

# Bayesian Linear Unmixing (BLU)

## Toolbox User guide

– *Beta version* –

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This graphical user interface of the Bayesian Linear Unmixing (BLU) algorithm has been developed by Pierre BOURDET, Clément DECHESNE, Julien TALLON, Pierre-Antoine THOUVENIN and Yvan WALLY during a student project conducted under the supervision of Prof. Nicolas Dobigeon at INP-ENSEEIHT.

If you use this GUI and the BLU algorithm, please cite the original paper in your work:

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Thanks.

## Table Of Contents

I- Launch Unmixing Toolbox .....	3
II- Analysis Process .....	4
II-1- Run data analysis .....	4
II-2-a) First estimation .....	4
II-2-b) Bayesian estimation.....	7
II-2- Run Image Analysis .....	9
II-2-a) First estimation .....	9
II-2-b) Bayesian estimation.....	12
III- Particular Graphical Units .....	14
III-1- Interfaces .....	14
III-2- Image Analysis – Menu Bar .....	15
III-2-a) “Plot spectra” tab.....	15
III-2-b) “Sub-analysis” tab.....	17
IV- Exported Results .....	18
IV-1- Data Analysis.....	18
IV-1-a) .txt file .....	18
IV-1-b) .mat file.....	19
IV-2- Image Analysis .....	20
IV-2-a) .txt file.....	20
IV-2-b) .mat file.....	21

Figure 1 : Openning window .....	3
Figure 2 : Data analysis interface .....	4
Figure 3 : File tab .....	4
Figure 4 : Load file .....	5
Figure 5 : File loaded .....	5
Figure 6 : Pop up-menu method of first estimation.....	5
Figure 7 : Launching buttons .....	5
Figure 8 : Plot results.....	6
Figure 9 : Parameters' pannel .....	7
Figure 10 : MCMC iterations .....	7
Figure 11 : Plot results from Bayesian estimation.....	8
Figure 12 : Image analysis interface .....	9
Figure 13 : File tab .....	9
Figure 14 : File Loaded.....	9
Figure 15 : Plot results.....	10
Figure16 : Launching buttons .....	10
Figure 17 : Parameters' pannels.....	11
Figure 18 : Plot results.....	11
Figure 19 : Pop up-menu method's choose .....	12
Figure 20 : MCMC iterations .....	12
Figure 21 : Bayesian estimation plot results .....	13
Figure 22 : Back button .....	14
Figure 23 : Close button .....	14
Figure 24 : Displaying parameters.....	14
Figure 25 : Plot spectra tab .....	15
Figure 26 : Pot pixel figure.....	15
Figure 27 : Plot all spectra figure.....	16
Figure 28 : Image rescaled.....	17
Figure 29 : Area loaded .....	17
Figure 30 : txt file results.....	18
Figure 31 : mat file results.....	19
Figure 32 : txt file image results .....	20
Figure 33 : mat file image results .....	21

## I- Launch Unmixing Toolbox

To launch the Unmixing Toolbox Graphic Interface, you have to compile the file `Main_interface.m` with MATLAB interface.

The first interface makes you choose between two options:

- Data Analysis: to unmix data from .txt or .mat files.
- Image Analysis: to unmix data from .envi or .mat images files.

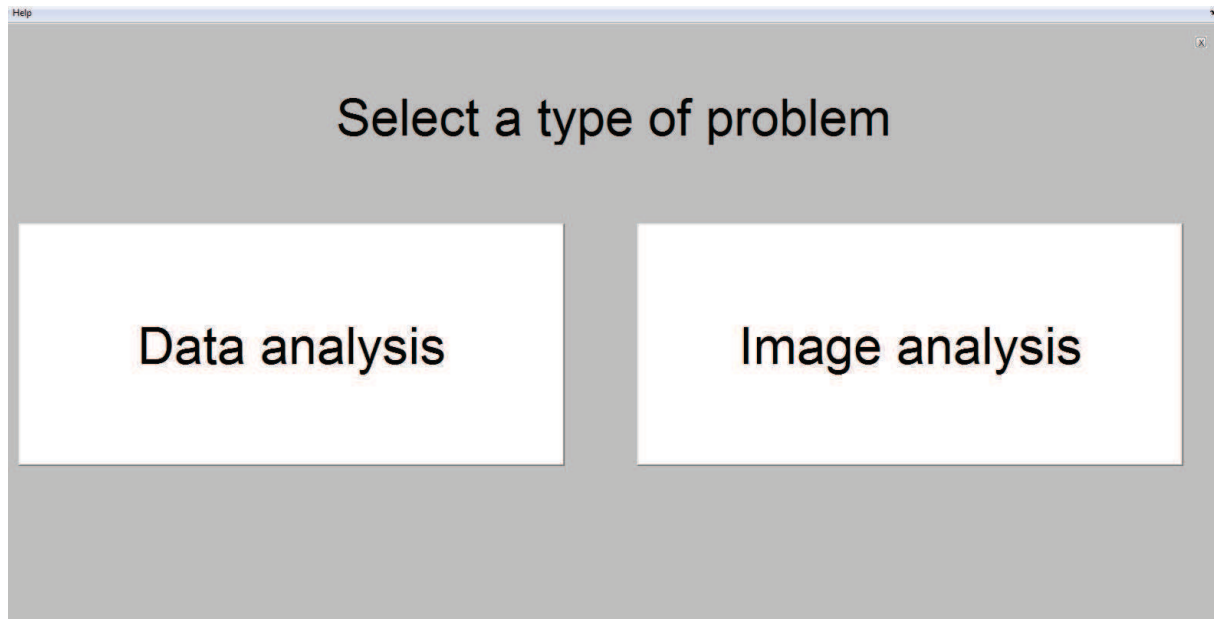


Figure 1 : Opening window

## II- Analysis Process

### II-1- Run data analysis

#### II-2-a) First estimation

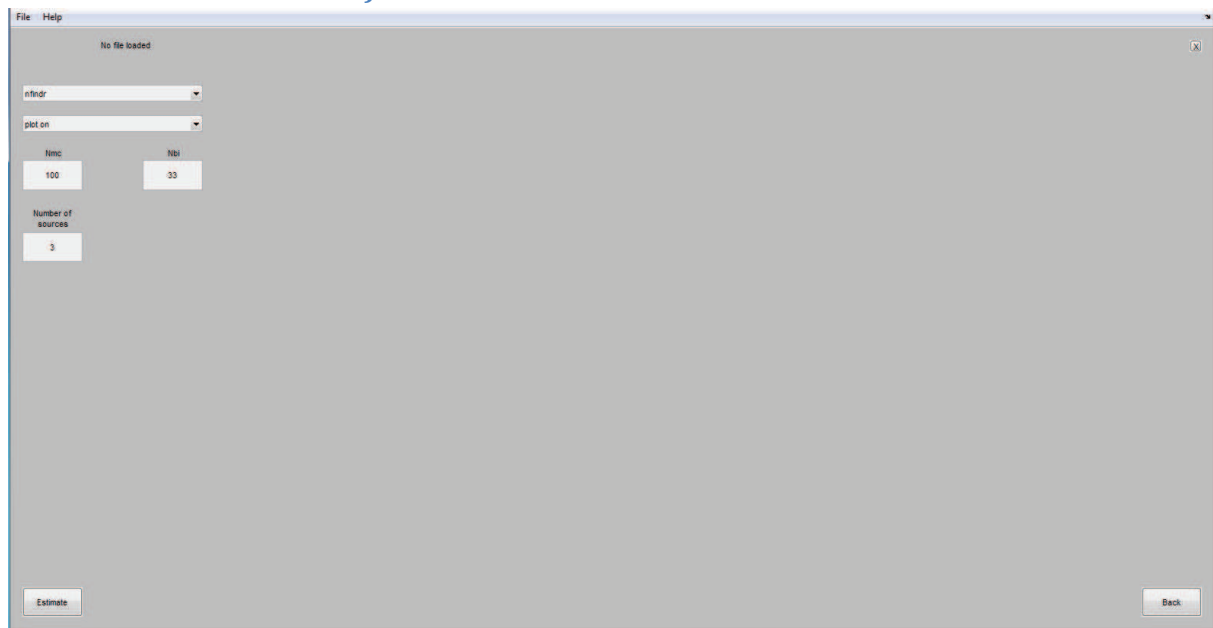


Figure 2 : Data analysis interface

First, the file which contains the data to unmix needs to be uploaded inside the interface.

While you can see this message: “No file loaded”, no data has been uploaded then estimation will not work.

If you load a .mat file, the image of interest inside the variable needs to be called “Y”, while this is not true, MATLAB displays an error message.

You may upload the file by clicking on the “file” tab and on “load file” tab from the menu bar on the interface as shown in Figure 3 and then choose the path of your file and its name as shown in Figure 4.

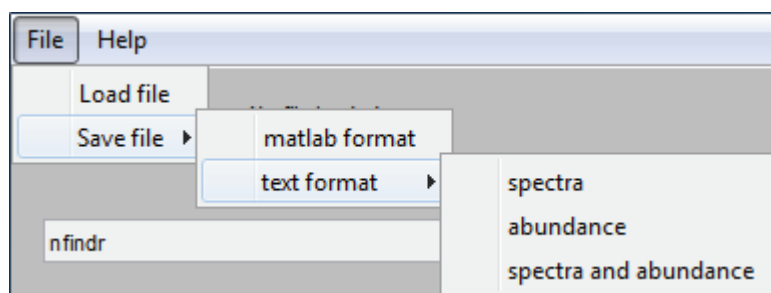


Figure 3 : File tab

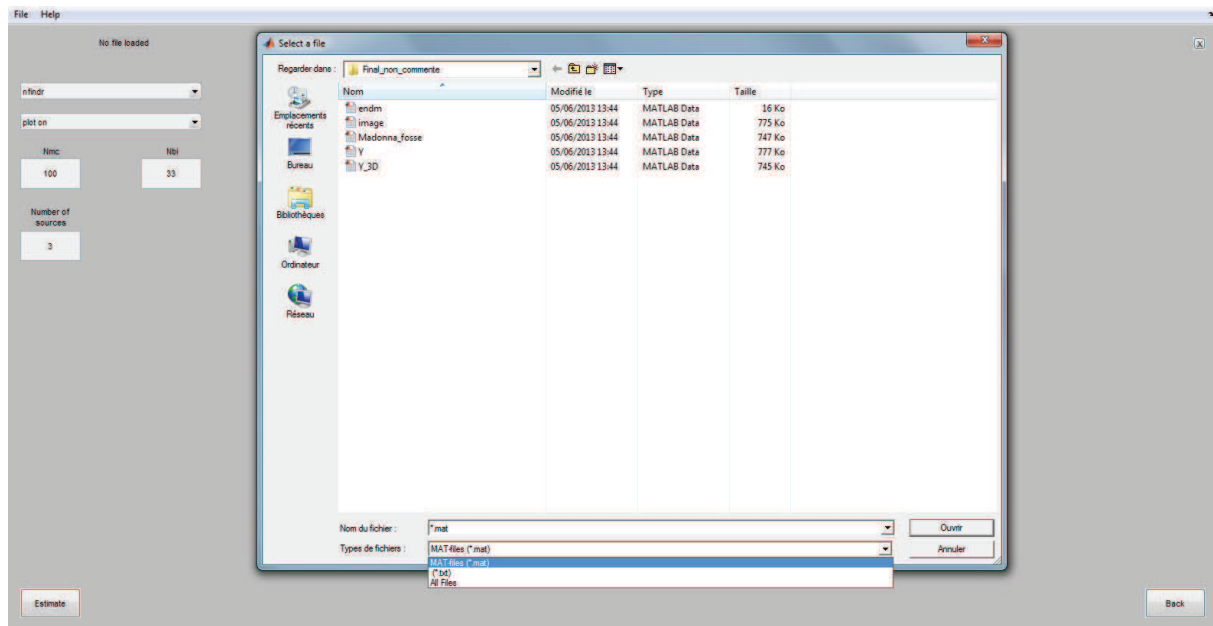


Figure 4 : Load file

Since “[Filename].txt is uploaded” or “[Filename].mat loaded” isn’t written on the left high corner, the upload has not been made, as shown in Figure 5.

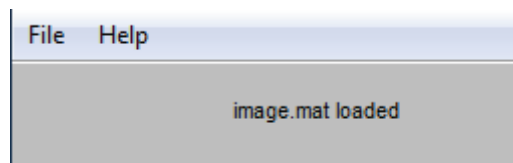


Figure 5 : File loaded

Don’t forget to choose the number of spectra you are searching in the field reserved and your estimating method in the following pop-up menu:

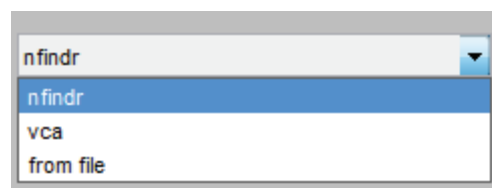


Figure 6 : Pop up-menu method of first estimation

When this is done, you may launch the first estimation of the spectra from the data pushing up the button “Estimate” as shown in Figure 7.

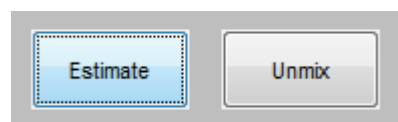


Figure 7 : Launching buttons

When the results are plot (Figure 8) , the button “Bayesian Unmixing” appears and allows you to refine the estimation given by vca or nfindr spectra estimations.

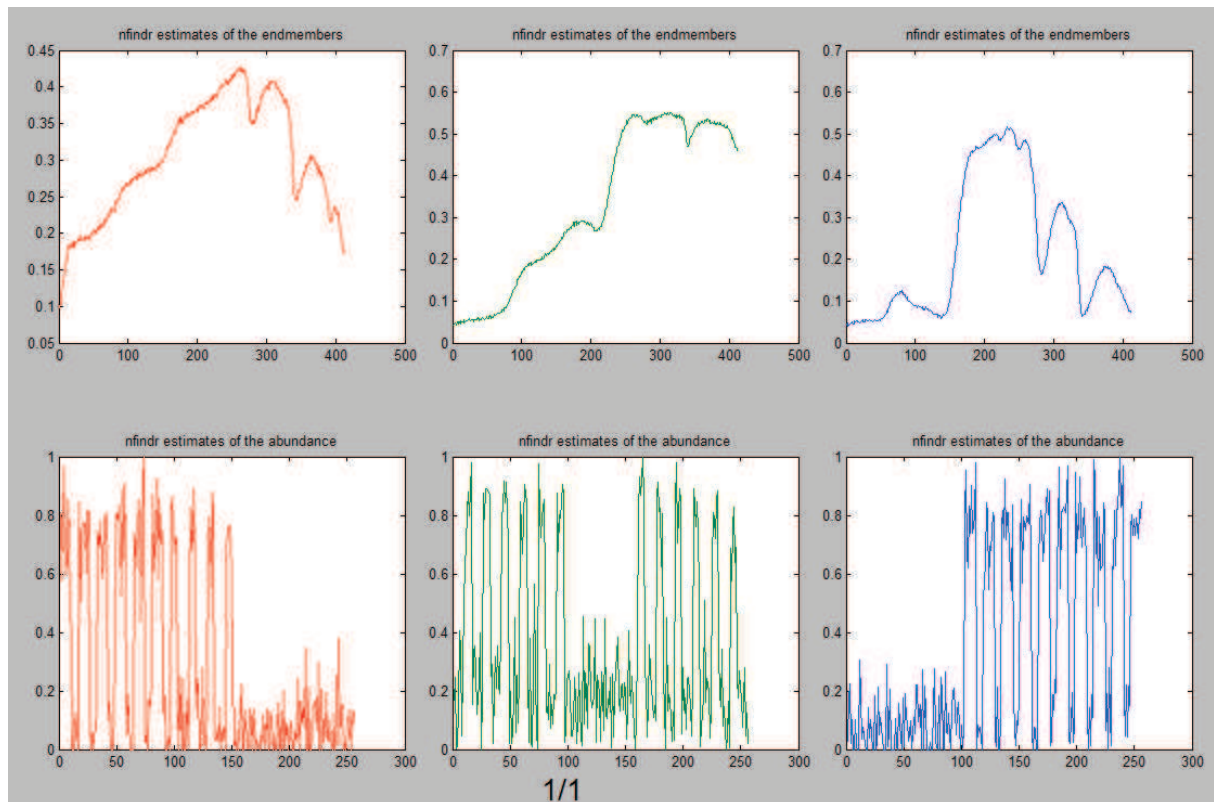
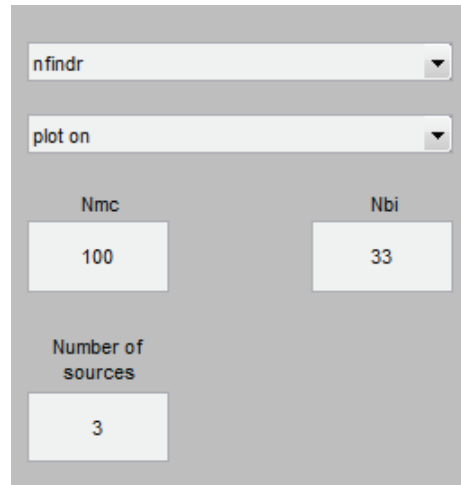


Figure 8 : Plot results

You might need to export the results of the first estimation, so in this case the exportation of the results works like after theII-2-b) Bayesian estimation by clicking on the submenu “Save file” under the menu bar “File”.

## II-2-b) Bayesian estimation



The Parameters' pannel contains the following settings:

- nfindr**: A dropdown menu.
- plot on**: A dropdown menu.
- Nmc**: A text box containing the value **100**.
- Nbi**: A text box containing the value **33**.
- Number of sources**: A text box containing the value **3**.

Figure 9 : Parameters' pannel

“Nbi” indicates the minimum number of iterations before registering the iterations. “Nmc” indicates the number of iterations of Monte-Carlo-Markov-Chains algorithm which needs a least number of iterations to converge (Figure 9).

Intermediate results are plot: the last estimation of spectra is plot in the left axes field and in the second field, you can see the cloud of spectra contained in the image in the R-1 dimension space of interest of the spectra. So you may watch the evolution of the convergence of the algorithm (Figure 10).

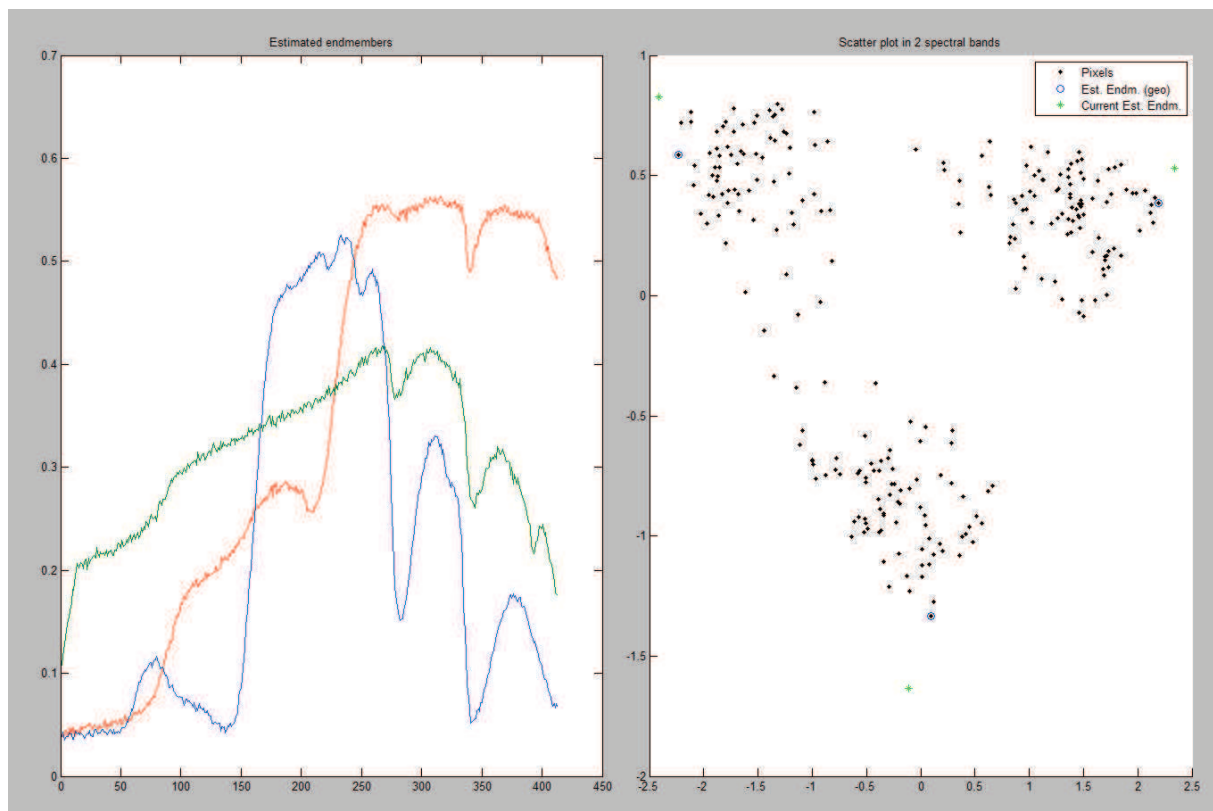


Figure 10 : MCMC iterations



When the waitbar is done, the results are plot in the interface. The three first spectra estimated can be seen with their abundances behind, and the others can be seen by clicking on the arrows on the side of the figures. You might watch the spectra with one plot per spectrum.

At the end of the Bayesian estimation, the same results than after the first estimation are plot but with the results refined by Bayesian estimation (Figure 11).

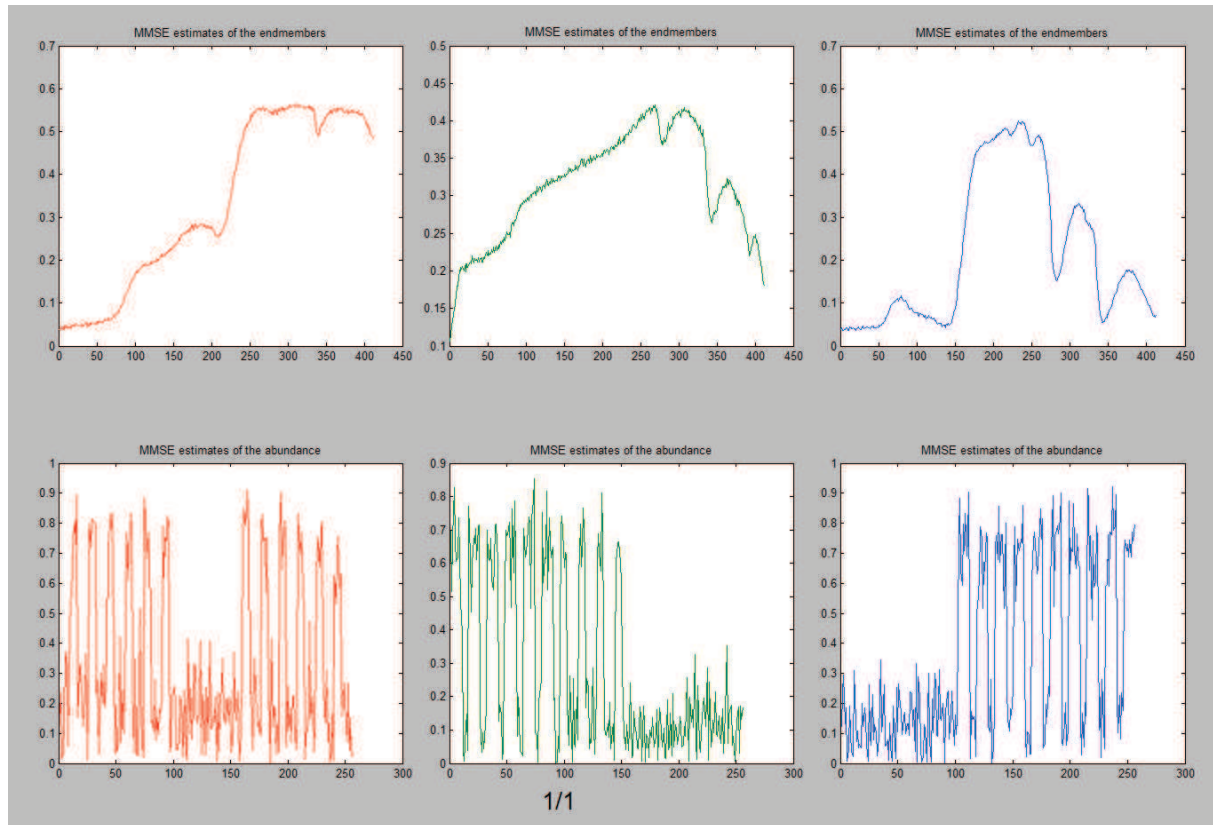


Figure 11 : Plot results from Bayesian estimation

You may export data results in .txt or .mat files with the details in part IV-1- Data Analysis.

## II-2- Run Image Analysis

### II-2-a) First estimation

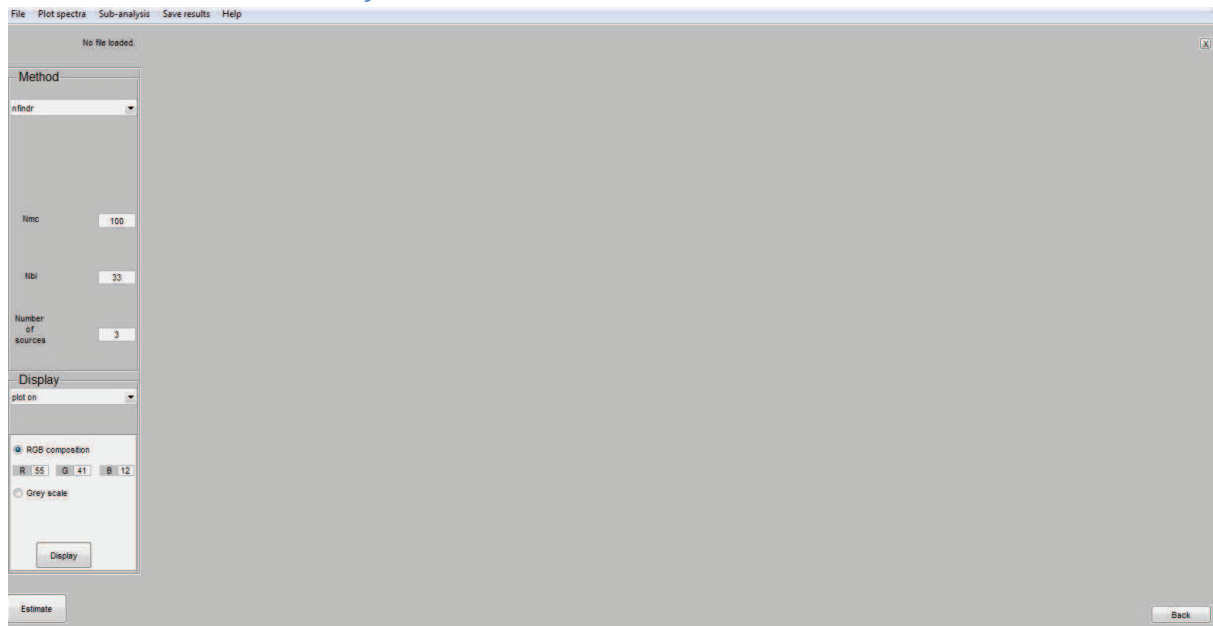


Figure 12 : Image analysis interface

First, the file which contains the image to unmix needs to be loaded inside the interface as shown in Figure 13.

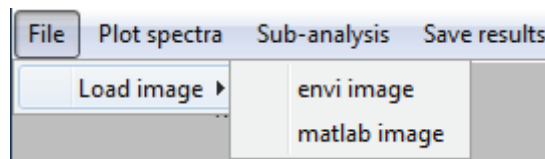


Figure 13 : File tab

While you can see this message: “No file loaded”, no data has been loaded then estimation will not work.

If you load a .mat file, the image of interest inside the variable needs to be called “Y”, while this is not true, MATLAB displays an error message.

Since “[Filename].envi is loaded” or “[Filename].mat is loaded” isn’t written on the left high corner, the load has not been made (Figure 14).

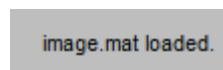


Figure 14 : File Loaded

When the file is loaded, you can visualize the image (Figure 15) and choose a part of it or watch spectra pixel by pixel as reported in III-2- Image Analysis – Menu Bar.

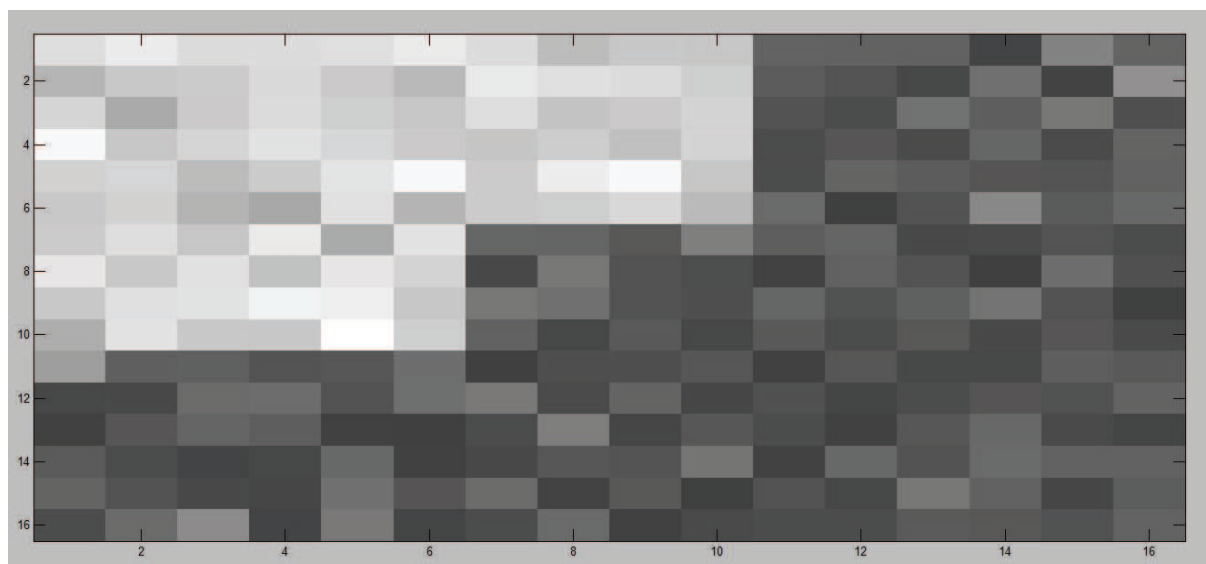


Figure 15 : Plot results

When this is done, you may launch the first estimation of the spectra from the data.



Figure16 : Launching buttons

The parameters associated with first estimation are the pop-up menu which chooses the method of estimation and the text field which determines the number of spectra you need to find. The other parameters have an impact only on Bayesian estimation.

Figure 17 : Parameters' pannels

Now you can launch the estimation by clicking on the button “Estimate” on the left bottom corner of the interface (Figure16).

When the wait bar is done, the results are plot in the interface. The three first spectra estimated can be seen with their map of abundances behind, and the others can be seen by clicking on the arrows on the side of the figures. You might watch the spectra with one plot per spectrum.

More details about the display parameters are available in part III-1- Interfaces.

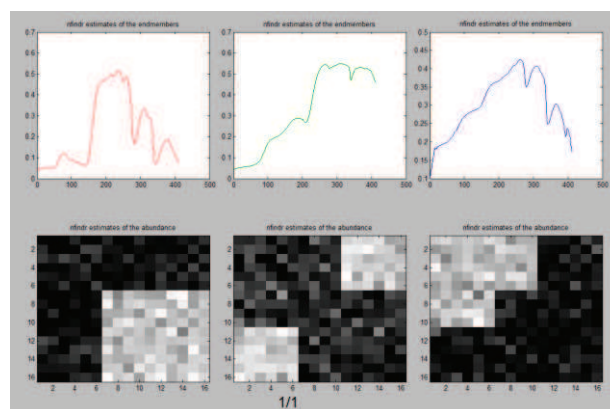


Figure 18 : Plot results

## II-2-b) Bayesian estimation

When the results are plot, the button “Bayesian Unmixing” appears and allows you to refine the estimation given by vca, nfindr spectra estimations, selected spectra or imported from file spectra (Figure 19).

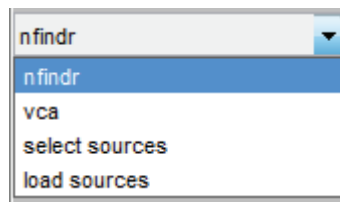


Figure 19 : Pop up-menu method's choose

“Nbi” indicates the minimum number of iterations before registering the iterations. “Nmc” indicates the number of iterations of Monte-Carlo-Markov-Chains algorithm which needs a least number of iterations to converge (Figure 20).

Intermediate results are plot: the last estimation of spectra is plot in the left axes field and in the second field, you can see the cloud of spectra contained in the image in the R-1 dimension space of interest of the spectra. So you may watch the evolution of the convergence of the algorithm (Figure 20).

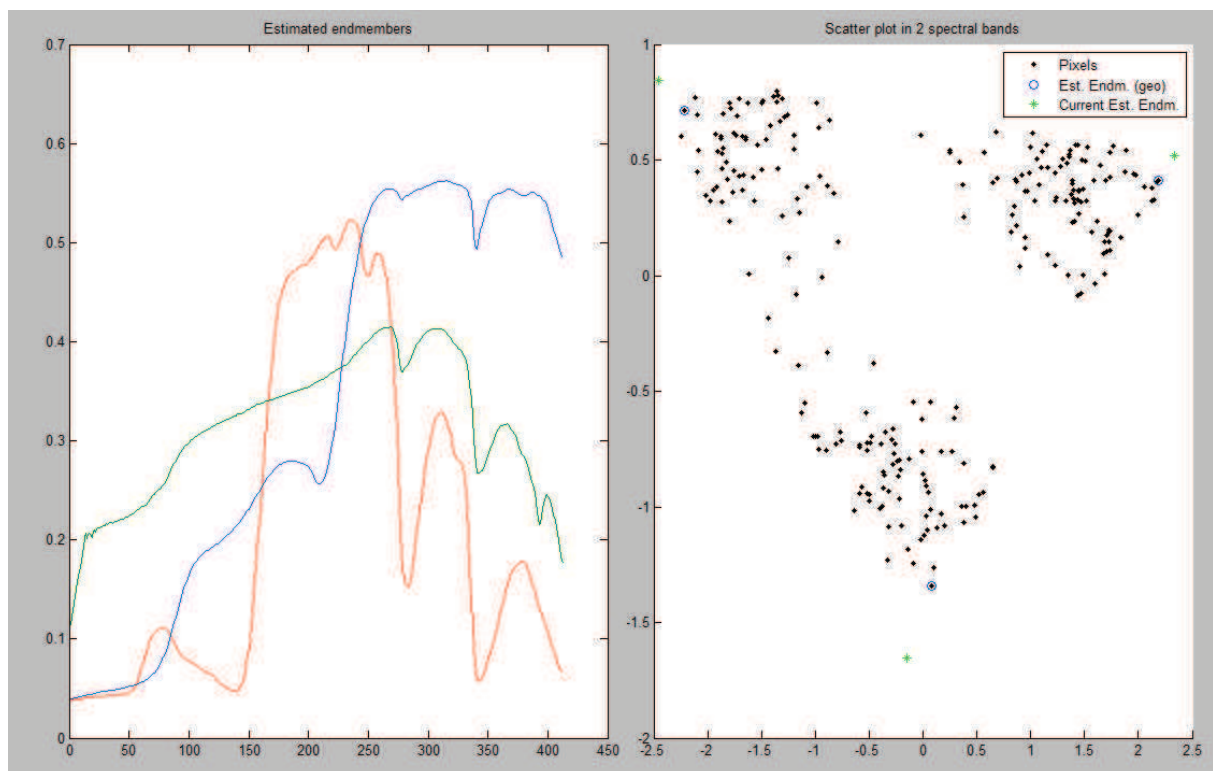


Figure 20 : MCMC iterations

At the end of the Bayesian estimation, the same results than after the first estimation are plot but with the results refined by Bayesian estimation (Figure 21).

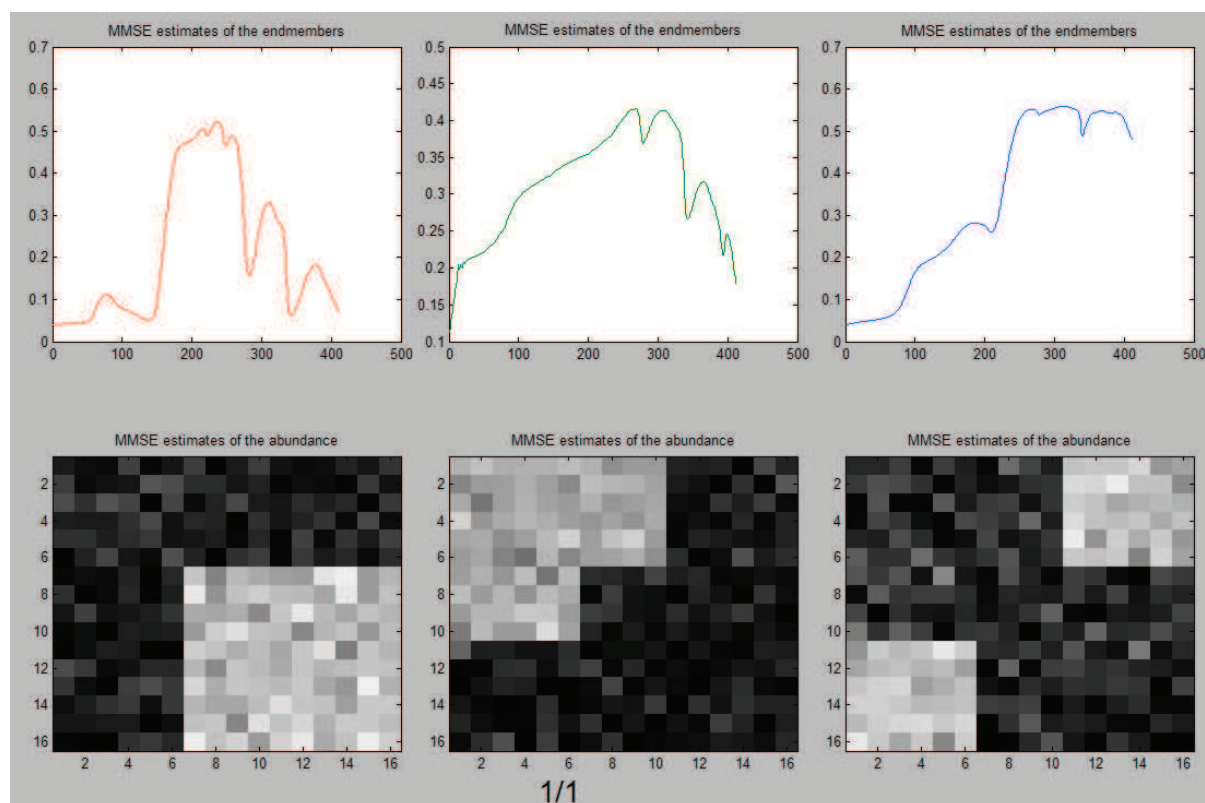


Figure 21 : Bayesian estimation plot results

You may export data results in .txt or .mat files with the detail in part IV-2- Image Analysis.

## III- Particular Graphical Units

### III-1- Interfaces

Two buttons may be used in the interfaces shown in Figure 22 and Figure 23.

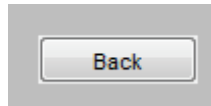


Figure 22 : Back button



Figure 23 : Close button

“Back” allows you to come back to the main interface where you choose the type of your data to unmix and resets all the algorithms.

“X” allows you to close the whole interface.

In the image analysis interface, you may make some arrangements of the displaying of the image to unmix (Figure 24).

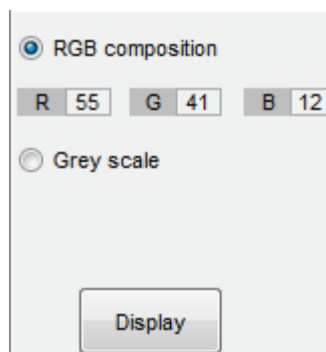


Figure 24 : Displaying parameters

First, you should choose between “RGB composition” or “Grey scale” that chooses the display mode (B&W or with colors), then choose your parameters of the RGB composition or the scale in grey tones and finish by pushing “Display” button that will display the image.

## III-2- Image Analysis – Menu Bar

### III-2-a) “Plot spectra” tab

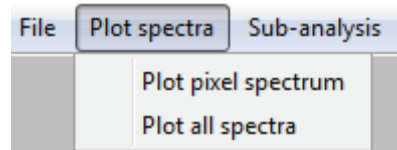


Figure 25 : Plot spectra tab

“Plot pixel spectrum” allows you to choose a pixel inside the image to unmix displayed and display its spectrum:

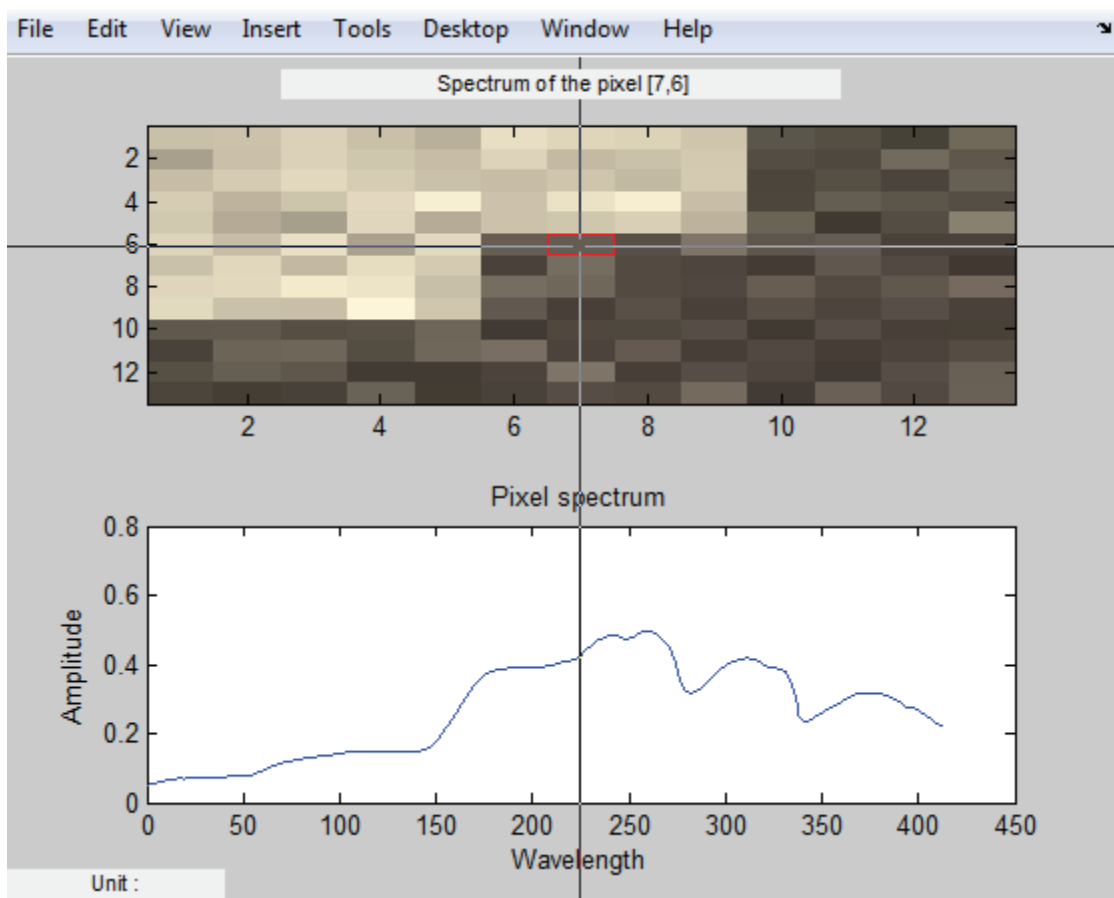


Figure 26 : Pot pixel figure

You can avoid the cursor by clicking on right mouse button.



“Plot all spectra” plots all the spectra of each pixel in the same axis field (Figure 27).

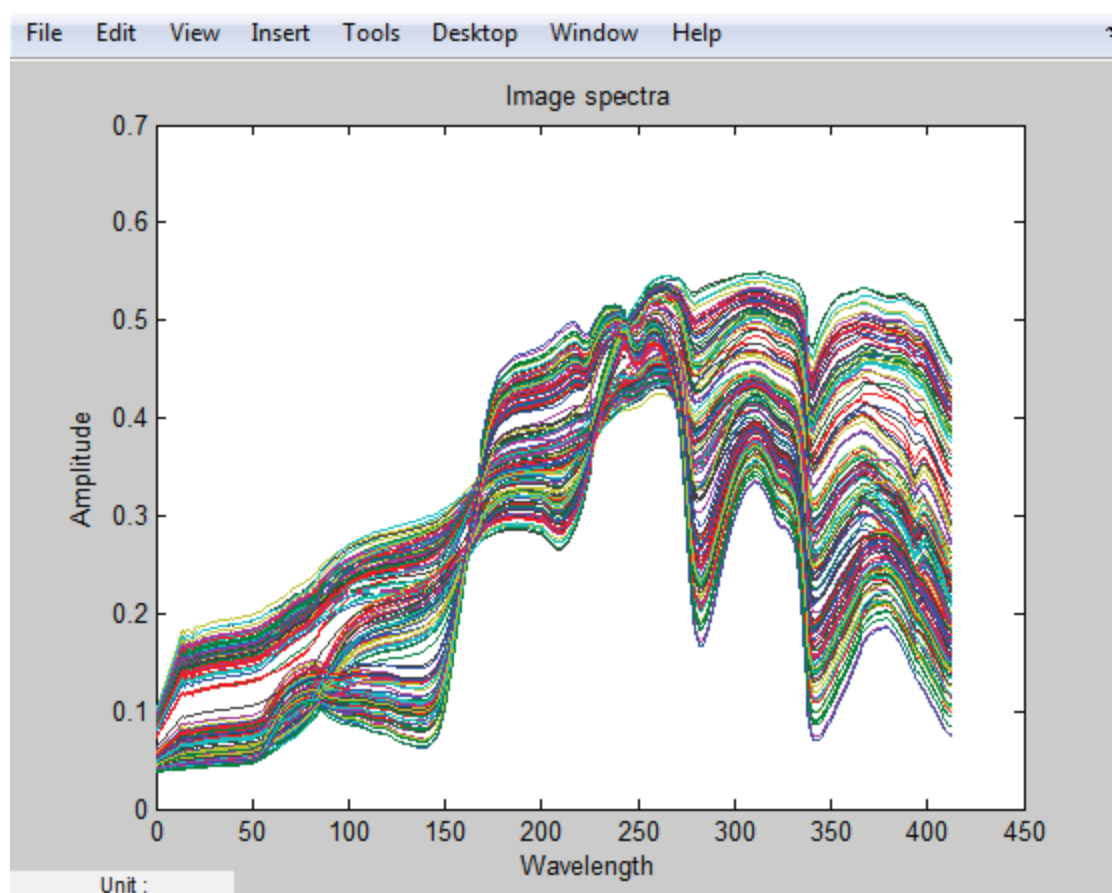


Figure 27 : Plot all spectra figure

### III-2-b) "Sub-analysis" tab

"Select area" allows you to rescale the image to analyze by repairing the area of interest from top left corner to bottom right corner with two left mouse clicks.

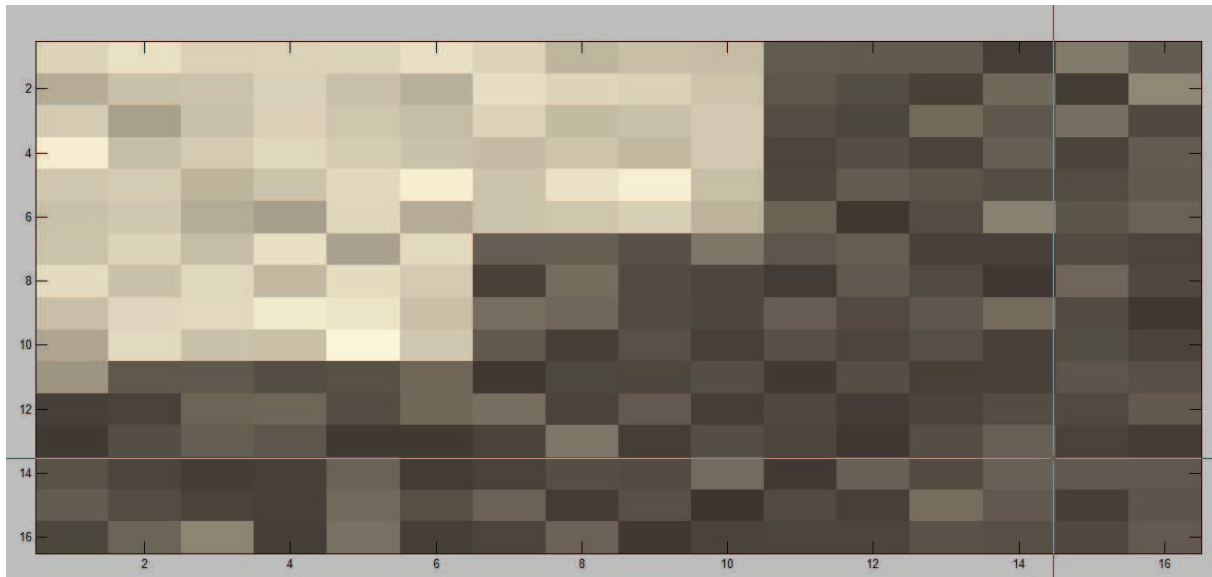


Figure 28 : Image rescaled

You may cancel your selection in « sub-analysis » tab and choose « Cancel selection ».

Moreover, while you do not see Figure 29 in top left corner of the interface written, you lack one or more corners of the area to select.

Area loaded.

Figure 29 : Area loaded

## IV- Exported Results

### IV-1- Data Analysis

#### IV-1-a) .txt file

By clicking on “Save abundances”, “Save spectra” or “Save both”, you may export by .txt file the data mentioned above.

Here is an example of spectra and abundances .txt files (Figure 30) extracted by the file unmixed above in part II-1- Run data analysis.

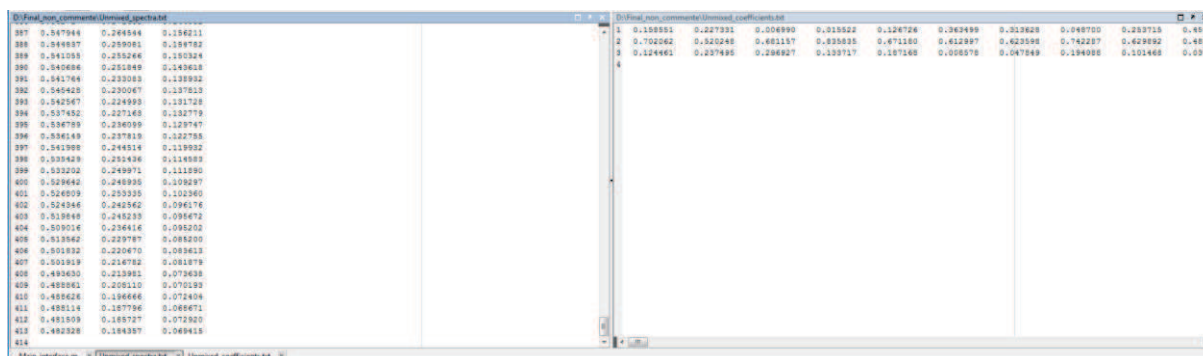


Figure 30 : txt file results

**Remark:** Dimensions of spectra matrix [lines\*columns]:  $[P \times R]$ . Dimensions of abundance matrix:  $[R \times L]$ . Where dimensions of matrix to unmix:  $[L \times P]$  and R the number of sources chosen by the user.

You may find a log file at the same path with some informations about the exported results and the algorithm.

#### IV-1-b) .mat file

By clicking on “Save results” and then “matlab format”, you may export by .mat file the data mentioned above.

Here is an example of spectra and abundances .txt files (Figure 31) extracted by the file unmixed above in part II-1- Run data analysis.

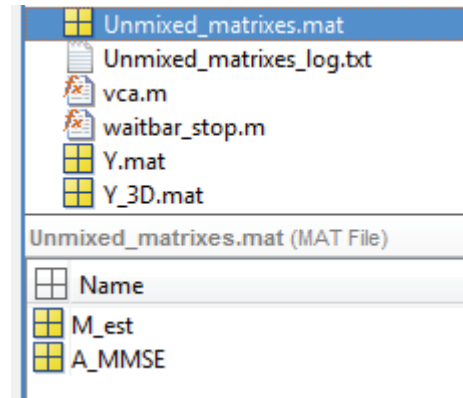


Figure 31 : mat file results

Remark: Dimensions of spectra matrix  $M\_est$  [lines\*columns]:  $[P \times R]$ . Dimensions of abundance matrix  $A\_MMSE$ :  $[R \times L]$ . Where dimensions of matrix to unmix:  $[L \times P]$  and  $R$  the number of sources chosen by the user.

## IV-2- Image Analysis

### IV-2-a) .txt file

By clicking on “Save abundances”, “Save spectra” or “Save both”, you may export by .txt file the data mentioned above.

Here is an example of spectra and abundances .txt files (Figure 32) extracted by the file unmixed above in part II-2- Run Image Analysis.

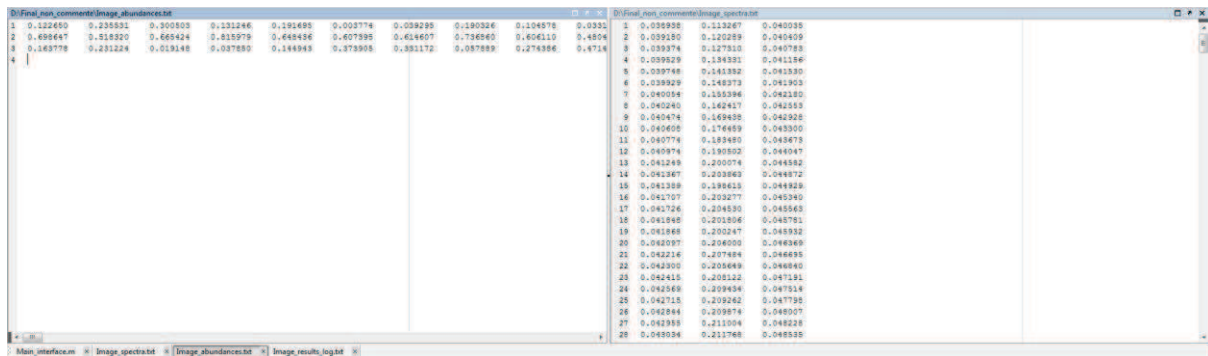


Figure 32 : txt file image results

**Remark:** Dimensions of spectra matrix [lines\*columns]:  $[L \times R]$ . Dimensions of abundance matrix:  $[R \times (P \times B)]$ . Where dimensions of matrix to unmix:  $[L \times P \times B]$  and R the number of sources chosen by the user.

You may find a log file at the same path with some informations about the exported results and the algorithm.

#### IV-2-b) .mat file

By clicking on “Save results” and then “matlab format”, you may export by .mat file the data mentioned above.

Here is an example of spectra and abundances .txt files (Figure 33) extracted by the file unmixed above in part II-2- Run Image Analysis.

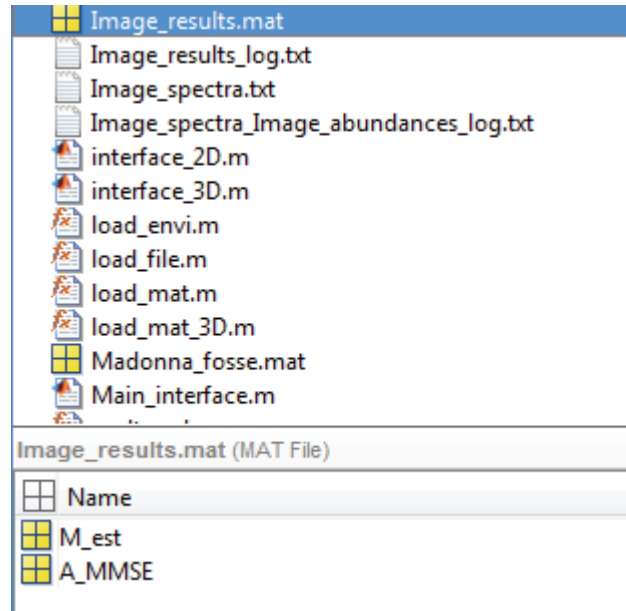


Figure 33 : mat file image results

Remark: Dimensions of spectra matrix A\_MMSE [lines\*columns]:  $[B \times R]$ . Dimensions of abundance matrix M\_est:  $[R \times (L \times P)]$ . Where dimensions of matrix to unmix:  $[L \times P \times B]$  and R the number of sources chosen by the user.