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# A Computationally Efficient Activation Model for Noninvasive Imaging of Cardiac Depolarization

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*Abstract*— **The computer model based computation of the cardiac activation sequence in humans has been recently subject of successful clinical validation. This method is of potential interest for guiding ablation therapy of arrhythmogenic substrates. However, for obtaining clinical acceptance computation times of a few minutes are desirable. This has fundamental impact on the degree of detail which can be used in the model. The central point of this paper is the efficient computation of simulated ECG data (forward problem), which is needed for each iteration step of the inverse problem solver. The computational optimizations are obtained by consequently using the biophysical properties of the source sensor relationship (lead field). The developed method is applied for imaging the activation sequence in a patient with a left posterior atrioventricular pathway (WPW). The computation time was 92 seconds on a Pentium 3 GHz CPU. The distance from the first onset of activation in the computed activation map to the successful ablation site was 11 mm.**

*Keywords*—**Cardiac modeling, inverse problem**

## I. Introduction

The inverse problem of electrocardiography (ECG) is a model based back projection of body surface ECG mapping data onto a cardiac source pattern. Recently, the successful validation of such approaches in humans was reported [1], [2]. For a clinical application, however, the source pattern has to be computed with a short computation time to obtain acceptance. This has severe implications for the model underlying the computation limiting the degree of detail which can be used in the approximation.

Activation time imaging is an iterative method for computing the depolarization sequence. At each iteration step the measured ECG data are compared with the ECG data simulated for the actual guess of the activation pattern. The guess is then improved by minimizing a cost function [3]. Thus, the method needs the solution of the forward problem at each of typically over ten thousand iteration steps. The scope of this study is to present a computationally efficient evaluation of an activation model which reduces the computation time to a few minutes.

## II. Method

### A. Model Scope

The basic idea of activation time imaging is to minimize the difference of the measured ECG data $\mathbf{\Phi}$ and the simulated ECG data $\mathbf{\Psi}$. The computation of the simulated ECG needs a proper model. Here, a lead field matrix $\mathbf{L}$ relating the membrane potentials in $P$ source points to the ECG in $N$ electrodes is obtained by applying the boundary or finite element method (BEM or FEM). The $P$ membrane potentials at $K$ time steps are stored in the source pattern matrix $\mathbf{V}(\boldsymbol{\tau})$. This notation should indicate that the source pattern is fully determined by an activation vector $\boldsymbol{\tau}$ (solution of the inverse problem). The simulated ECG $\mathbf{\Psi}$ (forward problem) is obtained by the product

$$\mathbf{\Psi} = \mathbf{L}\mathbf{V}(\boldsymbol{\tau}). \tag{1}$$

In order to stabilize the inverse solution with respect to noise and error in the model a regularization term of Tikhonov second order is added. Thus, the cost function has the form:

$$\frac{1}{f_s}\left\|\mathbf{\Phi} - \mathbf{L}\mathbf{V}(\boldsymbol{\tau})\right\|^2 + \lambda^2\left\|\Delta\boldsymbol{\tau}\right\|^2 \rightarrow \min . \tag{2}$$

Here, the first term is called residual error and the second is the regularization term with the regularization parameter $\lambda$. In order to make the choice of $\lambda$ insensitive to the sampling frequency $f_s$ of the ECG data the residual error is scaled by the sampling frequency.

### B. Computational Demands

Details on the optimization method used for computing cardiac activation times can be found elsewhere [3]. Shortly, a conjugate gradient method with the Polak-Ribiere formula for computing the direction of search is used for minimizing the cost function. Here, cost function evaluation and the computation of its gradient is by far the computationally most expensive part. The cost function contains two terms: the norm of the difference of measured and simulated ECG data (residual error) and the regularization term. As the evaluation of the regularization term of Tikhonov second order needs only the multiplication of a sparse regularization matrix with the activation vector it can be neglected when estimating the computation time.

The computational demanding task is the computation of the forward solution at each iteration step. The computation of the product (1) needs $N \times P \times K$ floating point multiplications. From the patient data presented in [2] and [3] we find that $N$ is 62 for the Amsterdam ECG mapping array, $P$ is typically about 500 to 1000 and $K$ is 50 to 100 if the ECG data is sampled at 500 Hz (the depolarization interval lasts 100 to 200 ms). Thus, this step requires about 5 million flops. This takes approximately 100 ms on a Pentium 3 GHz CPU. At least the same time is needed for computing the cost function gradient. Having in mind that more than ten thousand iterations are needed for computing an inverse

solution we estimate a computation time of 30 minutes. This is unacceptable if the imaging method should guide a curative treatment like catheter ablation. Note that there is no potential for a parallelization of the program code due to the iterative nature of the algorithm.

*C. Efficient Activation Model*

The focus of this paper is to present a method which uses the particular biophysical properties of the matrices for speeding up the computation of the matrix product by more than an order of magnitude.

Note that the scope of the model is the computation of the activation sequence from body surface ECG data. Thus the applied activation function does not need to represent such detail of the action potential as ionic current models do. It is sufficient to model activation by a step like function, with a known amplitude $\Delta v$ of, e.g., 90 mV for the ventricles. Due to the relatively coarse mesh grid used with models applied to the inverse problem a discrete source point corresponds to a tissue area (BEM) or volume (FEM) with a diameter of about 1 cm. As it takes a few milliseconds to activate a patch of this size the rise time parameter $T$ is typically larger than the rise time of a single cell. A well established activation function $V_p(t)$ is the sigmoidal step function [3], [4]

$$V_p(t)=\begin{cases} v_0 & \text{for} \quad t-\tau_p \le -T \\ v_0+\dfrac{\Delta v}{2}\left(\dfrac{t-\tau_p}{T}+1\right)^2 & \text{for} \quad -T < t-\tau_p \le 0 \\ v_0+\Delta v-\dfrac{\Delta v}{2}\left(\dfrac{t-\tau_p}{T}-1\right)^2 & \text{for} \quad 0 < t-\tau_p \le T \\ v_0+\Delta v & \text{for} \quad T < t-\tau_p \end{cases}, \qquad (3)$$

with the resting potential $v_0$ and the local activation time $\tau_p$ at the source point $p$. For a time step $k$ we can write $t=k/f_s$.

There is a remarkable biophysical property which helps speeding up the matrix product computation. If for a given time step $k$ all source points have the same membrane potential (i.e., all at resting potential or all at plateau potential) the ECG for this time step $k$ is zero in all leads. This effect is responsible for the genesis of the isoelectric segments in the ECG and mathematically reflected by the fact that all row sums of $\mathbf{L}$ are zero. Thus, any constant added to all $P$ action potentials will not affect the computed ECG. Consequently, any value can be assigned to the resting potential $v_0$ in (3). For saving computation time it is of advantage to have as many zeros as possible in the source pattern matrix $\mathbf{V}(\boldsymbol{\tau})$. We can achieve this by choosing either the resting or the plateau potential zero. In our implementation the plateau potential is set to zero by choosing $v_0=-\Delta v$.

Thus, almost half of the source pattern matrix elements will equal zero. A second possibility for saving computation time is to check for an isoelectric segment in the simulated ECG at the begin of the depolarization interval. The smallest activation time in the vector $\boldsymbol{\tau}$ is termed $\tau_{min}$. We now find from (3) that for all time steps $k<k_0$, with $k_0=f_s(\tau_{min}+T)$ the entire source region is at the resting potential. Thus, additional computation time can be saved by avoiding the computation of time steps $k<k_0$.

Finally, we observe that the contribution of a source point $p$ to the simulated ECG is equal for all time steps $k_0 \le k \le k_{p1}$, with, $k_{p1}=f_s(\tau_p+T)$ as $V_p(t)$ remains constant in this interval. Thus, the contribution is computed only once and added multiple times to the simulated ECG data matrix. Only for the short interval $k_{p1}<k<k_{p2}$, with $k_{p2}=f_s(\tau_p+T)$ the contribution of the source point $p$ to the ECG has to be computed independently for each time step. A pseudo-code for the fast matrix product computation is listed below.

```
function simulateECG(activation vector τ , lead field L)
  initialize the simulated ECG Ψ(n,k) for all n, k with zero
  compute source pattern V(p,k) for all p, k
  get the smallest activation time τ_min from τ
  compute k_0 rounding towards plus infinity
  for all source points p do
    compute k_p1 rounding towards plus infinity
    compute k_p2 rounding towards minus infinity
    for all electrodes n do
      comment: compute resting potential contribution x
      x=−L(n,p)×Δv
      for k=k_0 to k_p1 do
        Ψ(n,k)= Ψ(n,k)+x
      od
      comment: compute ECG during sigmoidal activation
      for k=k_p1 to k_p2 do
        Ψ(n,k)= Ψ(n,k)+ L(n,p)× V(p,k)
      od
    od
  od
```

The matrix product needs three nested loops. The outermost loop indexes all source points. The next loop indexes all electrodes. The innermost loop considers the time intervals and optimizations described above.

As outlined in [5] the evaluation of the cost function gradient brings as many components of new information for an optimization problem as there a unknowns (here, source points $P$). Thus, a fast gradient evaluation taking less time than $P$ function evaluations will speed up the optimization routine.

For an efficient computation of the residual error gradient we will first make the following definitions: we write $v'_p(k)$ for the partial derivative of the activation function $V_p$ (3) by $\tau_p$ at time step $k$. Outside the interval $k_{p1}<k<k_{p2}$ the derivative is zero. For the lead field matrix column $p$ we write $\mathbf{l}_p$. Finally we introduce $\mathbf{d}(k)$ for the differences of the measured ECG $\boldsymbol{\Phi}$ and the simulated ECG $\boldsymbol{\Psi}$ in all leads at time step $k$. Note that this result was already computed during the cost function evaluation. The component $p$ of the residual error gradient is then given by:

$$\frac{1}{f_s}\frac{\partial}{\partial \tau_p}\left\|\boldsymbol{\Phi}-\mathbf{L}\mathbf{V}(\boldsymbol{\tau})\right\|^2 = -\frac{2}{f_s}\sum_{k>k_{p1}}^{<k_{p2}} \mathbf{d}^T(k)\mathbf{l}_p v'_p(k) \qquad (4)$$

where the superscript $^T$ denotes the transpose. Thus, as the interval $k_{p1}<k< k_{p2}$ contains only a few samples (typically about five), the evaluation of the residual error gradient needs even less time than the residual error evaluation alone.

## III. Patient Data

### A. Measurement Protocol

In order to test our method with respect to a potential clinical application, we investigated data from a 24 year old male patient who underwent radio-frequency ablation of an atrio-ventricular accessory pathway (WPW-syndrome). The measurement protocol is shortly summarized as follows: the individual torso geometry was assessed by MRI imaging using a 1.5 T Siemens Magneton Vision Plus Scanner. The end diastolic ventricular geometry was taken from ECG-gated oblique cine mode images recorded with 6 mm slide thickness and spacing. The torso geometry (skin surface and lungs) were obtained from T1-FLASH-mode scans with 10 mm slide thickness. All scans were performed during breath-hold in expiration. From this data a boundary element computer model was built up containing the ventricular surface (697 source points *P*, 10 mm mean node spacing) the blood masses in the ventricular cavities, the lungs, and the skin surface. Seven anterior and five posterior markers were used to couple all geometrical data to the computer model. The patient was moved to the catheter laboratory and a 62-lead electrode array was applied. The electrode and marker locations were measured with a magnetic digitizer (Fastrak, Polhemus Inc., Colchester, Vt., USA). The Mark 8 ECG amplifier (Biosemi V.O.C, Amsterdam) was used to record the signals at a sampling rate of 2048 Hz and with a bandwidth of 400 Hz.

During the diagnostic part of the inverse procedure electro-anatomical mapping was performed for estimating the location of the accessory pathway. The bundle was localized in a left posterior position. Here, the coronary sinus (CS, a venous vessel in the left posterior and left lateral atrio-ventricular groove) was mapped for assessing left ventricular activation via the venous system. Mapping and annotation of the intra-cardiac signals took about 45 minutes. As the invasive diagnosis revealed a left sided pathway the combined mapping and ablation catheter was forwarded in the left ventricular chamber via the femoral artery. Two radio frequency deliveries were necessary to interrupt the accessory pathway. The distance between the two ablation sites was 18 mm. The therapeutic part of the invasive procedure took about 20 minutes. After a waiting period of 30 minutes (exclusion of a pathway recovery) the mapping catheter was removed and the 7 anterior marker positions were measured in order to couple the intracardiac data to the computer model.

### B. Model Application

For the inverse computation the ECG data bandwidth was reduced to 150 Hz according to the AHA recommendation [6] and the data was down-sampled to 500 Hz. A target beat was manually selected and the signal was baseline corrected prior to the ECG P-wave. The data in the time interval of ventricular depolarization (123 ms, 62 time steps) was used as input for activation time imaging. After removing channels with a low signal quality 55 of 62 leads were used as input for the inverse computation.

The starting activation time vector for the optimization routine was determined by the critical point theorem [7]. Here, an effective rank of 19 was determined for the measured ECG data matrix. As proposed in [3] a coupled regularization scheme was applied. This means that regularization was started with a relatively high value ($\lambda^2=10^{-11}$). Then the regularization parameter is reduced iteratively by diviving $\lambda^2$ by $\sqrt{10}$ at each iteration step. The solution obtained from the previous step was used as the starting vector for the actual step. As observed in [3] this reduces the influence of the regularization parameter on the computed activation map.

The computation time for 9 values of $\lambda$ was 92 s (21500 cost function calls). Thus the time needed for a single cost function evaluation and computation of its gradient was less than 4.3 ms. As the rise time parameter was selected to be 3 ms there were typically only 3 time steps in the computationally most expensive interval $k_{p1}<k< k_{p2}$. Thus about 95% of all time steps were computed with the computational optimizations described above contributing to the save in computation time.

The activation map computed at $\lambda^2=3.2\times10^{-15}$ is shown in Fig. 1. The distance from the location of the first activation onset in the computed map to the site of successful pathway ablation was 11 mm.

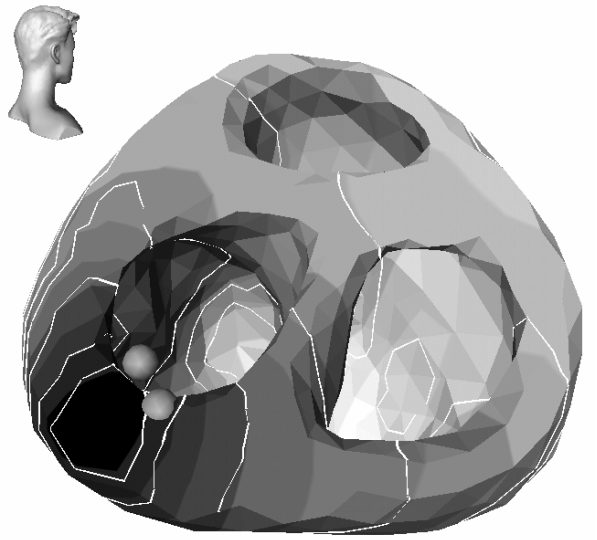

Fig. 1. The computed activation map is shown in a right lateral to posterior oblique view. Note the head icon for orientation. Dark marks early and light shading late activation. Isochrones are plotted in steps of 10 ms. First onset of activation is computed in a left posterior basal position at about 1 cm distance from the two ablation sites (spherical gray markers)

## IV. Discussion

Every model is an approximation of the reality and thus, every cardiac model will provide only a simplified picture of the true (individual) organ. In this context a clearly defined application or scope of the model is needed for specifying the necessary detail of the approximation. The application of the model presented here is noninvasive imaging of cardiac activation. A striking property of models applied in this field is an astonishingly coarse level of approximation (about 1 cm grid spacing, assumption of isotropic conduction) [2], [3], [4].

There are two arguments which justify the relatively coarse mesh grid typically applied: computation time and information content of the measured data. To our experience the computation time depends approximately by fourth order on the reciprocal of the node spacing applied. If we, e.g., halve the grid spacing $\Delta x$ the BEM mesh will contain four times more nodes as before ($P \sim \Delta x^{-2}$). The time needed for a single cost function evaluation is proportional to $P$ but as the number of iterations needed by the conjugate gradient increases approximately linear with $P$ we have a quadratic dependency with respect to $P$. Thus halving the grid spacing increases computation time by a factor of 16. We estimate on the other hand that the effective rank of the ECG data matrix is in the order of 20 and the number of linearly independent time steps is about 50 at a signal bandwidth of 150 Hz. Thus, it seems unlikely that using much more than 50×20 source points will truly improve the spatial resolution of the method.

As it was shown in [4] activation time imaging can cope with a relatively high degree of error in the model. Such errors are unavoidable when constructing volume conductor models of individual patients. However, it should be stressed at this point that according to [4] activation time imaging is less sensitive to model error as other approaches but not completely insensitive. Thus, one can expect that future model improvements such as modeling of individual fibrous structures might additionally stabilize the computed activation maps. This might be of particular interest for more complex activation patterns as, e.g., reentry.

The amazing stability of activation time imaging with respect to model errors enables the use of simplified activation functions. The central point of this study was the presentation of an activation model which enables the computation of an inverse solution in less than 2 minutes on an ordinary personal computer. A limitation of our study is that a comparison with formerly used activation models is missing. The major reason for this is that the optimizations in the activation model where developed over the years. Our current software differs from former versions in much more points (e.g. the programming language was changed from Fortran to C++, the optimization strategy is now a conjugate gradient instead of a Quasi-Newton method). This hampers the possibility of investigating only the effect of the activation model. However, from the data presented one can estimate that a single cost function evaluation takes less than 5 ms while the matrix product in (1) takes alone about 100 ms. As the computation time needed by the optimizer seems negligible, the speed up is more than a factor of twenty.

As an example for a potential clinical application the ventricular insertion of an atrio-ventricular accessory pathway was imaged in a WPW-patient with a spatial resolution of about 1 cm. Here, the clinical time span needed for the diagnosis of a left sided pathway was 45 minutes. The inverse computation of the activation map took only slightly more than one minute.

Considering that the computation of the start vector by the critical point theorem takes also about a minute and taking some time for signal processing (target beat selection, baseline correction) into account it is still realistic to reduce this time span to a few minutes.

The current resolution seems sufficient to describe the accessory pathway location in anatomical terms (left, right, anterior, posterior, lateral, septal). Clinically, this information is already helpful. For positioning the ablation catheter the signal from the catheter tip and the stability of the catheter position will be the key parameters also in the future.

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