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Spectral approach to time domain Diffuse Optical Tomography for breast cancer: Validation on meat phantoms

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ABSTRACT

Time Domain Diffuse Optical Tomography (TD-DOT) performed at multiple wavelengths can be used to non-invasively probe tissue composition. Then, tissue composition can be related to breast tissue and lesion type. Thus, TD-DOT could be used for therapy monitoring for breast cancer. We developed a software tool for multi-wavelength TD-DOT and performed a validation on meat phantoms to mimic tissue heterogeneity. An inclusion of different meat was exploited to mimic the presence of a lesion in the breast. Results show good localization of the inclusion, but poor quantification of the reconstructed breast composition. The use of a morphological prior constraint, providing information on inclusion geometry and position, significantly improves both localization and composition estimate.

Keywords: Diffuse Optical Tomography, Time Domain, Reflectance, Breast cancer

1. INTRODUCTION

Diffuse Optical Tomography (DOT) is an emerging tool for tissue imaging. Using a defined pattern of sources and detectors, a wide volume can be investigated, and absorption and scattering properties can be estimated. Those can be used to perform clinical diagnostic evaluation as well as therapy monitoring for breast cancer [1,2]. Though, other parameters can be retrieved that are more directly linked to tissue composition: the main chromophores of the tissue. In the case of breast, these are lipids, water, collagen, oxy- and deoxyhemoglobin. Following this approach, multiple wavelengths are needed, exploiting the wavelength dependency of each chromophore absorption spectra, to separate single contributions to the overall absorption coefficient. We combined this multi-wavelength (or spectral) approach to Time Domain DOT (TD-DOT), thus taking advantage of the decoupling of the absorption and scattering effects. Thus, we developed a spectral TD-DOT software tool and performed a validation on beef and pork meat phantoms embedding an inclusion made of different kind of meat. The heterogeneity of the meat cuts was exploited to mimic the heterogeneity of human breast, thus obtaining a more realistic testing environment than provided by phantoms of common use (*e.g.*, resin or silicone). Measures were performed in reflectance geometry. We also tested a morphological prior constraint to exploit the information on localization and geometry of the inclusion to improve the overall reconstruction quality [3].

2. MATERIALS AND METHODS

The TD-DOT algorithm is divided in the forward model, describing photon propagation within the tissue and the inverse problem, *i.e.* the concentration estimation from the photon time distribution. Light propagation is modelled by the analytical solution of the diffusion equation in a semi-infinite homogeneous medium, and through a perturbative approach when considering heterogeneities [4]. The wavelength dependency of the optical properties is exploited by

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expressing the absorption coefficient at a specific wavelength as $\mu_a(\lambda_i) = \sum_j^N \varepsilon_j(\lambda_i) C_j$, where $\varepsilon_j(\lambda_i)$ is the j-th extinction coefficient for the j-th chromophore, at the i-th wavelength, and C_j is the concentration of the j-th chromophore. The reduced scattering coefficient is modelled according to the empirical approximation to Mie theory: $\mu_s'(\lambda_i) = a(\frac{\lambda_i}{\lambda_0})^{-b}$, where a is the scattering amplitude related to the concentration of scattering centers and b is the scattering power related to their size [5]. The phantoms are composed by a thick slab of meat, while the inclusion is a 1 cm^3 cube of different meat set in the slab center, with its upper face at 1 cm depth. Three configurations were investigated: *i)* lard and ham *ii)* veal and lard *iii)* lard and tendon, respectively as bulk and inclusion. We will focus on the first configuration as it mimics a common situation: a malignant lesion with higher content of blood respect to an adipose background tissue. Measures were performed using a rectangular pattern (20 mm x 40 mm) with 4 measure spots on each long side, equally spaced. The wavelengths were adequately chosen to (at least partly) highlight different component contributions to the absorption spectra: 635 nm and 670 nm were selected for deoxyhemoglobin (Hb) and collagen, 830 nm for oxyhemoglobin (HbO_2), 915 and 940 nm for lipids, 980 nm for water, 1030 nm and 1065 nm for lipid and collagen. Laser light provided by a supercontinuum pulsed source was coupled to an optical fiber. Another optical fiber collected the re-emitted light, guiding it to a silicon photomultiplier detector. Photon time distributions were built using the time-correlated single photon counting technique [6].

3. RESULTS AND DISCUSSION

As an example of the results obtained, we will focus our discussion on the reconstructed HbO_2 maps of the ham in lard phantom. The average concentration of HbO_2 in lard and ham meats (measured separately on a bulk volume of each meat type) resulted to be 2.8 μM and 7.2 μM, respectively. Figures 1 and 2 are composed of different subplots, each referring to a different depth along the z coordinate, from 0 mm (*i.e.,* the surface) to 30 mm in 2 mm steps. The X and Y axis of each subplot correspond, respectively, to the x and y coordinate in space. The overall quality of the reconstruction is assessed by localization and quantification. The former is quantified by the error of the reconstructed position of the center of mass of the inclusion respect to the known position; while the latter by the error of the reconstructed HbO_2 values within a region around the center of mass respect to the measured one.

Figure 1 shows artifacts especially on the surface (the first subplots) resembling the sources and detectors pattern. This could be related to a poor matching of the optical fibers with the meat surface. At the same time, the reconstructed inclusion is blurred and spread along the x-y plane. The z coordinate of the inclusion is reconstructed at a shallower position than real. The reconstructed values are strongly underestimated with quantification error in the inclusion as high as 50%.

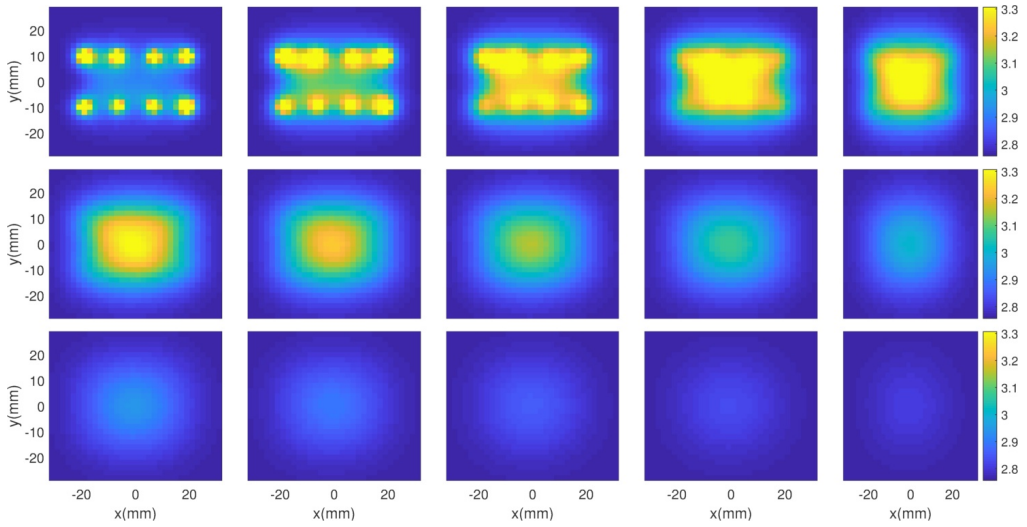

Figure 1. Reconstructed HbO_2 maps. There are strong artifacts on the surface and quantification is poor.

Figure 2 is obtained exploiting a morphological prior constraint on the geometry and position of the inclusion. Clearly, localization improves dramatically as the top of the inclusion is correctly set 1 cm from the surface, while it extends to 2

cm. Also, the morphological constraint strongly reduces the surface artifacts. At the same time, quantification improves as the reconstructed value in the inclusion ($6.5\ \mu M$) is closer to the measured one (10% error).

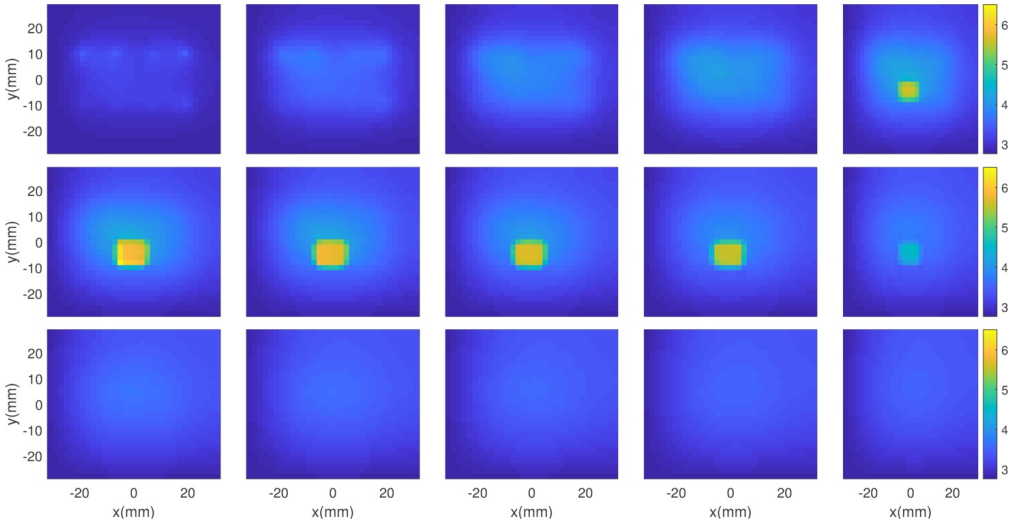

Figure 2. Reconstructed HbO_2 maps with the use of the morphological constraint. Surface artifacts disappear, and quantification improves.

The developed spectral TD-DOT software tool was validated on different meat phantoms. Generally, localization is reached, but results are dramatically improved when using the morphological constraint. Surface artifacts are removed, and blurring is dampened. Quantification benefits as well but an underestimation error persists (even though much smaller). The obtained results are promising and work into improving quantification needs to be done.

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