

SMolESY-select

USER'S GUIDE

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1. Intro - about the SMoESY-select

SMoESY-select is a freely available algorithm implemented into a graphical user interface (GUI) created in MATLAB programming suite (2019b/update 7, Mathworks). SMoESY-select provides the fully automated assignment/NMR signals alignment/relative quantification of 22 serum/plasma metabolites. The software is built on a fully automated supervised workflow, namely, the user is able to evaluate the results of each assignment/alignment step and directly export the relative quantification (i.e. integral values in arbitrary units) of the metabolites into a report (.csv format). All integrals are normalized to **one** proton (^1H), however, the integral values of five metabolites (i.e. creatinine, tyrosine, phenylalanine, choline, histidine) are produced by the integration of their corresponding *smoothed* signals by default. For each assigned ^1H -NMR spin system, user is able to see the corresponding metabolite's chemical structure as well as the chemical groups where the assigned NMR signal(s) belong to. Moreover, the GUI provides the automated alignment of all assigned spin systems ^1H -NMR signals for both standard 1D NMR and SMoESY spectra. Overall, SMoESY-select is a user friendly interface

2. Preparing spectra folder

1D-¹H-NMR spectra (e.g. 1D-NOESY) should be in one folder as indicated in **Fig. 1**. Under each spectrum title (e.g. Spectrum 1, Spectrum 2 in **Fig. 1**), the experiment folder should be numerical (e.g. 1 in **Fig. 1**). Please **ensure that only 1 experiment folder exists**.

Please note that **no non-spectral folders should be inside the parent NMR data folder**.

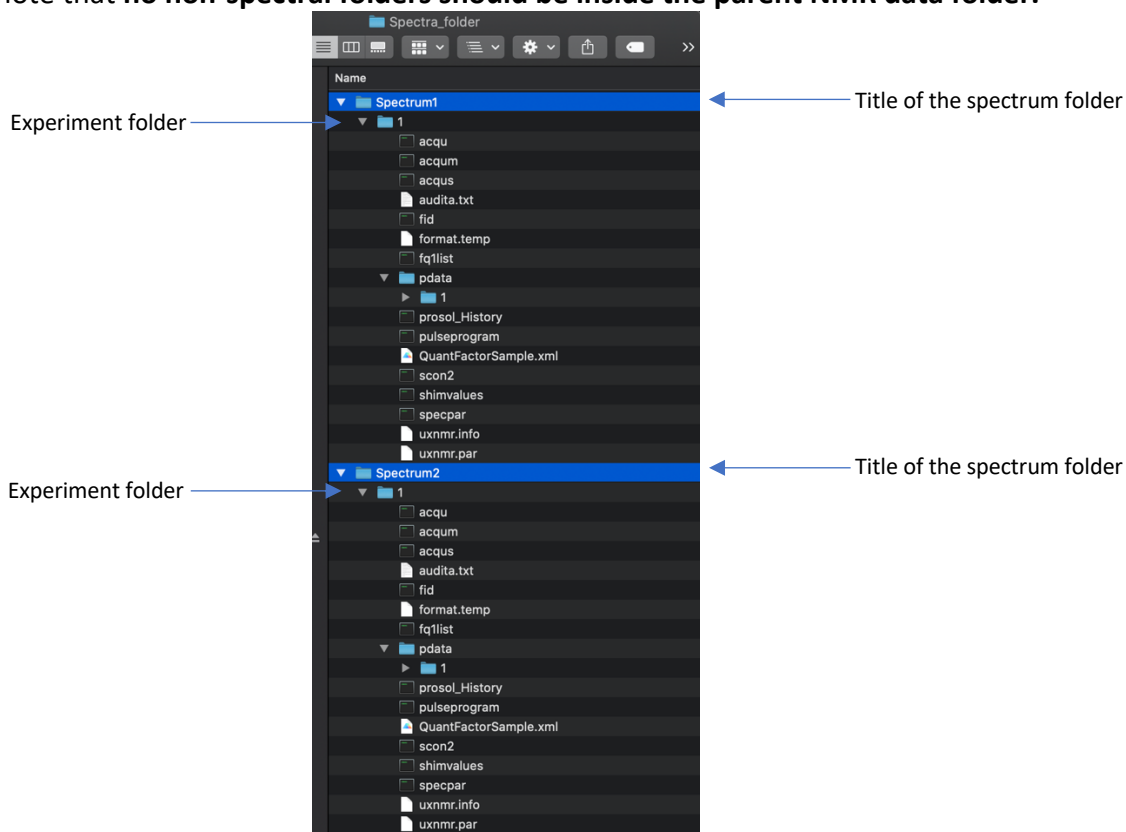


Figure 1. Spectra containing folder; In this example the spectra folder contains two 1D-NOESY plasma spectra with the depicted structure.

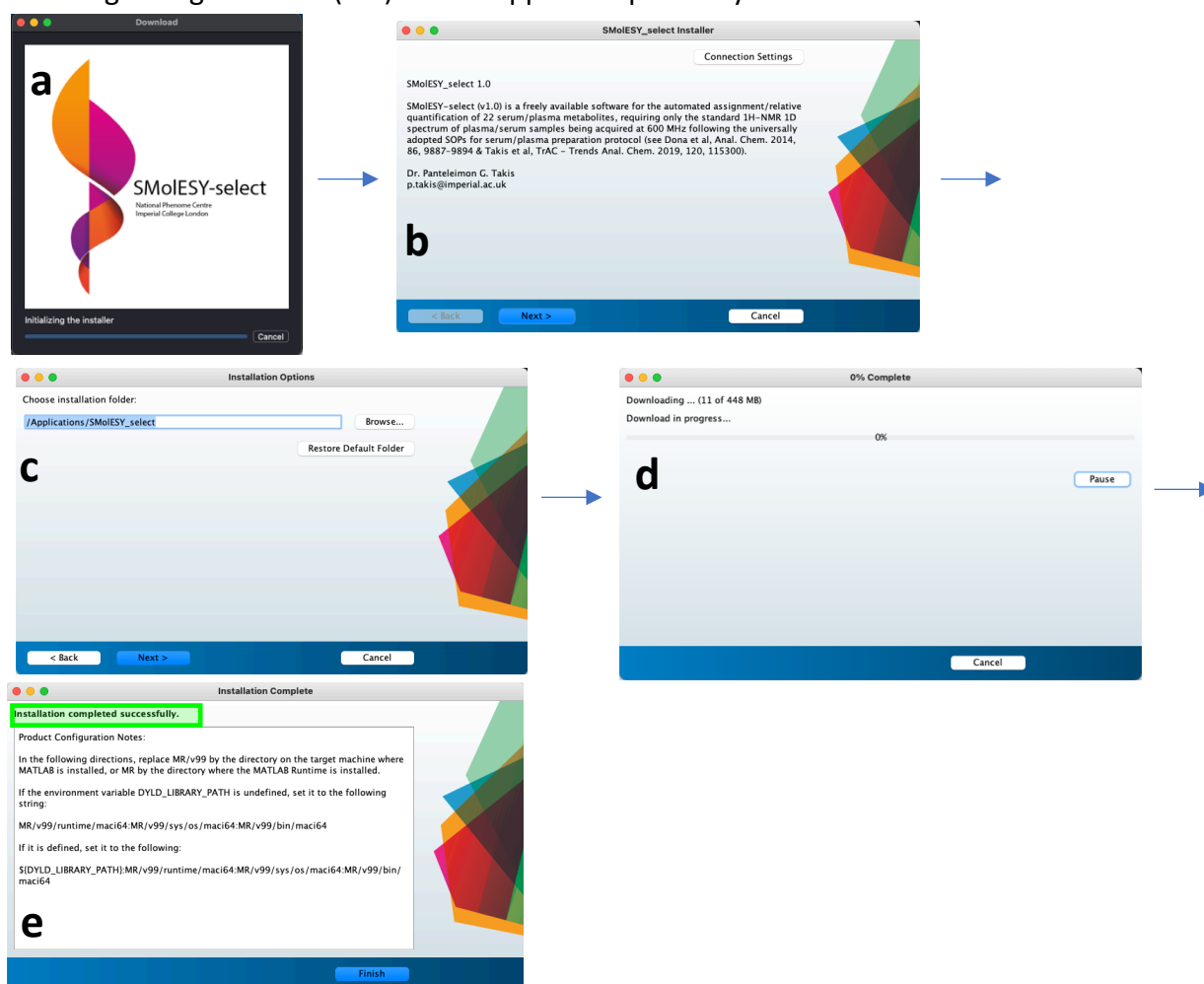
3. Preparing output folder

Before running the GUI, the user should create a folder, where all results will be exported by the GUI.

4. Installing/Running SMolESY-select

i) Installing/running SMolESY-select by the compiled file for MacOS

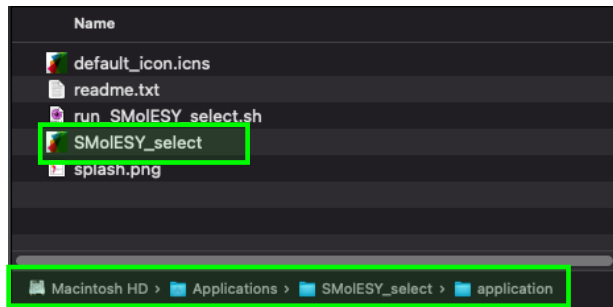
After downloading the software folder from <https://github.com/pantakis/SMolESY-select>, in the folder “Compiled_for_MAC_OS”, double click the file “SMolESY-select_installer.app”. Then follow the on-screen instructions (internet connection is required) for downloading/installing the MATLAB RUNTIME modules in order to run the software. The following dialog windows (a-e) should appear sequentially on screen:



→ In panel c, please ensure that the installation folder is: **/Applications/SMolESY_select**

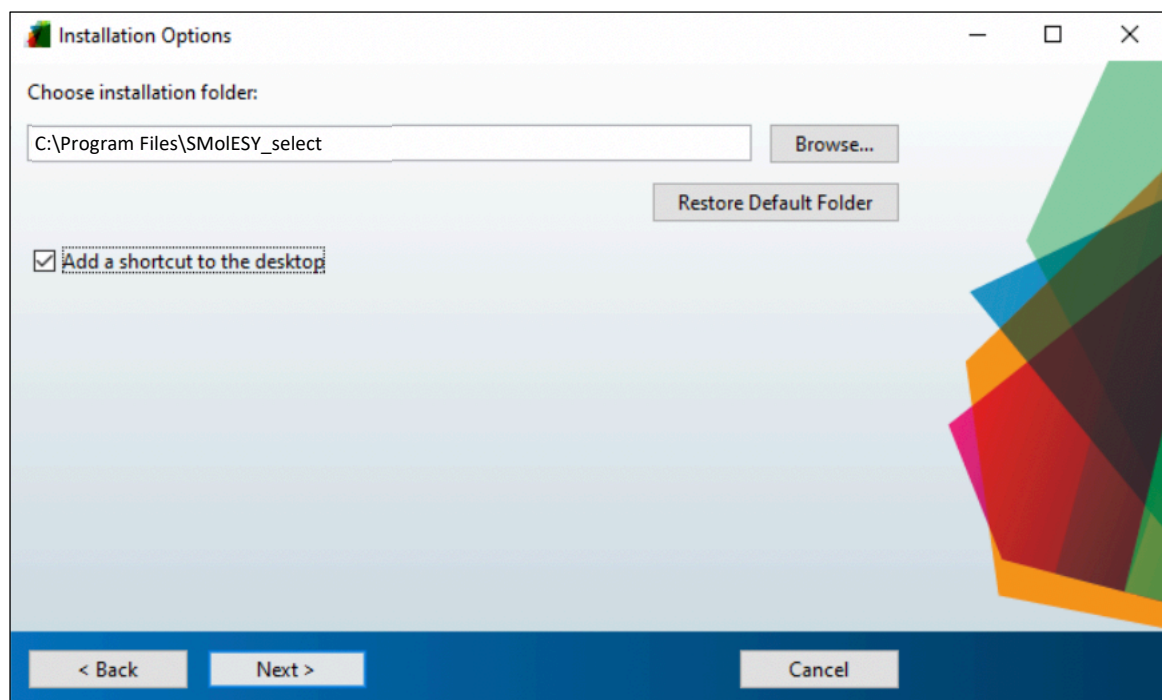
→ In panel e, ignore the Product Configuration Notes, once the installation is completed successfully.

→ To launch the application please double-click the “SMolESY-select.app”, which should be located in the folder: “**../Applications/ SMolESY_select /application**”, as you could see below:



ii) Installing/running [SMoESY-select](https://github.com/pantakis/SMoESY-select) by the compiled file for Windows

After downloading the SMoESY-select folder from <https://github.com/pantakis/SMoESY-select>, in the folder "Compiled for Windows", double click the file "SMoESY-select_installer.exe". Then follow the on-screen instructions (internet connection is required) for downloading/installing the MATLAB RUNTIME modules in order to run the toolbox as indicated above (i.e. for Mac OS). Please ensure that you create a desktop shortcut of the software in order to launch it as shown below:



5. Loading ^1H -NMR spectra

Pressing the button “**Define NMR spectra folder**”, a dialog window opens (**Fig. 2**) in order to define the parent folder containing all NMR spectra to be loaded into the SMoIESY-select.

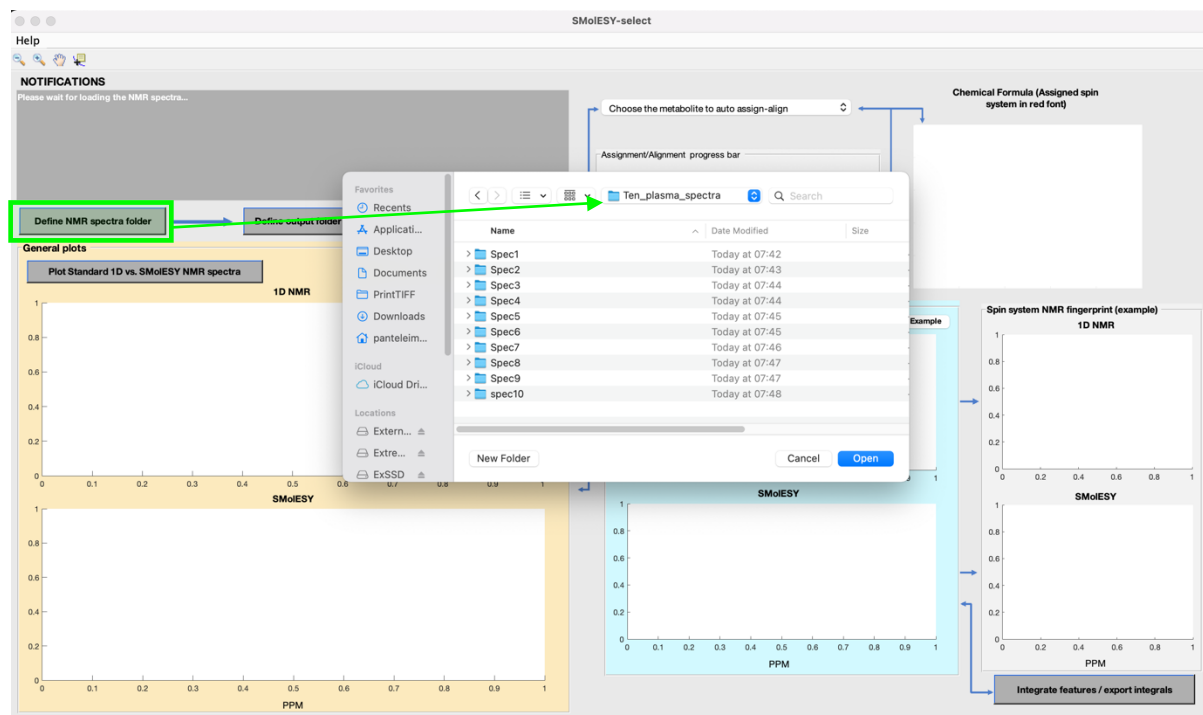


Figure 2.

→NOTE 1

The “NOTIFICATIONS” box, informs the user for the problematic (**Fig. 3a**) or successful (**Fig. 3b**) reading/loading of the NMR data by the software.

a NOTIFICATIONS

ERROR: NMR real and/or imaginary data cannot be found or read correctly. Please check the structure of the NMR spectra containing folder, which should be as indicated in the User's Guide file.
Reminder: Imaginary spectral data is needed to run SMoIESY-select software.

b NOTIFICATIONS

NMR real/imaginary data is successfully read and loaded on the SMoIESY-select software.
Please define the [Output_folder].

Figure 3.

6. Define output folder

Pressing the button “ **Define output folder** ”, a dialog window opens (**Fig. 4**) in order to define the output folder where all processing, SMolESY data etc. will be exported by SMolESY-select.

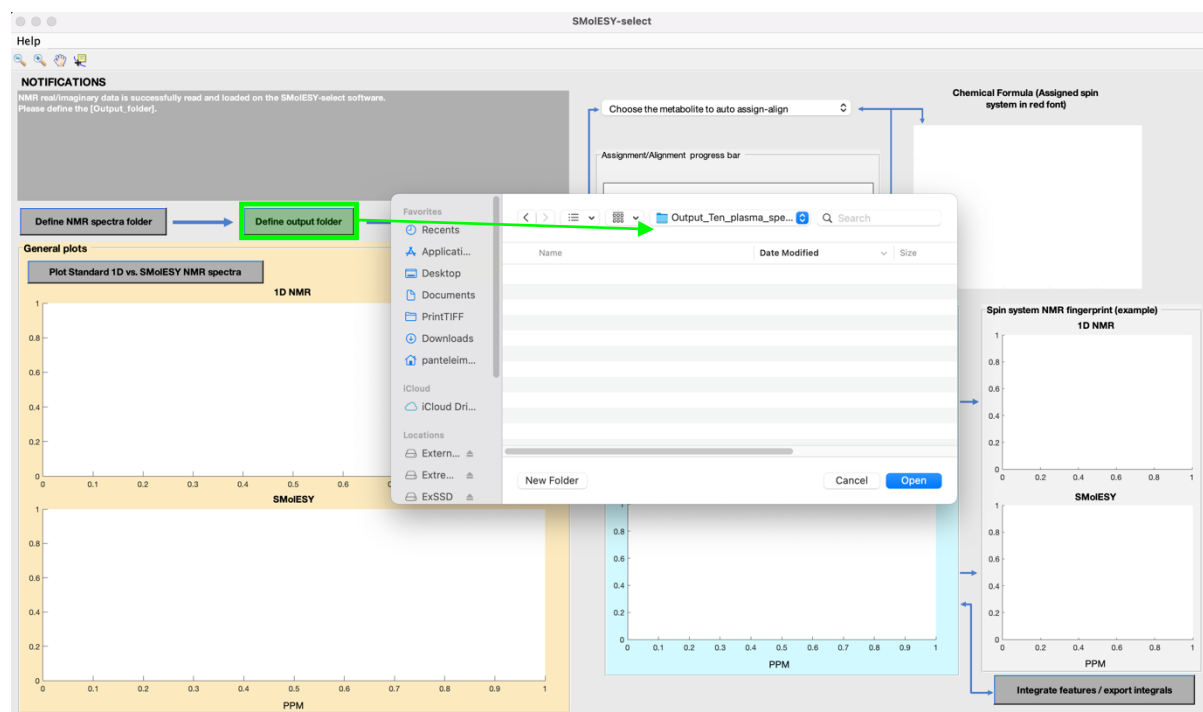


Figure 4.

7. Converting ^1H -NMR imaginary data into SMoIESY

Pressing the button “ **Transform to SMoIESY** ” (Fig. 5), the imaginary spectral data of the loaded ^1H -NMR (e.g. 1D-NOESY) spectra will be transformed into the SMoIESY.

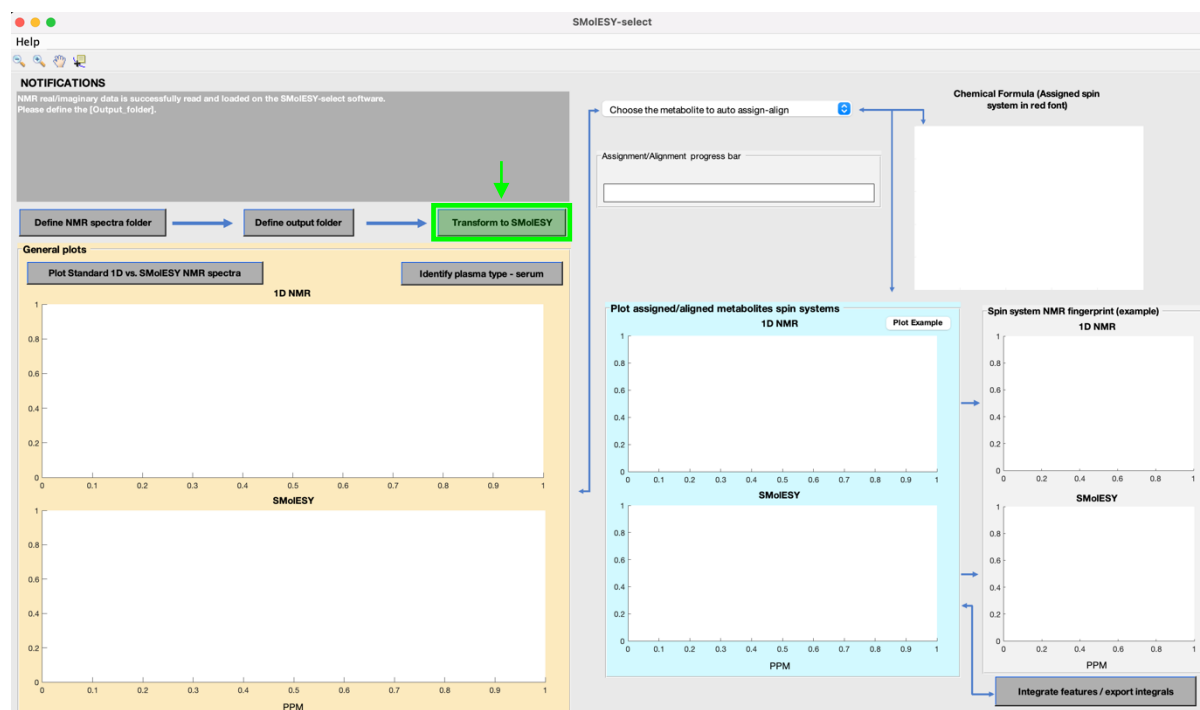


Figure 5.

→NOTE 1

The “NOTIFICATIONS” box, informs the user for any errors (Fig. 6a) or the successful (Fig. 6b) transformation of the ^1H -NMR data into SMoIESY.

a NOTIFICATIONS




ERROR: The transformation of the NMR spectra cannot be completed.

b NOTIFICATIONS

The transformation of the NMR spectra is completed. You could proceed with plotting the transformed spectra (mandatory step).

Figure 6.

8. Plotting ^1H -NMR and SMolESY data (mandatory step)

User should press the button “ **Plot Standard 1D vs. SMolESY NMR spectra** ” that plots both 1D ^1H -NMR and SMolESY data. This is a mandatory step since the algorithm calibrates the data while plotting them at Glucose anomeric proton. Please note that both ^1H -NMR and SMolESY data are plotted without being calibrated (**Fig. 7**). Moreover the user could explore the data by using zoom (“”), pan (“”) and data tips (“”) buttons in the SMolESY-select.

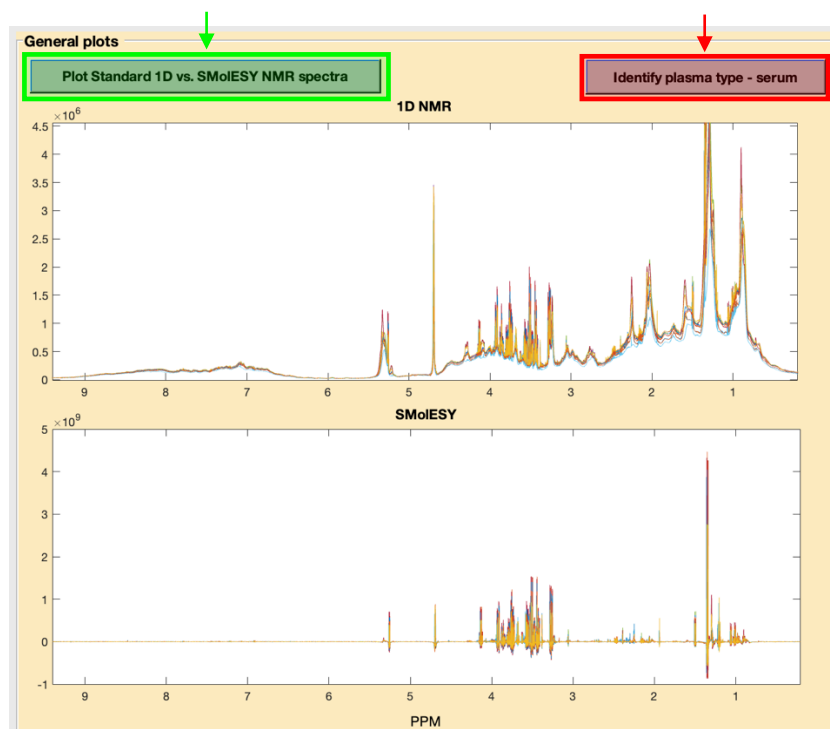


Figure 7.

→OPTIONAL

User could evaluate the type of blood product by pressing the button “ **Identify plasma type - serum** ”, namely if each sample is:

- i) Serum or heparin plasma
- ii) Plasma EDTA
- iii) Plasma citrate

SMolESY-select automatically identifies the presence or not of EDTA signals^[1] as well as calculates the ratio of citrate peaks integrals to noise and compares them with the maximum concentration observed by NMR in serum/plasma samples.^[2] Consequently, the user could be automatically informed about the type of the analyzed blood product biofluid. Results are printed in a .csv file (Fig. 8) and exported to the output folder initially defined by the user.

Spectra titles / Sample type -->	Plasma_EDTA	Plasma_Citrate	Plasma_Heparin_OR_Serum
Spec1	NO	NO	YES
Spec2	NO	NO	YES
Spec3	NO	NO	YES
Spec4	NO	NO	YES
Spec5	NO	NO	YES
Spec6	NO	NO	YES
Spec7	NO	NO	YES
Spec8	NO	NO	YES
Spec9	NO	NO	YES
Spec10	NO	NO	YES

Figure 8.

9. Start the automated assignment

In the drop list menu, the user could select any spin system (**Fig. 9**) from the 22 metabolites or ALL spins systems (**Fig. 9** red highlighted) and SMoIESY-select will start the automated assignment.

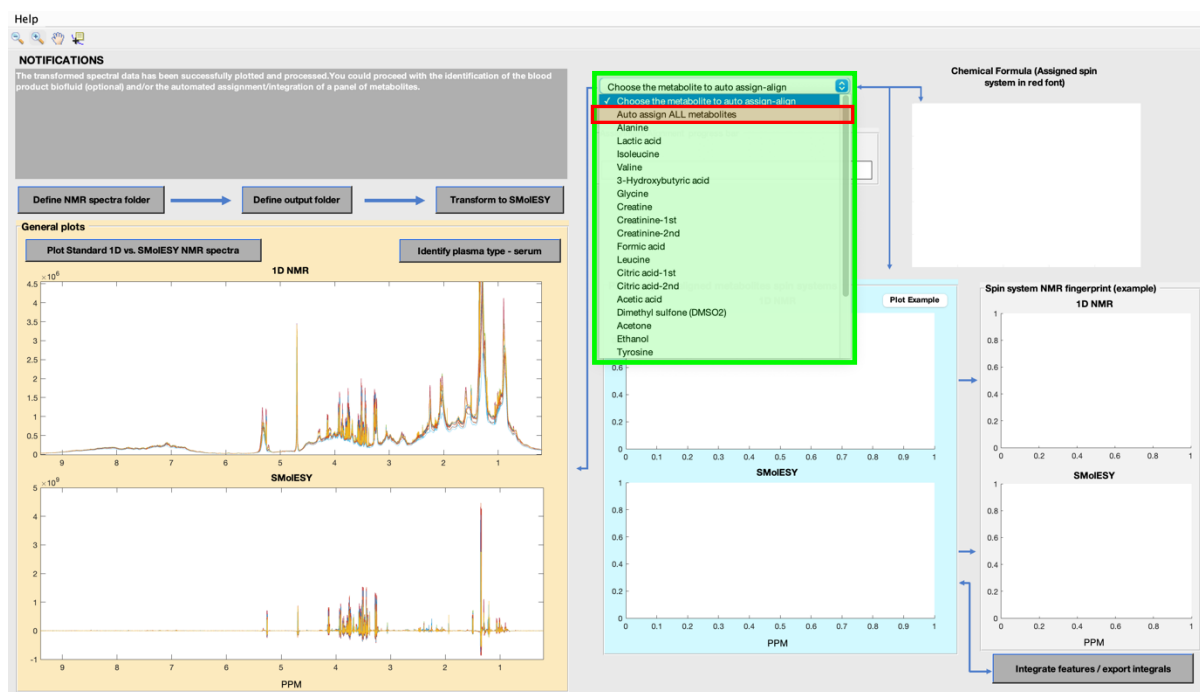


Figure 9.

When choosing a unique metabolite/spin system, the chemical structure of the metabolite along with the assigned NMR signals of selected protons (highlighted in **bold red font**) (see the example of Glutamine in **Fig. 10**).

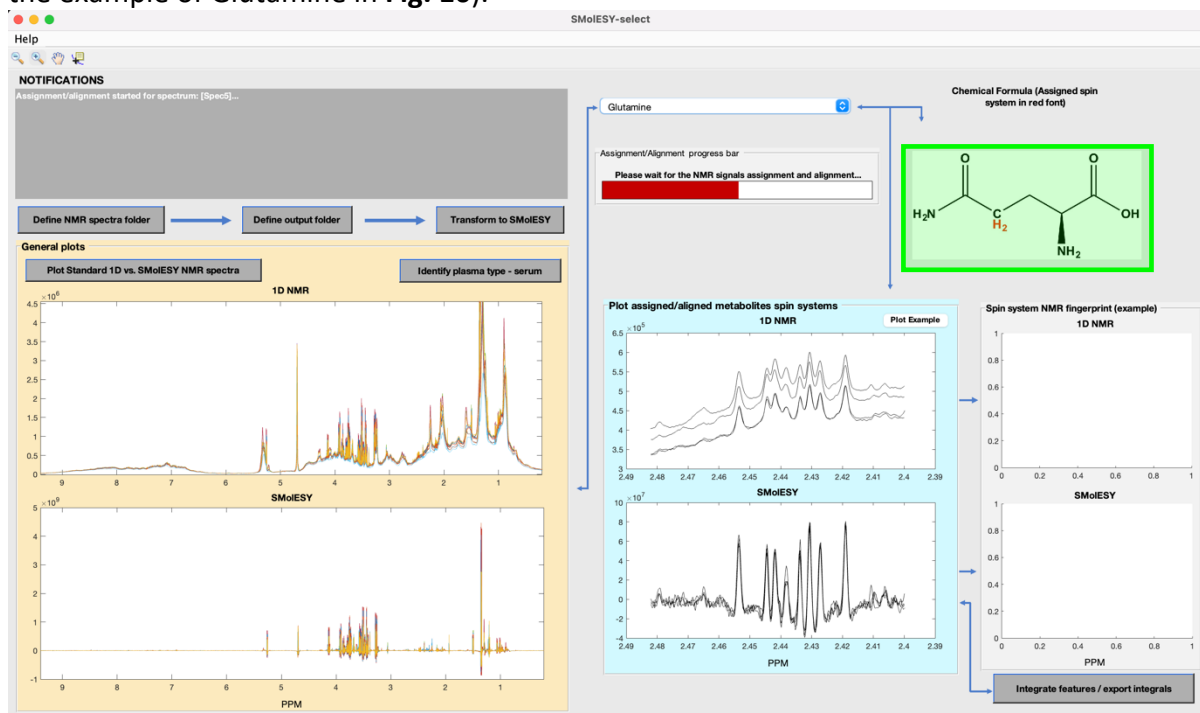


Figure 10.

During the automated assignment, the user is able to supervise the progress for each spin system assignment per spectrum (**Fig. 11a**) as well as evaluate the assignment due to the alignment/plotting of NMR signals per ^1H -NMR and SMoESY spectrum (**Fig. 11b,c**). All assignments for the 22 metabolites per spectrum are also printed in the output folder per spectrum (**Fig. 12**) (the user is also notified in the “NOTIFICATIONS” box). When assignment is finalized for all spectra, the user is able to visually inspect which in which spectra the assignment failed (by coloring the spectrum in red) and when the spin system NMR signal(s) is(are) assigned/aligned (colored in black) (**Fig. 11d**). Furthermore, pressing the toggle button “ **Plot Example** ” the user could plot an example of the spin system’s ^1H -NMR and SMoESY signal(s) template (**Fig. 11e**) as well as point by vertical blue dashed blue lines all the components of the assigned/aligned spectra in both ^1H -NMR and SMoESY spectra (**Fig. 11f**).

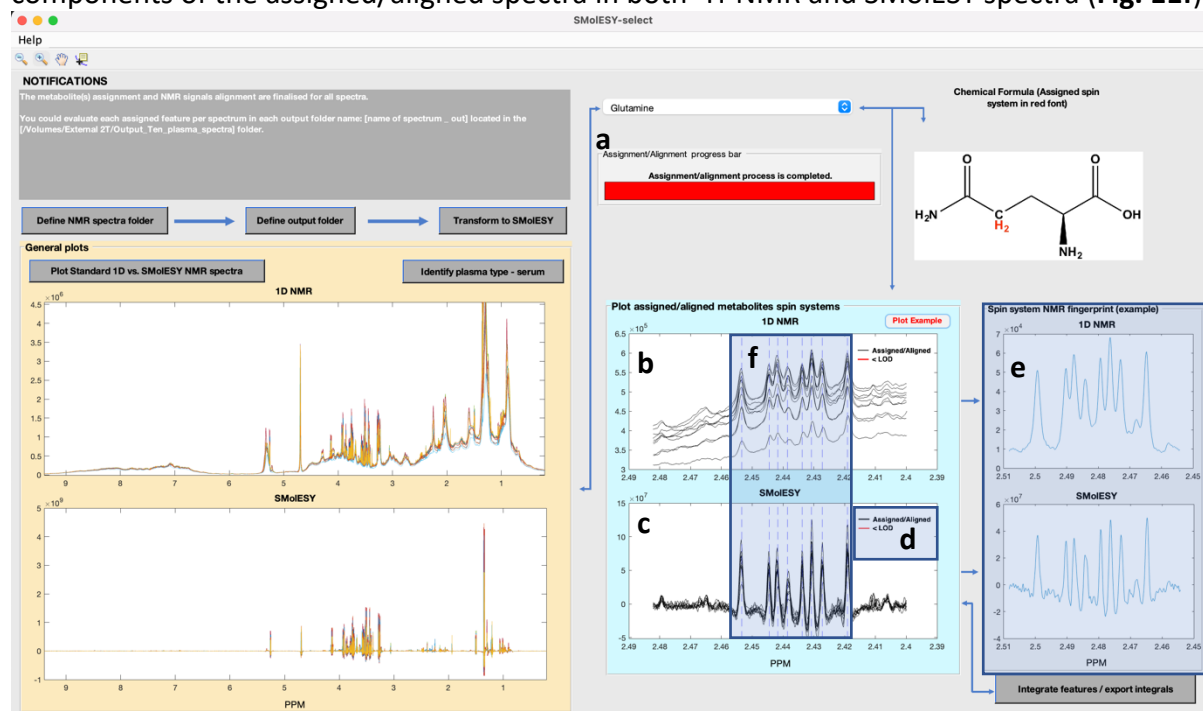


Figure 11.

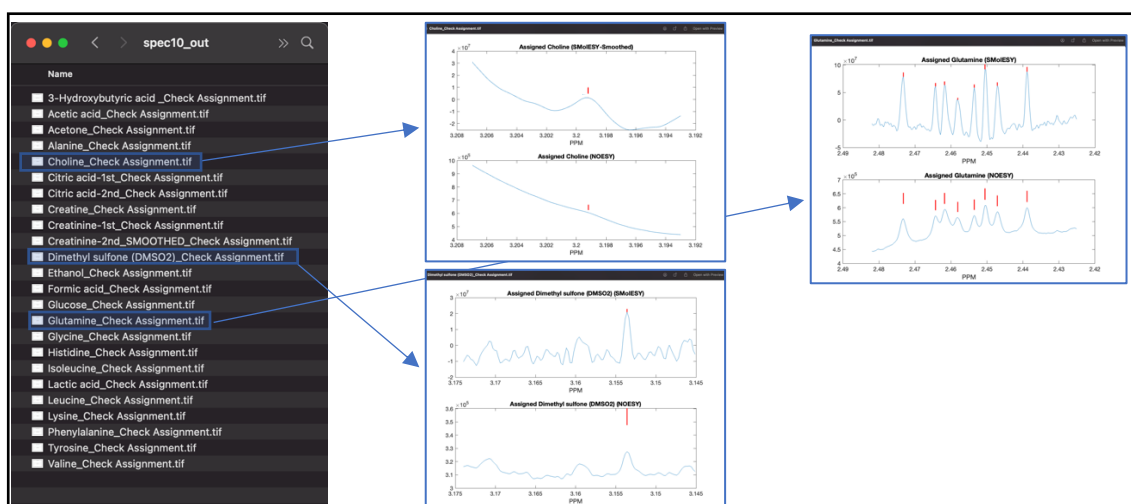



Figure 12.

→NOTE 1

If the metabolites signals are not assigned the red vertical dots are not plotted as shown in **Fig. 12**.

10. Start automated relative quantification (NMR signals integration)

After the completion of the selected or ALL metabolites automated assignment, user could press the button “  ” so as to automatically calculate the relative concentrations via integration and normalized to one proton for each metabolite or ALL metabolites (**Fig. 13**). Results are exported to a .csv file and user is notified in the “NOTIFICATIONS” box.

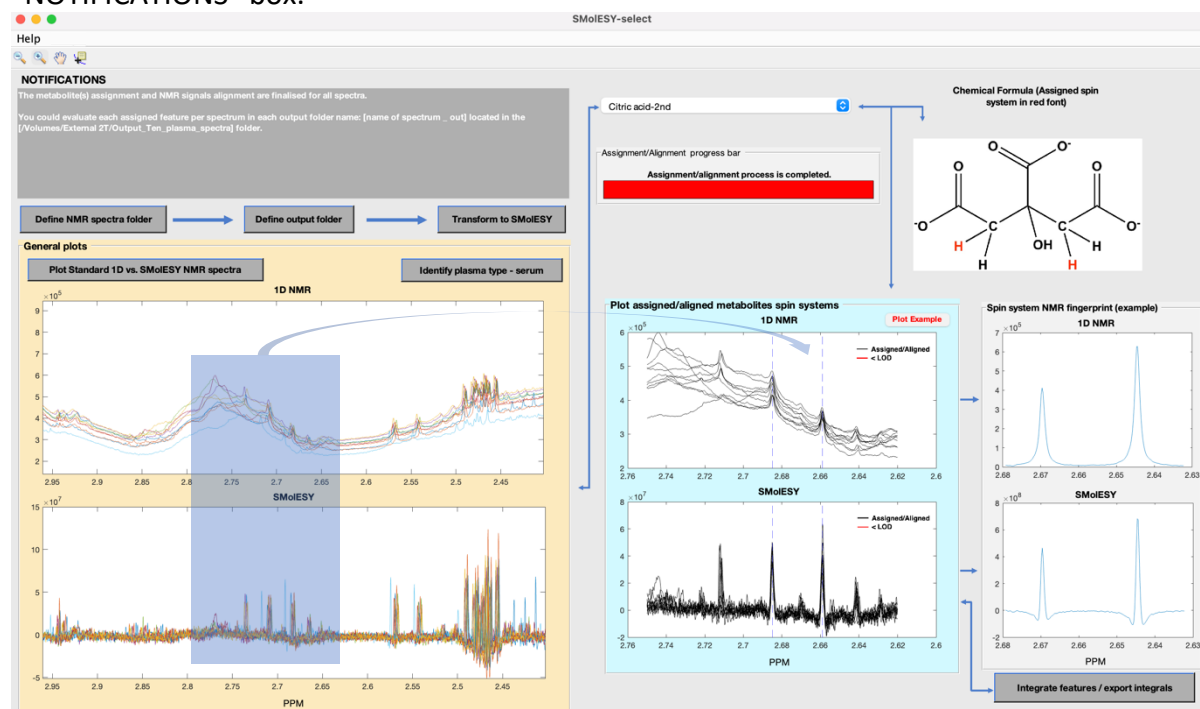


Figure 13.

→ NOTE 1

For the relative concentration results, algorithm automatically selects one or more predefined SMoESY components for each spin system as shown below in **Fig. 14.**, which showed the lowest risk of overlap tested in >8800 unique serum/plasma spectra and validated in various cohorts.

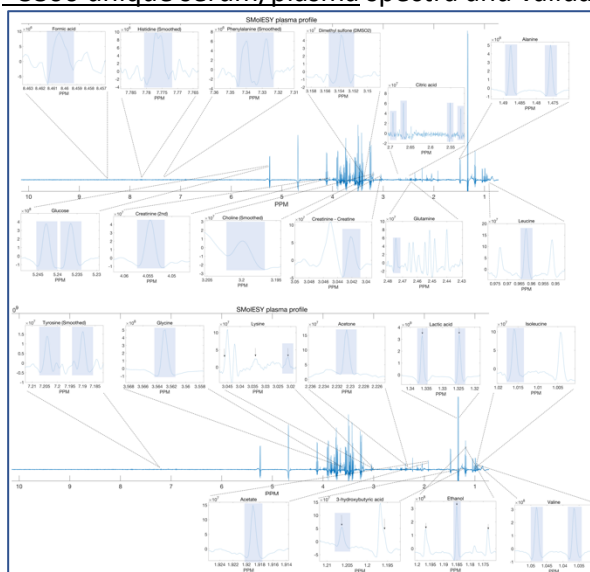


Figure 14.

11. Technical requirements - support

→ SMoLESY-select was created in MATLAB, 2019b – 2020b (MathWorks). The software code is compatible with MATLAB 2017b and above.

→ The compiled versions of SMoLESY-select for MAC_OS and WINDOWS, were created by MATLAB, 2020b and 2019b (MathWorks), respectively, and they were tested in macOS Big Sur (11.1 – 20C69) for both Intel and M1 (via Rosetta 2 emulator) proc. architectures, Catalina (10.15.2) and WINDOWS 10, where they are fully functional. For their installation, both compiled versions of SMoLESY-select need R2019b and R2020b 64-bit MATLAB Runtime, which is freely available by MathWorks:

(<https://uk.mathworks.com/products/compiler/matlab-runtime.html>).

MATLAB Runtime will be automatically downloaded/installed during the installation of both compiled versions of SMoLESY-select.

→ For troubleshooting and/or other technical information, contact Dr. Panteleimon G. Takis via e-mail: p.takis@imperial.ac.uk, with title of the e-mail: "Query for SMoLESY-select"

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