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CSIgui v2.0 – Help

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Introduction

CSIgui development started as a hobby project to quickly visualize MRI and MRSI data in Matlab. The original intent was to merge the MRI data into MRSI space to localize the spectral data. During development however, multiple functions were added, ultimately creating a backbone for raw MRS data processing. It supports single- and multi- dimensional data, can import different file types, process raw data and allows for specific processing tasks. This improved and sped up MRS data processing for me and now hopefully also for you.

Hovering your cursor on a button or in the menu shows additional information!

Install

Navigate to the CSIgui root directory in Matlab and run *"CSIgui.m"*, either via the command or current folder window.

The application will automatically add itself to your search path, enabling global use in Matlab by simply calling CSIgui.

Content

In the root directory the following is expected: "CSIgui.m", "CSIgui.fig", License, README.md and directory "Files".

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Load Data

Loading data in CSIgui is possible using two of the following methods: within the GUI by selecting "*File > Open*" in the top menu or by using specific input arguments in Matlab scripts or the Command window.

Supported data types:

.data/.list:	raw data stored in a two column float32 format and parameter list file.
.spar/.sdat:	data stored as VAX-CPX float and the Gyroscan NMRS parameter file.
*.dcm:	Images stored as Philips DICOM v4.2.
.par/.rec:	Images stored as Philips PAR/REC v4.2.
*.txt	Spectroscopy data stored as two columns; the real and imaginary parts.

Supported input arguments

CSIgui can be called as a regular function in Matlab. You can use CSIgui in combination with your own processing of data to easily view multidimensional spectral data. Examples are shown below.

```
>>> CSIgui( 'label' ,  var );
```

Supported input labels and corresponding variables

Label	Synonym	Input
data		structure output from csi_loadData() for loading list/data files
list		structure output from csi_loadList() or csi_loadData()
csi	spec | mrs	array of any size with spectra or fids.
labels		labels per dimension of the data array
filepath	fp	file path to spectroscopy data file as cell* – *.spar/sdat | *.list/data | *.mat
filepathi	fpi	file path to an image data file as cell* – *.dcm | *.par/rec

NB. *The file paths string variables are required to be a cell; {"D:\Example"}. See examples below.

Examples:

```
>>>   fp = "D:\Data\MyData\raw_001.data";
>>>   CSIgui(  { fp } ,  "filepath" );

>>>   fp = "D:\Data\MyData\raw_001.data";
>>>   fpi = "D:\Data\MyData\FFE.dcm";
>>>   CSIgui( { fp } , "filepath" , {fpi}, "filepathi");

>>>   load( "someSpectra.mat", "array" );
>>>   CSIgui( array, "mrs")
%% N.B. mrs, csi and spec labels all have equal functionality in CSIgui.
```

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Data Indexing

Summary of data handling of both MRSI and MRI data in CSIgui: dimensions, indexes, array sizes and CSI-space.

MRSI Indexing

CSIgui is compatible with MRSI arrays of all sizes, but data display is linked to size indexing. By default, the application expects the following dimensional indexing of the MRSI data:

Index 1:	Samples of a spectrum or FID;
Index 2/3:	The X and Y index of multi or single dimensional data.
Index >4:	Slice or Z index of multi or single dimensional data.

To correct any indexing differences of the MRSI data, the buttons "*Reorder*" or "*Auto Reorder*" can be used. For more details, see the "Processing" section below.

Example:

MRSI array of size: 1024 x 4 x 5 x 3 x 6;
Each spectrum of 1024 samples will be shown in a 2D plot of size 4x5 with slice selection of 1 to 3 and 1 to 6.

MRI Indexing

CSIgui expects the width and height of the image array to be the row and column index respectively e.g. the first and second index/dimension. Higher indexes/dimensions are handled as slices. Loading image data using the application itself is advised if merging of both MRSI and MRI data is requested.

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Displaying Data

Both the MRS and MRI data can be visualized separately or merged. All options are explained below.

View MRSI

Pressing the "*Show CSI*" button will open a 2D plot of the MRSI data. The second and third dimension of the MRSI data set will be shown as the X (width) and Y (height) in this plot. Other higher dimensions are accessible for display through a small automatically launched window called "*CSIgui display panel*".

A single spectrum can be viewed by selecting a spectrum of interest in the CSIgui 2D plot window. This opens a 1D plot of the clicked spectrum and allows separate processing of this displayed spectrum. The selected spectrum is highlighted in the 2D plot window. If correct x-axis scaling is required, enter frequency information by pressing the "*Frequency*" button in the "*set"* section of CSIgui.

View MRI

Pressing the "Show IMG" button will open up MRgui2, a separate application. This application displays multiple image types and enables scrolling through all images in a single image-type array.

Merging MRSI and MRI

Tested and validated on tra/sag/cor MRI data set in combination with transverse MRSI data sets only.

To merge the MRI data to MRSI space, coordinate information of both data sets is required. Pressing "*convert*" at the IMG options of CSIgui will calculate the coordinates of the images, calculate the coordinates of the MRSI data set and convert the images to MRSI space. Spatial information of MRSI data will be requested if unavailable. If no image header information is in memory, required parameters will be request too. Otherwise, the image coordinates are calculated automatically. The latter is applicable if the image data (dcm and par/rec files) is loaded using CSIgui's internal functions.

The desired image type for conversion must be given if multiple image types are available. Coordinate parameters can be entered separately by pressing the "*Coordinates*" button at the CSI and IMG section of CSIgui.

<u>MRSI coordinate parameters:</u>

1. Voxel size;
   The voxel size of each direction. For *.list/*.data files, use the acquisition voxel size, not the reconstruction voxel size.
2. Offset;
   Offset of the MRSI stack.

<u>MRI conversion parameters:</u>

1. Image type;
   Image type such as magnitude (M), phase (P) or specific maps (Ex. B0) to use for conversion to MRSI space.
2. Correct FFT method;
   Due to the FFT method, a half voxel shift is present. Setting this option to one (1) corrects for this offset. Default input is set to 1. Setting the option to zero (0) will disable the correction.

Miscellaneous data

CSIgui allows visualization of multi-dimensional calculated data as either a graph or a table.

Graph:

With respect to the x, y and z index on the second, third and fourth dimension, any additional dimension in the MRSI data set is concatenated. This mean every fifth dimension or above is combined to plot a line. To solve multiple slices e.g. the z-dimension, the create figure has a tab for each third-dimension index.

Table:

Allows option to save all data or solely the selected table-cells. Each additional dimension above the fourth dimension will be plotted below with the corrected indexing per array as a separate row.

Processing

Time management: not all functions are explained

Both MRSI and MRS data can be processed and analyzed by multiple available functions explained below. Hovering over each button in CSIgui and over specific menu items shows short explanations of the available options or requirement of set function.

In addition to these multi-voxel processing functions, a single spectrum can be processed separately by opening the spectrum of interest in the CSIgui 2D plot. For more information, see below.

MRSI functions

The functions are ordered according to different sections available in CSIgui.

RAW PROCESSING:

The function in this section is designed for file types which store raw MRSI data e.g. data stored in k-space domain. A different method of (pre-) processing is required.

1. Average
    - Data is averaged over the “aver” labeled dimension. If the label is not present, the user is asked to specify an index to average over. Useful if any number of sampled averages (NSA) are available.
2. Apodization
    - Apply apodization over the entire volume (each voxel in every dimension). A multi-dimensional hamming window is calculate using the size of indexes labeled as “Kx”, “Ky” and, if 3D, “Kz”. If no labels are present, the user is asked to specify at least two indexes. This function is useful if k-space is not sampled fully or to apply smoothening over the entire volume.
      Be aware; spatial apodization causes a small change in voxel size in all applicable directions.
3. FFT (spatial)

- Fast Fourier Transform over the “Kx”, “Ky” and, if present, “Kz” dimensions. If no labels are present, the user is asked to specify at least two indexes.

APPLY:

1. FFT
   - Fast Fourier Transform (forward) to convert the voxel data from frequency to spatial domain.
2. iFFT
   - Inverse Fast Fourier Transform (backward) to convert the voxel data from frequency to spatial domain.
3. Combine
   - Combine channels using different methods
     i. Manual
        1. Combine channels by summation or calculating the mean of all channels with the option to exclude specific channels.
     ii. WSVD
        1. Whitened singular voxel decomposition; the coils are combine by a noise weighting method.
           Source article: C. T. Rodgers et al. - Receive Array Magnetic Resonance Spectroscopy: Whitened Singular Value Decomposition (WSVD) Gives Optimal Bayesian Solution.
4. Zerofilling
   - Add trailing zeroes to data in the time domain. Target sample size is requested and has to be equal or greater than the actual sample size.
5. Apodization
   - Apply apodization to all voxels in the data set. Data required to be in the time domain before applying.
6. Autophasing
   - Apply a zeroth order phase correction at a given range in the spectrum. This algorithm will maximize the real part of the spectrum in this range.

CALCULATE:

1. T2
   - Calculate T2 by fitting the exponential decay function to a variable number of echoes. This function requires the echo dimension to be on the fifth index and will calculate T2 for all voxel.
     For now, the maximum signal of the spectrum is used for the fit and will later be upgraded to fit per metabolite as specific ranges. Data will be shown as graphs which includes the maxima over all echoes, the resulting fit values, the T2 value plus the confidence intervals of the fit and the coefficient of determination (R^2). All T2 values will be saved automatically to a *.mat file named with the date and time of calculating. Stored data includes the T2 values, R2 values, amplitude of the exponential fit and the confidence intervals. Formula used:

$$S = Amplitude \times e^{-(\frac{t}{T2})}$$

2. T1
    - Still under development. Proper estimating initial parameter values cumbersome.

3. SNR
    - Calculate the SNR for each spectrum using a variable noise mask size. Data can be visualized as either a graph, if multiple dimensions (e.g. index 5 or higher) are present or as a table. Formula used:

$$SNR = \frac{mean\left(max\left(real(spec)\right)\right)}{abs\left(std\left(spec(noise\ mask)\right)\right)}$$

      NB: Use of either the real or absolute part of the spectrum in the numerator can be chosen.
4. Max
    - Display the maximum of each spectrum. Data can be visualized as either a or as a table.
    - Visualize the maximum values of the full data set as a 3D scatter plot, with size and color normalized to the maximum maxima in the data.
5. Linewidth
    - Calculate linewidth at full width half max (FWHM). Values are returned in ppm if the frequency details are available (See Set > Parameters). Display as a graph or as a table. Calculated data can be exported to text file.

SET:

1. Parameters
    - Set the nucleus of interest, magnet strength, bandwidth and possible shift (in ppm) to calculate the following x-axis data; ppm-scale, time and frequency.
2. Coordinates
    - Set the voxel sizes in all applicable directions and any possible offset if the dimensional stack to calculate coordinates of for each voxel.
3. FID & Echo
    - Split FID and Echo data to enabling separate editing. This is specifically designed for the MESING sequence.
4. Window Ratio
    - Set 2D Plot window its ratio equal to voxel ratio
5. Plot Options
    - Set specific 2D plot options: Color scaling, Y-axis scaling, X-axis scaling (Zoom!)
6. Labels
    - Change the names e.g. labels of each dimension.

MRI functions

Functions in the MRI section of the GUI are focused on merging MRI with MRSI data. MRI data can be converted to MRSI space and display contrast of these images can be managed.

1. Coordinates (MRI)
    - Calculate coordinates for each voxel in the image data set. If no image header information from dicom or par files is present, required parameters are requested. See Displaying data > Merging MRI and MRSI for more information.
2. Convert
    - Convert the MRI data to the MRSI space. This requires coordinates of both data sets and missing information will be requested automatically. If multiple image types are present, the image type of interest to convert is requested.
3. Contrast
    - Set display contrast of the image when displayed simultaneously with the MRSI data.
4. Image in CSI
    - Display all the images used for the currently viewed CSI array. Only works if MR images are converted to CSI space.
5. Image & Grid
    - Create one figure with the 2D CSI voxel grid and the images. No spectra plotted. Solely for displaying and localization.

Individual spectrum

1. Phasing
    - Manual
        i. Apply manual phase correction in a separate GUI.
    - Automatic
        i. Automatically try to maximize the real part of the spectrum at a given interval or position. The interval must be given in sample points.
    - Phase all
        i. Manually phase the shown spectrum and apply the calculated correction to all other spectra in the data set.
2. FFT
    - Fast Fourier Transform (forward) to convert the spectrum from the frequency to the spatial domain.
3. iFFT
    - Inverse Fast Fourier Transform (backward) to convert the FID from the spatial to the frequency domain.
4. Apodization
    - Apply apodization to the spectrum. For proper use, the spectrum has to be in the time domain e.g. apply to the FID. Multiple apodization filters are present.
5. Zero Fill
    - Apply zero filling to the spectrum. For proper use, the spectrum has to be in the time domain e.g. apply to the FID. Target sample size is requested and has to be equal or greater than the current number of samples.
6. Linewidth
    - Calculate linewidth at FWHM of a specific peak of interest or in all peaks found automatically. Will show processing results of each peak in a separate figure.

7. SNR
    - Calculate the SNR of the spectrum. SNR value is displayed in the MRS information box in CSIgui.
8. Data Display
    - Set the unit of the displayed x-axis and the data type to be shown.
9. Replace voxel
    - Replace the spectrum in the dimensional data set with the processed single spectrum.
10. Export
    - Export the displayed spectrum to file; sdat/spar, text and mat-file.

Merging Voxels

Merge Voxels opens a separate window with the images and MRSI voxel grid plotted for each index in the (k)z-dimension. Select voxels of interest and press save to save data to file or merge to open the merge menu.

Merge menu:

- Set SNR filter on to include and/or exclude a peak at a specific SNR level
- Set SNR weighting to weight the averaging to peak of interest SNR.
- Apply frequency alignment prior to averaging by shifting each peak maximum to align.

View

CSIgui has a day and night mode with the latter being the default setting. Change the theme in the menu bar in View > Theme. To customize the color layout go to View > Set Custom Color and enable Custom color in View > Theme.

Exporting Data

Data

Exporting MRSI data can be found in the MRSI menu in CSIgui. Supported export file types are; sdat/spar, text and mat-file. Specific parameters will be requested for spar and sdat files.

Figure

CSIgui can automatically loop through all slice and attribute indexes and save each 2D MRSI plot as a separate image file.

Troubleshooting

No troubleshooting solutions available yet, though Matlab itself may help you out! 😉

Future Features

This is a to-do list and in no way a promise the function will end up in a stable release. Please contact me if you would like a custom function integrated in the GUI.

Contact

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