

ABSTRACT

We demonstrate the usability of bioresorbable phosphate glass fibers for time-domain diffuse optical spectroscopy (TD-DOS) in the short-wave infrared (SWIR) region of 950 – 1600 nm, with the use of an InGaAs detector. We first validate our measurements by comparing the optical properties of high-scattering solid silicone phantoms retrieved with these bioresorbable fibers with those by a standard Si fiber. We attempt to use the bioresorbable fibers to retrieve the absorption and reduced scattering spectra of a series of biological samples such as porcine muscle, porcine fat and bone, known to contain predominantly specific biomarkers such as – water, lipid and collagen respectively. These results have been published in an article in Biomedical Optics Express and can be found at –

Damagatla, Vamshi, et al. "Use of bioresorbable fibers for short-wave infrared spectroscopy using time-domain diffuse optics." Biomedical Optics Express 15.9 (2024): 5041-5052.

<https://doi.org/10.1364/BOE.531681>

DATASET OVERVIEW

In this dataset, we provide the information regarding the data, tools to read it, the acquisition methods, and analysis techniques, so as to provide a means for others to replicate our results or use them for other purposes. Briefly, the data set is divided into 4 folders to be read in that order for better understanding.

1) 1_Overview:

- a) **Index.JSON** – JSON file containing information about the files of the other folders, acting as an index for the dataset (all JSON files can be opened by notepad)
- b) **READ ME.pdf** – (currently opened file)

2) 2_Data:

- a) **Meta_data**: Contains experimental metadata
 - **Info.JSON** – JSON file containing information on the experimental setup, the samples, data acquisition, etc
 - **Table.xlsx**: Digital “Labbook” of the experimental data files and their acquisition/ analysis parameters
- b) **Raw_data**: The raw data acquired, directly as part of measurements

- **.DAT** – Raw data containing the acquired curves to be read for analysis that can be read using the codes in Tools section

3) **3_Tools:**

- a) **Read_matlab.m** – MATLAB script to read the raw data files into a MATLAB matrix and visualize the data
- b) **Read_python.py** – PYTHON script to read the raw data files into a PYTHON numpy array and visualize the data
- c) **Testfile** – Testfile to check the functioning of the codes

4) **4_Analysis:**

- a) PH25_scattering.txt: Reduced scattering spectra of PH25 phantom shown in Fig. 2(a)
- b) PH50_scattering.txt: Reduced scattering spectra of PH50 phantom shown in Fig. 2(b)
- c) PH25_absorption.txt: Absorption spectra of PH25 phantom shown in Fig. 2(c)
- d) PH50_absorption: Absorption spectra of PH50 phantom shown in Fig. 2(d)
- e) Processed_bone: Absorption and reduced scattering spectra of processed bone sample in Fig.3
- f) Porcine_muscle: Absorption and reduced scattering spectra of porcine muscle sample in Fig.4
- g) Processed_fat: Absorption and reduced scattering spectra of processed fat sample in Fig.5

All the .TXT files have also been converted into .XLSX and the data are presented as the graphs, as visible in the published article.

(NOTE: All JSON files can be opened in notepad or any text editor)