

Tensor-based MRSI GUI: Matlab based Graphical User-Interface for Residual Water Suppression and tissue type differentiation in MRSI signals

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Introduction:

This document is the user manual of the MATLAB based graphical user interface (GUI) for residual water suppression and tissue type differentiation in Magnetic Resonance Spectroscopic Imaging (MRSI) signals. The algorithms for residual water suppression and tissue type differentiation are described in [1] and [2], respectively.

This GUI requires two additional MATLAB toolboxes: Tensorlab [3] and Simple Matlab Solver for L1-regularized Least Squares Problems [4]. Before starting, make sure that these toolboxes are installed in MATLAB. In this GUI, all tensor-based analysis is done using “Tensorlab 3.0” package [3].

Folder contents:

“Tensor-based MRSI GUI” contains the following files

- 1) All required MATLAB code for using the GUI.
- 2) User manual named “MRSI_GUI_user_manual” for the GUI
- 3) One example MRSI dataset named “CSI_spectro_35_SENSE_11_2_raw_act”
- 4) One background MRI image (for representation only) named “aa_rep_img”.
- 5) Software License Agreement file. Note that the license specifying the conditions under which this code is distributed admits academic use only. If used for commercial purposes, contact Sabine Van Huffel.

Load

Load: To Load the MRSI data

Supported Format:

- {'spar','.sdat','.SPAR','.SDAT'} → philips data
- '.mat' → SPID format

Other formats can be loaded by installing SPID software toolbox [5] [6].

- {'rda','.RDA'} → siemens data
- {'ima','.IMA','.dcm'} → siemens DICOM data
- {'txt'} → jMRUI or 3DiCSI data

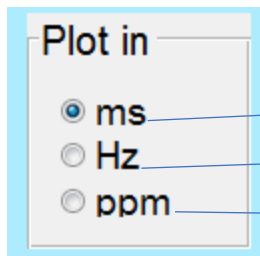
Load img

Load img: To load one slice of background MRI image.

Supported Format:

- '.mat' → Matlab data matrix
- '.jpg' → JPEG images
- '.png' → portable network graphics

Note: Here the loaded MRI image slice is assumed to be co-registered and aligned

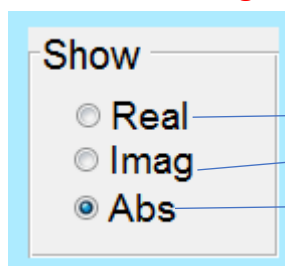


To plot time domain FID in milliseconds

To plot frequency domain Spectrum in Hertz

To plot frequency domain Spectrum in ppm

with the MRSI voxel grid. No co-registration or alignment is performed by this GUI

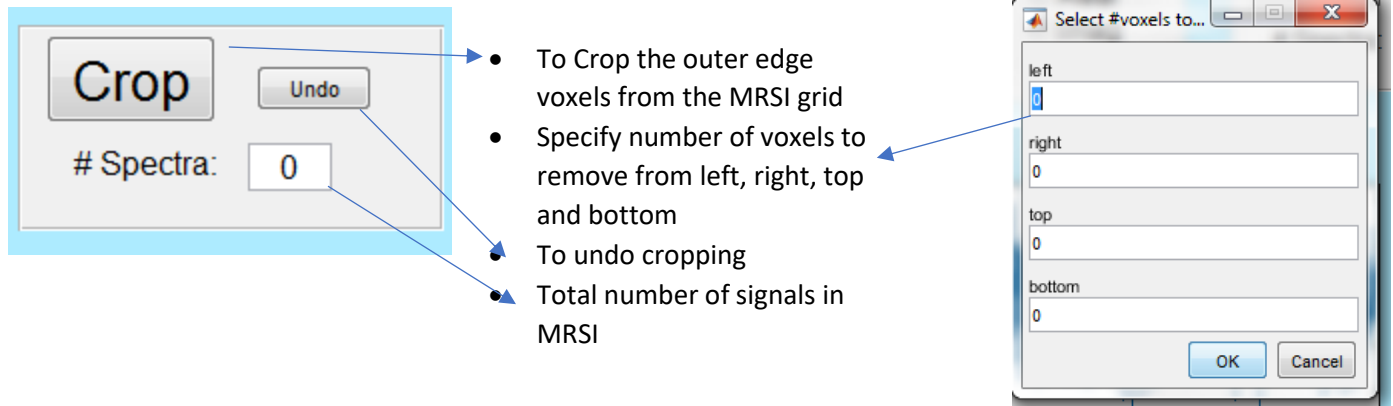


To plot real part of the signal

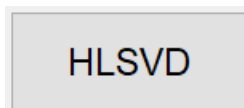
To plot imaginary part of the signal

To plot absolute value of the signal

Residual Water Suppression:

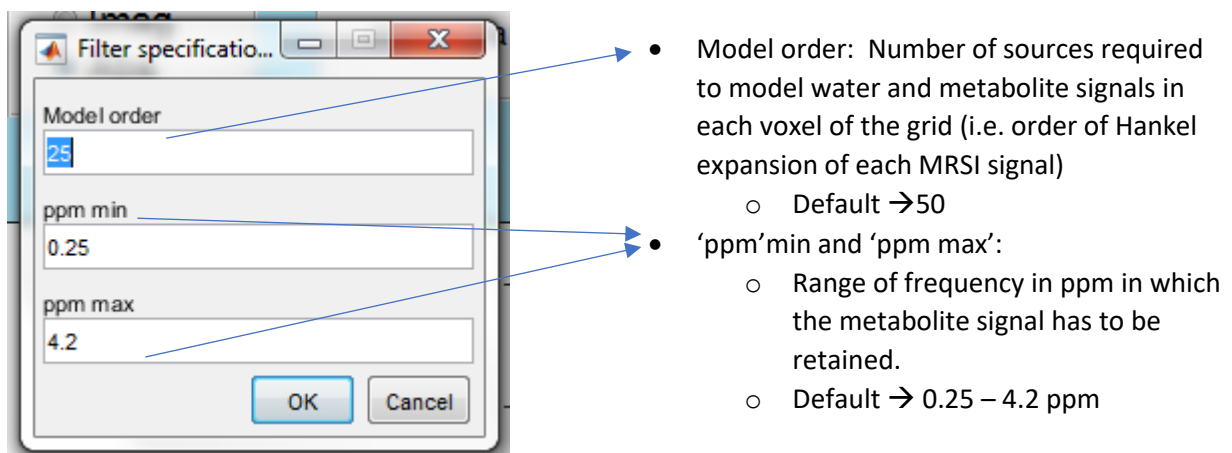


MRSI signals contain information for estimating metabolite concentrations from in-vivo in a non-invasive fashion. Along with clinically relevant components MRSI signals also contain unwanted components such as water, baseline etc. In general, residual water is suppressed before doing any analysis in a pre-processing step. This GUI provides three methods to suppress residual water in MRSI: HLSVD, Hankel-tensor and Löwner-tensor. For details of the water suppression algorithm the user is referred to [1].



HLSVD: To suppress residual water using Hankel Lanczos singular value decomposition (HLSVD) method. The HLSVD implementation is part of the SPID software toolbox [5] [6] which is based on [7].

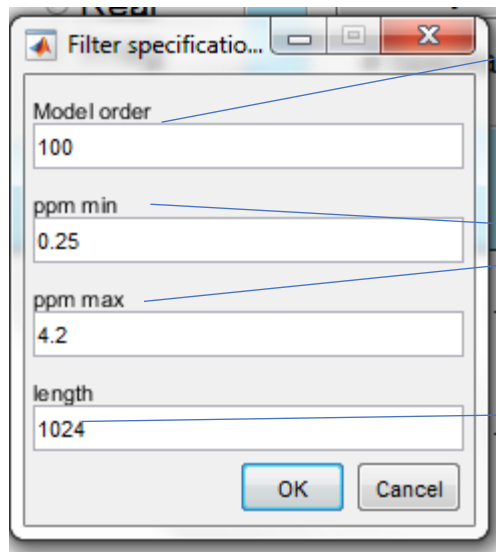
Input required by HLSVD method:



Hankel

Hankel: To suppress residual water using Hankel-tensor method.

Input required by Hankel-tensor method:

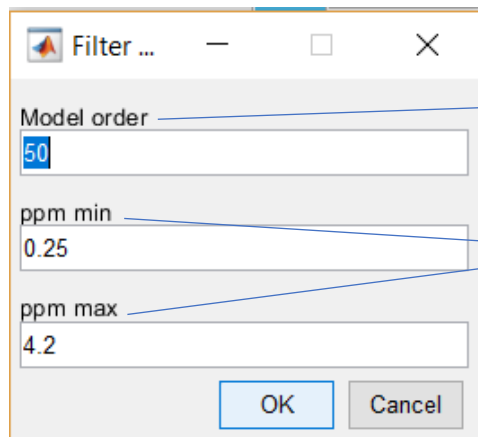


- Model order: Number of sources required to model water and metabolite signals over all voxels in the grid (i.e. order of MLSVD of tensor comprising all Hankel expansions of each MRSI signal as slices)
 - Default → 100
- 'ppm' min and 'ppm max':
 - Range of frequency in ppm in which the metabolite signal has to be retained.
 - Default → 0.25 – 4.2 ppm
- length:
 - length of FID in samples used to construct Hankel matrix. Remaining samples longer than "length" are discarded.

Löwner

Löwner: To suppress residual water using Löwner-tensor method.

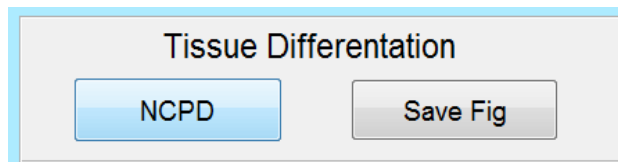
Input required by Löwner -tensor method:



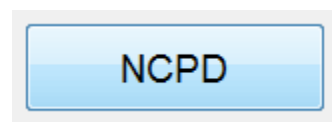
- Model order: Number of sources required to model water and metabolite signals in each voxel of the grid (i.e. the number of first-order rational functions). Additionally, 4 baseline sources modelling a 4-th order polynomial are also included.
 - Default → 50
- 'ppm' min and 'ppm max':
 - Range of frequency in ppm in which the metabolite signal has to be retained.

Tissue type differentiation using non-negative canonical polyadic decomposition (NCPD):

Magnetic resonance spectroscopic imaging (MRSI) reveals chemical information that characterizes different tissue types, e.g. in brain tumors. This GUI implements a Non-negative canonical polyadic decomposition (NCPD) based algorithm to differentiate various tissue types and to extract the tissue-specific profiles and their

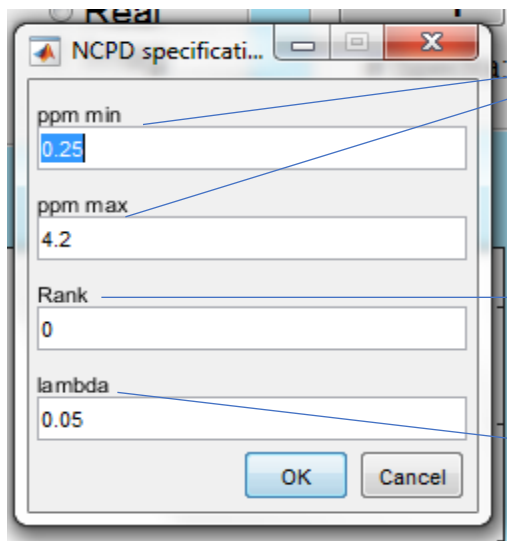


corresponding distribution. For details of the algorithm, the user is referred to [2].



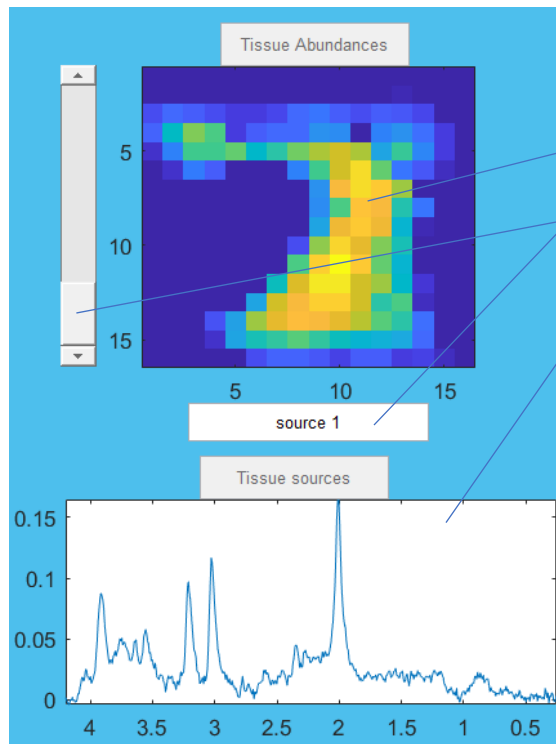
NCPD: To perform tissue type differentiation.

Input required by NCPD algorithm:



- 'ppm' min and 'ppm max':
 - Range of frequency in ppm in which the metabolite signal of interest is retained.
 - Only this region is used for analysis
 - Default → 0.25 – 4.2 ppm
- Rank:
 - Number of tissue sources.
 - $R < 1$, number of sources is estimated automatically.
- lambda
 - L1- regularization weight applied on abundancies.
 - Default → 0.05

NCPD Results:



- Source label, can be modified by user.
- Distribution map of each source.
- Spectrum of each source.
- Slider to see different sources.

Save Fig

To save the figure of abundance map and spectrum of individual sources obtained from NCPD algorithm.

Save

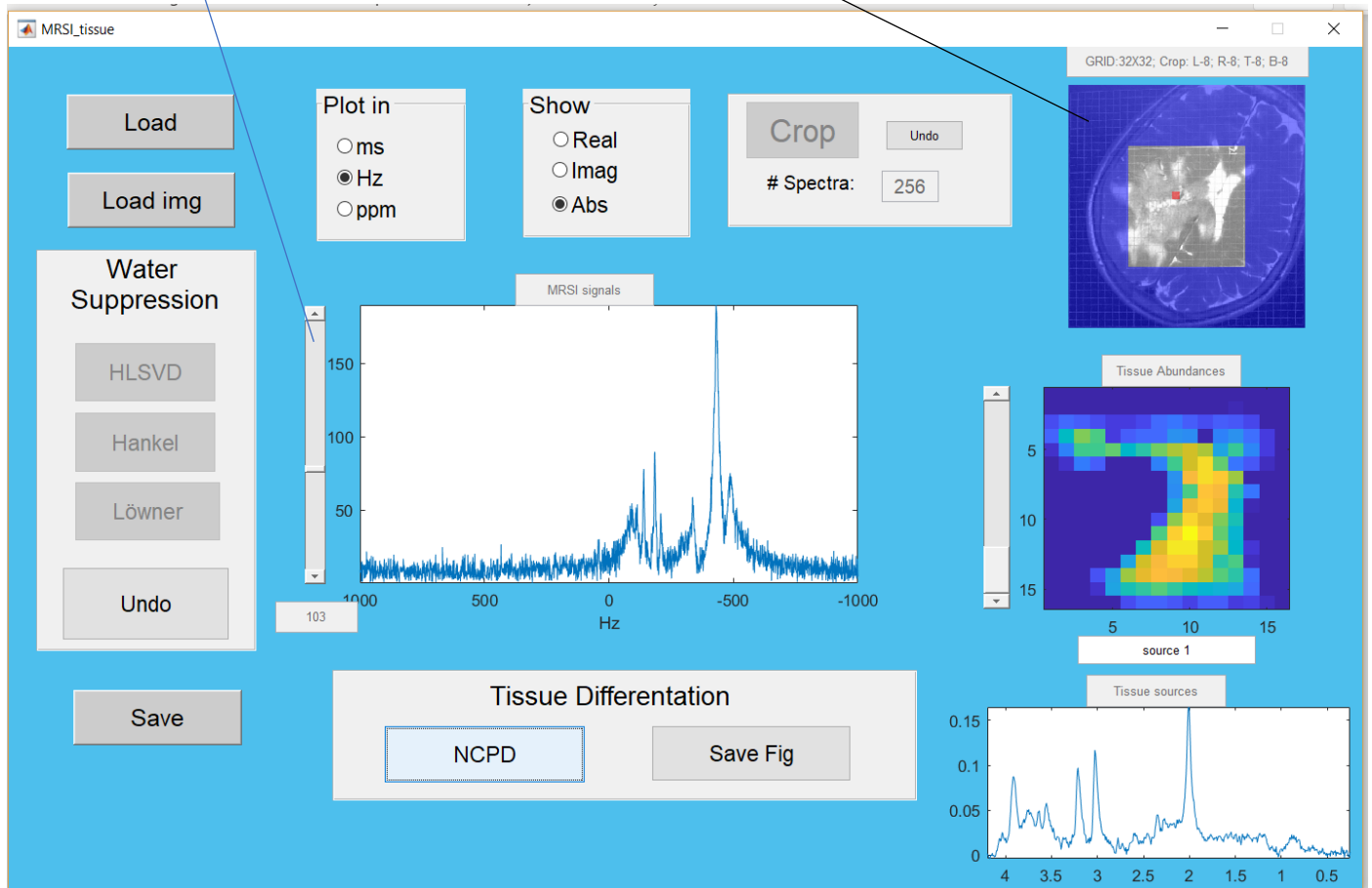
To save the processed signals. Will be saved in '.mat' format, can be loaded again to view the results. The results of NCPD algorithm are saved in `process_info.abundances` and `process_info.sources`.

Note: Save option will save only processed signals and original signals are not saved. Therefore, undo operations of the processed signals are not possible after loading again.

Voxels in MRSI grid:

blue: Cropped voxels, red: Voxel that is displayed.

Slider to view different voxels in the GRID



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