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Fitting a Spectral Model for Component Analysis in Diffuse Optical Tomography

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ABSTRACT

Time Domain Diffuse Optical Tomography (TD-DOT) at different wavelengths can be used to retrieve tissue reconstructing the components of a two-region system starting from self-normalized time-dependent measurements performed in reflectivity geometry over multiple wavelengths. The proposed method performs a fit of a limited number of tissues parameters providing a good quantification of the components' concentrations by applying a FEM-based Diffusion approximation of the TD-DOT direct model.

Keywords: Finite Element Method, Diffusion Equation, FEM, TD-DOT, Spectral Fit.

1. INTRODUCTION

Time Domain Diffuse Optical Tomography is a valuable tool for analyzing the composition of human breasts[1,2]. In breast cancer screening, asserting the nature of possible lesions can be vital for early identification of the malignant ones. The chromophores which are usually related to breast cancer are i) oxy- and ii) deoxy-hemoglobin, iii) lipids, iv) water and v) collagen, which, all together, allow to identify a tumor from a benign inclusion. Knowing the concentration of such chromophores, it is possible to retrieve the absorption spectra of a given tissue. On the same line, based on semi-empirical laws, the scattering spectra of a tissue in the visible and near infrared (NIR) range are described with two parameters related to the microscopic structure of a tissue[3]. Then, inputting the concentrations of the most relevant chromophores and basic information on the scatterers, we can define a forward model that describes the fluence's propagation in breast tissues by means of the Diffusion Equation. Thus, the output fluence, in the case of a two-region system probed with a N wavelengths, can be approximated by a set of N Diffusion Equations stemming from 7 parameters per region: 5 concentrations of chromophores and 2 parameters describing the scattering. We ran a series of fits based on these considerations for an experimental setup of 8 wavelengths, 8 sources and 8 detectors in a reflectance geometry. Tests were performed on homogenous and heterogenous simulations to which noise has been added and later have been convoluted with an experimental Impulse Response function (IRF).

2. METHODS

It is possible to relate the absolute values of absorption coefficients to the concentration of chromophores present in tissues. A linear relation can be written [4], so that: $\mu_a(\lambda) = \sum_j^N \varepsilon_j(\lambda) C_j$, where ε_j is the extinction coefficient over the spectrum of the j^{th} chromophore and C_j is its concentration. A spectral law can be observed also on the scattering coefficients. Empirical evidence, partly explained by Mie's scattering theory, shows that scattering fairly depends on the wavelength of the probing photons by the λ-law: $\mu'_s(\lambda) = a\left(\lambda/\lambda_0\right)^{-b}$, where a and b are semi-empirically defined parameters, respectively dependent on concentration and size of the scattering centres in tissues and λ_0 is a reference wavelength for which the parameters are defined. The wavelengths that have been used to perform the experiment were

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635, 670, 830, 915, 940, 980, 1030 and 1065 nm, so to cover all the characteristic features in the absorption spectra of the components considered.
The combination of the previous expressions offers room for directly retrieving the composition of tissues from optical data, instead of first reconstructing the optical coefficients. Our approximated forward model is then structured in:

i) a first fast part aimed at retrieving the optical coefficients from the previous equations by means of experimental extinction coefficients;
ii) a consequent second step starting from the optical coefficients to get the output fluence solving the Diffusion Equation by means of the Finite Element Method;
iii) a last part convolving the result with the IRF to take the experimental setup into account.

The fit procedure aims at finding the correct input parameters by iteratively minimizing an appropriate Loss Function describing the discrepancy between the experimental measurements and the results of the forward model previously defined. A first assessment of the method has been performed by simulating a homogenous system of $64\times48\times32$ mm^3 discretized by a mesh of cubic elements of side 2 mm. Temporal discretization has been performed by means of a time step of 25 ps for a total number of 130 steps, the mass matrix and stiffness matrix were assembled by using the Implicit Euler Scheme. The FEM computation was implemented with TOAST++ and speeded using GPU-acceleration[5]. The output of the simulation was then made more realistic by adding the Poisson noise corresponding to a photon count of 1×10^6 and by convolving it by an experimentally measured Impulse Response Function. The fit was performed assuming the whole system could be approximated by only 7 parameters: 5 chromophores' concentrations and 2 scattering parameters.

3. RESULTS AND DISCUSSION

The method, for the homogenous case, converged after approximately 21 iterations starting from values 10 times smaller than the nominal ones.
Results for the homogenous system can be found in Table 2 and show that a good agreement is reached between the simulated and the reconstructed ones. We stress the addition of Poisson noise in order to avoid inverse crime. A second test has been performed by trying to fit 14 parameters for a two-region model as defined in Figure 1. , where an inclusion of 1 cm^3 was simulated at 1 cm under the surface. The fit was performed of 7 parameters per region: 5 chromophores' concentrations and 2 parameters describing the scattering behavior. The parameters simulated assumed higher concentrations of the chromophores and higher scattering inside the inclusion with respect to the bulk with a varying contrast of 1.5 for the scattering power b**,** 2 for oxyhemoglobin, lipids and collagen and 3 for deoxyhemoglobin and water. No other heterogeneity was assumed at this stage. Fits were performed by assuming to know exactly the inclusion geometry used during the simulations. Retrieved parameters show a good agreement with the simulated ones as expected. Results are shown in Table **1.** However, we can observe a slightly worse reconstruction of the chromophores' concentration in the inclusion, with an overestimation of the concentration of lipids and water while water and oxyhemoglobin are underestimated instead. Next steps will aim at validating the presented procedure with silicone and meat phantoms to mimic at best experimental conditions and tissues' heterogeneities.

Table 1. Results of the homogenous reconstruction. The simulated parameters were taken from characteristic concentration and scattering values found in human breast [6].

	Hb (μM)	**HbO_2** (μM)	**Lipid** (mg/cm^3)	**H_2O** (mg/cm^3)	**Collagen** (mg/cm^3)	a (mm^{-1})	b
Simulated	1.91	8.8	575	270	108	1.2883	1.2641
Reconstructed	1.904	8.811	574.24	269.99	108.04	1.2884	1.2647

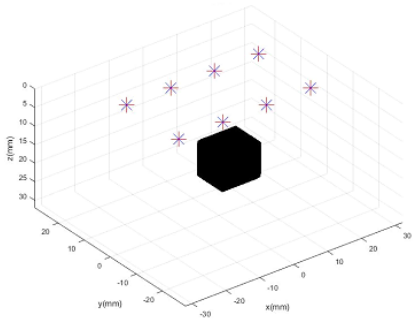

Figure 1. Two-regions definition used in the simulations and fit. The black region identifies a cubic inclusion of side 10 mm and set 10 mm under the surface. This same binary map was used for the fit for the meat phantom even though the delimitations of the region were known only approximately. Blue and red stars indicate the position of (coincident) sources and detectors.

Table 2. Results of the fit in the case of a simulated inclusion as described in Figure 1. The two-regions delimitation was the same in simulation and reconstruction.

	Hb (μM)	**HbO_2** (μM)	**Lipid** (mg/cm^3)	**H_2O** (mg/cm^3)	**Collagen** (mg/cm^3)	**a** (mm^{-1})	**b**
Simulated Bulk	1.91	8.8	575	270	108	1.2883	1.2641
Reconstructed Bulk	1.928	8.807	574.535	270.00	107.5	1.2887	1.2659
Simulated Inclusion	3.82	26.4	1150	810	216	3.68649	1.8933
Reconstructed Inclusion	3.6	26.5	1168.3	794.5	224.3	4.0718	2.0278

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