4)$$

and to $\xi_i, \xi_i^* \geq 0$, where ξ_i and ξ_i^* (in the following, denoted jointly as $\xi_i^{(*)}$) are the slack variables that account for the excess of the residuals over insensitivity ε, and I_1 (I_2) is the set of samples for which $\varepsilon \leq \xi_i^{(*)} \leq e_C$ ($\xi_i^{(*)} > e_C$). By following the usual SVM formulation methodology, Lagrangian functional L_{PD} can be written down [2, 3], and by making zero its gradient with respect to the primal variables, we obtain

$$\mathbf{w} \quad = \quad \sum_{i=1}^{N} (\alpha_i - \alpha_i^*) \varphi(\mathbf{x}_\mathbf{i}^\mathbf{v}) \qquad (5)$$

$$0 \quad = \quad \sum_{i=1}^{N} (\alpha_i - \alpha_i^*) \qquad (6)$$

where α_i, α_i^* denote the Lagrange multipliers that correspond to (3), (4), respectively. Matrix notation is introduced in $\mathbf{y} = [\mathbf{y_1}, \ldots, \mathbf{y_N}]^{\mathbf{T}}$, $\alpha^{(*)} = [\alpha_\mathbf{1}^{(*)}, \ldots, \alpha_\mathbf{N}^{(*)}]^{\mathbf{T}}$,

and $\mathbf{V}(i, j) = < \varphi(\mathbf{x_i^y}), \varphi(\mathbf{x_j^y}) >$, and then, the dual problem consists of maximizing

$$-\frac{1}{2} (\alpha - \alpha^*)^T (\mathbf{V} + \gamma \mathbf{I}) (\alpha - \alpha^*) + \\ + (\alpha - \alpha^*)^T \mathbf{y} - \varepsilon (\alpha + \alpha^*)^T \mathbf{1} \qquad (7)$$

with respect to $\alpha_i^{(*)}$, and constrained to (6) and to $0 \leq \alpha_i^{(*)} \leq C$. After this quadratic programming (QP) problem is solved, and according to (1), (5), (6), the estimated output for a new observation $\mathbf{x}$ can be easily shown to be given by $\hat{y} = \sum_{i=1}^{N} \eta_i < \varphi(\mathbf{x}_i^v), \varphi(\mathbf{x}^v) > + b_r$, where $\eta_i = (\alpha_i - \alpha_i^*)$. This solution has an sparse expression for an adequate choice of $\varepsilon > 0$, as it only depends of the observations with $\eta_i \neq 0$, and hence they are called the *support vectors*, which contain all the information that is necessary for the model.

To avoid the explicit calculation of dot products in feature spaces, Mercer's kernel are used, which are bivariate functions $K()$ equivalent to calculating a dot product in a possibly infinite dimensional feature space [2], this is, $K(\mathbf{x}, \mathbf{y}) = < \varphi(\mathbf{x}), \varphi(\mathbf{y}) >$. Examples of widely used Mercer's kernels are the following:

- The *linear kernel*, given by $K(\mathbf{x}, \mathbf{y}) = < \mathbf{x}, \mathbf{y} >$. In this case, the regression function has a linear form that can be calculated explicitly as $\beta = \sum_{i=1}^{N} \eta_i \mathbf{x}_i$.
- The *Gaussian kernel*, given by

$$K(\mathbf{x}, \mathbf{y}) = \exp\left(-\frac{\|\mathbf{x} - \mathbf{y}\|^2}{2\sigma^2}\right)$$

where σ is the width parameter.

Therefore, we can use in this model a Mercer's kernel, and the final solution of SVM regressor can be readily expressed as

$$\hat{y} = \sum_{i=1}^{N} \eta_i K(\mathbf{x}_i^v, \mathbf{x}^v) + b_r \qquad (8)$$

In general, two kinds of free parameters must be chosen: cost function free parameters $\{\gamma, C, \varepsilon\}$, and kernel free parameters $\{\sigma, \delta\}$. A possible method for setting them is a sequential search of the appropriate value for each, basing on bootstrap bias-corrected training error, as proposed in [4], and this is the approach followed in this work.

3. Experiments and results

Observations were available from an animal model database. The methodological details of the animal experiments used for the present study have been reported elsewhere [5]. In brief, the CDMM velocity images and simultaneous hemodynamical measurements of E_{max} were available in 9 animals (pigs). For each acquired beat, CDMM images were first aligned, in order to bound the region of interest (ROI) both in the spatial domain (between
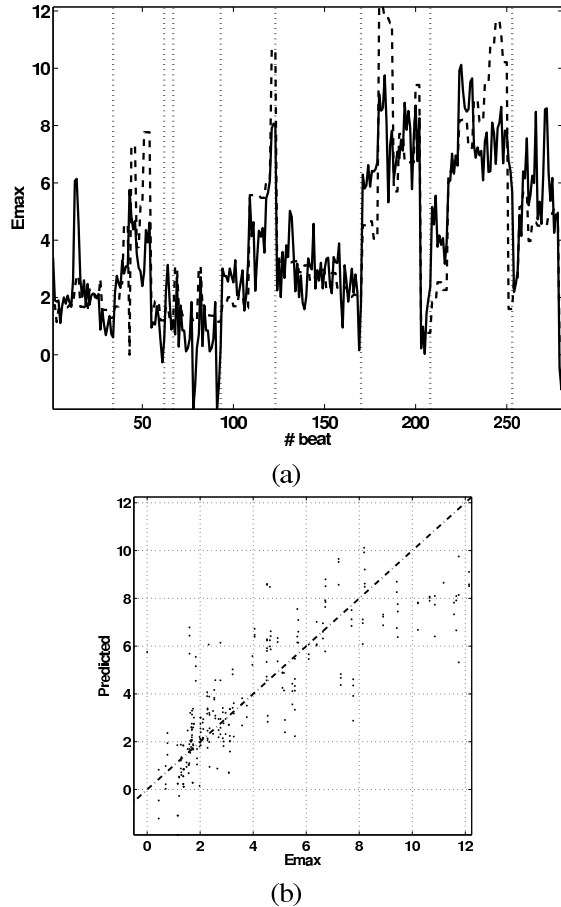
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Figure 1. Predicted values of E_{max} with linear kernel. (a) Noninvasive prediction for each observation (continuous) and catheter measurement (dashed). Vertical lines represent observations from different animals. (b) Noninvasive prediction vs catheter measurement.

parameters $\{\gamma, C, \varepsilon\}$, as well as kernel parameter σ for the RBF kernel. Free parameters were adjusted for providing the minimum bootstrap mean squared error, by following a procedure similar to that proposed in [4], and using B=10 resamples. In order to measure the agreement between hemodynamical measurements of E_{max} and the measurements provided by SVM-SR, intraclass correlation coefficient (R_{ic}) was used as merit figure for each regressor.

Table 2 shows the R_{ic} values when estimating E_{max} for each regressor, as well as for the whole set of the independent outputs. The highest performance ($R_{ic} = 0.81$) was achieved by the linear kernel, and surprisingly, the RBF kernel did not improve the approximation performance, as opposite to what one should expect, given the underlying nonlinear relationships among variables. Figure 1 depicts the predicted E_{max} for each observation, as provided by its own independently trained machine. Though the accuracy in the prediction was limited, a visible good trend to follow the actual output value could be observed.

Because the linear kernel exhibited a higher prediction accuracy, we explored the least squares solution for comparison purposes, but extremely poor performance was obtained (mean $R_{ic} = 0.16$). This proved that the problem can not be trivially solved by any linear coefficient fitting, and that the SVM approach exhibited very good regularization properties. Also, in order to determine if an increase in the detail of the image representation could improve the performance, resolutions of $2^5 \times 2^5$ and $2^6 \times 2^6$ were explored, with no significant improvement ($R_{ic} = 0.80, 0.79$).

Finally, the averaged coefficients for the nine regressors were obtained, as represented in Fig. 2. There was a clear coherence among the coefficients obtained for each of the leave-one-pig-out regressor, so that the variance for each model was reduced (not shown). Given that velocities leaving the apex are codified as negative, and viceversa, we can observe that positive coefficients correspond to a index decrease, and these are at the beginning of the systole along all the spatial domain and at the end of the systole close to the outflow tract and close to the apex. The rest of the coefficients are negative, and accordingly, they will contribute to the index increase.

4. Conclusions

An innovative approach has been presented for characterizing noninvasively and quantitatively the left ven-

the apex of the left ventricle and the outflow tract) and in the temporal domain (from the beginning to the end of systole). Each ROI was first interpolated using bivariate tensor product splines, and then downsampled to a grid of $2^4 \times 2^4$ pixels, which was an initial trade-off between a moderate computational burden required and a minimally acceptable representation of the velocity field in the image.

Given that intra-subject measurements are expected to be strongly dependent, we considered the following training and test strategy. All the available measurements in all but one pig were considered for training, and the measurements for the pig out were used as independent test set; this procedure was repeated for the 9 available pigs. Table 1 shows the number of observations in each train and test set for each of the nine leave-one-pig-out regressor.

The linear and the RBF kernels were explored. For each regressor, the required free parameters were adjusted in the training set. Searched free parameters were cost function

Table 1. Number of training (middle) and test (down) observations for each regressor (up).

#1	#2	#3	#4	#5	#6	#7	#	#9
247	253	276	255	251	234	243	236	253
34	28	5	26	30	47	38	45	28

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Table 2. Values of R_{ic} for each SVM regressor from velocity (V), with $d = 4$ (linear and Gaussian kernel).

	V lin	V Gauss
#1	0.37	0.67
#2	0.58	0.41
#3	0.54	0.16
#4	0.61	0.36
#5	0.83	0.72
#6	0.30	0.53
#7	0.75	0.45
#8	0.55	0.34
#9	0.76	0.32
Total	0.81	0.67

tricular function. Instead of either an (often unavailable) physical description based approach or an indirect noninvasive parameter, the possibility of approximating the implicit physical description between the CDMM images and a given cardiac index through learning form examples has been proposed. The accuracy obtained in the estimation, though acceptable for a first approach, needs to be improved. We could observe that the sequential search of the three-four free parameters sometimes became suboptimal, which could be the cause for RBF kernel not outperforming the linear kernel. Other conventional search strategies were explored, without success. As an exhaustive search is not currently feasible for medium and large scale problems, a better free parameter search strategy will surely improve the accuracy of SVM. Another interesting technical direction is the exploration of other appropriate Mercer's kernels, that can deal more efficiently with increased detail in the input space. Without doubt, the inclusion of more images in more animals will improve the performance.

Acknowledgements

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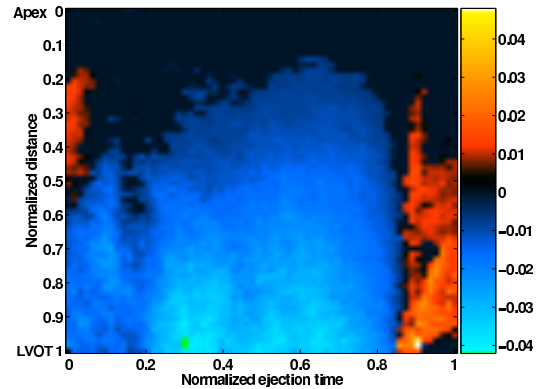
(a)
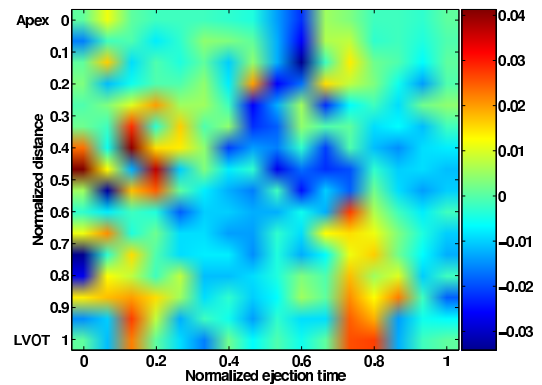
(b)

Figure 2. Linear SVM coefficients representation. (a) Example of centered Doppler M-mode image. (b) Map of averaged coefficients for E_{max} regressor.

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