DEVELOPMENT OF OPEN SOURCE TOOL TO DERIVE SPECIFIC ABSORPTION COEFFICIENT OF BIOCHEMICAL PARAMETERS BY SEGMENTATION OF SPECIES SPECTRA

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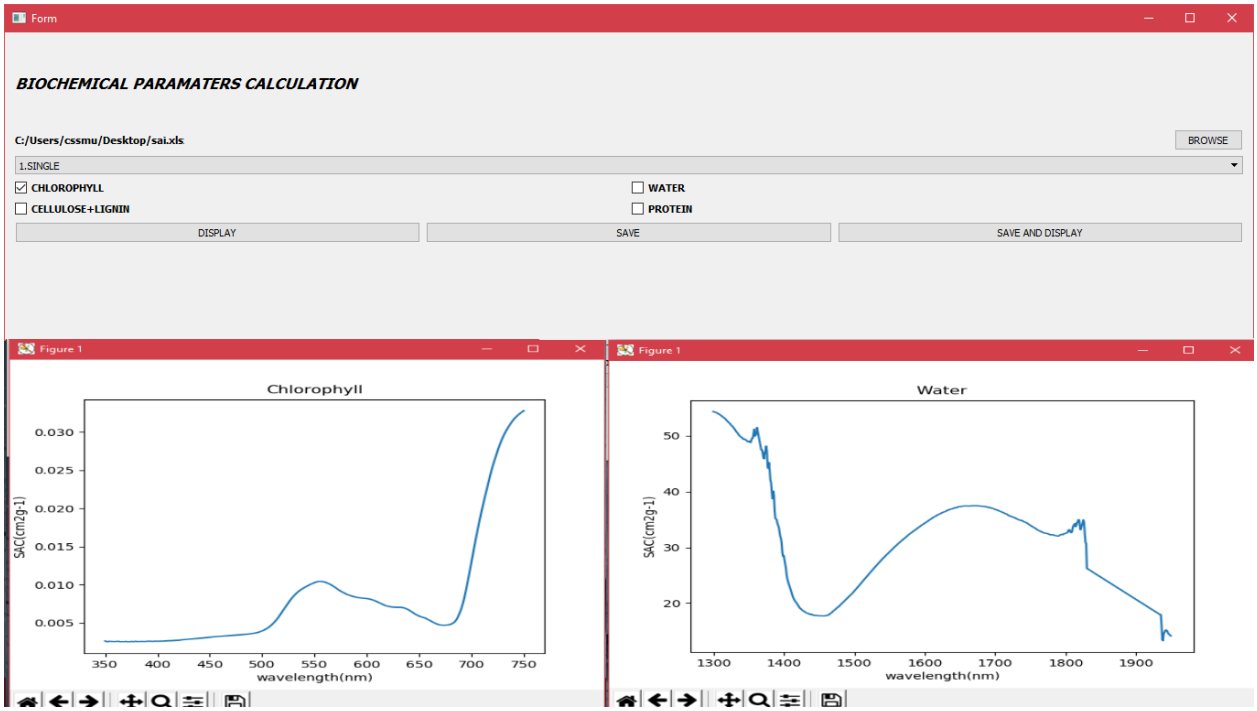
Abstract:

Hyperspectral remote sensing (HRS) has number of applications in the field of forestry and agriculture (Govender et al., 2006). HRS data have been used for the studies such as species forecasting, estimating the stress condition of the species, discriminating similar species using biochemical and biophysical parameters (Ray and Dadhawal, 1995). The spectrum of a tree species is influenced by leaf structure and pigments, water content, biophysical and biochemical parameters. One of the main use of the biochemical parameters is to find the health condition of the tree species. The concept arises with the values or range of the biochemical properties that are recorded for each species. Generally such studies are done at varied spatio-temporal scales with different samples for the same species. This way the stressed and the healthy tree species can be differentiated. Currently, there are few countable studies related to the biochemical parameters and health condition of the trees as it is practically difficult to conduct field survey at every season and also feasibility for the biochemical analysis is highly expensive. Fourty et al. (1995) analyzed the optical properties of the leaves and decomposed absorption spectra of vegetation into six specific absorption coefficients (s.a.c) having the characteristics of protein, cellulose, hemicellulose, lignin, starch, and sugar. However, in reverse, the estimation of the biochemical constituents was poor. This model is developed on the basis of leaves spectrum that include a wide range of internal cellular structures and biochemical compositions. Generally, leaf absorption was modeled using pigment concentration and the corresponding specific absorption. The leaf chemistry do change drastically the structure of the spectrum. The literature is very unclear about the origin of the absorption; most of the time it is ignored, and the articles presenting negative values are ignored. But the reality is NIR absorptance typically increases with biochemical concentration. Referring to the context, the current study proposed to develop a tool that analyze the reflectance of the spectrum with respect to the biochemical parameter by determining the specific absorption coefficients. The study promises to group the leaf spectrum (5-10 samples) and estimate the leaf biochemistry with reasonable accuracy. The study concentrates on a tool development where specific absorption and the coefficient of the biochemical parameters can be retrieved. The derived s.a.c are validated from the measured and the estimated leaf biochemical properties. The input for the tool can be a leaf/ canopy/satellite derived spectrum. The tool basically calculates the biochemical parameters

viz., chlorophyll, water, protein cellulose and lignin. The input for this tool is excel sheet containing wavelength ranging from 350nm to 2500nm (but also varies depending on the type of field spectroradiometer used or satellite data) and corresponding reflectance value from 0 to 1. Tool will calculate the s.a.c for each biochemical parameter by dividing spectra into segments like, for chlorophyll the wavelength ranges from 350-750nm, water ranges from 1300nm – 1450nm & 1778nm-1949nm, protein ranges from 1700nm -1750nm and cellulose + lignin ranges from 2000 – 2500. The tool basically developed takes single file as well as batch files. The tool shows the output as a graph figure and generates an excel file. Where in graph x-axis represent the wavelength in nm (Nano meters) and y-axis represents the SAC in $cm^2.g^{-1}$. But for a batch file the tool cannot display the graph because of the memory high memory requirement. The tool is developed using object-oriented python programming language. The front end of the tool is developed using PyQT5 of Python wrapper around the QT framework for creating graphical user interfaces, or GUIs. The QFileDialog.getOpenFileName() method of QFileDialog class will prompt for open file dialog box to select input excel file in the system which has wavelength and reflectance. The selected excel file is accessed using the openpyxl module of python, through which program can read and write the data from excel. Since, openpyxl module is used the index will start from 1 rather starting from 0. If the input file is a single spectrum file it will save the data i.e., s.a.c into the same file otherwise for batch files QFileDialog.getSaveFileName() method will prompt for save dialog box which will take the path and name where it has to save the output in excel file format which contains wavelength and corresponding reflectance and s.a.c. The Check_File () function of program will validate data present in the file with the following parameters i.e., the first column is the wavelength and so on with the reflectance values that ranges from 0-1. The program will calculate specific absorption coefficient $k_0(\lambda)$ i.e., equation (2) defined in Jacquemoud (1996). The tool's button will the trigger function associated with it when they are clicked. The Display button will show the output in the form of graph (Fig1).



Similarly save button will save the data in the form excel file. If the user wants to see and save the data they can click the save and display button which will save as well as show the output in graph. If user want to know more about the tool they can press the help button. User can only choose one or more biochemical parameter at a time by checking the corresponding check box button.

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