Instruction on running the code to read Tarragona's data file

IMPORTANT: Before running the main program as a Matlab script named 'Broadband_Tarragona.m', the user must first acquire its inputs from another Matlab script named 'tarragona_intensityread.m' to estimate the number of time stamps or number of spectra in the reference intensity file.

Step 1: Type the following in the Matlab Command Window:

```
[result]=tarragona_intensityread(Input_ref,0,1,2);
p2 = result.num_spectra ;
```

Step 2: Type the following in the Matlab Command Window:

```
[result]=tarragona_intensityread(Input_insult,0,1,2);
p4 = result.num_spectra ;
```

Step 3: Now run the main program by typing the following in the Matlab Command Window:

```
[Raw_data,Results]=Broadband_Tarragona(Input_ref,1,p2,Input_insult,1,p4);
```

Step 4: Select the default button from the menu for wavelength range.

Step 5: Select the recommended method to estimate pathlength.

Step 6: Input 0 and press 'Enter' to skip estimating the residual for particular time stamps.

A text file is generated containing NIRS data such as concentration changes of oxygenated haemoglobin (HbO2), deoxygenated haemoglobin (Hb), redox state of cytochrome c oxidase (CtOx), total haemoglobin (HbT) and the difference of haemoglobin (HbDiff); pathlength estimated at wavelength 840nm (pathlength840); pathlength estimated at wavelength 740nm (pathlength740); Absolute concentration of Hb (Absolute Hb).

Please note:

The Input_ref is the Tarragona's reference intensity file including its path.
e.g.: C:\....\Input_ref.tdf

The Input_insult is the Tarragona's insult intensity file including its path
e.g.: C:\....\Input_insult.tdf

Walk through example (including some basic theory):

Assume there are two Tarragona's intensity files: one is the reference intensity (LWP183_ref.tdf) while the other one is the intensity measured during insult (LWP183_insult.tdf).

1. Following step 1) by typing the following into the Matlab Command Window, we get p2 = 23

   [result]=tarragona_intensityread('C:\Users\tzhu\Desktop\Broadband\Code_Tarragona_Broadband System\LWP183_ref.tdf',0,1,2);

   p2 = result.num_spectra ;

2. Following step 2) by typing the following into the Matlab Command Window, we get p4 = 155

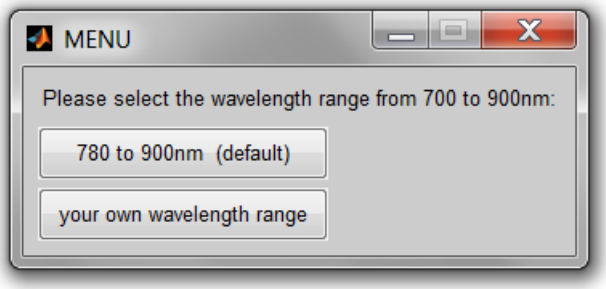
   [result]=tarragona_intensityread('C:\Users\tzhu\Desktop\Broadband\Code_Tarragona_Broadband System\LWP183_insult.tdf',0,1,2);

   p4 = result.num_spectra ;

3. Following step 3) by typing the following into the Matlab Command Window:

   [Raw_data,Results]=Broadband_Tarragona('C:\Users\tzhu\Desktop\Broadband\Code_Tarragona_Broadband System\LWP183_ref.tdf',1,p2,
   'C:\Users\tzhu\Desktop\Broadband\Code_Tarragona_Broadband System\LWP183_insult.tdf',1,p4);

4. The program generates a menu asking the user to select the wavelength range as shown as in the figure below. The user could select the default wavelength range which is 780 to 900nm, or enter a preferred wavelength range by click the 'your own wavelength range' button.



   If the user prefers to define the wavelength range himself, the following will appear on the Matlab Command Window as:

   Enter the minimum lambda:

   The program is waiting for the user input for the minimum wavelength. Once the user enters the wavelength number, press enter to confirm:

   e.g.: Enter the minimum lambda: 740

   Please note if the user enters the minimum wavelength to be less than 740nm, a warning message would be generated as indicating the following in the Matlab Command Window:

Warning: The specific extinction coefficient will not be corrected by wavelength dependent factor!

Now, the program is waiting for the user input again for maximum wavelength as:

Enter the maximum lambda:

Once the user enters the wavelength number, 900 in this case, press enter to confirm.

5. The program generates another menu asking the user to select the method of calculating the pathlength as shown below:

The recommended method of estimating the pathlength is obtained at 840nm/740nm by fitting the second differential of the absolute attenuation spectra to the second differential of the water absorption spectra (Matcher *et al*., 1994) between 700 to 900 nm (assuming average cerebral water content of 85%). Or the user is also given a choice to enter his own pathlength in the unit of cm.

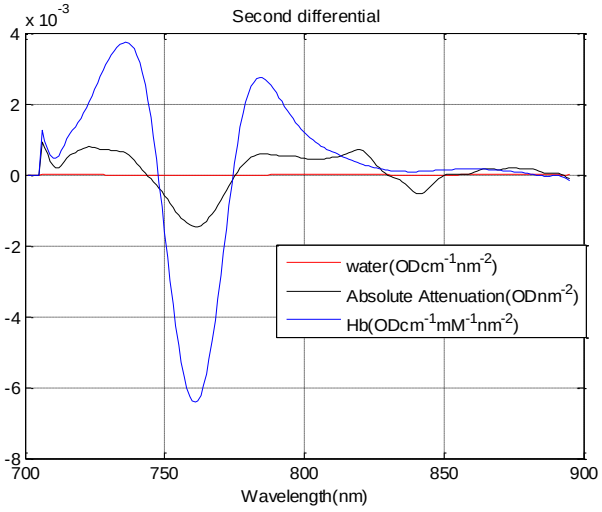
If user selects to 'Manually input pathlength yourself' button, the following will appear on the Matlab Command Window as:

Enter the pathlength(cm):

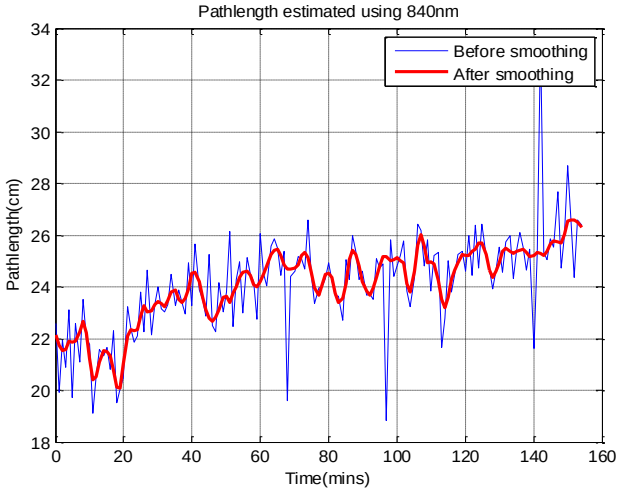
The program is waiting for the user input. Once the user enters the pathlength, press enter to confirm:

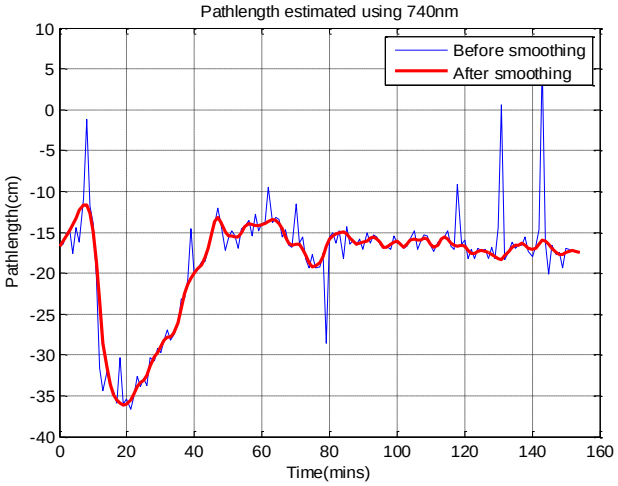
e.g.: Enter the pathlength(cm): 21

If the user selects the '740nm and 840nm (recommended)' button, the program would automatically generate plots of second differential of water, absolute attenuation and deoxygenated haemoglobin (Hb) between 700 to 900nm for different time stamps. One example of the second differential at time stamp = 155minute is shown below:



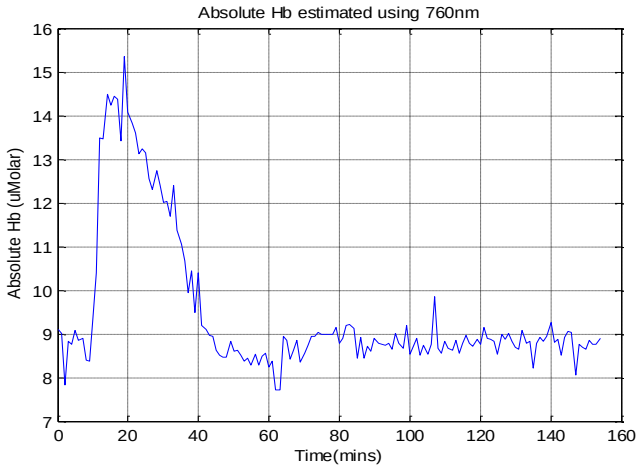
Also, two separate figures of pathlength estimated using 840nm and 740nm for a total of 155 minutes are given as the following:





Please note that the values of pathlength estimated using 740nm are negative. These are due to the negative second differential of water at wavelength 740nm. To improve on estimation of concentration changes, the program uses the pathlength estimated at wavelength 840nm (as it has similar results as compared to the pathlength estimated in Tarragona) to calculate the concentration changes of oxygenated haemoglobin (HbO2), deoxygenated haemoglobin (Hb), redox state of cytochrome c oxidase (CtOx), total haemoglobin (HbT) and the difference of haemoglobin (HbDiff).

6. Next, the program estimates the absolute concentration of deoxygenated Haemoglobin (Hb). It is obtained at 760nm by fitting the second differential of absolute attenuation spectra to the second differential of water and Hb absorption spectra (Matcher and Cooper, 1994) between 700 to 900 nm (assuming average cerebral water content of 85%). The result of the absolute concentration of Hb is provided as a figure as shown below:



7. Once the pathlength is estimated, the program is continued to calculate the concentration changes of HbO2, Hb and CtOx using the modified Beer-Lambert Law (Tachtsidis 2005). The general equation for calculating concentration changes can be expressed as:

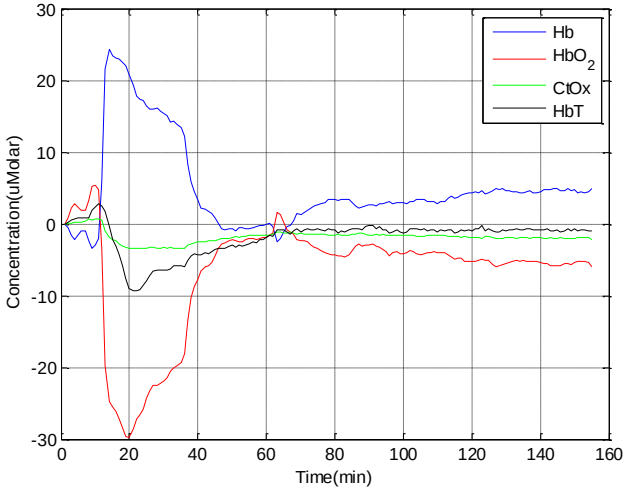
$$\begin{bmatrix} \Delta HbO_2 \\ \Delta HHb \\ \Delta CtOx \end{bmatrix} = \left(\frac{1}{\beta}\right)[\boldsymbol{\varepsilon}]^{-1}\Delta \boldsymbol{A}$$

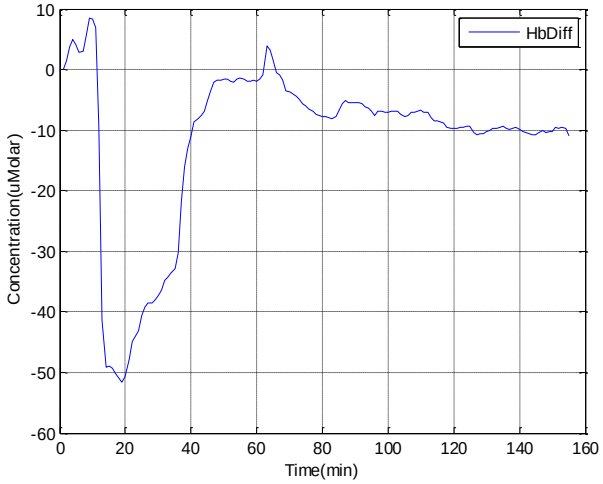
Where $$\boldsymbol{\varepsilon} = \begin{bmatrix} HbO_2(\lambda_1) & HbO_2(\lambda_2) & \dots & HbO_2(\lambda_m) \\ HHb(\lambda_1) & HHb(\lambda_2) & \dots & HHb(\lambda_m) \\ CtOx(\lambda_1) & CtOx(\lambda_2) & \dots & CtOx(\lambda_m) \end{bmatrix}$$

and $$\Delta \boldsymbol{A} = [\Delta \boldsymbol{A}(\lambda_1) \quad \Delta \boldsymbol{A}(\lambda_2) \cdots \quad \Delta \boldsymbol{A}(\lambda_m)]^{\boldsymbol{T}}$$

The pathlength is denoted as β, $\boldsymbol{\varepsilon}$ is the wavelength dependent factor corrected specific extinction coefficient and $\Delta \boldsymbol{A}$ is the change attenuation measured using wavelength range from λ_1 to $\lambda_m$nm.

The figure below shows the result generated for the concentration changes of Hb, HBO2, CtOx and HbT. The HbDiff is also generated in a separate figure below:





8. The residuals of change attenuation are calculated for the user's defined wavelength range using a 3-component fit (Matcher et al. 1995). The fit measures the difference between estimated change attenuation (from the results of concentration changes above) and measured change attenuation read from Tarragona. Because there are three concentration changes (Hb, HbO2 and CtOx), hence it is a 3-component fit.

   In this case, the program generates the residuals in a matrix form with columns indicating a total of number of time stamps (e.g.: 155 minutes), where each row represents the residuals of change attenuation for a particular wavelength. The result of residuals is shown at the workspace under the structure named 'Results'. Within the structure, a field named 'Residuals' contains the residuals of the 3-component fit which is denoted as 'ThreeFit'.

   Note: There are also other results such as the residuals of the 2-component fit, denoted as 'TwoFit'. This is similar to 3-component fit except the residuals are estimated when only considering the Hb and HbO2, thereby it is a 2-component fit.

9. The program then is awaiting the user input to see if the user would like to have residuals from specific time stamps. The following line is shown in the Matlab Command Window:

   Please enter the no. of datapoint you would like to select for calculating residual:(enter 0 to skip)

   In this case, input 0 and then press enter to skip this process. The program reads the user's decision and displays a message as:

   No points are selected for calculating residual!

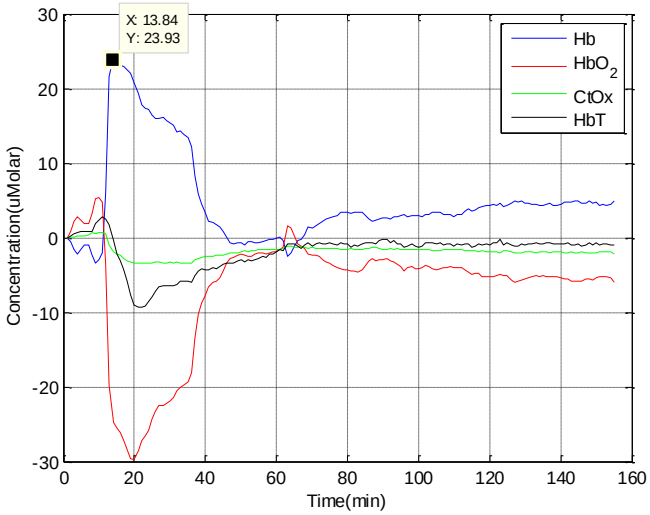
If the user would like the program to output residuals of change attenuation for particular time stamps, one could enter the number of data points (time stamps) in the Matlab Command Window such as:

Please enter the no. of datapoint you would like to select for calculating residual:(enter 0 to skip) 2

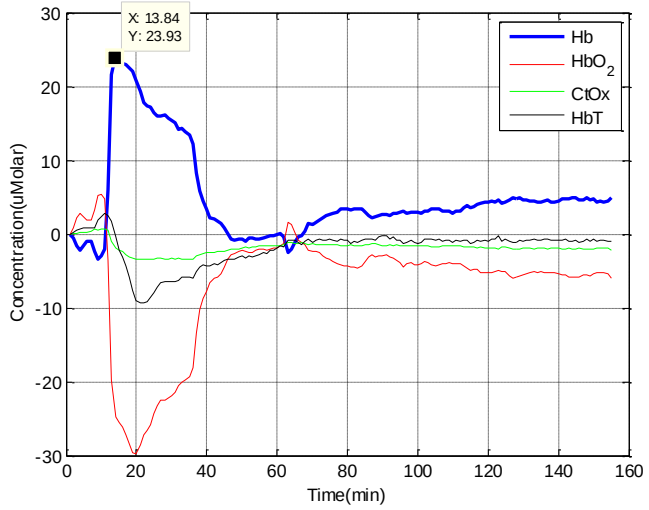
The program then displays the following message:

Please select the point(s), then press SPACE to continue

The user is asked to select the first data point from the plot of concentration changes of Hb, HbO2, CtOx and HbT. A data cursor allows the user to select particular data point from the plot by also displaying the x and y values as shown in the figure below:



The x value indicates the time in minute while the y value indicates the concentration changes of the selected chromophore, In this case, the selected chromophore is Hb and the first data point is selected at time stamp = 13.84 minute (rounds up to approximately 14 minute). If one wants to remove this data point, simply select a new data point before pressing 'SPACE' to confirm his selection. The program also highlights the selected chromohpore once 'SPACE' is pressed:



The program now is awaiting the second data point with displaying the same message:

Please select the point(s), then press SPACE to continue

Once a second data point is selected, the program is terminated. The calculated residuals for the two selected time stamps are displayed under the name, 'Selected_Residuals', with 3-component and 2-component fit results. Each fit result contains the time stamps that were selected and the residuals for those time stamps, denoted as 'ErrorLambda'.

For more information about the program, please contact: tingting.zhu.09@ucl.ac.uk

Reference:

- Matcher, SJ, Cope, M, and Delpy, DT. Use of the water absorption spectrum to quantify tissue chromophore concentration changes in near infrared spectroscopy. Physics in Medicine & Biology 39, 177-196.1994
- Matcher, S.J., Cooper, C.E. Absolute quantification of deoxyhaemoglobin concentration in tissue by near infrared spectroscopy. Phys Med Biol 39, 1295-1312, 1994
- S. J.Matcher , C. E.Elwell , C. E.Cooper, M. Cope and D. T.Delpy, "Performance comparison of several published tissue near-infrared spectroscopy algorithms," Analytical Biochemistry, vol. 227, no. 1, pp. 54-68, May 1995
- Ilias Tachtsidis, "The Technique of near-Infrared Spectroscopy: Theory and Practical Aspects," in Experimental Measurements of Cerebral Haemodynamics and Oxygenation and Comparisons with a Computational Model: a Near-Infrared Spectroscopy Investigation. London, United Kingdom, 2005, ch. 4, pp. 108-135.