

An Application of Genetic Algorithms to Estimate both the Blood Perfusion and Geometric Parameters of Breast Tumors by Thermal Analysis

Antônio Márcio Gonçalo Filho[1,2(✉)], Michelli Marlane Silva Loureiro[1(✉)], and Felipe Santos Loureiro[1(✉)]

[1] Federal University of São João del Rei, Av. Visconde do Rio Preto, s/no Colônia do Bengo, São João del Rei 36301-360, Brazil
{michelli.loureiro,felipe.loureiro}@ufsj.edu.br
[2] Accenture, Dublin, Ireland
antonio.marcio.filho@accenture.com
http://www.ufsj.edu.br

Abstract. This work presents the application of a genetic algorithm (GA) for solving the inverse bioheat transfer problem to estimate the position, as well as the blood perfusion of a breast tumor based on the skin temperature. A multi-layered breast cancer model is employed with the Pennes' bioheat equation being discretized by the finite element method. The input data consist of the skin temperature of the target breast tumor. The evolution process generates a set of meshes for representing the breast with the tumor and tries to minimize the temperature difference on the skin surface between the target model and the model generated from the GA. Three different GA strategies were tested, and the results were satisfactory and reached a model close to the expected target.

Keywords: Genetic algorithms · Bio-heat transfer · Inverse problem · Finite elements method

1 Introduction

Tumor detection is a common problem in computational applications. After collecting patient data, it is possible to apply a wide range of search algorithms to locate the tumor position within the tissue. Many machine learning algorithms have been applied to solve such a problem, e.g., neural networks, support vector machines, Bayesian networks, clustering, fuzzy logic and decision trees [1,8]. This work aims at applying a genetic algorithm (GA) to estimate the position (center and radius) and the blood perfusion of a circular tumor within the

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modelled breast tissue, proposed by [13]. This work is based on the methodology presented in [6], that used genetic algorithm in a rectangular shaped tissue model, and the one presented in [5]. The temperature field, collected at the outer portion of the tissue, is calculated via the Penne's Bio-Heat Transfer Equation (acronym PBHTE). The genetic algorithm then tries to estimate the aforementioned parameters within the tissue by generating a population of cancerous breast models that can fit within the expected target model. Those populations are evolved, and after a number of generations, the model that most approaches to the target model is then returned.

Wahab's breast cancer model describes the breast as a semicircle with an underlying circular tumor. This model has three different layers of tissue, representing fat, mammary gland and muscular tissue. Here, the open-source finite-element mesh generator software Gmsh [4] is used to create the mesh of each GA individual model. Afterwards, the temperature field of each individual is computed by the finite element method through an in-house code. The objective function minimizes the temperature difference on the skin surface between the GA model to the target model. Continuous operators are applied during the evolutionary process, and individuals with most resemblance to the target model are selected with both generating offsprings, proceeding to the next generation via elitism.

2 Related Work

This work applies the methodology of Gonçalo et al. [6] and Gonçalo [5] in the Wahab's [13] breast cancer model. Gonçalo et al. work uses a steady-state genetic algorithm to estimate a tumor within a simple rectangular cancerous tissue model. In this model, the temperature field is calculated by the PBHTE, described by Harry H. Pennes in [11], which can be stated as: given Ω as the tissue domain; k as the thermal conductivity; ρ_b as the density of the blood; c_b as specific heat of the blood; ω_b as the blood perfusion and Q_m as the metabolic heat generation, find the tissue temperature T such that

$$\nabla \cdot k\nabla T + \omega_b \rho_b c_b (T_a - T) + Q_m = 0, \text{in } \Omega, \tag{1}$$

where T_a is the arterial temperature. This equation is used to calculate the temperature in the computational domain of the model.

In the work of Gonçalo et al. [6], each individual created by the GA was evaluated taking into account the difference between the target temperature on the skin surface used as reference and the respective skin temperature calculated within the model. This objective function can be stated as

$$J(\mathbf{x}_r, r) = \frac{1}{2} \sum_{i \in \eta_{\Gamma_S}} (\hat{T}_i - T_i(\mathbf{x}_r, r))^2 \tag{2}$$

where J is the error of each individual; $\mathbf{x}_r$ is the center of the circular tumor in the two-dimensional space, and r its radius; T_i is the computed temperature of the node i on the skin surface labeled as Γ_S, and $\hat{T}_i$ is the target temperature of

the model in the same node. The model used is based on [13], which describes a three-layered breast cancer model, with fat, mammary gland and muscular tissue.

Other works, including [10] utilizes dual reciprocity, combined with genetic algorithms, to estimate the location of a tumor using the skin temperature analysis through an inverse methodology considering the PBHTE. [2] utilizes curve fitting techniques to estimate the position of a breast cancer by non-invasive means. 2D and 3D breast models taking into account the PBHTE are discretized by the finite volume method. Das's model only has a single healthy tissue and the breast tumor. The referred work's algorithm tries to estimate the depth, in centimeters, the size and the blood perfusion through the solution of the inverse bio-heat transfer problem. This work is further expanded in [3], where the analysis also tries to find the angular and radial position of the breast model tumor. Melo et al. [9] employed a binary-coded GA to estimate the blood perfusion of a rectangular tumor considering the PBHTE and the finite element method. A detailed study on the effect of the GA parameters into the analyzed problem was also presented.

2.1 Breast Cancer Model

A breast cancer geometric model, based on Wahab's model, was created to be employed as a guideline for the mesh generator. The model is described in [13] as a semi-circle with four distinct tissue layers, namely: fat, mammary gland, muscle, and the tumor considered as a circle inside the gland layer. This model is used as a reference to the Gmsh to create a mesh of the model. In his work, Wahab proposed three different models of breast cancer, while referencing Sudharsan [12] with his own proposed model for the composition percentage of each tissue layer. Each of the models has the composition percentage as described by Table 1. This work uses the extremely dense model of breast cancer as reference.

Table 1. Composition of each healthy tissue in Wahab's breast cancer model, using Sudharsan's model as a reference for comparison.

Tissue composition (%)	Muscle (D_1)	Gland (D_2)	Fat (D_3)
Extremely dense (ED)	20	70	10
Heterogeneously dense (HD)	20	60	20
Scattered fibroglandular (SF)	20	40	40
Predominantly fatty (PF)	10	20	70
Sudharsan's model	26.5	54.1	19.4

The physical properties of each layer, as described by Wahab, are shown at Table 2. Those properties are considered in the PBHTE to calculate the temperature field in the model through the finite element method.

Table 2. Physical properties of each tissue layer, as described by Wahab.

Physical properties	Muscle (D_1)	Gland (D_2)	Fat (D_3)	Tumor (T_1)
Thermal conductivity (W/m °C)	0.48	0.48	0.21	0.48
Metabolic heat generation (W/m^3)	700	700	400	8720
Blood perfusion (1/s)	0.8e−3	0.5e−3	0.2e−3	0.1e−1
Blood specific heat (J/kg °C)	4200	4200	4200	4200
Blood density (kg/m^3)	1060	1060	1060	1060

3 Methodology

This work follows the one in Gonçalo et al. [6] to calculate the temperature raise through the modelled tissue. The problem is formulated as an inverse problem, where the temperature measured on the skin surface is used to determine how parameters of the input model should be in order to estimate both center and radius, and the blood perfusion of the yet unknown breast tumor. To estimate such parameters, this work uses a Genetic Algorithm (GA) in which each genotype is comprised of the radius r of the tumor, its center x_r and y_r, and its blood perfusion ω. The target of the function is a set of calculated skin temperature of a reference model, and the objective is to minimize the temperature difference on the skin surface between each individual model generated and the target model through Eq. 2.

3.1 Model Generation Through Gmsh

To generate Wahab's breast cancer model mesh, the open-source software Gmsh was used. To create the mesh, the geometric model, represented in Fig. 1, is defined as described below:

- An outer semi-circle of diameter 14.4 cm defines the outermost boundary (skin surface) of the model.
- An inner semi-circle of diameter 13.4 cm, separates the fat outer layer D_3 from the inner mammary gland layer D_2.
- The innermost ellipse defines the muscle layer and has 2.2 cm y-radius and 6.7 cm x-radius.
- A circle inside the middle layer, defined as the mammary gland layer, represents the tumor. Its radius is variable, though the target (reference) model uses it as having 1 cm radius.

Each layer with its own physical properties is defined as a separate group that, during the evaluation process, will receive different levels of refinement in the mesh. The input model for each mesh is represented in Fig. 2, which is also the target model for the GA. After processing by Gmsh, the final generated mesh is represented in Fig. 3(a).

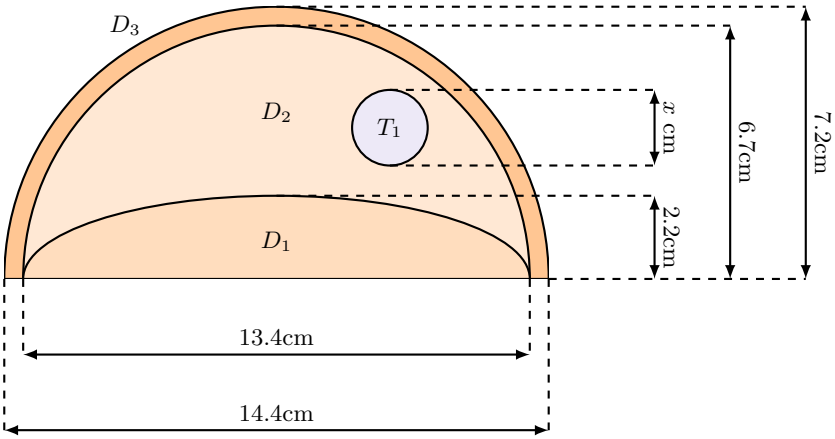


Fig. 1. Breast cancer model based on Wahab's model used as mesh generation reference. D_1 is the muscular layer; D_2, the mammary gland; D_3 the fat layer; and T_1 the tumor.

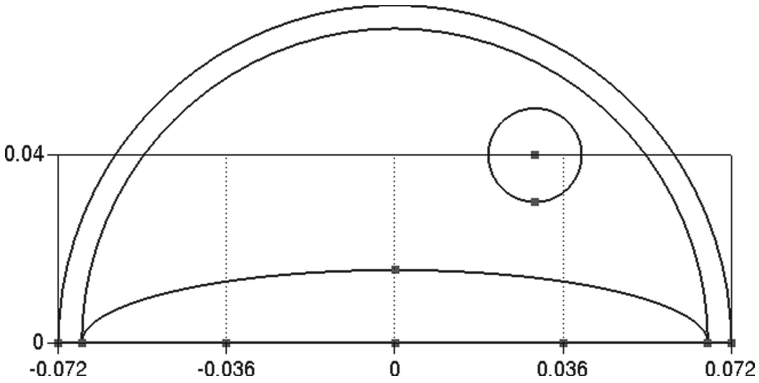


Fig. 2. Geometric model used as input for mesh generation on Gmsh. This model is also the reference model for the objective function on the GA.

3.2 Genetic Algorithm

Three different strategies of GA were used on this work: a classic generational GA; a steady-state algorithm; and an operator-independent strategy, developed for this problem. All of them use the same objective function, defined by Eq. 6, which will be discussed on Sect. 3.3. Each individual in the GA has its genotype defined by the tumor radius, its respective centre on a bi-dimensional plane and its blood perfusion. Each strategy can be described as follows:

– Generational GAs are the most traditional form of GA and use a random set of individuals that evolve, based on the Darwin's evolution theory, by selecting

the best individuals of each generation and applying a set of operators to pass the best genotypes to the next generation.
- Steady-state GAs do not apply the concept of "generations" between populations of generated individuals. All the operators are applied within the same population, and each new generated individual substitutes the worst ones.
- A third strategy, developed and based on the generational GA, create different groups of individuals based on the operator applied to create each individual, then merge all those groups to create a new generation. This method isolates the effect of each operator in the process, making easier to determine the influence of each operator within the population. This strategy was developed due to the heavy influence of the crossover over the mutation in this real inverse problem.

Other techniques, applied on all three strategies, include elitism, which tries to keep the best individuals for the next generation, and it is a default method in steady-state GAs, where most of the population, except the very worst individuals, is within the elitism margin; and partial re-initialization of the population, which creates random individuals on-the-fly for some of the generations. Both strategies can be described as tools that help the algorithm's performance [7].

All the GAs used in this current work are real GAs and use real numbers on the genotype of the individuals. As such, the operators used to solve the problem also considers the rational nature of the problem. The arithmetic crossover generates a couple of individuals y_1 and y_2 based on the Eq. 3, where x_1 and x_2 are the selected parents, and α is an uniformly distributed random value between x_1 and x_2, weighting randomly which parent will have more influence on each offspring value.

$$\begin{aligned} y_1 &= \alpha x_1 + (1-\alpha)x_2 \\ y_2 &= \alpha x_2 + (1-\alpha)x_1 \end{aligned} \tag{3}$$

Similarly, the mutation also uses a randomly uniform value around the value of the x_i parent genotype to generate the y_i value, as shown in Eq. 4. This value limited by γ_i, which varies differently for the centre, the blood perfusion and for the radius.

$$y_i = y_i + \alpha, \quad \alpha \in [-\gamma_i, \gamma_i] \tag{4}$$

The selection for the next generation in the generational and operator independent strategies is carried out by tournament, which chooses an n number of random individuals, then selects the one of those for the next generation with probability of p_1 for the best evaluated individual, then consecutively decreasing probability p_i for the rest of the individuals, following Eq. 5.

$$p_i = p((1-p)^{i-1}) \tag{5}$$

3.3 Evaluation

The evaluation process uses a modified version of Eq. 2, with the addition of the blood perfusion variable ω as input for the skin temperature calculation, and

compares the skin surface temperature of the target model with the one of each generated individual model as represented by Eq. 6.

$$J(\mathbf{x}_r, r, \omega) = \frac{1}{2} \sum_{i \in \eta_{\Gamma_S}} (\hat{T}_i - T_i(\mathbf{x}_r, r, \omega))^2 \tag{6}$$

Each individual generated by the AG has its own temperature field computed on the nodes of the mesh through the PBHTE, described by Eq. 1, using the finite element method. The individuals that approaches the most from the target model's skin surface temperature curve are considered the best, thus having better chance of being selected for the next generations and to generate offspring through the operators.

4 Testing and Experimental Results

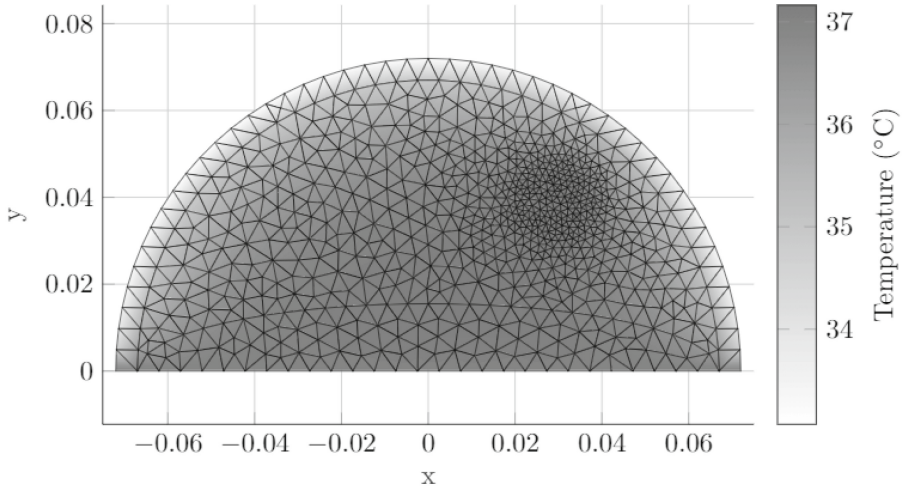
Using the model represented in Fig. 3(a) as the target model and the parameters described at Table 3, each GA strategy was tested in order to find evidence that the method could estimate the centre and the radius, as well as the blood perfusion of the tumor inside Wahab's model. Table 3 shows the parameter configuration for each of the algorithms tested. The method was developed under OCTAVE software and ran on a Intel® Core i7-4790 at 3.60 GHz, with 16 GB DDR3 RAM memory.

Table 3. Final parameter configuration used for the testing of each GA strategy.

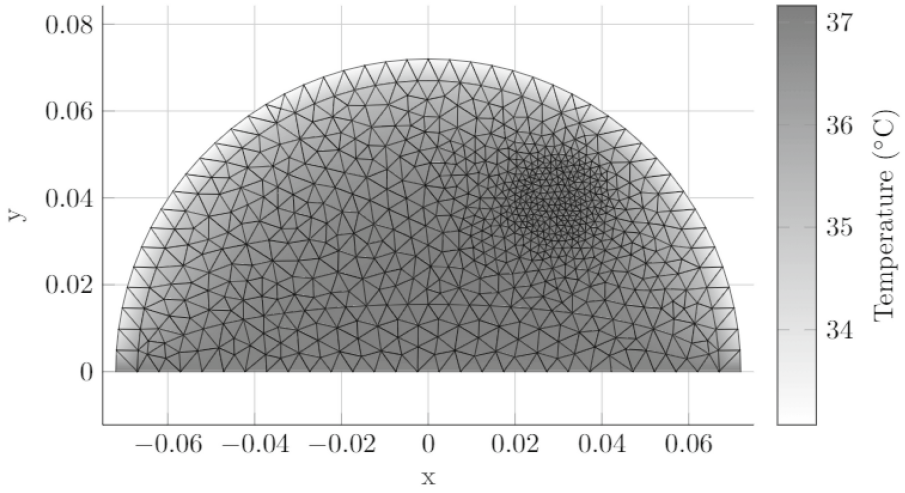
Parameter	Generational	Steady-state	Operator-independent
Number of executions	15	15	15
Number of iterations	200	5000	200
Population size	200	200	200
Crossover rate	0.8	0.8	0.8
Mutation rate	0.01	0.1	0.1
Elitism rate	0.1	-*	0.1

*Steady-state algorithm does not have elitism rate.

Table 4 shows the resulting model characteristics generated by each strategy, its genotype for centre, radius and blood perfusion, and its respective objective function. All three strategies generated individuals very close to the target model, with the objective function value varying between 2.3456e−08 and 2.7460e−09, and the operator independent GA performing a little better than the others. Each generated best model for each strategy is represented at Fig. 3.

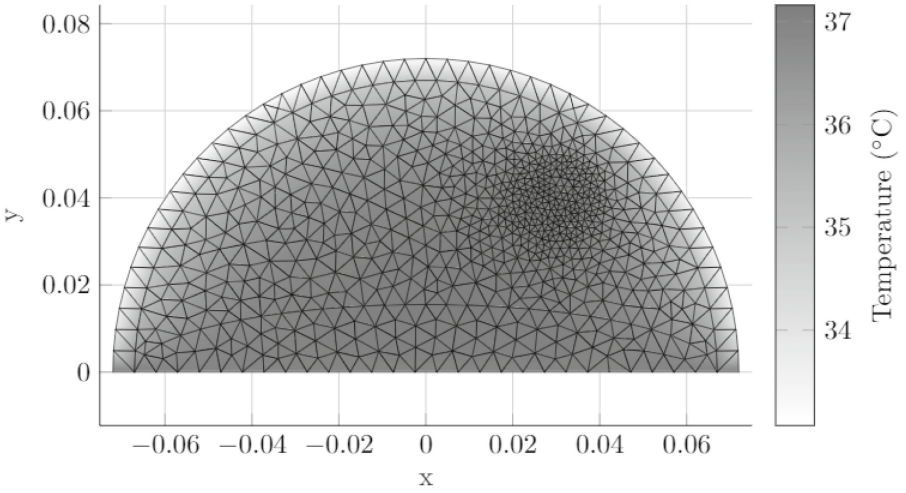


(a) Target model

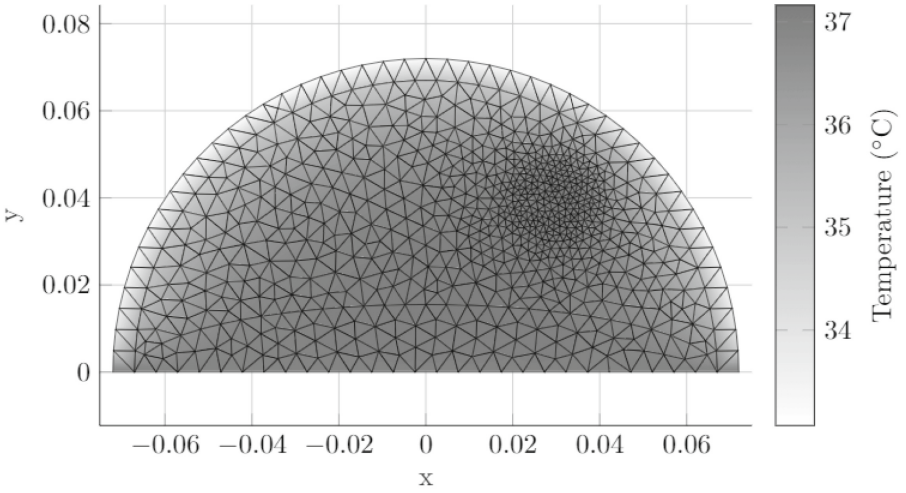


(b) Generational GA

Fig. 3. The target model used for reference and each generated model temperature map by different strategies used in this work.



(a) Steady-state GA



(b) Operator-independent GA

Fig. 3. (*continued*)

Table 4. Results for the three GA strategies in comparison to the target model used as reference for the objective function. r is the radius, x_r and y_r defines its centre and ω indicates the blood perfusion.

Model	r	x_r	y_r	ω	$J(\mathbf{x}_r, r, \omega)$
Target	1.0000e−03	3.0000e−02	4.0000e−02	1.0000e−02	–
Operator independent GA	9.9980e−03	3.0001e−02	4.0001e−02	1.0022e−02	2.7460e−09
Steady-state GA	9.9976e−03	3.0006e−02	4.0010e−02	9.8934e−03	1.6576e−09
Generational GA	9.9991e−03	3.0014e−02	4.0022e−02	9.6939e−03	2.3456e−08

5 Conclusion

The application of three different GA strategies on the inverse problem showed some evidence that the method could potentially work on tumor detection. The used breast cancer model, being more complex than other similar works, approaches more of a real problem than more simple and geometric abstract models. The solution of the PBHTE through FEM permits the GA to have precise metrics on determining simultaneously the geometric parameters and the blood perfusion of the tumor in the 2D model, and could as well help doctors to develop protocols for the detection of tumors based on thermal analysis.

6 Future Work

Future works that include the application of the current methodology on more realistic models, as well as 3D models, could determine real applications of the methodology proposed by this present work. The number of physical properties, layers of tissues, and other variables could also be increased to reach even more precise models.

References

1. Cruz, J.A., Wishart, D.S.: Applications of machine learning in cancer prediction and prognosis. Cancer Inf. **2**, 117693510600200030 (2006)
2. Das, K., Mishra, S.C.: Non-invasive estimation of size and location of a tumor in a human breast using a curve fitting technique. Int. Commun. Heat Mass Transf. **56**, 63–70 (2014)
3. Das, K., Mishra, S.C.: Simultaneous estimation of size, radial and angular locations of a malignant tumor in a 3-d human breast-a numerical study. J. Therm. Biol. **52**, 147–156 (2015)
4. Geuzaine, C., Remacle, J.F.: Gmsh: a 3-d finite element mesh generator with built-in pre-and post-processing facilities. Int. J. Numer. Meth. Eng. **79**(11), 1309–1331 (2009)
5. Gonçalo, A: Application of genetic algorithms for the solution of the inverse bioheat transfer problem for the detection of breast tumors (2018). Graduation final project (in Portuguese)

6. Gonçalo Filho, A.M., Nogueira, L.L., Silveira, J.V.C., Loureiro, M.M.S., dos Santos Loureiro, F.: Solution of the inverse bioheat transfer problem for the detection of tumors by genetic algorithms. In: Gervasi, O., et al. (eds.) ICCSA 2017. LNCS, vol. 10405, pp. 441–452. Springer, Cham (2017). https://doi.org/10.1007/978-3-319-62395-5_30
7. Kora, P., Yadlapalli, P.: Crossover Operators in Genetic Algorithms: A Review (2006)
8. Kourou, K., Exarchos, T.P., Exarchos, K.P., Karamouzis, M.V., Fotiadis, D.I.: Machine learning applications in cancer prognosis and prediction. Comput. Struct. Biotechnol. J. **13**, 8–17 (2015)
9. Melo, A.R., Loureiro, M.M.S., Loureiro, F.S.: Blood perfusion parameter estimation in tumors by means of a genetic algorithm. Procedia Comput. Sci. **108**, 1384–1393 (2017)
10. Partridge, P., Wrobel, L.: An inverse geometry problem for the localisation of skin tumours by thermal analysis. Eng. Anal. Boundary Elem. **31**(10), 803–811 (2007)
11. Pennes, H.H.: Analysis of tissue and arterial blood temperatures in the resting human forearm. J. Appl. Physiol. **1**(2), 93–122 (1948)
12. Sudharsan, N., Ng, E., Teh, S.: Surface temperature distribution of a breast with and without tumour. Comput. Meth. Biomech. Biomed. Eng. **2**(3), 187–199 (1999)
13. Wahab, A.A., Salim, M.I.M., Ahamat, M.A., Manaf, N.A., Yunus, J., Lai, K.W.: Thermal distribution analysis of three-dimensional tumor-embedded breast models with different breast density compositions. Med. Biol. Eng. Comput. **54**(9), 1363–1373 (2015). https://doi.org/10.1007/s11517-015-1403-7