31st Annual International Conference of the IEEE EMBS
Minneapolis, Minnesota, USA, September 2-6, 2009

Improved Infrared Thermography Based Image Construction for Biomedical applications using Markov Chain Monte Carlo method

V. Umadevi, S. Suresh and S. V. Raghavan

Abstract— **Breast Thermography is one of the scanning techniques used for breast cancer detection. Looking at breast thermal image it is difficult to interpret parameters of tumor such as depth, size and location which are useful for diagnosis and treatment of breast cancer. In our previous work (ITBIC) we proposed a framework for estimation of tumor size using clever algorithms and the radiative heat transfer model. In this paper, we expand it to incorporate the more realistic Pennes bio-heat transfer model and Markov Chain Monte Carlo (MCMC) method, and analyze it's performance in terms of computational speed, accuracy, robustness against noisy inputs, ability to make use of prior information and ability to estimate multiple parameters simultaneously. We discuss the influence of various parameters used in its implementation. We apply this method on clinical data and extract reliable results for the first time using breast thermography.**

I. INTRODUCTION

A non-invasive, non-ionizing & inexpensive screening technique for checkups at regular intervals, facilitating early detection and possible cure is suitable for Breast cancer. Breast Thermography, one such scanning technique gives the surface temperature of the body part being scanned. Tumor is a mass of cancerous cells having higher metabolic rate; hence surface temperature of the skin regions closer to the tumor will be higher than the normal skin surface. In effect, a tumor can be modelled as a heat source embedded inside human tissue. Surface temperature of the skin affected by tumor or heat source can be used for extraction of tumor parameters - depth, size and location. Finding parameters of a heat source embedded inside tissue, using surface temperature data is a challenging "ill-posed" inverse problem [4].

In our previous work we proposed a framework called Infrared Thermography Based Image Construction for Biomedical applications (ITBIC) [11] to approximate the size of the tumor by observing contour formations on the image. It was intended as an adhoc, but clever and quick tool for practitioners, and was lacking robustness in terms of accuracy and a sound theoretical basis, with reference to the forward model. The tumor was modeled as a 2-D disc passing heat through radiation only. Currently we model the tumor as a 3-D sphere within a cubical block of tissue. Heat transfer process within the human tissue is modeled using Pennes Bio-Heat transfer equation [1]. Construction of Temperature field from the heat source within the tissue affected by heat source is shown in [2], [4]. The inverse problem of estimating radius of the sphere and location within the cube from the surface temperatures is generally very complicated. Finite Element [5], [10] methods have been previously applied for extraction of tumor parameters. Li et al [8] have proposed that the Monte Carlo method can be applied to solve the inverse problem of bio-heat transfer.

Moving toward the holistic ITBIC framework, we have applied the MCMC method to estimate the tumor parameters with the more realistic forward model described above. We have established this method's feasibility to inverse bio-heat transfer problems. Our method surpassed all previously used methods in tumor parameter estimation [5], [8], [10] in terms of accuracy and speed. It is computationally feasible as it takes a few 15 mins on an Intel P4 3.0 GHz machine, hence can be used by hospitals across the world. Some other advantages of this method are (a) it is robust against noisy temperature measurements (b) it not only gives a point estimate but also a measure of the uncertainty in our estimate (c) it provides a systematic approach to making use of the available prior information from experience or the patient's inputs. We apply our algorithm on actual clinical data and subject it to verification.

In section II we introduce the MCMC method in the context of Bayesian inferencing and explain our implementation. In section III we review estimation results of a single parameter, the size of the tumor. We analyze the performance with various metrics including uncertainty in output, output deviation from actual value etc., and discuss some aspects in its implementation. In section IV we discuss the results obtained in the extraction of multiple parameters namely tumor size and location. In section V we discuss the parameter estimation from clinical data. We submit our conclusions and discuss avenues for future research in section VI.

II. THE MCMC METHOD & THE FORWARD PROBLEM

The MCMC method and Bayesian inferencing have been described in this section. First, we define the forward problem, and explain the sampling and the algorithm.

A. Forward problem

The forward model has been framed using the Pennes Bio-heat transfer equation (1) for steady state heat flow within the tissue assuming conduction, convection and metabolic heat generation of tumorous tissue. Table I gives the values of the parameters of (1). COMSOL [7] software was used for simulation. The mesh had around 3500 base points and 20000 tetrahedral elements with other parameters like element quality and volume ratio up to accepted standards.

V. Umadevi and Prof. S. V. Raghavan is with Network Systems Laboratory, Department of Computer Science and Engineering, IIT Madras, Chennai, India {umadevi,svr}@cs.iitm.ernet.in

S. Suresh is with Department of Mechanical Engineering, IIT Madras, Chennai, India santhosh.suresh1@gmail.com

978-1-4244-3296-7/09/$25.00 ©2009 IEEE

TABLE I

PENNES EQUATION PARAMETERS

Parameter name	Symbol	Tissue	Tumor
Thermal conductivity (W/m)	k	0.42	0.42
Blood perfusion rate (l/s)	ω_b	$18e^{-8}$	$9e^{-6}$
Density (kg/m^3)	ρ_b	920	920
Specific heat of blood (J/kg.K)	c_b	3000	3000
Arterial blood temperature (K)	T_b	310	310
Metabolic heat generation rate (W/m^3)	Q_{met}	450	29000

Let $\boldsymbol{x}$ be the input vector, and $\mathbf{T}$ be the output. We can assume the forward model to be the function F, where the output is a set of temperatures corresponding to predetermined positions on the surface of the tissue. We have, $\mathbf{T} = F(\boldsymbol{x})$.

$$k\left(\frac{\delta^2 T}{\delta x^2}+\frac{\delta^2 T}{\delta y^2}+\frac{\delta^2 T}{\delta z^2}\right)+\omega_b\rho_b c_b(T_b-T)+Q_{met}=0 \quad (1)$$

B. Bayesian inferencing

Bayes' conditional probability equation that relates experimental data $\mathbf{T}$ and parameter $\boldsymbol{x}$ is as follows:

$$P(x|T)=\frac{P(T|x)P(x)}{P(T)} \quad (2)$$

P(x|T) is posterior probability density function (PPDF), P(x) is the prior distribution function, P(T) is a normalizing constant, P(T|x) is the likelihood function, given by,

$$P(T|x)=\frac{1}{(\sqrt{2\pi}\sigma)^n}\exp\left(-\frac{(T_{meas}-F(x))'(T_{meas}-F(x))}{2\sigma^2}\right) \quad (3)$$

T_{meas} refers to the vector of measured temperature values of dimension n and σ is described later. Parameters are estimated from posterior distribution as:
(a) Maximum a Posteriori (MAP) $\hat{x}_{MAP} = arg\ max_x(P(x|T))$
(b) Mean estimate $\hat{x}_{MEAN} = E(P(x|T))$

C. Sampling

PPDF is usually of a non-standard form, so numerical sampling becomes necessary. Metropolis-Hastings (MH) sampling algorithm[9] used has been explained below:

1. Initialize x_0
2. for $i = 1$ to N
   a. Draw a sample $u \sim U(0,1)$
   b. Draw a sample $x^* \sim q(x^*|x_i)$
   c. If $u < A(x^*, x_i)$ $x_{i+1} = x^*$
   d. else $x_{i+1} = x_i$

Where N is the total number of samples, u is a random number generated from the standard uniform distribution $U(0,1)$, q($x^*|x_i$) is proposal density function given as the probability of drawing x^* from a sample distribution of $N(x_i, \sigma)$ where σ is 5% of x_i and A is the acceptance ratio defined as $A(x^*, x_i) = min\{1, \frac{p(x^*).q(x_i|x^*)}{p(x_i).q(x^*|x_i)}\}$. For more details on the above concepts, see [8], [9].

III. SINGLE PARAMETER ESTIMATION

We considered the tissue to be a homogeneous cube of size 0.072 m $\times$0.072 m $\times$0.072 m with an embedded spherical tumor placed at the it's center. An overview of the system is given in Fig. 1. The forward function F used in the MH block is the one described in section II-A where $\mathbf{T}$ is a mesh of 5×5 measurements spread uniformly across the top surface of the cube. T_{meas} was calculated as $r = r_{act}$ in the above model. In this section we analyse implementation and results of Single Parameter estimation in detail.

A. The algorithm output

The algorithm is given a seed value r_0, our guess at the radius. The output is a set of N samples of the radius value, which is expected to converge to the actual value i.e. after a certain number of iterations, the x_i settle down around r_{act}, which is actual tumor radius. The randomwalk nature of the samples has been shown in Fig. 2. We measure the accuracy of the output in terms of the Standard Deviation (SD) of the resulting distribution of samples. The Burn in is the number of iterations the algorithm takes to get close enough to the actual value. The MAP described in section II-B is also used as a metric. Table II shows some estimated tumor radii against corresponding actual radius.

B. Performance against the various parameters

In this section, we describe the influence of implicit MCMC parameters on the performance of the algorithm and provide insight on their selection and usage.

1) Parameter σ_{ins}: σ_{ins} refers to the σ mentioned in (3). Table III that the optimal result in terms of SD metric is when σ_{ins} is 0.15. Although the Burn in fluctuates for various values of σ_{ins}, we notice that for very low values, the randomwalk is too confined and gets lost, while, for a slightly

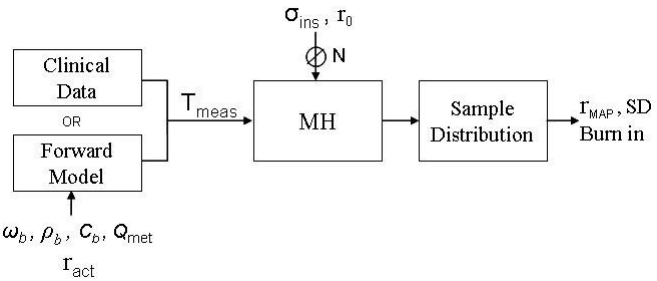


Fig. 1. Block diagram of overall system implementation

TABLE II

PERFORMANCE OF ALGORITHM USING N=100, $r_0 = 0.005m$, σ_{ins}=0.15

Actual Tumor radius (m)	Estimated Tumor radius (m)	SD of output
0.0050	0.0050	0.0006
0.0075	0.0075	0.0005
0.0100	0.0100	0.0016
0.0125	0.0127	0.0018
0.0150	0.0150	0.0019
0.0175	0.0175	0.0029
0.0200	0.0202	0.0030

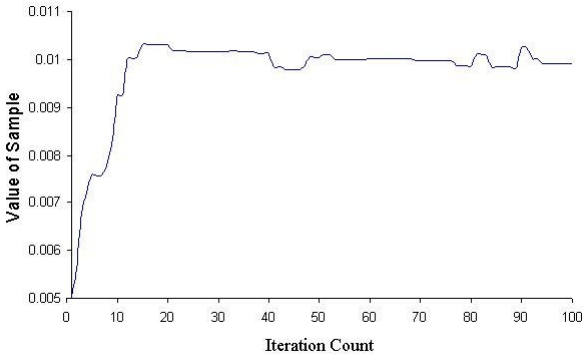


Fig. 2. Randomwalk for the case $r_{act} = 0.01m$, $r_0 = 0.005m$, $\sigma_{ins} = 0.2$, N=100, $r_{MAP} = 0.01m$, SD= 0.0010, Burn in=10

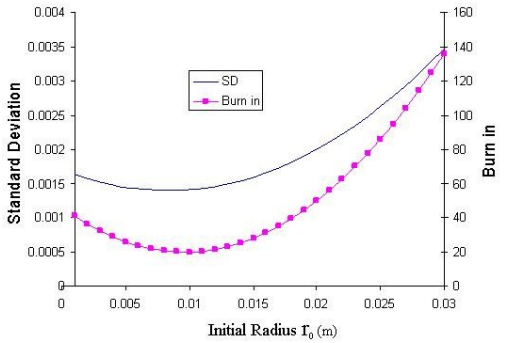


Fig. 3. SD vs Initial r_0 for the case of $r_{act} = 0.01m$

larger value, it is quite streamlined and accurate. However, it loses focus and delays reaching the actual value as the σ_{ins} increases beyond a point. In conclusion, for the range of measurements taken by contemporary thermography, σ_{ins} is recommended to be around 0.15.

2) Influence of initial value: The choice of the initial value is a tough one. As would be expected, the closer the initial value would be to the actual value of the radius, the better are the results. Here, we show that although the results are affected by initial value that is very far away from the actual value, the results are still within acceptable accuracy for unfairly faulty choice of initial value, in the context of breast thermography. Variation of SD and Burn in, against r_0, which are the measure of accuracy and computation time are shown graphically in Fig. 3 respectively.

3) Error in measurement (ξ): Our model also accounts for the possibility of error in the measured values of the temperatures. We measure the performance of the algorithm against measurement error(ξ) quantified as the standard deviation of the Gaussian noise added to the model output simulated with r_{act}, to give T_{meas}. Fig. 4 shows the algorithm is robust for unusually large amounts of error, of the order 0.5°C.

4) Mesh Accuracy: We subject different meshing sizes to tissue cube and tumor, and study their effects on the estimation of tumor radius. The results show that the error in the model takes over making further accuracy in meshing unnecessary. González [6] writes that the current state-of-the-art infrared temperature measurements have an accuracy of 0.05°C, consequently able to detect tumour radii of around 0.5 cm to 3 cm, correct to the tenth of a centimeter. For this level of accuracy seen as the standard, our current meshing seems sufficient. In our simulation, since the T_{meas} and samples use the same model, it does not affect the MCMC in any pronounced way by changing the meshing.

TABLE III

MAP, SD AND BURN IN FOR THE CASE OF N=100, $r_{act} = 0.01m$, $r_0 = 0.005m$ WITH σ_{ins} RANGING FROM 0.1 TO 1

Sl. no.	σ_{ins}	MAP	SD	Burn in
1	0.10	0.0103	0.0011	14
2	0.15	0.0099	0.0009	15
3	0.20	0.0096	0.0012	18
4	0.25	0.0096	0.0017	34
5	0.30	0.0097	0.0014	32
6	0.40	0.0100	0.0012	09
7	0.50	0.0101	0.0013	21
8	0.60	0.0098	0.0015	20
9	0.70	0.0052	0.0027	65
10	0.80	0.0098	0.0018	26

C. The concept of Prior information

We supplied our algorithm with prior information and studied its effect in estimation of parameters. The inverse of the standard deviation of the prior probability distribution (σ_p) can be a measure of the information. Fig. 5 shows the result metrics against σ_p. Clearly, a better informed prior not only causes quick convergence but also higher levels of accuracy as would be desireable today.

IV. Multiparameter estimation

In this section we discuss the estimation of tumor size and location. The seed value is taken as $r_0 = 0.005$ m and $x_0 = y_0 = z_0 = 0.02$ m. Table IV summarizes the performance of the algorithm for various cases of actual tumor size and location while Fig. 6 gives a sample randomwalk showing that the algorithm converges to actual values.

V. Verification with actual clinical data

In this section we discuss the estimation of tumor parameters with clinical data. A cancerous Breast Thermal

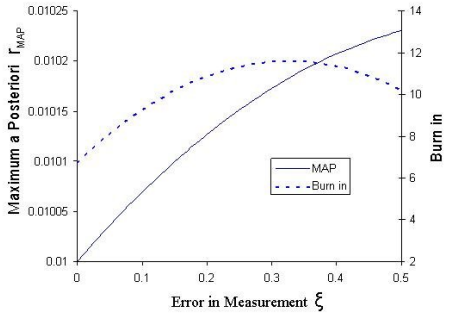


Fig. 4. MAP and Burn in vs Sigma Error for the case of $r_{act} = 0.01m$

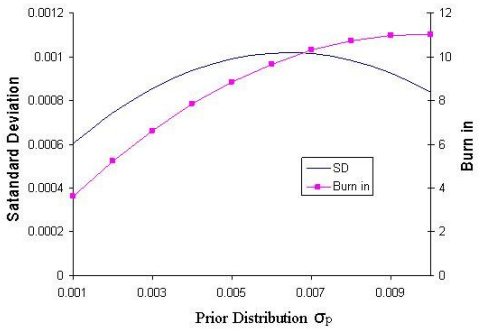


Fig. 5. SD and Burn in vs σ_p of Prior distribution

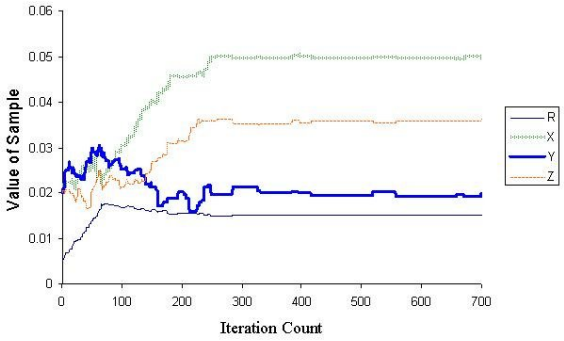


Fig. 6. Multiparameter estimation: Randomwalk for the case [r_{act} x_{act} y_{act} z_{act}] = [0.015 0.05 0.02 0.036], MAP [r x y z] = [0.015 0.05 0.0192 0.0358]

image (or Thermogram) is shown in Fig. 7(a). The actual and simulated temperature profiles for a reduced 5×5 mesh are shown in 7(b) and 7(c) respectively. Our algorithm not only converges to a constant radius value which is quite close to the "thermal" radius of the tumor, it is also able to simulate the effects of the tumor, within it's own limitations. It is remarkable that such a crude model can give conclusive results with minimal computational cost.

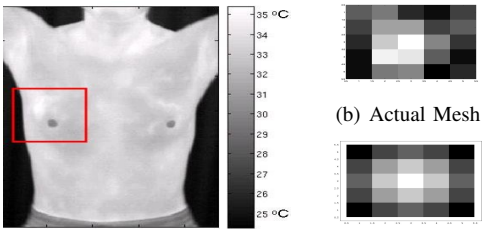
VI. Conclusion & Future Work

In conclusion, we have established the capacity of this method to give quick, dependable results against erroneous data in tune with the accuracy standards today [6]. Pidaparti's ANN based method [10] gives about 10% error with noisy data while our algorithm gives less than 2% error for up to 10% noise with slightly lesser number of iterations. Using a

TABLE IV

Multiparameter estimation: cases with N=700

Case	Tumor parameter:	r (m)	x (m)	y (m)	z (m)
1	Actual values	0.01	0.036	0.036	0.036
	Estimated values	0.01	0.034	0.037	0.034
	SD of output	0.00076	0.0049	0.0078	0.0045
2	Actual values	0.02	0.028	0.024	0.03
	Estimated values	0.02	0.028	0.023	0.03
	SD of output	0.0029	0.0020	0.0014	0.0034
3	Actual values	0.015	0.05	0.02	0.036
	Estimated values	0.015	0.05	0.019	0.036
	SD of output	0.0018	0.0091	0.0028	0.0059



(a) Cancerous Breast Thermogram (b) Actual Mesh (c) Simulated Mesh

Fig. 7. Clinical Validation

tenth of the number of iterations as Paruch [5], we get less than 1% error while their time consuming Genetic Algorithm based system gives around 5% error.

Our work would encourage further research into the multitude of possibilities that arise by applying MCMC methods in Bio-medical applications. Though our model is a simplistic description of the human tissue with limited mesh size, it gives sufficiently accurate results. Modelling the skin surface shape to a sphere and the shape of the tumor, which is usually an extremely irregular shape can also be considered. In the era of growing Artificial Intelligence, one can expect a sensor to be dynamically updating itself about the tumor via Breast thermal imaging, being sent by wireless communication to a computer, which would inturn pass on the instructions to a cyberknife to dynamically kill the tumor cells without side effects. This is another major step in that theme of research, which we have fondly termed as ITBIC.

References

[1] H. H. Pennes, Analysis of tissue and arterial blood temperature in resting human forearm, *Journal of Applied Physiology*, vol. 1, no. 2, 1948, pp. 93-122.

[2] E. Y. K. Ng, N. M. Sudharsan, "Effect of blood flow, tumour and cold stress in a female breast a novel time-accurate computer simulation", Proc. of the Institution of Mechanical Engineers, Part H: Journal of Engineering in Medicine, vol. 215, no. 4, 2001, pp. 393-404.

[3] H. Qi, P. T. Kuruganti, Z. Liu, "Early Detection of Breast Cancer using Thermal Texture maps", IEEE Symposium on Biomedical Imaging: Macro to Nano, Washington D.C., 2002, pp. 309-312.

[4] Z. S. Yu, K. Y. Li, S. P. Zhang, "The Noninvasive Reconstruction of Inner Heat Source and Temperature fields in Biological body by Boundary Element Method", in Proc. of 1st International Conference on Bioinformatics and Biomedical Engineering, 2007, pp. 849-852.

[5] M. Paruch, E. Majchrzak, Identification of tumor region parameters using evolutionary algorithm and multiple reciprocity boundary element method, *Engineering Applications of Artificial Intelligence*, vol. 20, issue 5, 2007, pp. 647-655.

[6] F. J. González, Thermal simulation of breast tumors, Instrumentación Revista Mexicana De Física, 53 (4), 2007, pp. 323-326.

[7] COMSOL Multiphysics, Version 3.4, Burlington, MA, 2007.

[8] K. Y. Li, Y. G. Dong *et al* The noninvasive reconstruction of 3D temperature field in biological body by Monte Carlo Method, *Journal of Neurocomputing*, vol. 72, issue 1-3, 2008, pp. 128-133.

[9] S. Parthsarathy, C. Balaji, Estimation of parameters in multi-mode heat transfer problems using Bayesian inference - Effect of noise and a prior, *International Journal of Heat and Mass Transfer*, vol. 51, issues 9-10, 2008, pp. 2313-2334.

[10] M. Mittal, R. M. Pidaparti, Breast Tumor Simulation and Parameters Estimation using Evolutionary algorithms, *Modelling and Simulation in Engineering*, vol. 2008, issue 2, 2008, pp. 756436-756441.

[11] V. Umadevi, S. V. Raghavan, "Infrared Thermography Based Image Construction for Bio-Medical Applications",Proc. of 3rd International Conference on Bioinformatics and Biomedical Engineering, Beijing, June 2009.