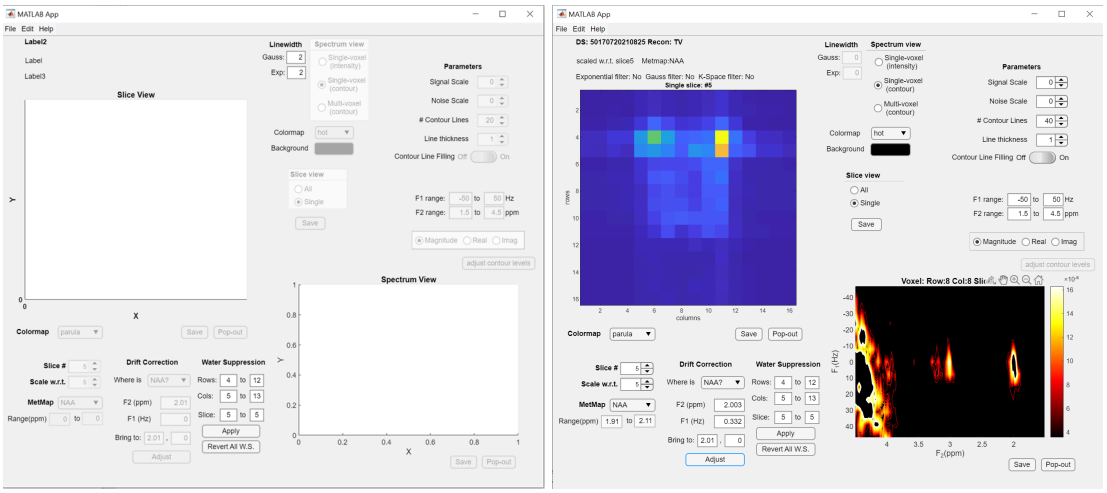
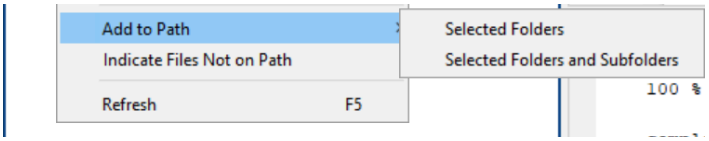
Display



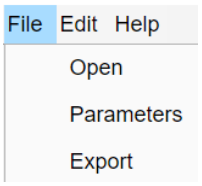
Application Interface

1. **Input “displayapp” in the MatLab command line**
   Make sure the app’s root folder is added to the path: Go to the file explorer panel, right-click and select “Add to Path” >> “Selected Folders and Subfolders”



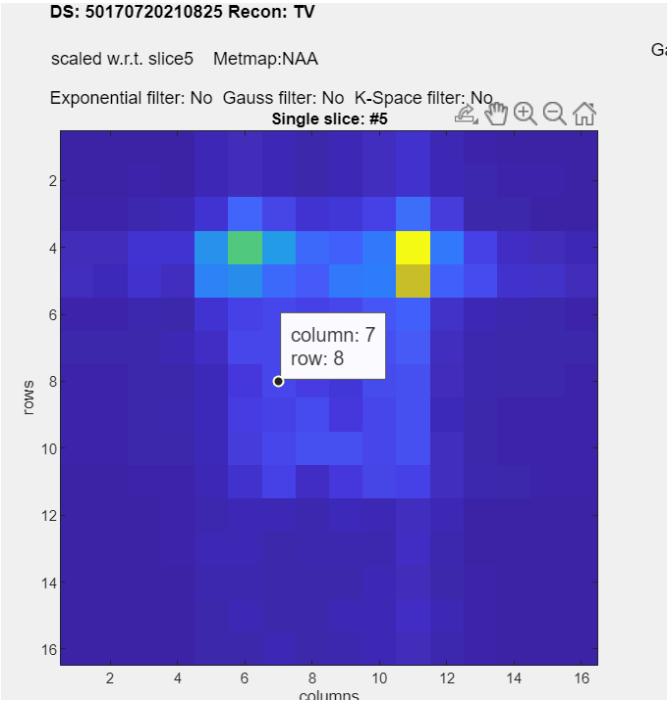
Adding root folder to path

2. **Once the app is open, go to “File >> Open” and select the reconstructed dataset**



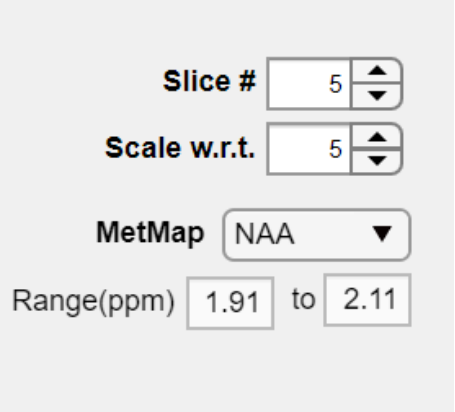
Opening reconstructed data

3. **Adjust the following on the panel for optimal display of the 5D dataset:**
   a. Slice-view section



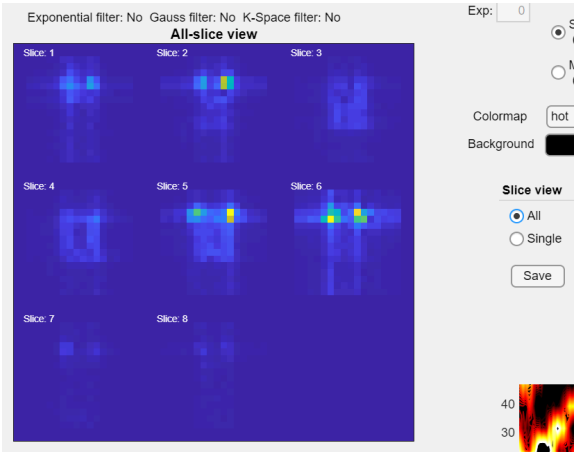
Viewing single slice (slice #5) and data info. Use cursor to see voxel position

Colormap: change display colormap for the slice views (default: parula)
Save: save the current single slice view
Pop-out: display the current slice in a separate window



Adjust settings for single-slice display

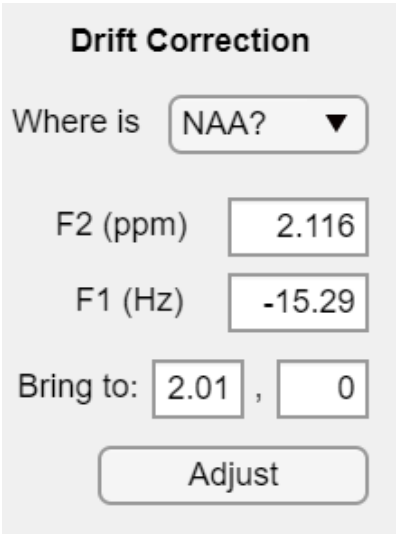
Slice: choose which slice to display (1-8, default: 5)
Scale w.r.t.: colormap scaled with respect to which slice (1-8, default: 5)
MetMap: Metabolite map to be displayed (default: NAA)
Range(ppm): F2-axis range where the metabolite's peak is found (default: for NAA 1.91 to 2.11)



Displaying all slices.

Slice view: toggle between seeing all of the slices or just individual slice
Save: save all-slice view with all metabolite maps

b. Drift correction (circular shift based on peaks' positions in the spectrum):

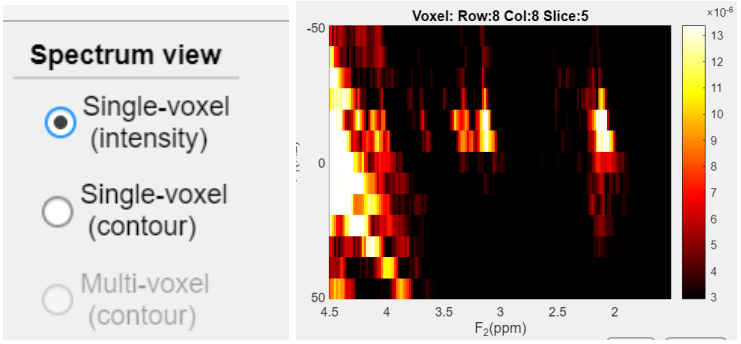


Where is: adjust all peak positions using this metabolite as the reference point
Bring to: where that metabolite peak's center should be
The app would search for the point with the highest contour level within the F2 range of that metabolite, and display its current location in F2 (ppm) and F1 (Hz), select "Adjust" to bring the peak center to the desired location.

c. Water suppression:

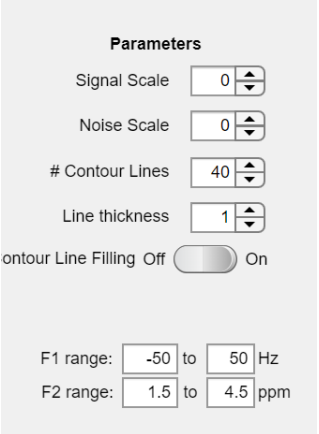
Performed water suppressions on the selected voxels by selecting “Apply” (range defined by rows, cols, slice, inclusive).
Select “Revert All W.S.” to revert all the water suppressions.

d. Spectrum-view section



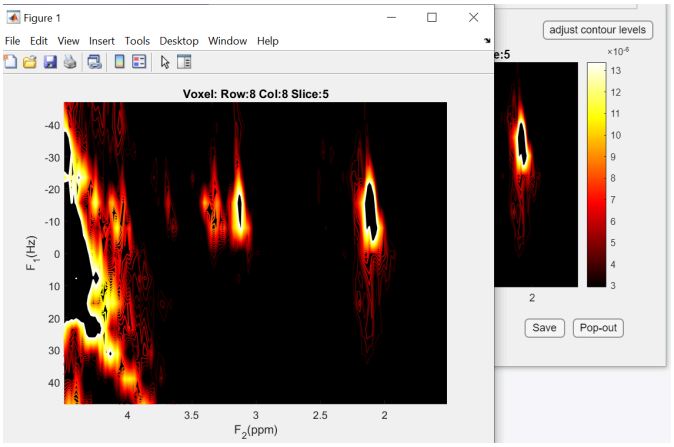
Single-voxel intensity plot

Toggle between intensity and contour plots for single-voxel spectrum
(See “4. Generating reports” section for the “Multi-voxel (contour)” option)



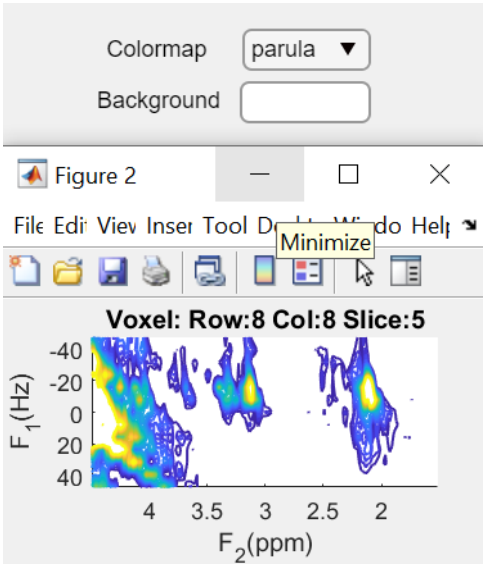
Spectrum display settings

F1 range/F2 range: adjust spectrum axis ranges
(default: F1: -50 to 50 Hz, F2: 1.5 to 4.5 ppm)
Contour Line Filling: toggle between on and off (default: Off)
#Contour Lines: number of contour lines (default: 40)
Line thickness: contour line thickness (default: 1)
Signal Scale/Noise Scale: adjust to visualize peaks clearer



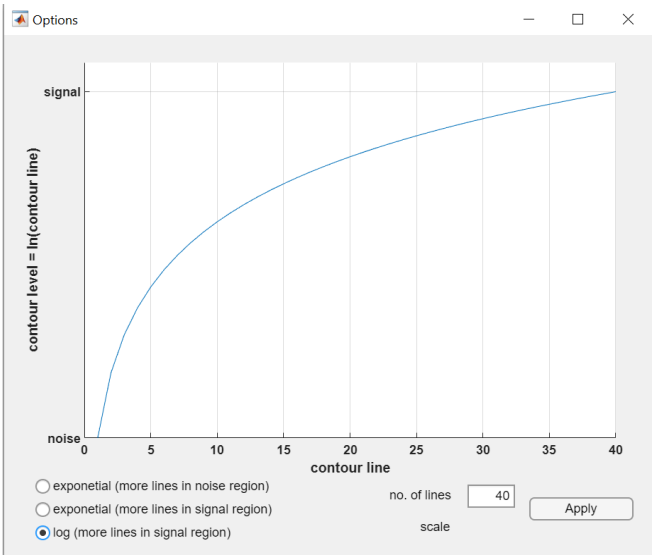
Pop-out: display in a separate window for more options

Save/Pop-out: save or display in a separate window the spectrum



Adjusting colormap and background for the spectrum

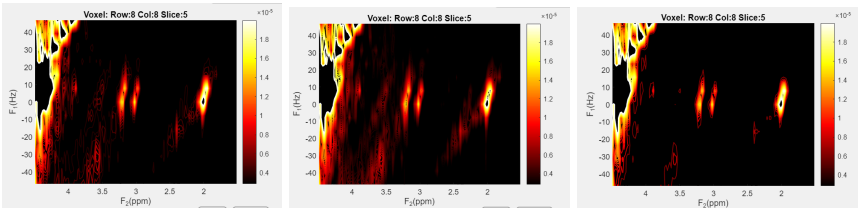
Colormap/Background: colormap and background color of the spectrum (default: hot/black)



Interface for contour line settings

Adjust contour levels:

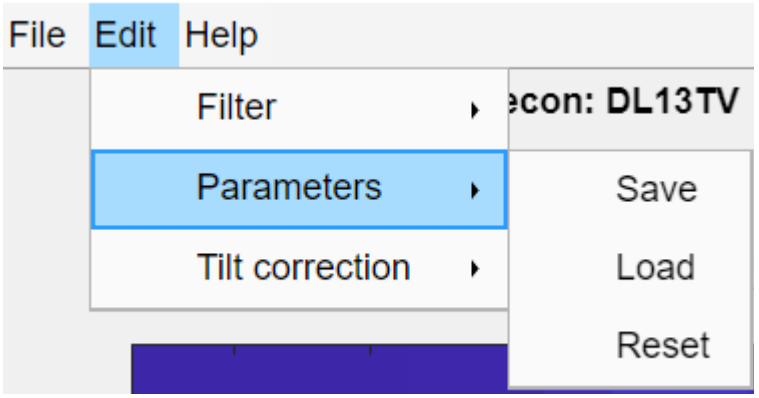
adjust and apply how contour levels are calibrated, line number, and scale in a pop-out window.



From left to right: exponential (more lines in signal), exponential (more lines in noise), log (more lines in signal)

e. Saving, loading, and resetting display options

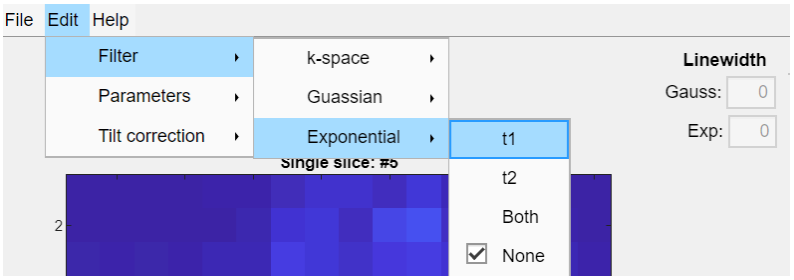
Go to “Edit >> Parameters” on the top menu



Top menu: save, load, and reset parameters

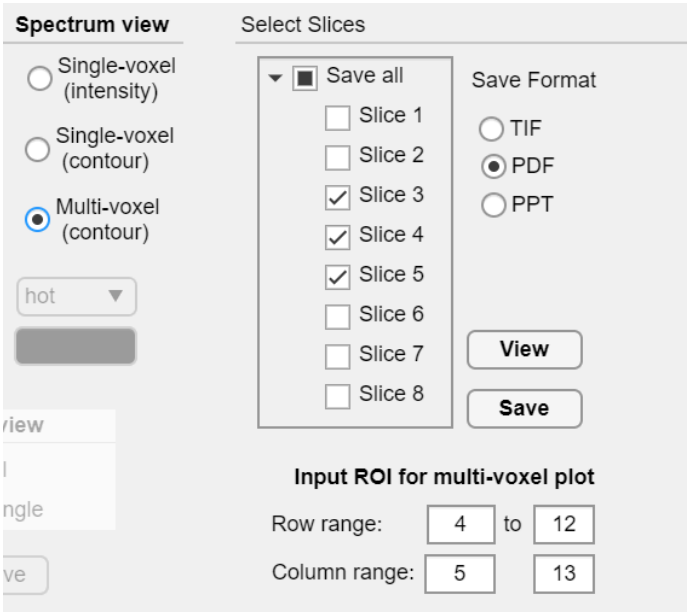
f. Applying tilt correction and filters

Go to “Edit >> Filters/Tilt Correction” and use Linewidth to adjust the strength of the Gaussian/Exponential filters.



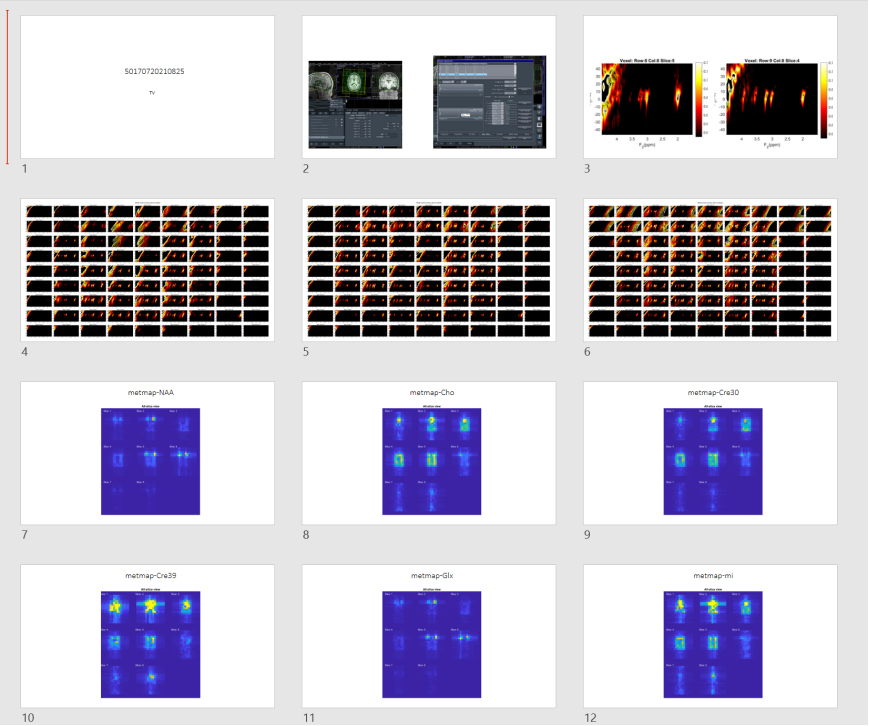
Filters, tilt-correction

4. Generating reports



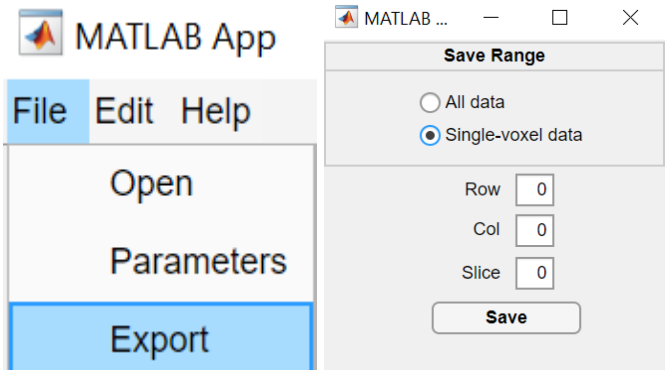
Options for generating report

Toggle to “Multi-voxel (contour)” in the spectrum view section
Select which slices to save
Select “Save all” to tick all eight slices
Select Save Format (default: PDF). The generated report would also include scan information, voxel localization images, and all metabolite maps in all-slice views.
Select the ROI for the multi-voxel plot (default: Rows: 4 -12, Columns: 5 - 13)
Select “View” or “Save” to either view output images or save as the selected format



Example generated powerpoints

5. Saving data



Use pop-out window to save data

Go to the top menu and select “File >> Export”
Toggle between the two options and select “Save”:

“Save all data”:

save the entire dataset with tilt correction, water suppression, and filter data.

“Select single voxel data”:

allow input of row, col, and slice (row, columns, and slice, see spectrum display title for position) to save individual voxel
(Usually saved as “dataset name-region-row-column-slice, e.g., 50170820200517-FG-4-6-6)

Quantitation

1. **Water and fat suppression (in batch):**
   Open the batch_suppress.m file
   Set the root folder containing the single-voxel data after “path = “
   The code would first tilt the data (
   (on dimensions and early, late placement)
   Perform water suppression ()
   Tilt the data back and save the struct “w_sup”(water suppressed) under the original single-voxel data
   Tilt the data again and perform fat suppression as well
   Then tilt the data back and save the struct “wf_sup”(both fat and water suppressed) alongside “recon”(original)

2. **Create basis**
   Change path name, etc.

3. **Adjust voxel phase**
   Load data into workspace
   AJ_JPRESS_v2(), change name to struct (w_sup/wf_sup/recon)

4. **Profit Quantitation**
   Change save file name and path

5. **Saving and reading quantitation results**
   Read ratio_table from work_space