An Online Modeling and Image Reconstruction Tool for Optical Imaging based on NIRFAST

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Abstract: Model based image reconstruction in Optical and Molecular imaging is rapidly becoming an optimal method due to the flexibility and robustness of this method to problem specific cases. An online imaging and Finite Element modeling tool for optical imaging has been developed which allows the user to run problem specific cases, as well as providing an online tutorial for light propagation in tissue. This online package, based on NIRFAST is presented and is being made available to users worldwide to allow further development of this novel imaging technique.

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1. Introduction

Diffuse optical tomography (DOT) is a non-invasive imaging technique that has been under development for the past 20 years for the detection and characterization of functional changes within the biological tissue [1]. Due to the relatively low absorption of hemoglobin, water and lipid at wavelength range of 650 nm – 1000 nm, near infrared (NIR) light can transmit through several centimeters of tissue to allow tomographic detection of light transmission. Using the measured NIR signal, together with the known spectral absorption and scatter coefficients of tissue, it is possible to extract functional information about the tissue being imaged.

In most DOT imaging studies, the majority of the work has relied on the use of model based image reconstruction. A large number of different models can be used to predict light propagation within tissue, including stochastical, analytical and numerical. Numerical models have the potential of being able to model complex geometries as well as complex heterogeneous media, but have historically required longer computation times. But, perhaps the most promising reason for adoption of numerical approaches is to facilitate the combination of NIR tomography with standard clinical imaging systems, using pre-defined tissue geometries as the input domain. A number of different numerical models have been developed and used with specific application in DOT, including finite elements [2, 3], finite difference [4], finite volume [5] and boundary elements [6].

A number of models and image reconstructions are available, open source, to allow users worldwide to develop, adapt or validate their individual algorithms. Two of the most commonly available codes are (1) TOAST which is a software suite for image reconstruction in optical diffusion tomography. It contains binary command line tools for numerical modeling of light transport and parameter recovery, as well as MATLAB compatible library files to allow a more user friendly environment (http://web4.cs.ucl.ac.uk/research/vis/toast/) and (2) NIRFAST which is a MATLAB based toolbox that also includes capabilities for Multi-modal NIR imaging, Fluorescence, spectral and Bioluminescence imaging (http://www.NIRFAST.org).

NIRFAST relies on the availability of MATLAB, which is a generic, script based scientific package. A major advantage of this is that the package is platform independent and can be run on any workstation regardless on the operating system. Although MATLAB is well known and accepted as a preferred software for prototyping, it lacks computational speed in instances whereby multiple, repeatable functions are required. To overcome this, NIRFAST has been written, in part, using compiled high-level programming languages that provide computational speed comparable to those written entirely in high-level languages. There is however the assumptions that most labs and researchers worldwide would have access to MATLAB, which is proprietary software and this may not be true for smaller research groups. Additionally, most three dimensional, spectral, and multi-modal image reconstructions require access to powerful hardware to allow problem solving in realistic time.

To address this problem, we have developed an online web application which allows the use of NIRFAST to the researchers without access to MATLAB. Specifically, this online package is designed to allow users some built-in 2D and 3D models in order to investigate light propagation in tissue. Additionally, the users can import and export models and solution from this package to allow validation of self developed software.

2. Methods

The application is based predominantly on the Java Server Pages (JSP) technology. NIRFAST's functionality is accessed though the Java Runtime class method, first documented by Klimke [7]. This enables the Web application to receive complete standard and error output from NIRFAST. All functionality can be accessed using one of the mainstream Web Browsers (IE, Mozilla Firefox) and is available as a Graphical User Interface, in a fashion familiar to Web users. Images (before and after reconstruction) can be presented either as JPEGs generated by NIRFAST or as structures generated by Java2D and Java3D and embedded in the Web Page as Java Applets. This adds interactive features, such as zoom and rotation, and is especially useful in 3D. Streaming of reconstruction data to the Web page is achieved using the Direct Web Remoting library (http://directwebremoting.org). The Apache Commons FileUpload (http://commons.apache.org/fileupload/) package provides basic functionality for import of user generated models. Tutorials for new users are based on tutorials for the Matlab only version of NIRFAST. The package is being deployed on a powerful server computer connected to the Internet to allow remote execution of complex image reconstruction for expert users. A CPU usage limiter will balance the load generated by multiple users running image reconstruction at the same time.

3. Results

The developed online package has the same functionality of NIRFAST, but is at present restricted to single and multiple wavelength optical tomography. In order to demonstrate its functionality, two cases are presented (1) Single wavelength and (2) Spectral model. All methods and algorithms used have been previously described elsewhere [3].

A 2D circular mesh with a radius of 43 mm with background optical properties of $\mu_a = 0.01$ mm^{-1} and $\mu_{s'} = 1.0$ mm^{-1} has been used for the generation of forward data. Within this mesh, 3 anomalies were placed, each having a radius of 7.5 mm, located as shown in Figure 1 (top row). Each anomaly was assumed as having either 2 times the background absorption or reduced scatter or 2 times the background absorption and reduced scatter. The boundary data were generated with a computational time of 5 seconds. To avoid inverse crime in image reconstruction a second mesh was for image reconstruction. Simultaneous images of absorption and scatter were reconstructed iteratively until the difference between the forward data and the reconstructed data did not improve by more than 2% when compared to the previous iteration. The final images, corresponding to 14 iterations, are shown in Figure 1
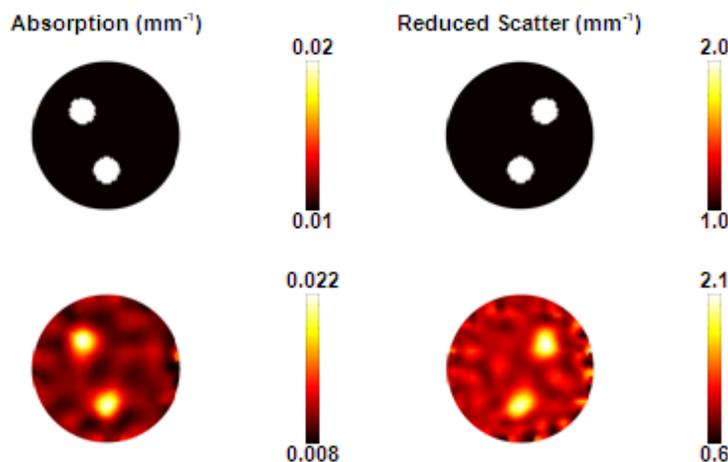

Figure 1. Top row: The forward model shows the true distribution of internal optical properties. Bottom row: Reconstructed images of optical properties are shown using single wavelength data. The images were reconstructed from noisy simulated data.

(bottom row) and were obtained with a computation time of 76 seconds.

For the spectral case, the background properties were assigned to have those typical of breast adipose tissue which consisted of oxygenated hemoglobin (HbO) of 0.012 mM, deoxygenated hemoglobin (Hb) of 0.005 mM, water content (H$_2$O) of 47%, scattering amplitude of 1.34 and scatter power of 0.56. Within this mesh, 5 anomalies, each having a radius of 7.5 mm, were placed as shown in Figure 2. The boundary data were generated for a total of 7 wavelengths (661, 735, 761, 785, 808, 826 and 849 nm) with a computational time of 47. Simultaneous images of all chromophores were reconstructed iteratively until the difference between the forward data and the reconstructed data did not reduce by more than 2% as compared to the previous iteration. The final images, corresponding to 9 iterations, are shown in Figure 2 and were recovered with a computation time of 580 seconds.
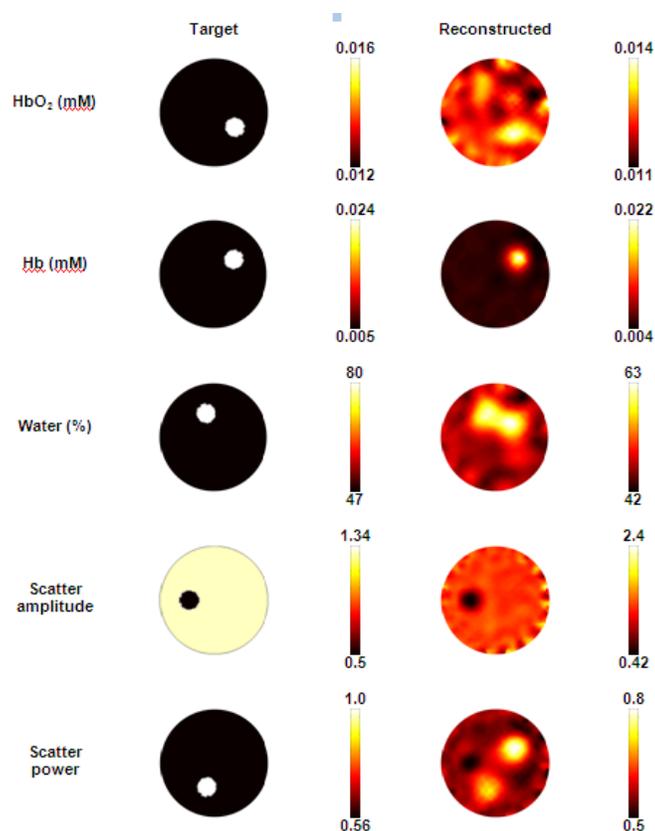
Figure 2. The forward model shows the true chromophore distributions (left column) and the reconstructed spectral images (right column) using 7 wavelengths of measurement data. The images are reconstructed from noisy simulated data

4. Conclusions

In this work, the online application for NIRFAST is presented. The capability of NIRFAST has been demonstrated through examples that allow single wavelength, as well as multi-wavelength spectral modeling and image reconstruction. Further work is under investigation to explore a general framework for the application of spatial information, which may be readily available from other imaging modalities, for example MRI or CT, that will allow more accurate and perhaps more computationally efficient image reconstruction algorithms.

NIRFAST is a MATLAB® based toolbox which also includes capabilities for Multi-modal NIR imaging, Fluorescence, and Bioluminescence imaging. NIRFAST is currently available for academic research for free, via the URL link:

http://www.NIRFAST.org

5. Acknowledgements

6. References

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