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The single moving dipole source for electrocardiography inverse problem in 3D human model

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Abstract. Computing electrical source in the heart from potentials on the body surface is an ill-posed problem of electrocardiogram (ECG). It is so difficult to get an exact solution of this problem. To solve this ECG inverse problem, a numerical analysis is used for forward problem with a specific source model. Then, the solutions of ECG inverse problem is reached by using an iterative technique, Newton or downhill simplex, to find the best source whose potentials best match to the observed potentials in a least square sense. Such methods, however, often converge to a local minimum and their results are affected by initial parameters. In this paper, source is considered as a moving single equivalent dipole and genetic algorithm, an efficient and robust optimization method, is proposed to estimate parameters of source. In addition, some improvements are introduced to enhance performance of conventional genetic algorithm. A 3D volume conductor model of human body is constructed base on an anatomic atlas for numerical test. A comparison between our approach and one using downhill simplex method is implemented. The results show that our approach is stable and may provide a good scheme for solving the ECG inverse problem.

Keywords: Bioelectric, Electrocardiography (ECG), Inverse problem, Finite Element Method, Genetic Algorithm, Optimization Method.

1. Introduction

The bioelectric current sources arise from excitable cells undergoing an activation process. Activation of cardiac tissue can be characterized as the process in which cells undergo rapid depolarization. The depolarization process causes a propagation of excitation waves to move through the myocardium (the muscular of the heart); these waves in turn procedure an extracellular potential field. This potential field depends on geometry and conductivity of the volume conductor and the distance from, orientation to and intensity of the source current [1].

Inverse problems are usually to discover the unknown causes from known consequence. On the other hand, the problem in which the field and the conductor are known but the source is unknown, is

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called inverse problem[1]. In medical applications of bioelectric phenomena, the inverse problem has clinical importance. For instance, in everyday clinical diagnosis the cardiologist and the neurologist seek to determine the source of the measured bioelectric signals. The possible pathology affecting the source provides the basis for their diagnostic decisions - that is, the clinical status of the corresponding organ.

The ECG inverse problem is the bioelectric inverse problem in which the potential values at a limited number of measurement points on boundary are known and we have to reconstruct the unknown sources generating these data. Solving the ECG inverse problem is made difficult, because it is often ill-posed in the Hadamard sense [1]. The solution does not depend continuously on the data, small errors in the measurement of the torso potentials or thorax geometry can yield unbounded errors in the solution.

Because of its importance and usefulness, it has attracted numerous researchers to devote themselves to it in the past decades (Rudy, Mesinger and Rapport 1988, Huiskamp and van Oosterom 1989, Furukawa et la 1989, T. Musha et la 1998, Jaakko Malmivuo and Robert Plonsey 1995, Gulrajani et la 1988, etc). And several methods are developed for this problem such as solving Gabor-Nelson equations directly (Nelson 1981), combination of Brody shift equaiton and Levenberg Marquardt method (Gulrajani 1985) [2,3]. Recently, a new approach which yields a more precise solution, has been studied to get the solution of inverse problem by combination of a numerical analysis for forward problem, such as Finite Element Method (FEM), Boundary Element Method (BEM), Finite Difference Method (FDM), etc. with an iteration technique such as downhill simplex iteration (T. Musha 1999), simulated annealing (Gerson 1994), Newton-Raphson or Levenberg Marquardt (Xanthis 2006) etc[4,5]. These methods, however, may not perform consistently and also sensitive to the noise in the data. This study proposed using genetic algorithm, an efficient and robust method, to estimate the parameters of electrical source in the heart.

To solve this problem, the best we can do is to build a parametric model and try to adjust the unknown parameters based on the available observation. In this paper, the electrical source is considered as a single moving dipole (e.g 3 parameters for position, 3 parameters for orientations and magnitude) lying within entirely a finite, inhomogeneous volume conductor to simulate the electrical activity of the heart. Simulation models of a volume conductor (model of thorax) are built from a classical anatomic atlas [6] and stereo matching technique [7].

First, we use a numerical method to solve the forward problem. Because our discussion is limited to inverse problem in inhomogeneous volume conductor, finite element method (FEM) [8, 9] is exclusively used in this problem. By this approach, the volume conductor (solution domain) is discretized into number of finite elements that are connected via nodes. At each node, the governing differential equation is approximated by an algebraic expression, called interpolation function. These interpolation functions are then substituted into the integral equation, integrated and combined with the results from the solution domain to obtain a system of equations. Finally, the system is solved for unknown variable.

Next, Genetic Algorithm (GA) [12] is applied to compute the parameters of location, orientation and magnitude of a set of dipoles whose potential fields best match to measurement potentials in a least squares sense. Mathematically, it is a very difficult problem because the geometry of the model is inhomogeneous and its objective function is very complex. GA is a relatively effective approach for this problem. Although GA might not find the best solution, it can find a near perfect solution with acceptable time.

In GA, each solution, called chromosome, is encoded as a bit string (binary form). In the first step of GA, an initial population of random chromosomes is generated. A new population is formed by GA operators such as: selection, evaluation, crossover and mutation, and replaces the current population in the next generation. This process repeats in the specified number of iterations, and chromosomes will be developed generation by generation under control of objective function to reach the best solution. Because the conventional GA has a very poor local performance, some improvements have been added to enhance its performance.

A 3D simulation is constructed from a set of classical anatomic atlas for numerical testing. A significant effort is devoted toward making the forward problem adaptive to the specific Human subject on which measurements are performed [6]. Also, the currently established model matches the internal structure of a standing person. Then, the elements from this model are gained by using Deform 3D software [14].

Moreover, to estimate the performance of our approach, our results are compared with a traditional approach using downhill simplex method [15] (T. Musha et la, 1999). The comparison shows that our results were more accurate and stable than those recovered by T. Musha method. And it shows that our algorithm is the effective approach to dipole localization.

2. Modelling

2.1. Problem formulation and solution

Mathematically, most bioelectric field problems can be formulated in terms of Poisson's equation as following [1]:

$$\nabla . s \nabla \Phi = I_v \quad \text{in } \Omega. \tag{1}$$

Where, Φ is the potential field, σ is the electrical conductivity tensor, I_v is the current per unit volume within the volume conductor Ω and "∇." is the divergence operator. The forward problem would be solved Eq. (1) for Φ with given a known description of I_v, and the Neumann boundary condition (Eq. 2) and the Dirichlet condition (Eq. 3)[1]:

$$s \nabla \Phi . n = 0 \quad \text{on } \Gamma_T \tag{2}$$

$$\Phi = \Phi_0 \quad \text{on } \Sigma \subseteq \Gamma_T \tag{3}$$

Because of the complex geometries and inhomogeneity of volume conductor, it is very difficult to find an exact solution of this problem. Most numerical techniques for solving this kind of problem require that the continuous domain (volume conductor) be broken up into discrete elements, called mesh or grid, and then solutions of the volume conductor problem can only be obtained by employing a particular numerical approximation method.

In our study, we apply the finite element method to solve this problem. The primary idea of this method is discretizing the solution domain into elements which is characterized by interpolation function. The governing differential equation is approximated by a system of equations.

The FEM is started by Poisson's Eq. (1) with boundary conditions (2), (3). Such problem can be formulated in terms of minimizing the potential energy function, Π:

$$\Pi = \int_{\Omega} \frac{\sigma}{2}\left[\left(\frac{\partial\phi}{\partial x}\right)^2 + \left(\frac{\partial\phi}{\partial y}\right)^2 + \left(\frac{\partial\phi}{\partial z}\right)^2\right] d\Omega - \int_{\Omega} I_V \phi d\Omega \tag{4}$$

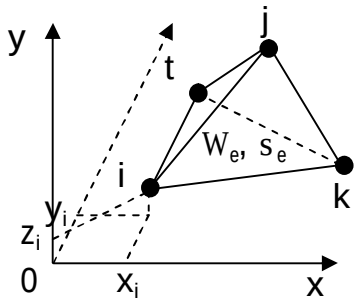


Fig. 1. A tetrahcedron element.

The first step in FEM is discretization. For sake of simplicity, we use tetrahedron elements and the linear approximation function of potential within a typical tetrahedron element is represented by the following equation [8]:

$$\phi(x,y,z) = a + bx + cy + dz \tag{5}$$

The solution domain is divided into triangle elements $\Omega = \cup\Omega_e$. In each triangular element, Ω_e, the unknown coefficients *a, b, c, d* can be found from three independent simultaneous equations of potentials $\phi_i, \phi_j, \phi_k, \phi_t$ at four nodes $\{i, j, k, t\}$ (Figure 1) by substituting each of these four equations and its corresponding node coordinate into equation (5):

$$\begin{aligned}
\phi_i(x,y) &= a + bx_i + cy_i + dz_i \\
\phi_j(x,y) &= a + bx_j + cy_j + dz_j \\
\phi_k(x,y) &= a + bx_k + cy_k + dz_k \\
\phi_t(x,y) &= a + bx_t + cy_t + dz_t
\end{aligned} \tag{6}$$

Where, (x_i, y_i, z_i), (x_j, y_j, z_j) ,(x_k, y_k, z_k), (x_t, y_t, z_t) are correlatively the co-ordinates of nodes *i, j, k, t.*

In matrix form:

$$\begin{Bmatrix} \phi_i \\ \phi_j \\ \phi_k \\ \phi_t \end{Bmatrix} = \begin{bmatrix} 1 & x_i & y_i & z_i \\ 1 & x_j & y_j & z_j \\ 1 & x_k & y_k & z_k \\ 1 & x_t & y_t & z_t \end{bmatrix} \begin{Bmatrix} a \\ b \\ c \\ d \end{Bmatrix} \tag{7}$$

Which is equivalent to:

$$\begin{Bmatrix} a \\ b \\ c \\ d \end{Bmatrix} = \begin{bmatrix} 1 & x_i & y_i & z_i \\ 1 & x_j & y_j & z_j \\ 1 & x_k & y_k & z_k \\ 1 & x_t & y_t & z_t \end{bmatrix}^{-1} \begin{Bmatrix} \phi_i \\ \phi_j \\ \phi_k \\ \phi_t \end{Bmatrix} = [N_e]\{\phi_e\} \tag{8}$$

Where, N_e is the inverse matrix of coefficient matrix. $\phi_e = \{\phi_i, \phi_j, \phi_k, \phi_t\}^T$ is potential vector of the e-th element. From the equation (5), we have:

$$\begin{Bmatrix} \frac{\partial \phi}{\partial x} \\ \frac{\partial \phi}{\partial y} \\ \frac{\partial \phi}{\partial z} \end{Bmatrix} = \begin{Bmatrix} b \\ c \\ d \end{Bmatrix} = [B_e] \begin{Bmatrix} \phi_i \\ \phi_j \\ \phi_k \\ \phi_t \end{Bmatrix} = [B_e]\{\phi_e\} \tag{9}$$

Where, B_e is a [3x4] matrix which is extracted from the matrix N_e. The energy function associated with a single triangular element may now be determined:

$$\Pi_e = \int_{\Omega_e} \frac{\sigma_e}{2} \phi_e^T B_e^T B_e \phi_e d\Omega - \int_{\Omega_e} I_v [1 \quad x \quad y \quad z] N_e \phi_e d\Omega$$
$$= \left(\frac{1}{2} \phi_e^T k_e \phi_e - h_e \phi_e \right) \tag{10}$$

Where, the superscript T denotes transposition.

$k_e = \int_{\Omega_e} s_e B_e^T B_e d\Omega$ is a [4x4] element matrix.

$h_e = \int_{\Omega_e} I_v [1 \quad x \quad y \quad z] N_e d\Omega$ is a [1x4] element vector

The energy function may be recast as following:

$$\Pi = \sum_{e=1}^{M} \Pi_e = \sum_{e=1}^{M} \left(\frac{1}{2} \phi_e^T k_e \phi_e - h_e \phi_e \right) \tag{11}$$

Where, M is the number of elements on mesh.

The condition for the minimum of Π is :

$$\delta\Pi = \frac{\partial \Pi}{\partial \phi_1} \delta\phi_1 + \frac{\partial \Pi}{\partial \phi_2} \delta\phi_2 + ... + \frac{\partial \Pi}{\partial \phi_N} \delta\phi_N = 0 \tag{12}$$

Which is equivalent to:

$$\frac{\partial \Pi}{\partial \phi_i} = 0 \qquad \forall i=1,\ldots,N \tag{13}$$

Where, N is the number of nodes on mesh. Let us introduce the following vectors and a matrix where element vectors and matrix are simply placed:

$$\{\Phi\} = \{\{f_1\}, \{f_2\}, ...\}$$
$$\{H\} = \{\{h_1\}, \{h_2\}, ...\}$$
$$[K] = \begin{bmatrix} [k_1] & 0 & 0 \\ 0 & [k_2] & 0 \\ 0 & 0 & ... \end{bmatrix}$$

The total potential energy can be rewritten in the following form by contribution of element vectors and matrix:

$$K\Phi = H \tag{14}$$

The matrix K contains all geometry and conductivity information of the model. Because the basic function is nonzero in a few intervals and the number of nodes in mesh is great, the matrix K is a sparse and large. Solving linear equation system (6) with the specific boundary conditions, we can calculate the potential at every node within volume conductor. Then, the solution of forward can be calculated by formulation:

$$\Phi = K^{-1}H \tag{15}$$

2.2. Solution of inverse problem

The solution of ECG inverse problem can be reached by using FEM for forward problem in conjunction with GA in estimation the parameters of dipole sources [16]. Genetic Algorithms (GA) are capable of searching for global in functions which cause difficulty for gradient based methods [10, 11]. Principal advantages of GA are domain independence, non-linearity and robustness. Because of these characteristics, GA is suitable for this problem.

2.2.1. Parameters and representation

In this paper, we encode the solutions as bit strings. The length of string depends on the required precision.

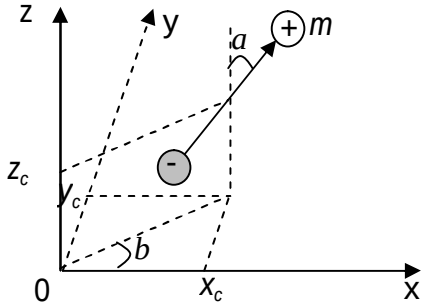


Fig. 2. Parameters of a dipole.

The source is considered as a moving single dipole which has the following independent variables: position of dipole $r(x_c, y_c, z_c)$, orientation (a, b) and magnitude, m.

For sake of simplicity, in our calculation, we assumed that length of dipole, d, is a constant (in our experiment, d = 0.1cm). A chromosome which composed of the parameters of dipole (x_c, y_c, z_c, a, b, m) is encoded as the following:

01...0	10…1	11…0	00..1	01..1	11…1
x_c	y_c	z_c	a	b	m

Fig. 3. Representation of a chromosome

2.2.2 Equivalent dipole source

In our parametric model, the source is considered as an equivalent current dipole lying within entirely the heart. The equivalent dipole is known as a single dipole which best approximates the electrical phenomenon.

The equivalent current dipole is expressed with three co-ordinates *r(x, y, z)* (Fig 2) and three components of its dipole moment p(p_x, p_y, p_z). The best-fitting dipole is found by optimal algorithm such that mean squared difference between the dipole-calculated potentials $\Phi_{cal} = (\Phi_{1,cal}, \Phi_{2,cal}, ..., \Phi_{N,cal})$ and the observed potentials $\Phi_{obs} = (\Phi_{1,obs}, \Phi_{2,obs}, ..., \Phi_{N,obs})$ at *N* electrode sites is minimized. Since the potentials are proportional to the dipole moment p, one has :

$$\Phi_{obs} = A(r).p \tag{16}$$

Where A(r) is a transfer matrix from a given unit dipole at *r* onto the torso potentials at the electrode sites; this matrix depends on the dipole location and the torso model. p and r are the dipole moment and location, respectively. To calculate Φ_{cal}, the expected value of Φ_{obs}, in a iterative fashion, an initial moment p and position r are arbitrarily selected:

$$\Phi_{cal} = A(r).p \tag{17}$$

The squared error between Φ_{obs} and Φ_{cal} is defined as:

$$S(r, p) = (\Phi_{obs} - \Phi_{cal})(\Phi_{obs} - \Phi_{cal}) \tag{18}$$

An equivalent dipole which best fit Φ_{obs} is obtained by minimizing *S(r,p)*. For a given dipole location *r*, the squared error is minimized for an optimal dipole moment given as

$$p_{opt} = A(r)^t A(r)]^{-1} A(r)^t \Phi_{obs} \tag{19}$$

Substituting the formula for p_{opt} into *S(r,p)* gives

$$\begin{aligned} S(r, p_{opt}) &= (\Phi_{obs} - \Phi_{cal})^t (\Phi_{obs} - \Phi_{cal}) \\ &= \Phi_{obs}{}^t \{E - A(r)[A(r)^t A(r)]^{-1} A(r)^t\} \Phi_{obs} \end{aligned} \tag{20}$$

Where E is a N-D unit matrix. Because p_{opt} is a function of *r*, $S(r,p_{opt})$ depends on *r* only and it is gain minimized by genetic algorithm.

2.2.3. Evaluation function

Theoretically, the solution is only true if the entire distribution of potential on the surface is known, but it is impossible. In fact, input signals for inverse problem come from a finite number of electrodes placed on the body surface. It was proved that the number of electrodes between 32 and 200 is sufficient to present adequately the entire surface-potential distribution [5] (R. S. Macleod and D. H. Brooks 1998) and enough to locate dipole source.

Therefore, the evaluation function (or called objective function), is formed to represent the difference between the observed potential fields and the calculated potential fields at the limited nodes and have the following equation:

$$f = \sqrt{\frac{\sum_{i=1}^{N_0} \left(\Phi_i - \Psi_i\right)^2}{\sum_{i=1}^{N_0} \Psi_i^2}} \tag{21}$$

Where, N_0 is the limited number of selected nodes on boundary. Φ_i, Ψ_i are correlatively calculated and measured potentials at these nodes. Our problem is finding the dipole whose potential fields minimize this evaluation function.

2.2.4. Genetic algorithm

The genetic algorithm to define the source of ECG inverse problem may be summarized as follows (Figure 4):

Step 1: Generating an initial population of random chromosomes. To increase diversity of population, the chromosomes are chosen so that they are different from each other.

Step 2: For each individual chromosome in the current population, applying the forward problem to compute the potential fields within the volume conductor by Eq. (7) and evaluation function is computed at the selected nodes on the boundary by Eq. (21).

Step 3: Using the GA operators to create a new population for the next generation: selection, crossover and mutation.

Selection operator: Using the tournament selection. Only one individual from each subgroup whose evaluation function is lowest is chosen to reproduce for candidate population.

Crossover operator: 2-point crossover is used with probability, pc , for each chromosome. Also, a selection algorithm is applied to reduce identical chromosomes.

Mutation operator: The purpose of this operator is to allow the GA to avoid the local minima. Each chromosome involves a probability, pm , that an arbitrary bit will be changed from its original state.

The new population generated with these operators replaces the old population. The step 2 and step 3 are repeated with this population until a termination condition is satisfied.

Step 4: The generational process is repeated until a termination condition has been reached. In our program, the process will be terminated after a finite number of iterations.

Step 5: Solution of inverse problem is the chromosome which minimizes the evaluation function in the current population of the last generation.

However, conventional GA has a very poor local performance because of the random search. To get a good solution, great computational costs are inevitable.

Some improvements are necessary to enhance performance of GA. In this section, we introduce some important modifications that can dramatically improve the performance of the conventional GA [10-12].

Elitist strategy: Two sets of solutions are stored in our algorithm: a current population and an elite set. The elite set keeps the best solutions at each generation. After the genetic operators are implemented, the elite set is updated by choosing the best individuals of new population. By preserving the good solutions, we can avoid losing some excellent solution.

Hybrid Algorithm: In many cases, the association of GA with other heuristic algorithms can significantly improve the performance of conventional GA. In this study, we propose a hybrid

algorithm which combines GA with a local search procedure (hill climbing). To reduce the computational cost, the local search procedure is applied only for the elite set.

Selection and crossover operator: In our algorithm, we use tournament selection. The size of subgroup, GroupSize, can make GA result in different solutions. When GroupSize is great (the subgroup is large), the competition is intense, some outstanding solutions in the population have greater chance to survive, the population will be dominated rapidly by these outstanding solutions and lead to premature convergence. Thus, in the beginning of GA, we set GroupSize a small value to limit the competition and increase it in the subsequent generations in order to stimulate the evolution.

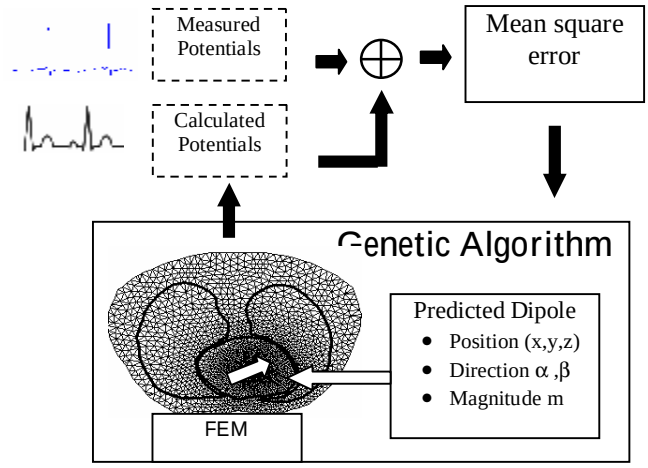


Fig. 4. Scheme of source localization.

3. Experimental method

A three dimensional (3-D) volume conductor model is created from the images of thorax which obtained from the visible human viewer project [6] and stereo matching technique [7].

The model is constructed into 31 layers (starts from 300th cross section to 600th cross section). The actual distance between successive cross-sections is 1cm.

One of the main strength in our approach stems from the approximately developed body volume conductor model. This reflects the complicated internal structure at the expense of a lot of manual preprocessing efforts for the definition of the approximate general tetrahedral elements. Our approach enables the effective solution of the inverse problem which requires multiple solution of the forward problem. To realize how important this is, just recall that the inverse problem non-linearity is handled through iterative solution of a version linearized around a continuously updated solution. One may argue that this approach involves a compromise in the forward problem accuracy, well this is generally true but the effort is directed toward limiting the inaccuracies within the measurement efforts. Moreover, a significant effort is devoted toward making the forward problem adaptive to the specific Human subject on which measurements are performed. Also, the currently established model matches the internal structure of a standing person. Differently modified models for the subjects lying on their left and their right side as asked by medical examinations, will be developed next.

The 3D volume includes regions with different conductivities [17]. The conductivities of the body tissues in this study are shown in the Table I as the following:

Table I. Conductivities of body tissues

Element	Conductivity (S/m)
Thorax	0.21
Lung	0.04
Heart	0.10
Blood	0.6

For the application of the FEM, the volume conductor is divided into tetrahedral elements by Deform 3D software. This is a powerful process simulation system designed to analyze the three-dimensional (3D) flow of complex metal forming processes [13]. In our experiment, we used a computer with Window XP, 2GB RAM, 2.26 GHz Chipset.

Using this software, a list of nodes or co-ordinates and triangular surfaces for human body structure is created. From these data, Deform 3D software will generate a 3D-mesh model with precision depending on user's requests (Figure 5).

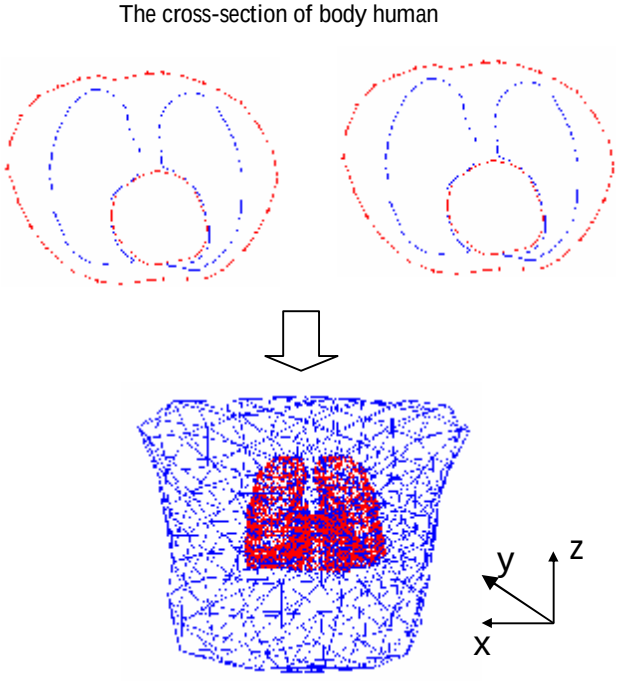


Fig. 5. Three-dimension mesh model.

In our experiment, the model is divided into M=27072 tetrahedral elements and N=5626 nodes. Because the electric field around the source becomes very strong, the mesh points required for FEM are concentrated near source to increase the accuracy in calculation.

In this simulation, the evaluation function is estimated at N_0=111 electrodes placed surround the body. These electrodes were enough to locate the single dipole source [4]. Some parameters using in GA are shown in Table II.

Table II. Parameters of GA

Parameter	Attribute
Precision	10^{-5}
Bit length	15
Crossover probability (p_c)	0.95
Mutation probability (p_m)	0.015
Population Size	3000
Iteration	1000
Elite Size	2
Group Size	2

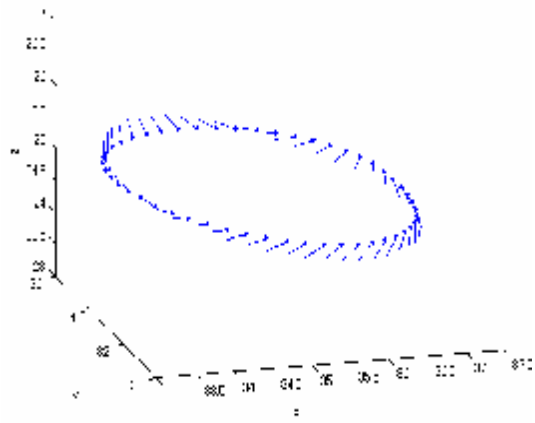


Fig. 6. Assumption trajectory of dipole.

We assume the actual trajectory of dipole to be a circle, which has radius, r = 2cm and lies on a plane with normal vector, $\vec{n}$ = (*0.5, 0.7, 1.1*), and center point, (x_0, y_0, z_0) = (*35, 33, 25*) (Fig 6). The formulations of position, orientation and magnitude of dipole in respect to time, t , are represented by equations:

$$x(t) = r * \cos(2pt) + x_0$$
$$y(t) = r * \sin(2\pi t) + y_0$$
$$n_x * (x - x_0) + n_y * (y - y_0) + n_z (z - z_0) = 0$$
$$m(t) = 0.1 * \cos^2(2\pi t) + 1$$
$$\alpha(t) = 2\pi t$$
$$\beta(t) = 2\pi t^2$$

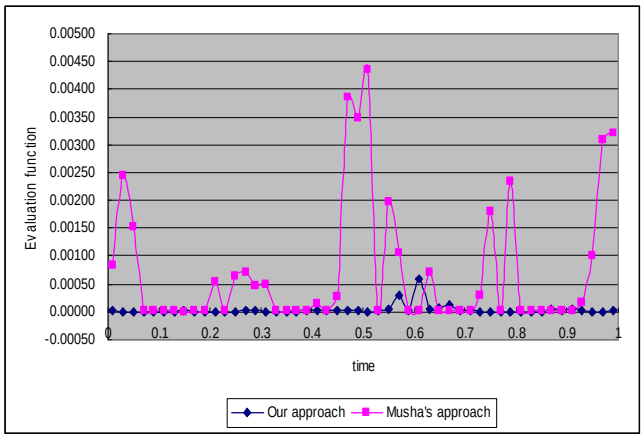
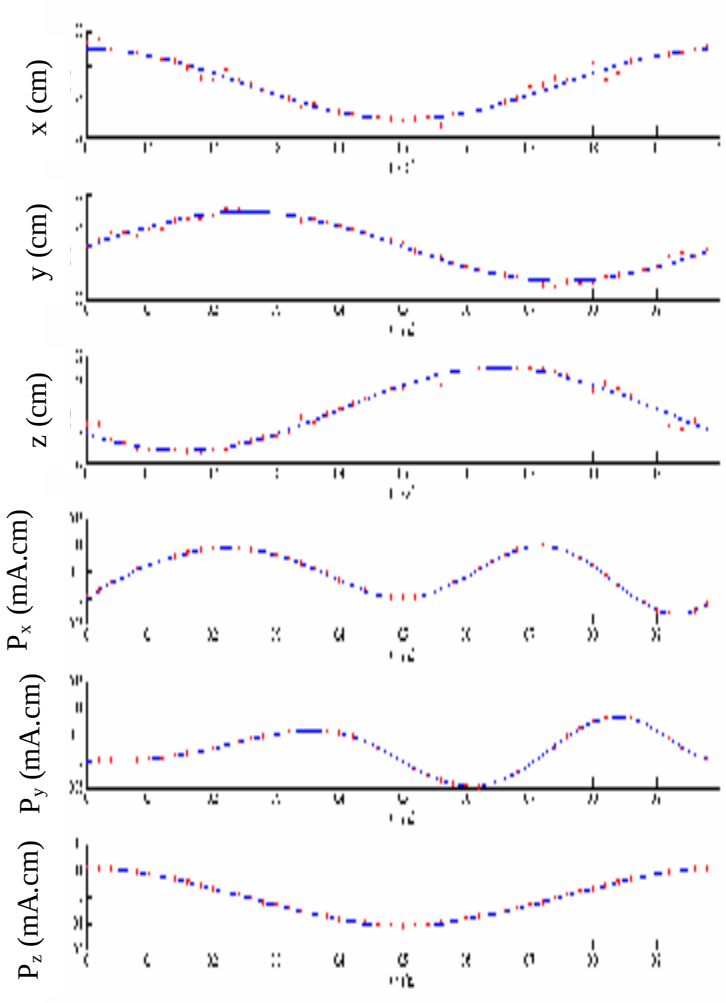
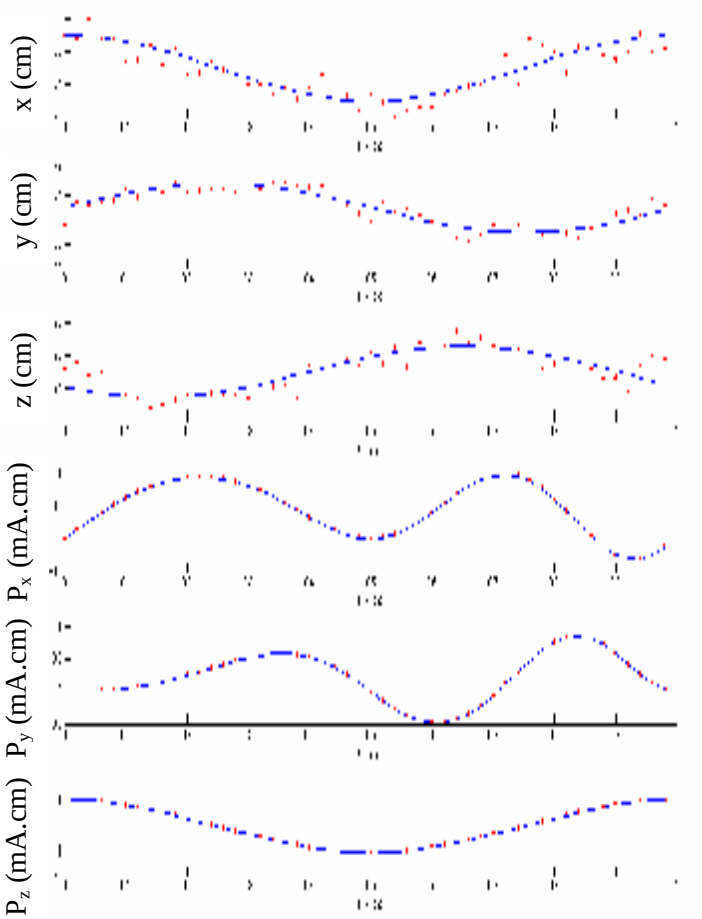


Fig. 7. Evaluation function.



(a) Our approach



(b) T. Musha's approach

Fig. 8. Component parameters of the dipole source.

The dipole moments are also changed by time and calculated by the following equations:

$$P_x(t) = d * m * \sin(\alpha) * \cos(\beta)$$

$$P_y(t) = d * m * \sin(\alpha) * \sin(\beta)$$

$$P_z(t) = d * m * \cos(\alpha)$$

In the experiment, we chose 50 (N_p = 50) dipoles at time points t = {*0, 0.02, 0.04, …, 0.98*}. The length of dipole is a constant (d = 0.1cm). With the parameters of GA as in table II and parameters of FEM, the execution time (in elapsed CPU seconds) is approximately 60 seconds per dipole.

In T. Musha's approach, we used randomly 1000 different initial simplexes, and the maximum number of iterations is 5000. In this case, the execution time to determine one dipole is approximately 0s. The program was run at least 3 times with each approach to confirm the stability of program. And the result has been analysis at the next section.

Fig. 7 shows the values of objective function at selected time points in our approach and T. Musha's approach. Our approach always converged to the global minimum regardless of the starting parameter estimates while simplex often converged to the different solutions for different starting parameter estimates.

T. Musha and et als applied the downhill simplex method to estimate the parameters of dipole source. This technique requires only function evaluations, not derivatives and it must be start not just with a single point, but with N points, defining a set of initial simplex.

A simplex is the geometrical figure consisting, in N dimensions, of *N+1* points (or vertices) and all the interconnecting line segments, polygonal faces, etc. In three dimensions, a simplex is a tetrahedron, not necessarily the regular tetrahedron. In general we are only interested in simplexes that are nondegenerate, i.e that enclose a finite inner N-dimensional volume. If any point of a nondegenerate simplex is taken as the origin, then the N other points define vector directions that span the N-dimension vector space.

Then, it takes a series of steps, most steps just moving the point of simplex where the function is largest, optimum point though the opposite face of the simplex to a lower point. The termination criteria can be delicate in any multidimensional minimization routine.

Fig. 8 shows some other measures of parameters of dipole. The assumed results are represented with blue lines (solid line) and calculated results are represented with red lines (dot line). The parameters calculated by our approach are shown in Fig 8a. Fig. 8b shows the results of T. Musha's approach. Obviously, our parameters are closer to the parameters of assumption dipoles than those gaining from his approach.

4. Results and discusion

In order to investigate the solution method, we define function *Err* as a measure of difference between assumed and calculated solution in the simulation:

$$Err_f = \sqrt{\frac{\sum_{i=1}^{N_p} \left(f_i^c(t) - f_i^a(t) \right)^2}{N_p}} \tag{22}$$

Where, superscripts *a, c* denote assumption and calculated values, respectively. Np is the number of dipoles. The error of solution in the simulation models can be judged by the average of distance between assumed and calculated dipole location as following:

$$E = \frac{D}{N_p} \tag{23}$$

Where, D is the summed Euclidean distances of calculated and assumed dipoles and has equation as following:

$$D = \sum_{i=1}^{N_p} \sqrt{(x_i^c - x_i^a)^2 + (y_i^c - y_i^a)^2 + (z_i^c - z_i^a)^2} \tag{24}$$

Table III shows some errors computed by equations (22) and (23).

Table III. Some errors of dipole components

Parameter	Our apporach	Musha's approach
Err_x (cm)	0.22453	0.72628
Err_y *(cm)*	0.15717	0.60383
Err_z *(cm)*	0.14650	0.66305
E_r *(cm)*	0.21412	1.06150
Err_{Px} *(mA.cm)*	0.03426	0.70728
Err_{Py} *(mA.cm)*	0.38662	0.27002
Err_{Pz} *(mA.cm)*	0.02256	0.88154
E_P *(mA.cm)*	0.30087	0.63321

We used 50 dipoles with the different orientations, magnitudes and positions as above. These dipoles are enough to estimate the goodness of our approach. The source localization was carried out three times to confirm the reliability of the obtained solution.

The results in Table III show that the errors of dipole locations are acceptable. The average of position errors is approximate 0.22cm, and the average of dipole moment errors is about 0.3mA.cm.

Also, the execution time is reasonable, one dipole running on one computer consumed approximately 60 seconds for calculation. Although, in our approach execution time is longer than T.Musha's one, it's still acceptable to get a good solution.

These analysis results point out that this approach is a promising way to get stable and high accurate solution.

5. Conclusion

In this paper, we represented an efficient and robust method to solve the ECG inverse problem in bioelectric field by finite element method in conjunction with genetic algorithm. We have first introduced finite element method to solve the forward problem. The solution of inverse problem is solved by genetic algorithm. We also introduce some additional features to overcome the disadvantages of conventional genetic algorithm.

The performance of our approach was evaluated based on a 3D realistic torso model and compared with a traditional approach using downhill simplex method proposed by T. Musha. Computer simulation results show that our approach is very effective and stable. The results are as good as what we expected. The further work along this stream is ongoing. Our method in this paper is also suitable for ECG source localization.

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