

The Use of a Single Continuous Regularization Parameter for the Generalized Eigensystem Method

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Abstract

We have previously proposed the generalized eigensystem (GES) method as an alternative to Tikhonov regularization for various types of inverse problems. In those studies, we truncated the number of modes used in GES to stabilize the inversion. However, often there is a significant decrease in performance when the number of modes to use is estimated using only the available data. We have modified our formulation of GES to use the same expansion vectors as before, but now the stabilization is performed by the inclusion of a single continuous regularization parameter. In this study we compare the performance of GES using the optimal modal truncation and two different methods for choosing the single continuous regularization parameter.

1. Introduction

We have previously introduced the generalized eigensystem (GES) method as an alternative to Tikhonov regularization for solving the inverse problem of electrocardiography [1, 2, 3, 4]. Recently we introduced the minimum distance to origin (MDO) method as a method for estimating the number of modes to use in GES [3] based only on measurable data. We compared GES using MDO to choose the number of expansion modes with Tikhonov regularization using the composite residual and smoothing operator (CRESO) for choosing the single continuous regularization parameter. In that study, zero order GES with MDO outperformed zero order Tikhonov with CRESO, but there was a large degradation in performance for GES when using MDO to choose the number of modes compared to the optimal choice of modes.

In this paper we present an alternative formulation for GES that makes it similar to Tikhonov regularization in that at each time instant we seek a *single* continuous regularization parameter. Specifically, instead of determining the exact number of modes to use in order to stabilize the inverse, we first take a sufficient number

of expansion modes, then impose a low pass filtering characterized by a Tikhonov type parameter t to weaken the instability effect of higher order modes.

2. Experimental data and model

For this paper, data was collected during an *in-vivo* experiment on swine. The swine model was used because of its similarity to humans in the anatomical arrangement of heart, lungs, bone, muscle, etc. For this experiment, bipolar pacing electrodes were sewn to the heart surface (the epicardium) in six different locations, and an epicardial sock was placed over the heart surface and over the pacing electrodes. The epicardial sock had effectively nine columns of six electrodes arranged about the heart. The chest was then sewn shut and unipolar recordings of epicardial potentials were made from the epicardial sock electrodes while the heart was paced from the six sites (Prucka Engineering, Houston, Texas).

A finite element model of the region from the epicardium to the torso was constructed using the I-DEAS finite element package (SDRC, Ohio) from CT scans made of the swine. For this study we assumed a homogeneous model with 41,430 nodes and 212,366 linear tetrahedral elements. The finite element model had 1748 nodes on the epicardium. In order to project the measured epicardial potentials at the 54 electrodes to the torso, we performed Laplacian interpolation from the measured electrodes to estimate the potentials at the remaining finite element nodes on the heart surface [5]. Using standard finite element techniques [3] a transfer matrix relating the (measured and estimated) epicardial potentials at all nodes on the heart surface to finite element nodes on the body surface was constructed. Specifically, our transfer matrix related the potentials at all 1748 epicardial nodes to 96 finite element nodes on the torso (body) surface which we assumed to be the measurement locations. These 96 torso surface locations were fairly evenly spaced near the heart on the pig torso.

The time segments analyzed consisted of the QRS portion of the cardiac cycle beginning just after the pacing spike. The rms values of the measured epicardial potentials as a function of time for the portion of the QRS analyzed in this paper is displayed in Figure 1 for the six pacing sites. As the figure illustrates, the duration of the QRS varies as the source of the ventricular depolarization is varied, from a minimum of 75 milliseconds to 120 milliseconds.

In order to simulate modeling and measurement errors, white Gaussian noise was added to the computed body surface potentials. Once the body surface potentials were computed, the segments of time to be analyzed were determined, and the corresponding body surface potentials were determined. The rms value of the body surface potentials over the entire time period to be analyzed was determined as

$$RMS = \sqrt{\frac{1}{96N} \sum_{k=1}^{96} \sum_{i=1}^N (b_k^i)^2} \quad (1)$$

where N is the number of sample points in the QRS to be analyzed, b_k^i is the i^{th} sample point in the QRS at the k^{th} location. Once the RMS value was determined, zero mean white Gaussian noise with standard deviations of

$$\sigma = RMS * f \quad (2)$$

was added to the body surface potentials, where f was varied. Specifically, f was 0.05 for the 5% noise level used throughout this paper, although other levels of noise were also examined.

3. Inverse algorithms

The zero order generalized eigensystem method can be formulated as the solution to the following minimization problem

$$\min_{\hat{h}} \Pi = \|\hat{b} - b\|^2 + t \|\hat{h}\|^2 \quad (3)$$

where b is a vector of known (measured) body surface potentials, \hat{h} and \hat{b} are estimates of the potentials on the heart surface (the *epicardium*) and body surface, respectively, and t is the regularization parameter. In general, we attempt to match the estimated body surface potentials with the measured body surface potentials, while penalizing epicardial estimates with large magnitude. The regularization parameter t indicates the relative weight given to the two terms, and needs to be estimated based on measurable data.

For the generalized eigensystem methods, we assume

$$\hat{b} = \Phi_B \alpha \quad (4)$$

$$\hat{h} = \Phi_H \alpha \quad (5)$$

where Φ_B and Φ_H are suitably chosen matrices whose columns contain the expansion vectors, and α is a vector of expansion coefficients. Note that the expansion vectors on the epicardium and body surface are related through the transfer matrix Z ,

$$\Phi_B = Z \Phi_H \quad (6)$$

For zero order regularization, minimizing Π leads to the expression for α

$$(\Phi_B^T \Phi_B + t \Phi_H^T \Phi_H) \alpha = \Phi_B^T b \quad (7)$$

We can compute the generalized singular value decomposition of the pair Φ_B and Φ_H as

$$\Phi_B = U C X^T \quad (8)$$

$$\Phi_H = V S X^T \quad (9)$$

where U and V are unitary matrices, S is a diagonal matrix with nonzero elements s_i , C is a diagonal matrix with nonzero elements c_i , and

$$C^T C + S^T S = I \quad (10)$$

Using these relationships, we can write the algebraic system (7) as

$$(C^T C + t S^T S) \tilde{\alpha} = C^T \tilde{b} \quad (11)$$

where $\tilde{\alpha} = X \alpha$ (X is defined by equations 8 and 9) and $\tilde{b} = U^T b$.

In this study we chose to use 54 expansion modes throughout, since there were 54 epicardial sensors. For this algorithm, a value of the regularization parameter t was chosen at each time step. Hence the the inverse problem was solved independently at each time step. Two different methods were examined for choosing this parameter.

3.0.1 Composite residual and smoothing operator

Originally proposed by Colli-Franzone [6], CRESO is a commonly used method for determining the regularization parameter for Tikhonov regularization in inverse electrocardiography [7, 8, 9]. CRESO finds the value of t that maximizes the difference between the derivative of the smoothing term $t \|\hat{h}\|^2$ and the fit to the body surface data $\|\hat{b} - b\|^2$. That is, we want to find the smallest value of t which maximizes the function

$$B(t) = t \|\Phi_H \alpha\|^2 - \|\Phi_B \alpha - b\|^2 \quad (12)$$

This can alternatively be formulated as finding the smallest value of t which minimizes the function

$$C(t) = \|\Phi_H \alpha\|^2 + 2t \frac{d}{dt} \|\Phi_H \alpha\|^2 \quad (13)$$

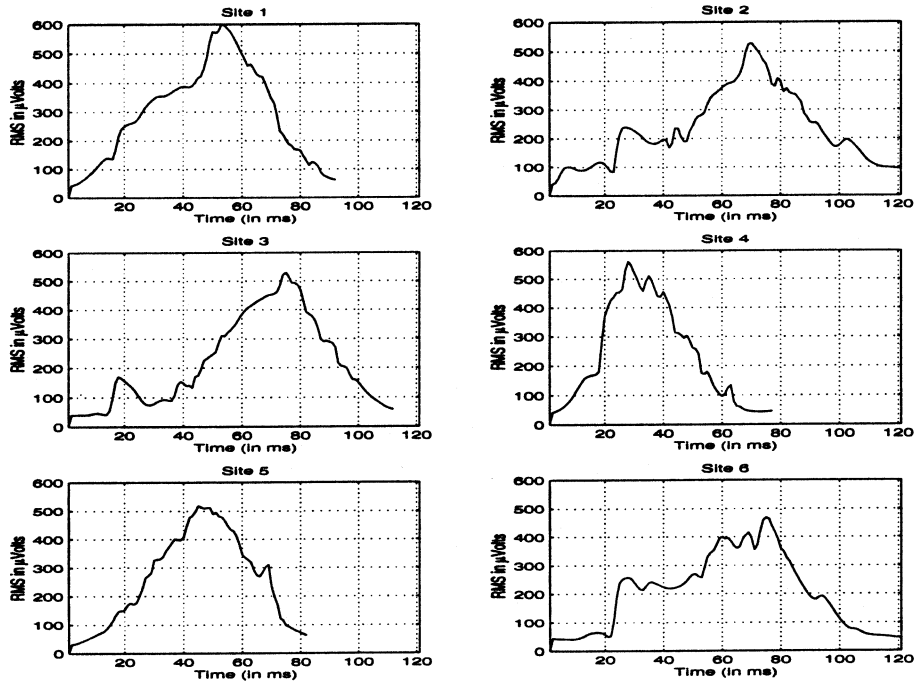


Figure 1. RMS values of measured epicardial potentials as a function of time for the six pacing sites. The QRS duration ranged from 75 milliseconds to 120 milliseconds.

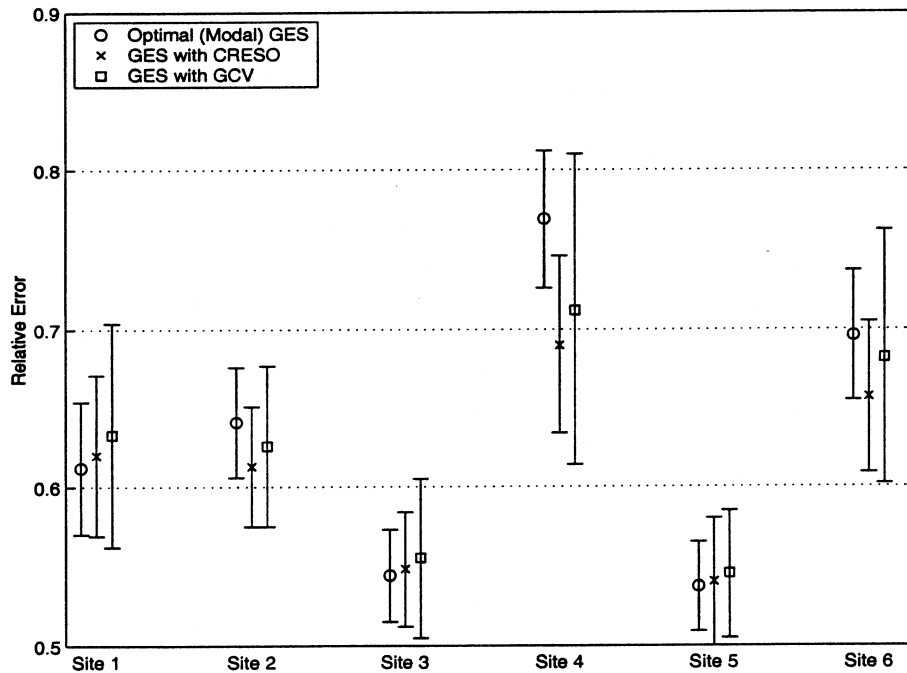


Figure 2. Relative errors (mean \pm standard deviations) for the six pacing sites for optimal modal truncation, using CRESO to choose the single regularization parameter, and using GCV to choose the single regularization parameter.

After some manipulation the function $C(t)$ to be maximized can be written as

$$C(t) = \sum_{i=1}^{N_c} \frac{s_i^2 c_i^2 \bar{b}_i^2}{(c_i^2 + ts_i^2)^2} \left[1 - \frac{4ts_i^2}{c_i^2 + ts_i^2} \right] \quad (14)$$

where N_c is the number of nonzero singular values c_i (for our problem $N_c < N_s$) and \bar{b}_i is again the i^{th} component of $\mathbf{U}^T \mathbf{b}$.

3.0.2 Generalized Cross Validation

The generalized cross validation method finds the value of the regularization parameter which minimizes the predicted errors in the observed data [10]. To use the generalized cross validation to estimate the regularization parameter t , we need to choose the value of t to minimize

$$V(t) = \frac{\|\hat{\mathbf{b}} - \mathbf{b}\|^2}{[\text{trace}(\mathbf{I} - \mathbf{A}(t))]^2} \quad (15)$$

where

$$\hat{\mathbf{b}} = \mathbf{A}(t)\mathbf{b} \quad (16)$$

$$= \mathbf{UC} [\mathbf{C}^T \mathbf{C} + t\mathbf{S}^T \mathbf{S}]^{-1} \mathbf{C}^T \mathbf{U}^T \mathbf{b} \quad (17)$$

With the assumptions above, the function $V(t)$ to be minimized in generalized cross validation reduces to

$$V(t) = \frac{\|\hat{\mathbf{b}} - \mathbf{b}\|^2}{\left[N_b - \sum_{i=1}^{i=N_c} \frac{c_i^2}{c_i^2 + ts_i^2} \right]^2} \quad (18)$$

where $\mathbf{b} \in R^{N_b}$.

4. Results and discussion

Figure 2 presents the results of twenty-five simulations with a five percent noise level for (1) the optimal modal truncation, (2) using CRESO to choose the regularization parameter, and (3) using GCV to choose the regularization parameter for the six different pacing protocols. The average relative error (over the size protocols) was 0.633 ± 0.036 for the optimal modal truncation, 0.611 ± 0.045 when CRESO was used to choose the regularization parameter, and 0.626 ± 0.065 when GCV was used to choose the regularization parameter. For the system studied the reformulation of GES with a single regularization parameter produces better results than the optimal modal truncation (when the known solution is used to produce the number of expansion modes). In addition, using CRESO to choose the regularization parameter produces smaller average errors and smaller standard deviations than when GCV is used.

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