*Chapter 5*

# CSIgui: an open-source view and processing tool for multi-dimensional MRSI data in MATLAB

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***Zenodo 2020***

**Keywords: MATLAB, Analysis, Processing, GUI, MRS data**

## Introduction

MR Spectroscopy (MRS) allows for non-invasive detection of all nuclei with a non-zero spin in the human body. Most sensitive is $^{1}$H MRS with the highest gyro-magnetic ratio ($\gamma_{1H}$ : 42.58 Mhz $T^{-1}$) and high natural abundance compared to other nuclei. Recent advances in producing homogenous RF transmit (Tx) fields at ultra-high magnetic fields (>7 tesla), i.e. the implementation of a birdcage body coil for X-nuclei transmit(Tx), in combination with an increasing number of RF receiver (Rx) coils made whole body MRS imaging of the less sensitive nuclei phosphorus ($^{31}$P), sodium ($^{23}$Na), deuterium ($^{2}$H) and more feasible *in vivo*. [1–3]

The number of receiver channels (Rx) is increased to acquire significant signal to noise ratio (SNR) for processing and ultimately clinical relevance.[4,5] In addition, larger fields of view are possible with the new transmit body coils which allow more homogeneous transmit fields ($B_1^+$).[6,7] This consequently increases the dimensionality of the spectroscopy data and current strategies which aim more and more for MR spectroscopic imaging (MRSI) further increase the acquired information density. As current MR systems cannot process this additional data stream, data processing must be done using raw data formats instead of common data formats such as dicom or spar and sdat.

Therefore, a research friendly tool to easily view multi-dimensional X-nuclei spectroscopy data and to analyze MRSI data with multiple RF channels, many voxels (due to the increased field of view), numerous sample averages and more.

CSIgui (Chemical shift imaging graphical user interface) development started as a necessity to visualize and analyse multi-dimensional MRSI data in MATLAB (The Mathworks Inc., Natick, MA). However, spectroscopy data is difficult to interpret without proper spatial localization of the voxels in MR image space. To allow proper localization a method to merge MRI data into MRSI space was added. This development continued and multiple conventional spectroscopy processing functions were added, creating a backbone for raw MRS data processing. It now supports single- and multi- dimensional data, can import different file types, process raw data and enables specific MRS processing tasks on individual spectra and bulk data.

## Download and Installation

The current CSIgui version is frozen and archived on GitHub and a published release accessible via Zenodo. ("github.com/Sugocy/CSIgui/releases/tag/vThesis" and "doi.org/10.5281/zenodo.3669640").

### Installation

Navigate to the CSIgui root directory in MATLAB and run *"CSIgui.m"*, either via MATLAB's command window or current folder window. The application will automatically add itself to the MATLAB search path, enabling global use in MATLAB by calling CSIgui.

### Content

In the root directory the following files and directory are expected: "CSIgui.m", containing the core code of the GUI "CSIgui.fig", License, README.md and directory "Files".

## Methods

After installation and running the command 'xxx' CSIgui starts with the user interface screen shown in figure 1. A detailed explanation of its algorithms is defined:

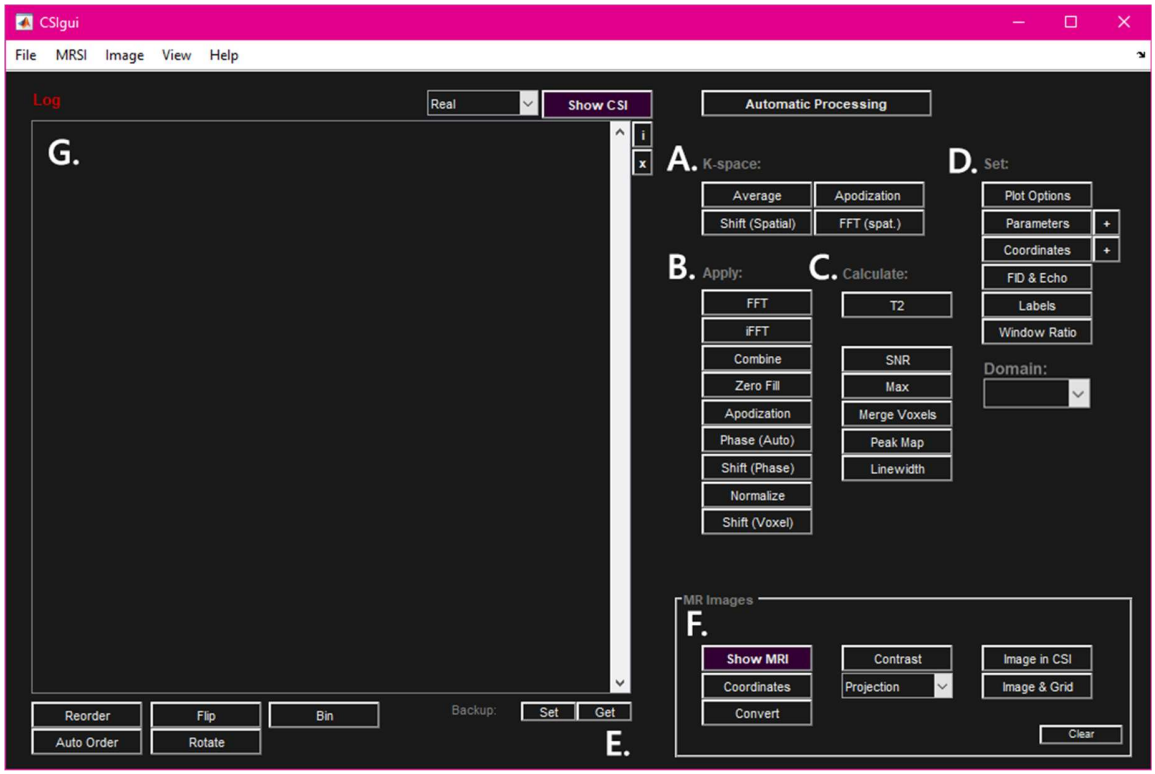


**Figure 1.** The main window of CSIgui with the different sections which are labelled with a letter in this figure. **(A. – C.)** The k-space, apply and calculate section that allows processing of MRS k-space data, applying processing functions to spectroscopy data or calculating values from the MRS data. **(D.)** A specific part of the GUI to set parameters and other information which is lacking in general raw data headers. **(E.)** The grey square shows MRI specific options such as viewing loaded images and converting MR images to spatial MRSI space. **(F.)** General data manipulation options are found in this section including creating a

backup of current MRS data, rotating the MRS data array and changing the order of the data dimensions.
**(G.)** List window that shows information loaded data and the logs of all operations in CSIgui.

## Load Data

Loading data in CSIgui is possible using two of the following methods. The first is within the GUI by selecting "*File > Open*" in the top menu and the second method is accessed by using specific input arguments in MATLAB scripts or the Command window. More in-depth details on MRS loading data can be found in the scripts "csi_loadData.m", "csi_loadList.m", "csi_readSDAT.m", "csi_readSPAR.m" and csi_readText in the CSIgui root directory "Files".

Supported data types:

| | |
|---|---|
| *.data/*.list: | raw data stored in a two column float32 format and the Gyroscan parameter list file as exported with Gyroscan release 5. |
| *.spar/*.sdat: | raw data stored as VAX-CPX float and the Gyroscan parameter file as exported with Gyroscan release 5. |
| *.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. |

### *Input arguments*

CSIgui can be called as a regular function in MATLAB and supports multiple input variables. This allows integration of CSIgui with other data processing scripts coded by the user to easily view multidimensional spectral data or to apply specific processing steps. 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*<br>– *.spar/sdat \| *.list/data \| *.mat |
| *filepathi* | *fpi* | file path to an image data file as cell*<br>– *.dcm \| *.par/rec |

**NB.** *The file paths string variables have to be passed to CSIgui as a cell-variable; {"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“);
```

## Data Indexing

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

### *MRSI Indexing*

CSIgui is compatible with MRSI arrays of all sizes within the available amount of random-access memory (RAM) in MATLAB. Displaying the data is linked to dimension indexing. By default, the application expects the following dimensional indexing of the MRSI data:

| | |
|---|---|
| Index 1: | Samples of a spectrum or free induction decay (FID); |
| Index 2/3: | The X (width) and Y (height) index of multi or single dimensional data. |
| Index >4: | Slice or Z index of multi or single dimensional data. |

To edit the order of the dimensions 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 datapoints will be shown in a 2D plot i.e. a slice, of size 4x5 with available slice selections 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. Higher dimensions of these 2D arrays are handled as separate slices. Loading image data using the application itself is advised if merging of both MRSI and MRI data is requested.

## Display Data

Both the MRS and MRI data can be visualized separately or merged.

### *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 transverse, sagittal and coronal MRI data sets 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 requested too. Otherwise, the image coordinates are calculated automatically. The latter is applicable if the image data (dicom and Philips par/rec files) is loaded using CSIgui's default 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>

| | |
|---|---|
| Voxel size: | The voxel size of each direction. For *.list/*.data files use the acquisition voxel size, not the reconstruction voxel size. |
| Offset: | Offset of the MRSI stack. |

<u>MRI conversion parameters:</u>

| | |
|---|---|
| Image type: | Image type such as magnitude (M), phase (P) or specific parameter maps E.g. B0 (maps, $T_1$ maps) to use for conversion to MRSI space. |
| FFT correction: | Half a voxel shift is present in any odd sized dimension of the data due to the FFT method used in MATLAB. 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.

### *Calculation 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 dimensions in the MRSI data set such as averages, RF channels, echoes or other attributes are concatenated. This means every fifth dimension or above are combined to plot a line. To allow visualization of calculated data from multiple slices e.g. the z-dimension, the created figure includes tabs for each slice.

*Table:*

Display calculated values in tables for each available 2D plot e.g. slice. Any additional dimensions in the MRSI data set such as averages, RF channels, echoes or other attributes are concatenated in its corresponding slice table. Data or only the data selection in the visible table can be saved to a file.

## Processing

Both MRSI and MRS data can be processed and analyzed by multiple available functions which are explained below. Hovering the mouse cursor over each button in CSIgui and over specific menu items shows short explanations of the available options or requirement of the functions. All options in the k-space, apply and calculate section apply to every individual spectrum in the dataset.

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, including: Raw Data Processing, Apply, Calculate and Set.

#### K-SPACE

The processing options in this section are designed for file types which store raw MRSI data i.e. data stored in k-space domain.

- Average

  Data is averaged over the “aver” labelled dimension. If the label is not present, the user is asked to specify an index to average over.

- Spatial Apodization

  Apply apodization over the entire volume (each voxel in every dimension). A multi-dimensional filter window is calculated using one of the available filter window algorithms: Hamming, Hann, flat top or Blackman. The size of indexes labelled as “Kx”, “Ky” and, if 3D,

"Kz" are used to define window size. If the proper labels are not present, the user is asked to specify at least two indexes. More in-depth details of the implemented algorithm can be found in the script "csi_apodization3D.m" in the CSIgui root directory "Files".
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 significant increase in voxel size in all applicable directions. [8]

- FFT (spatial)

Fast Fourier Transform from k-space domain to spatial domain over the "Kx", "Ky" and, if present, "Kz" dimensions using the default functions in MATLAB shown in equation 1, with "data" the MRSI data either in the spatial "x" or k-space "f" domain and the dimension to apply the transform over, "index" . If the proper labels are not present, the user is asked to specify at least two indexes. In addition, the option to choose the shift method to center the zero-frequency component of the spectra is available. The default option (2, automatic) uses the circular shift function for odd sized dimensions instead of the "fftshift" and its inverse functions. Options 1 and 0 use solely the circular or Fourier shift function respectively. More in-depth details of the implemented algorithm can be found in the script "csi_rawfft.m" in the CSIgui root directory "Files".

*IF* (SIZE OF K-SPACE DIMENSION IS ODD) **EQ. [1]**

data(x) = *FFTSHIFT*( *FFT*( *IFFTSHIFT*(DATA(F), INDEX ), [ ], INDEX ), INDEX)

*elseif* (size of k-space dimension is even)

data(x) = *circshift*( data(f), -1 × *ceil*( $\frac{size(\text{index})}{2}$ + 1) , index)

END

APPLY

- FFT

Fast Fourier Transform (forward) to convert the voxel data from time to frequency domain using default MATLAB functions shown in equation 2 with "data" the MRSI data either in the spatial "x" or frequency "f" domain. More in-depth details of the implemented algorithm can be found in the script "csi_fft.m in the CSIgui root directory "Files".

data(f) = *fftshift*( *fft*( data(x) ) ) eq. [2]

- iFFT

Inverse Fast Fourier Transform (backward) to convert the voxel data from frequency to time domain using default MATLAB functions shown in equation 3 with "data" the MRSI data either in the spatial "x" or frequency "f" domain. More in-depth details of the implemented algorithm can be found in the script "csi_ifft.m in the CSIgui root directory "Files".

data(x) = *ifft*( *ifftshift*( data(f) ) ) eq. [3]

- Combine

  Combine channels from multiple RF coils using one of two available methods.

  1. Manual: Combine channels by summation or calculating the mean of all channels with the option to exclude specific channels.
  2. WSVD: Whitened singular voxel decomposition; the coils are combined using a noise weighting method.[9] A noise component is required for this algorithm to calculate a noise covariance matrix between all channels. The noise can be calculated from the positive edge of the spectrum using a noise mask which size can be set in the WSVD options window or using the noise measurements per channel which are available if a list/data file is in memory. With the latter approach the noise mask size setting is not used. For more in-depth information the user can open the script "wsvd.m" located in the "Files" directory of CSIgui repository or read the source article.

- Zerofilling

  Add trailing zeroes to data in the time domain. Target number of datapoints is requested and must be equal or greater than the actual number of datapoints. More in-depth details of the implemented algorithm can be found in the script "csi_zeroFill.m in the CSIgui root directory "Files".

- Apodization (time domain)

  Apply 1D apodization to all voxels in the data set. The filter that will be applied to time domain data will be displayed in a new window and the user has the option to apply the filter or abort the operation. More in-depth details of the apodization algorithms can be found in the function "CSI_filterSpectra" in the main script of CSIgui.

- Phase (auto)

  Apply an automatic zeroth order phase correction using a given peak its frequency range in the spectrum. This algorithm will maximize the real part of the spectrum in the given range. More in-depth details of the implemented algorithm can be found in the script "csi_autoZeroPhase.m" in the CSIgui root directory "Files".

CALCULATE

All functions in this section apply to every individual spectrum in the dataset.

- T2

  Calculate $T_2$ 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 $T_2$ for all voxels. The maximum signal in the spectra at the data range given by the user will be used to calculate $T_2$ using equation 4 with the maximum signals S, the signal amplitude A and the corresponding echo times t. The data range option allows the user to select a peak signal of interest. Results will be shown as graphs which include the maxima over all echoes e.g. the measured data, the resulting fit values, the $T_2$ values plus confidence intervals of the fit and the coefficient of determination ($R^2$). All $T_2$ values will be saved automatically to a *.mat file named with current date and time. Stored data includes the $T_2$ relaxation time values, $R^2$ values, amplitude of the exponential fit and the confidence intervals. More in-depth details of the implemented fitting algorithm can be found in the script "T2_exp.m" in the CSIgui root directory "Files".

$$S = Ae^{-(\frac{t}{T2})} \qquad \text{Eq. [4]}$$

- SNR

  Calculate the SNR for each spectrum using a noise mask with variable size and using either the real or the magnitude part of the data using equation 5. The SNR will be calculated using the maximum signal intensity in the range specified by the user. Data can be visualized as a graph, if multiple dimensions (e.g. index 5 or higher) are present or as a table.

$$\mathrm{SNR} = \frac{mean\left(max\left(real(\mathrm{spec})\right)\right)}{abs\left(std\left(spec(\mathrm{noise\ mask})\right)\right)} \qquad \text{Eq. [5]}$$

  **NB:** Use of either the real or absolute part of the spectrum in the numerator can be chosen.

- Max

  Two methods to view the maximum value at a given range of a spectrum are available. The first method calculates and displays the maximum value of each spectrum and data can be visualized as either a graph or as a table. The second method displays the maximum values of the full data set as a 3D volumetric scatter plot with size and color normalized to the largest maxima in the calculated data.

- Linewidth

  Calculate the linewidth at full width half max (FWHM) for each individual spectrum in the data set. Values are returned in ppm if the frequency parameters are available (See Set > Parameters). Results can be displayed as a graph or as a table and can be exported to text file. More in-depth details of the implemented algorithm to calculate a linewidth at the half hight of a signal peak can be found in the script "csi_LineWidth.m" in the CSIgui root directory "Files".

- Normalized

  Normalize the MRS data set to either the maximum or minimum signal, a peak intensity, spectral noise or a custom value in the entire data volume or per voxel using the real part of the data.

- Shift (voxel)

  Shift the MRSI data set by a number of voxels by altering the grid coordinates or manipulating the index of the MRS data set.

SET

- Parameters

  Set the nucleus of interest, magnetic field strength, bandwidth and possible shift (in ppm) to calculate x-axis values for each spectrum with the option for unities time (s), frequency (Hz) and parts per million (ppm).

- Coordinates

  Set the voxel sizes in all applicable directions and any possible offset if the dimensional stack to calculate coordinates of for each voxel.

- FID & Echo

  Split FID and Echo data to enabling separate editing. This is specifically designed for the multi-echo spectroscopic Imaging (MESING) sequence.

- Window Ratio

  Set the 2D Plot window its size ratio equal to the voxel ratio of the MRSI data.

- Plot Options

  Set specific 2D plot options: Color scaling, Y-axis scaling and X-axis scaling. The latter allows zoom in on specific peaks in the 2D plot.

- 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.

- Coordinates (MRI)

  Calculate coordinates for each voxel in the image data set. If no image header information from dicom or par file is present, required parameters are requested. See Displaying data > Merging MRI and MRSI for more information.

- 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.

- Contrast

  Set display contrast of the image when displayed simultaneously with the MRSI data.

- Image in CSI

  Display all the images used for the currently viewed CSI array. Only works if MR images are converted to CSI space.

- Image & Grid

  Create one figure with the 2D CSI voxel grid and the images. No spectra plotted. Solely for displaying and localization.

### *Individual spectrum*

Individual spectra can be viewed by clicking on a voxel in the 2D plot window of CSIgui. A separate plot window showing the 1D data and a 1D options panel will open. Multiple processing options for the 1D data are available and explained here:

- Phasing

  | | |
  |---|---|
  | Manual: | Apply manual phase correction in a separate GUI. |
  | Automatic: | 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: | Manually phase the shown spectrum and apply the calculated correction to all other spectra in the data set. |

  The GUI for applying manual phase corrections can be used separately from CSIgui using the script “csi_PhaseCorrectionGUI.m”

- FFT

  Fast Fourier Transform (forward) to convert the spectrum from the time domain to the frequency domain using equation 2.

- iFFT

  Inverse Fast Fourier Transform (backward) to convert the spectrum from the frequency to the time domain using equation 3.

- Apodization

  Apply apodization to the data using an available 1D filter. The filter that will be applied to time domain data will be displayed in a new window and the user has the option to apply the filter or abort operation. More in-depth details of the apodization algorithms can be found in the function “CSI_filterSpectra” in the main script of CSIgui.

- Zero Fill

  Add trailing zeroes to data in the time domain. Target number of datapoints is requested and must be equal or greater than the actual number of datapoints. More in-depth details of the implemented algorithm can be found in the script “csi_zeroFill.m in the CSIgui root directory “Files”.

- 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 separate windows.

- SNR

  Calculate the SNR of the spectrum. SNR value is displayed in the MRS information box in CSIgui.

- Data Display

  Set the unit of the displayed x-axis and the data type to be shown.

- Replace voxel

  Replace the spectrum in the dimensional data set with the processed single spectrum.

- 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 as an overlay 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 spectrum using the maximum 1D cross-correlation between all peaks and the spectrum with the maximum signal.

## 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-files. Specific parameters will be requested for spar and sdat files. Saving the data as a mat-file allows the user to continue working in CSIgui by loading the mat-file in question when needed. In addition, the exported data in text format is compatible with JMRUI v4 and higher.

***Figures***

A displayed 2D MRS plot from CSIgui can be saved to file using the menubar options MRSI > Export > Figure. In addition, CSIgui can automatically loop through all slice and attribute indexes and save each 2D MRSI plot as a separate image file.

## GUI Appearance

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.

## Results

A few examples are shown that highlight the functionality and potential of CSIgui (fig. 1-5). The tool allows processing, visualization and localization of raw 3D CSI data as acquired in a $^{31}P$ loading phantom in combination with MR images (fig. 1). In addition, it is possible to view the data in between all processing steps which are explained. Application of CSIgui to heart and liver $^{31}P$ spectroscopic imaging data are shown in figure 2, where a coronal and transverse slice of two *in vivo* 3D CSI raw data sets, both acquired with a 16-channel receiver array can be seen. The different RF channels are combined using the WSVD algorithm implemented in CSIgui. Merging MRSI and MRI data allows localization of tissue specific voxels in the heart, liver and skeletal muscle including discrimination of different metabolite peaks (fig. 2B-C and 2E-F).

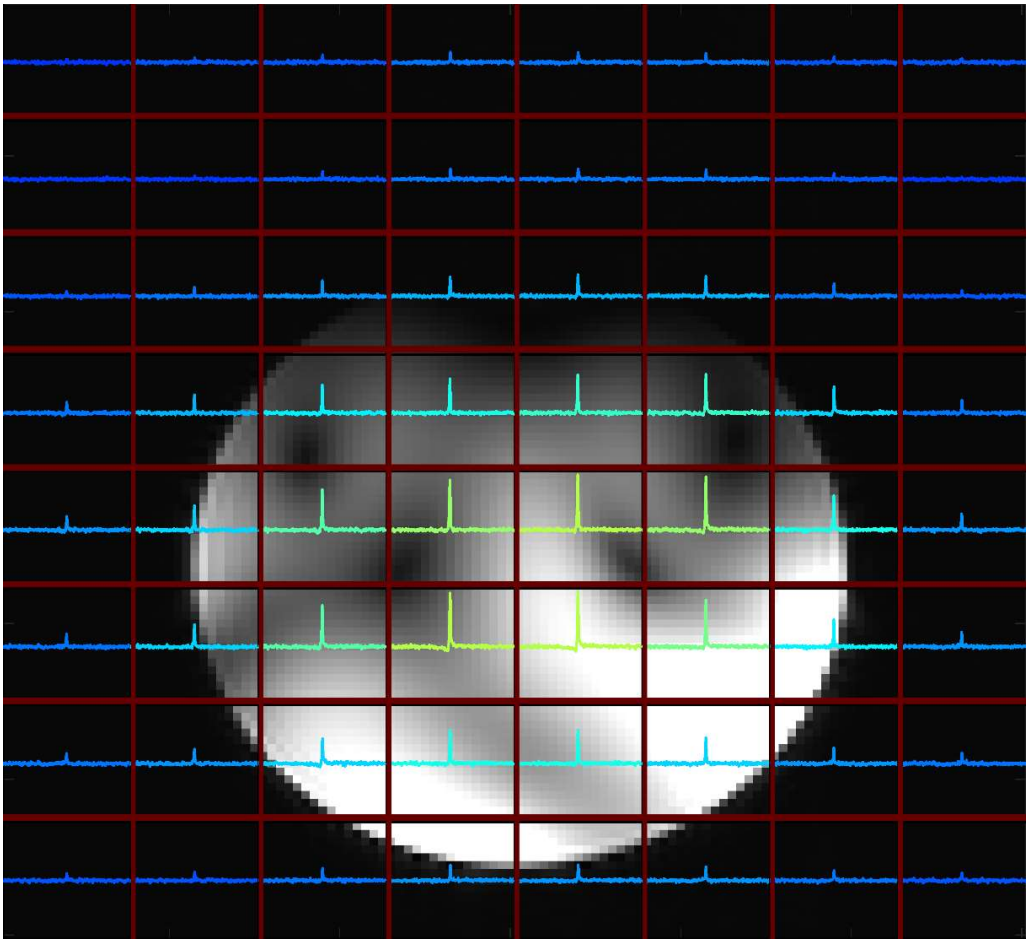

**Figure 2.** The 2D plot window of CSIgui showing a single slice from a 3D MRSI data set with a converted MR image in the background. The data were? acquired in a $^{31}P$ loading phantom containing a solution with a single $^{31}P$ metabolite using a 3D CSI protocol in combination with a $^{1}H/^{31}P$ dual transceiver coil in quadrature mode. Using CSIgui, raw data were loaded and indexed e.g. shaped to k-space. The data was averaged over the number of sampled averages dimension and spatially filtered using a 3D hamming window before

inverse Fourier transform of k-space to the spatial domain. The resulting FIDs from all voxels were apodized in the time domain using a Gaussian filter in a single operation. Zeroth order phase correction were applied automatically after Fourier transform to the frequency domain. The MRSI parameter file retrieved from the MR-system was loaded and frequency plus spatial parameters were set. This allowed converting the MR images to MRSI space and plot the resulting spectra on top of the calculated images.

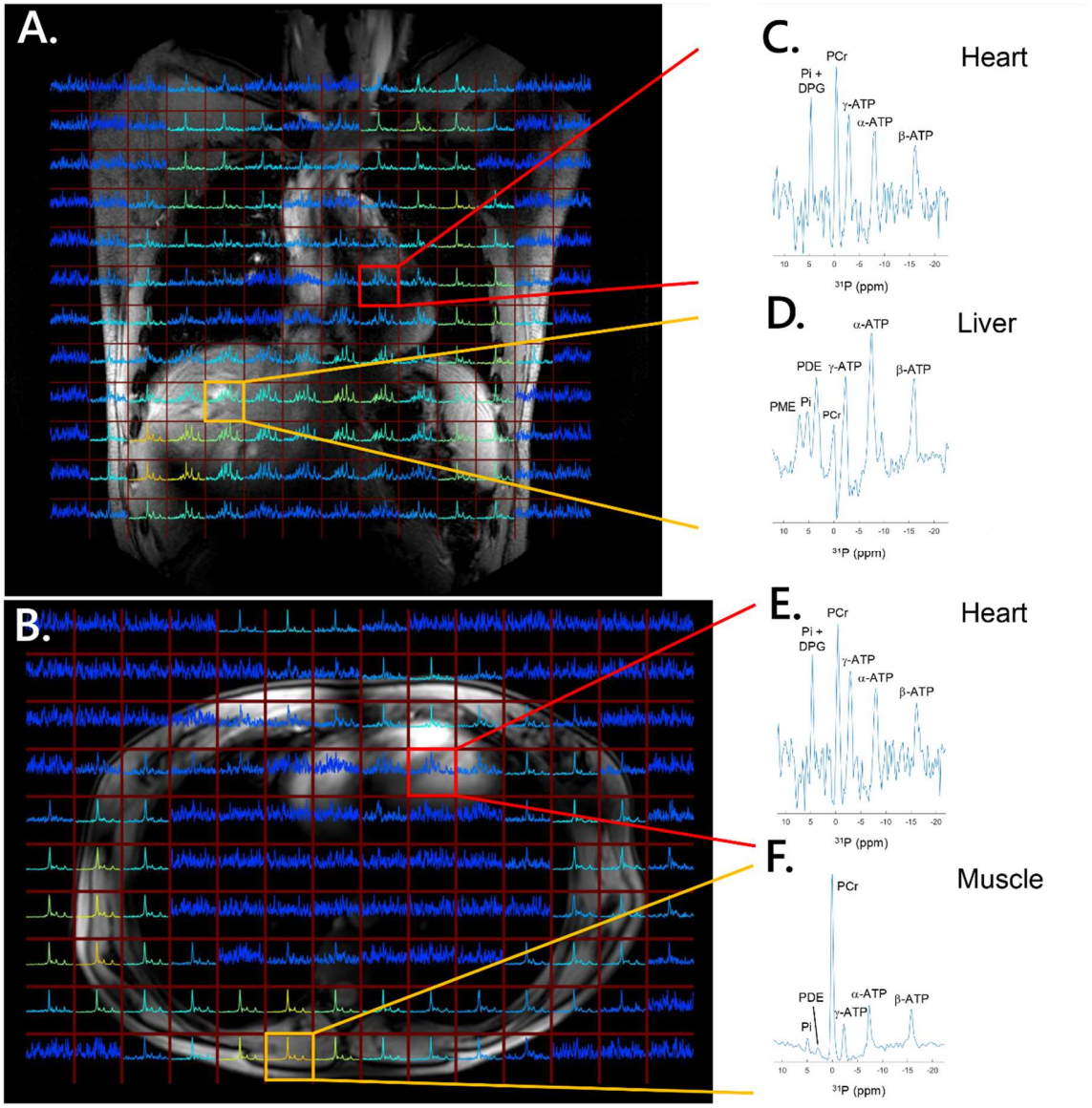


**Figure 3.** Collage of two *in vivo* 31P MRSI data sets of the heart and liver acquired with a 16-channel setup at 7 tesla and processed with CSIgui. **(A - B.)** A coronal and transverse MR image with a slice from the 3D CSI data set displayed on top. The heart, liver and skeletal muscle are visualized with the two red and two yellow squares respectively. The colors of the spectra are scaled to the

maximum signal amplitude in the data volume with a yellow, high signal to blue, low signal color gradient. The y-axis is scaled to the maximum per voxel. MR images acquired during the same session are converted to MRSI space and plotted with in the background of the MRSI data. **(C - F.)** Four individual spectra from the two 3D data sets showing spectra in the heart, liver, and skeletal muscle. Different metabolites can be discriminated after processing and localization and show tissue specific signal intensities.

Another example of CSIgui its functionality is the $T_2$ quantification of inorganic phosphate in a sphere embedded in a large body-size phantom seen in figure 4. The presented data serves a validation purpose for a multi-echo spectroscopic imaging protocol[6]. The displayed fit results are generated using CSIgui including the image and individual spectra of the FID and echoes. This functionality is also used for *in vivo* $T_2$ quantification of phosphocreatine in the gluteus maximus (fig. 5). It shows the use of the image display function in CSIgui in combination with the $T_2$ calculation output.

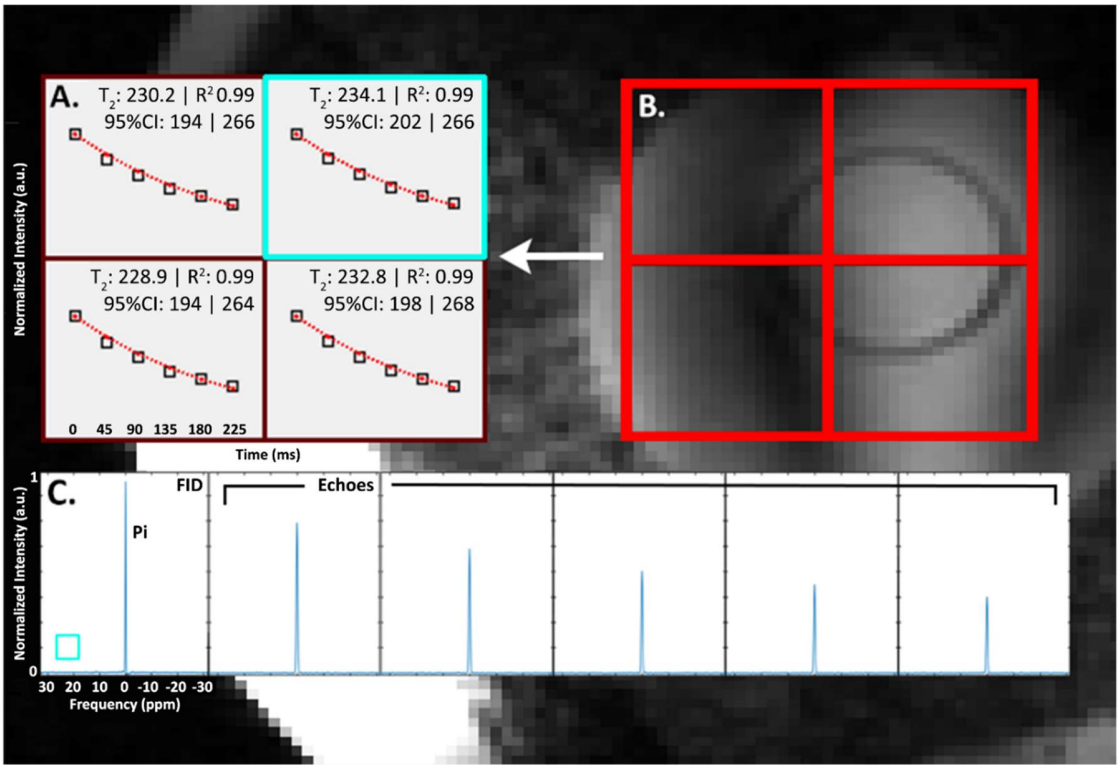


**Figure 4.** Multi-echo spectroscopic imaging data processed and presented for validation using CSIgui (Copied from chapter 4: "Low SAR 31P (multi-echo) spectroscopic imaging using a $^{31}P$ whole body birdcage coil at 7T"). **A)** *In vitro* $T_2$ measurement of inorganic phosphate in a body-sized phantom using a multi-echo spectral imaging sequence for each voxel in **B)** the red grid on the localizer image of the sphere which contains the metabolite. The normalized maximum peak value for the FID and each echo plus the corresponding fit are denoted as black squares and a red dotted line respectively. Both the line color and marker appearance were edited using CSIgui. Average $T_2$ over all four voxels for the Pi contained in the small sphere was 232 ± 35 ms. **C)** The

spectra of the FID and five echoes for the single voxel highlighted by the blue square, acquired using a $^{31}$P dual coil receiver in combination with a $^{31}$P body coil. The frequency scaling shown for the x-axis of the FID is equal for all other echoes.

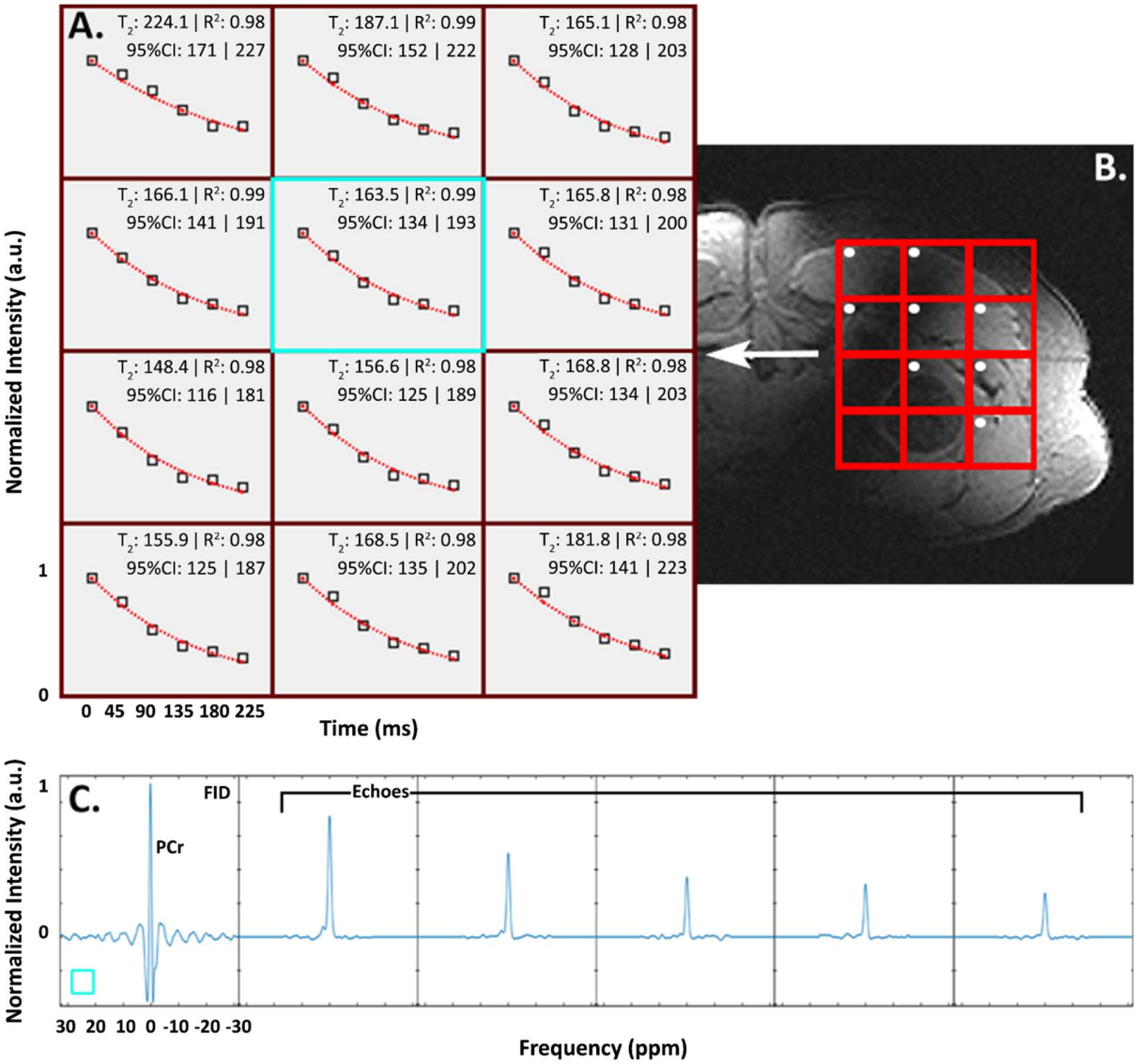


**Figure. 5.** *In vivo* multi-echo spectroscopic imaging data processed and presented using CSIgui. ((Copied from chapter 4: "Low SAR 31P (multi-echo) spectroscopic imaging using a $^{31}$P whole body birdcage coil at 7T"). **A)** *In vivo* $T_2$ fits of phosphocreatine using multi-echo spectroscopic imaging data from a single volunteer in voxels corresponding to the gluteal muscles as shown by the red grid in **B)** the $T_1$-weighted localizer image. Normalized maximum peak value for the FID and each echo are denoted as open squares and the red dotted lines represent the fit which are all set using CSIgui options. Echo times applicable to all voxels are shown in the bottom left. Average $T_2$ from all voxels with high muscle tissue content, denoted by the white dots, was 177 ± 35 ms. **C)** Spectra of the FID and five echoes for the voxel

highlighted by the blue square, acquired using a $^{31}$P dual coil receiver in combination with a $^{31}$P body coil. The frequency scaling shown for the x-axis of the FID is equal for all other echoes.

## Discussion

Magnetic resonance spectroscopy (MRS) focusses on physiological changes in the body rather than monitoring morphological changes using imaging modalities such as computed tomography (CT) and magnetic resonance imaging (MRI). Technological advances at ultra-high-field MRS (7T and higher) create opportunities to better monitor and therefore investigate chemical processes in detail such as the energy metabolism, phospholipid metabolism but also the acidity of the environment. However, the new data generated is not easily processed by currently available software. The default MR console software cannot process the increased number of dimensions and those processing steps are not fully accessible. Visualization of all the additional data dimensions such as RF channels, averages, cardiac phases, echoes and more is cumbersome with the current available tools such as 3DiCSI (Hatch Center for MR research, Columbia University), which is discontinued and jMRUI which is not suitable for merging MRSI and MRI data or multi-channel data.[10] New data structures and novel processing of advanced MRSI is either slow or even impossible to view as the software code of common software packages is not easily changed or its source code not accessible.

To overcome this issue, CSIgui was created in MATLAB. MATLAB is a higher programming language and commonly used in the research environment for image and data processing. The large default algorithm library saves time and eases scripting, however for visualization of these data sets specific coding is required. CSIgui allows visualization and processing of the multi-dimensional MR spectroscopic data, with all code available to the user to understand algorithms or change it to their preferences. The core methodology of the GUI code is documented and in combination with available example code users can easily add their own functionality to the tool. This allows development of the tool by peers in the field. In addition, the tool enables exporting data to data formats which are used in software such as jMRUI (MRUI Consortium, http://www.jmrui.eu) and LCModel (LCModel, http://www.s-provencher.com/lcm-test.shtml).

One general limitation of CSIgui is the lack of support for data formats from (N)MR vendors other than Philips and Gyroscan. This can be solved by creating an addition to the code using example code in the "CSIgui.m" file.

A learning curve is present in CSIgui especially if the user is not experienced with processing MRS data. For instance, the data domain is only tracked by the GUI when the user loads data using CSIgui. Otherwise the user must be aware when applying specific operations to the data such as 1D apodization or zeroth order phasing. In addition, converting MR images to MRSI space is also a complex step to verify by the user if specific artefacts such as fold over are present. However, the automatic processing option guides the user to apply each processing step in a correct order.

## Conclusion

The default MR software is currently unable to process the additional data streams that come with multichannel data. CSIgui allows processing and analysis of the large MRSI data sets in a common

research-oriented programming language, MATLAB. This allows the tool to be flexible in use with custom add-ons, custom processing code in MATLAB and in combination with other NMR tools used in the field.

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