

χ -sep toolbox GUI Manual

Information

- This tool is MATLAB-based GUI software for reconstructing Quantitative Susceptibility Map (QSM) and separating positive and negative susceptibility sources (χ -separation). Separating paramagnetic (e.g., iron) and diamagnetic (e.g., myelin) susceptibility sources co-existed in a voxel provides the distributions of two sources that QSM does not provide. Magnetic susceptibility maps generated by QSM or χ -separation offer important information for research or diagnosis. An inexperienced researcher (user) can easily conduct QSM and χ -separation processing through the tool's user-friendly interface.
- χ -sep toolbox Alpha version
- The χ -sep toolbox includes the following features:
 1. DICOM/NIFTI/MATLAB data compatibility
 2. **QSMnet**: Quantitative susceptibility mapping (QSM) reconstruction algorithm based on deep neural network (QSMnet; J. Yoon et al., Neuroimage, 2018)
 3. **χ -separation using R2' (or R2*)**: magnetic susceptibility source separation algorithms based on convex optimization that share similar contrasts and optimization parameters with either MEDI+0 (Liu et al., MRM, 2018) or iLSQR (Li et al., Neuroimage, 2015) algorithms. The toolbox also provides the option to use pseudo R2 map if R2 measurement is not available (using R2' is recommended for accurate estimation).
 4. **χ -sepnet using R2' (or R2*)**: a U-Net-based neural network that reconstructs χ -separation using R2' and phase. In case R2 is not measured, another neural network is trained to estimate χ -separation maps from R2* and phase.
- Last update: Mar-14-2023
- Reference:

H. Shin, J. Lee, Y. H. Yun, S. H. Yoo, J. Jang, S.-H. Oh, Y. Nam, S. Jung, S. Kim, F. Masaki, W. Kim, H. J. Choi, J. Lee. χ -separation: Magnetic susceptibility source separation toward iron and myelin mapping in the brain. Neuroimage, 2021 Oct; 240:118371.

M. Kim, H. Shin, C. Oh, H. Jeong, S. Ji, H. An, J. Kim, J. Jang, B. Bilgic, and J. Lee, "Chi-sepnet: Susceptibility source separation using deep neural network", 30th Annual Meeting of International Society of Magnetic Resonance in Medicine, 2022; 2464.

J. Yoon, E. Gong, I. Chatnuntawech, B. Bilgic, J. Lee, W. Jung, J. Ko, H. Jung, K. Setsompop, G. Zaharchuk, E.Y. Kim, J. Pauly, J. Lee. Quantitative susceptibility mapping using deep neural network: QSMnet. Neuroimage. 2018;179:199-206.
- χ -sep toolbox is powered by MEDI toolbox, STI Suite.
(MEDI toolbox and STI Suite are used for phase data processing, so if you are only interested in QSMnet, χ -separation, and χ -sepnet, you don't need them.)

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Name:

Affiliation:

Software:

Purpose:

INDEX

Requirements	6
Installation and integration with support tools	7
1. Add χ -sep toolbox path.....	7
2. Add MATLAB toolbox path.....	7
3. Add QSM toolbox path	8
4. Open χ -sep toolbox GUI.	8
Information of χ-sep toolbox GUI.....	9
1. Main window	9
2. Input data	10
3. Output data and directory	11
4. Parameters and process	12
Usage of χ-sep toolbox GUI.....	14
1. For whole processing from phase processing to χ-separation (R2' version)	14
① Execute χ -sep toolbox GUI.	14
② Load input data.	15
③ Set dropbox of output directory to 'NIFTI' and load output directory.....	17
④ Put common parameters of your data.	17
⑤ Set method of each process.	17
⑥ Run processing	18
2. For whole processing from phase processing to χ-separation (R2* version).....	20
① Execute χ -sep toolbox GUI.	20
② Load input data.	21
③ Set dropbox of output directory to 'NIFTI' and load output directory.....	23
④ Put common parameters of your data.	23
⑤ Set method of each process.	23
⑥ Run processing	25
3. For phase processing	26
① Execute χ -sep toolbox GUI.	26
② Load input data.	27
③ Set dropbox of output directory to 'NIFTI' and load output directory.....	28
④ Put common parameters of your data.	28
⑤ Set method of each process.	28
⑥ Run processing	29
4. For QSMnet and χ-separation (R2' version)	30

①	Execute χ -sep toolbox GUI.	30
②	Load input data.	31
③	Set dropbox of output directory to 'NIFTI' and load output directory.....	32
④	Put common parameters of your data.	32
⑤	Set method of each process.	32
⑥	Run processing	33
5.	For QSMnet and χ-separation (R2* version)	34
①	Execute χ -sep toolbox GUI.	34
②	Load input data.	35
③	Set dropbox of output directory to 'NIFTI' and load output directory.....	36
④	Put common parameters of your data.	36
⑤	Set method of each process.	36
⑥	Run processing	37

Requirements

MATLAB toolbox

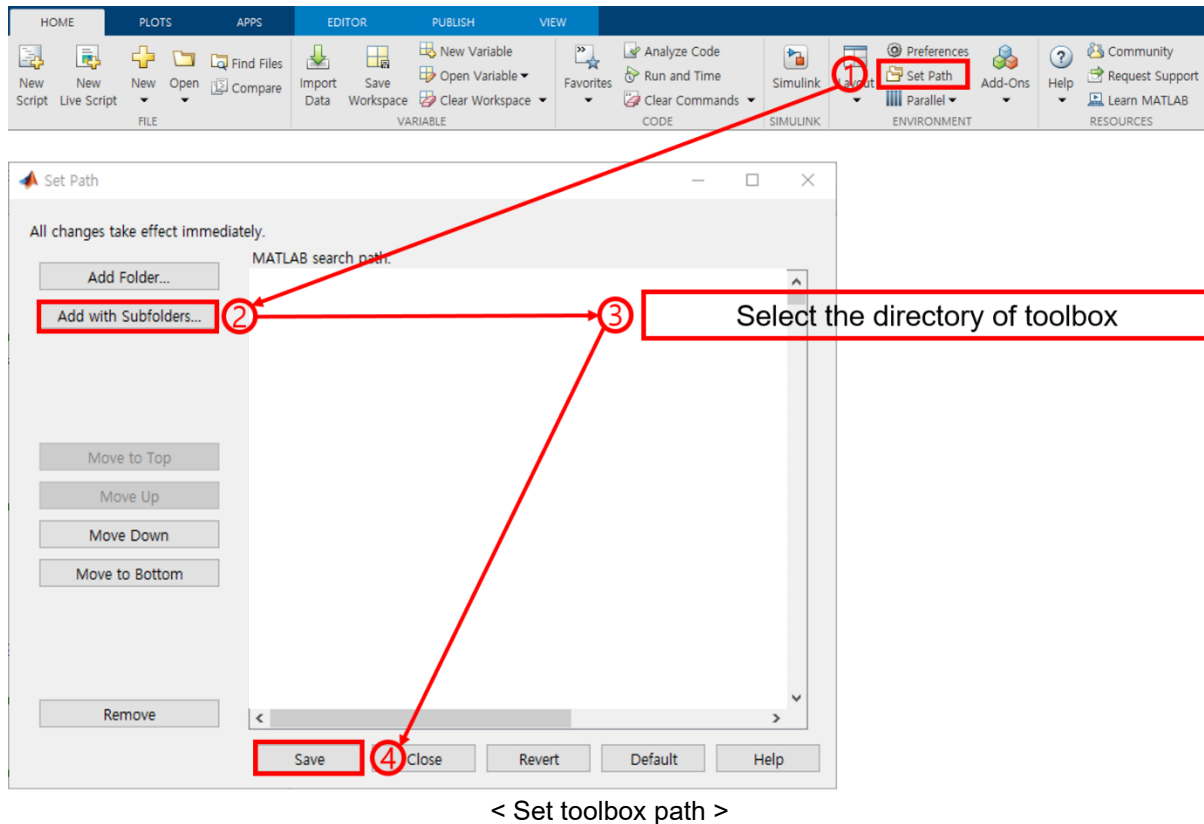
1. xiangruili/dicm2nii
(<https://kr.mathworks.com/matlabcentral/fileexchange/42997-xiangruili-dicm2nii>)
2. Tools for NIfTI and ANALYZE image
(<https://kr.mathworks.com/matlabcentral/fileexchange/8797-tools-for-nifti-and-analyze-image>)
3. Deep Learning Toolbox Converter for ONNX Model Format
(<https://kr.mathworks.com/matlabcentral/fileexchange/67296-deep-learning-toolbox-converter-for-onnx-model-format>)

QSM toolbox

1. STI Suite (Version 3.0)
(<https://people.eecs.berkeley.edu/~chunlei.liu/software.html>)
 2. MEDI toolbox
(<http://pre.weill.cornell.edu/mri/pages/qsm.html>)
- MEDI toolbox and STI Suite are used for phase data processing, so if you are only interested in QSMnet, χ -separation, and χ -sepnet, you do not need to install them.

Installation and integration with support tools

1. Add χ -sep toolbox path



- ① Click “Set Path”
- ② Click “Add with Subfolders”
- ③ Select the directory of Select the directory of “ χ -sep toolbox”
- ④ Click “Save”

2. Add MATLAB toolbox path

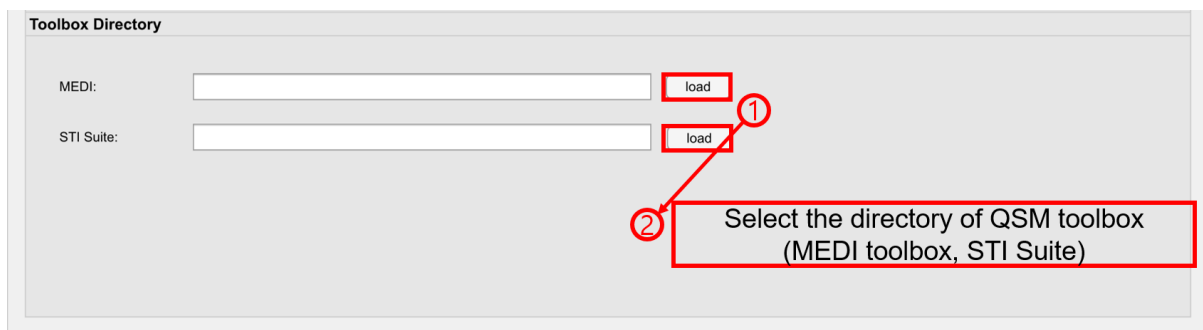
- ① xiangruili/dicm2nii: Add the directory path of dicm2nii in the same way as 1 (Add χ -separation tool path).
- ② Tools for NIfTI and ANALYZE image: Add the directory path of Tools for NIfTI and ANALYZE image in the same way as 1 (Add χ -separation tool path).
- ③ Deep Learning Toolbox Converter for ONNX Model Format: Download onnxconverter Add-on, and then install it.

3. Add QSM toolbox path

- ① STI Suite: Add the directory path of STI Suite in the same way as 1 (Add χ -sep toolbox path).
- ② MEDI toolbox: Add the directory path of MEDI toolbox in the same way as 1 (Add χ -sep toolbox path).

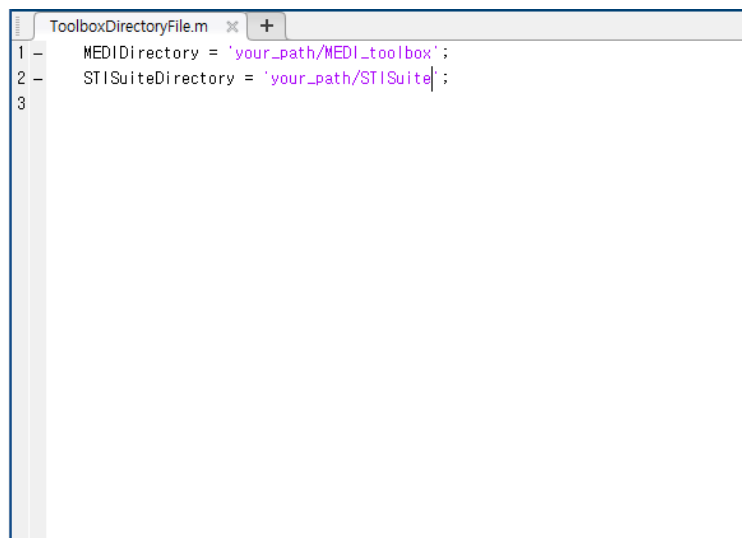
Alternatively, there are two ways to add QSM toolbox path.

- ① Load the QSM toolbox path from the common tab of the χ -sep toolbox GUI.



< Set QSM toolbox path in χ -sep toolbox GUI >

- ② Write the QSM toolbox path in ' χ -sep_toolbox_dir/initialize/ToolboxDirectoryFile.m'.



< Write the QSM toolbox path in ToolboxDirectoryFile.m >

4. Open χ -sep toolbox GUI.

- Type “Chisep” in MATLAB command.
- Click “GUI for chi-separation” button.

Information of χ -sep toolbox GUI

1. Main window

The screenshot displays the main window of the χ -sep toolbox GUI, which is divided into three main panels:

- Setting panel (Red background):** This panel contains tabs for 'Phase unwrapping', 'Background field removal', 'QSM', 'Chi-Separation', and 'Common'. The 'Phase unwrapping' tab is active. It includes an 'I/O' section with input fields for 'Magnitude:', 'Phase:', and 'Brain Mask:', each with a 'load' button and a 'Load' dropdown menu. Below this is an 'Output Directory:' field with a 'load' button and a 'NIFTI' dropdown menu. The 'Setting' section below has a 'Method:' dropdown menu set to 'Laplacian (STI Suite)' and a 'Pad Size:' input field with the value '[12, 12, 12]'.
- Display panel (Blue background):** This panel shows a tree view with 'InputData' and 'OutputData'. It includes a 'Data Type' input field, a 'Matrix Size' input field, and a 'Display' button.
- Start panel (Green background):** This panel contains a 'Processing' section with four checkboxes: 'Phase unwrapping', 'Background field removal', 'QSM', and 'Chi-Separation'. A large 'Start' button is located at the bottom right.

< χ -sep toolbox GUI main window >

Setting panel: You can set data I/O and parameters for process. This panel consist of 'Phase unwrapping', 'Background field removal', 'QSM', ' χ -separation', and 'Common' tabs.

Display panel: This panel displays briefly the data.

Start panel: You can select processes, then run it.

2. Input data

Data name	Unit	File format	Note	If select 'process',
Magnitude	-	DICOM, NIFTI, MAT	3D or 4D (multi-echo)	-
Phase	-	DICOM, NIFTI, MAT	3D or 4D (multi-echo)	-
Brain mask	-	NIFTI, MAT	3D	Generated by tool (Brain extraction based on the BET tool from the MEDl)
Field map	Hz	NIFTI, MAT	3D	Generated by tool (Phase unwrapping process)
Local field	Hz	NIFTI, MAT	3D	Generated by tool (Background field removal process)
QSM	ppm	NIFTI, MAT	3D	Generated by tool (QSM process)
R2'	-	NIFTI, MAT	3D	-
R2*	-	NIFTI, MAT	3D	Generated by tool (Auto-Regression on Linear Operations from the MEDl: multi-echo mag is needed)

< Information of input data >

- You can specify the format of input data with the dropdown. It can be loaded as NIFTI or MAT with the 'Load'. For Magnitude and Phase, they can be loaded as DICOM by selecting the 'Dicom' of the dropdown.

The screenshot shows the 'Phase unwrapping' tab selected. Under the 'I/O' section, there are three rows: 'Magnitude:', 'Phase:', and 'Brain Mask:'. Each row has a text input field, a 'load' button, and a dropdown menu. The dropdown menu for 'Magnitude' is open, showing three options: 'Load' (highlighted in blue), 'Dicom', and 'Load'.

< Example: a dropdown of magnitude >

- If the 'Process' is selected, Brain mask, Field map, Local field, QSM, and R2* can be generated.

The screenshot shows the 'Phase unwrapping' tab selected. Under the 'I/O' section, there are three rows: 'Magnitude:', 'Phase:', and 'Brain Mask:'. Each row has a text input field, a 'load' button, and a dropdown menu. The dropdown menu for 'Brain Mask' is open, showing three options: 'Load' (highlighted in blue), 'Load', and 'Process'.

< Example: a dropdown of brain mask >

3. Output data and directory

Data name	Unit	File format	Note
Field map	Hz	NIFTI, MAT	Generated by Phase unwrapping
Local field	Hz	NIFTI, MAT	Generated by Background field removal
Brain mask	-	NIFTI, MAT	Generated by Background field removal (V-SHARP)
QSM	ppm	NIFTI, MAT	Generated by QSM
χ -positive map	ppm	NIFTI, MAT	Generated by χ -separation
χ -positive map	ppm	NIFTI, MAT	Generated by χ -separation
χ -total map (pos + neg)	ppm	NIFTI, MAT	Generated by χ -separation

< Information of output data >

- You can define the format of data to save on the drop box next to the load button of the 'Output Directory'.
- If 'None' is selected, the output data is not saved.

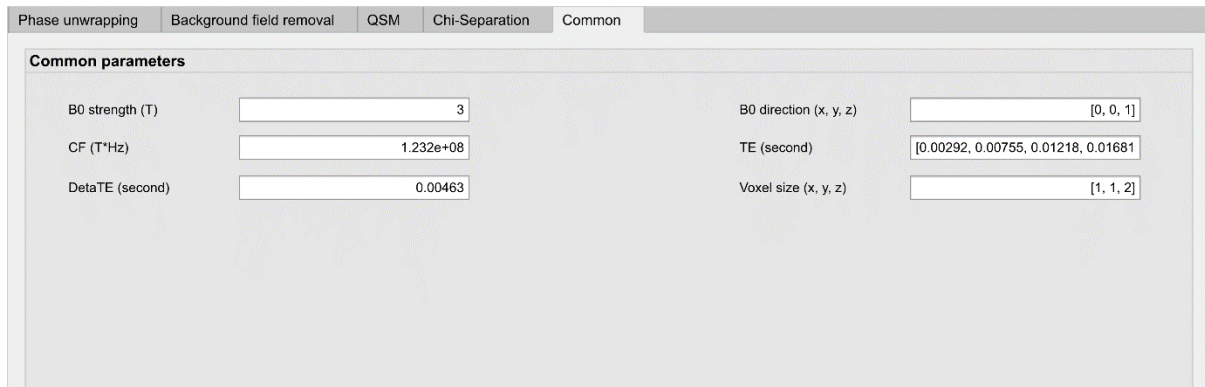
The screenshot shows a software interface with several tabs: 'Phase unwrapping', 'Background field removal', 'QSM', 'Chi-Separation', and 'Common'. The 'Common' tab is active. Under the 'I/O' section, there are input fields for 'Magnitude:', 'Phase:', and 'Brain Mask:', each with a 'load' button and a dropdown menu. Below these, there is an 'Output Directory:' field with a 'load' button and a dropdown menu. The dropdown menu is open, showing options: 'NIFTI' (selected), 'NIFTI', 'MAT', and 'None'. At the bottom, under the 'Setting' section, there is a 'Method:' dropdown menu with 'Laplacian (STI Suite)' selected.

< Example: a dropbox of output directory >

4. Parameters and process

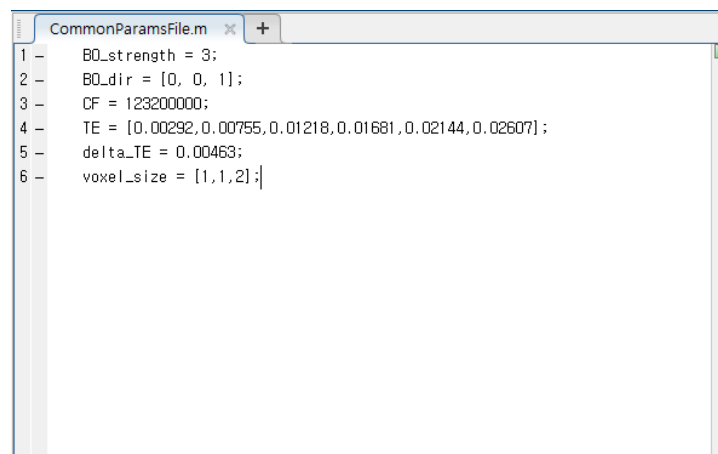
● Common parameters

- These are the six parameters of the data commonly used in various processes: B0 strength, B0 direction, central frequency (CF), echo time (TE), delta TE, and voxel size.
- There are two ways to set common parameters.
- The first way is to put the parameters of your data at the common tab of the setting panel.



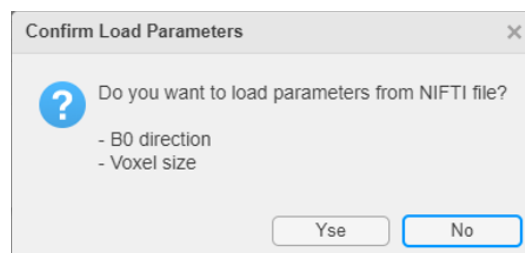
< A common tab of χ -sep toolbox GUI >

- The second way is to write them in ' χ -sep_toolbox_dir/initialize/CommonParamsFile.m' before running the tool.



< CommonParamsFile.m >

- Additionally, you can load them that exist in the header file when data with extension of NIFTI or Dicom is loaded.



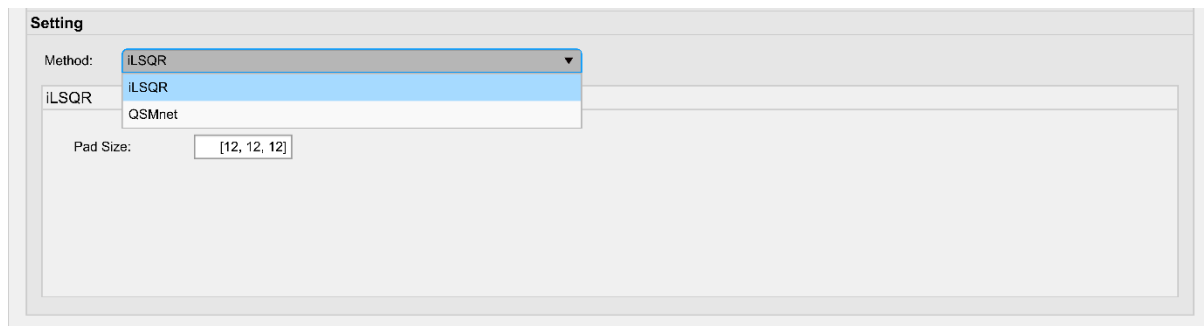
< A dialog asking whether to load the parameters existing in the header file >

- Processes

Process name	Method	Note
Phase Unwrapping	Laplacian-based method	-
Background Field Removal	V-SHARP	Generate QSM mask
QSM	iLSQR, QSMnet	You can select the reference tissue in QSMnet method
χ -separation	χ -separation _{L1} , χ -separation _{SA} , χ -sepnet	When you don't have R2, You can create pseudo R2 filled with nominal values for χ -separation methods. Also, you can run χ -sepnet trained by R2*.

< methods of processes >

- By controlling the drop box for Method, you can select the methods of process in the activated tab.
- A panel of the selected method appears and then you can put the parameters of the process.
- Since the processing time of χ -separation_{L1} and χ -separation_{SA} is much longer than that of deep learning-based methods for χ -separation, it is recommended to use the network method if you want to see the results quickly.
- **Warning:** Deep learning (QSMnet and χ -sepnet) is designed for 1 mm isotropic voxel size. Too different resolution can result in artifacts.



< Example: a dropbox of QSM method >

Usage of χ -sep toolbox GUI

1. For whole processing from phase processing to χ -separation (R2' version)

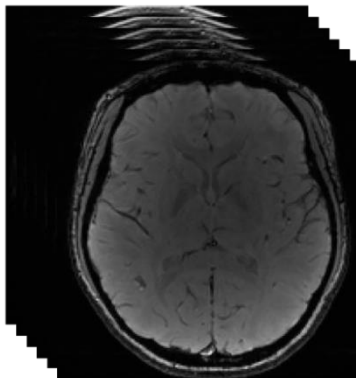
Exercise

- Perform whole processing implemented in the tool with one run from phase processing to χ -separation.
(MEDI toolbox and STI Suite are required for full processing.)

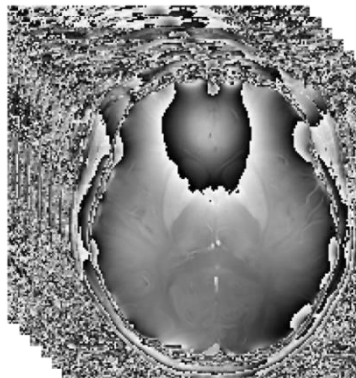
Input data

- Multi-echo GRE magnitude (4D: x, y, z, echo time)
- Multi-echo GRE phase (4D: x, y, z, echo time)
- R2prime (3D)

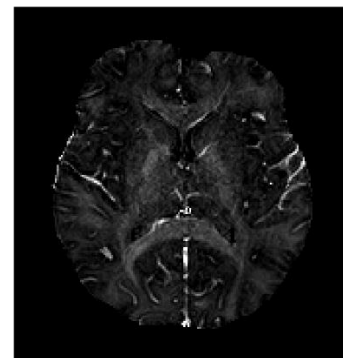
Magnitude



Phase



R2prime



Processes

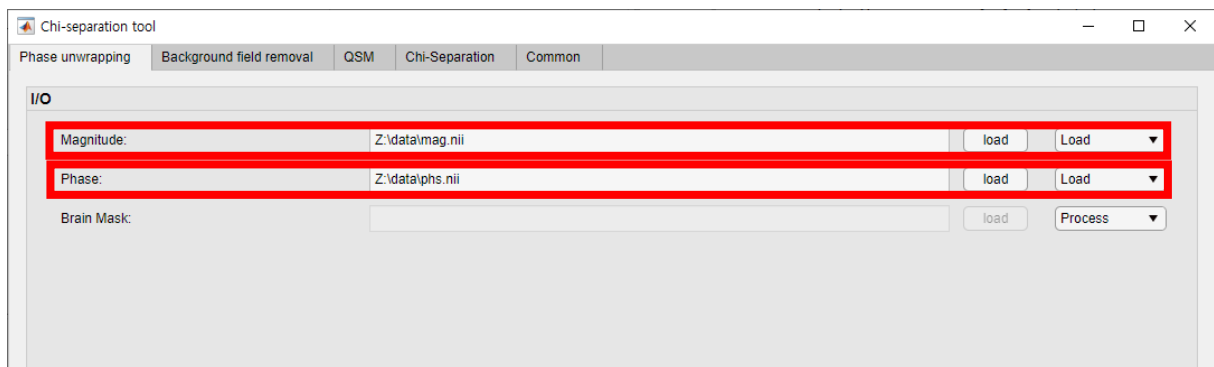
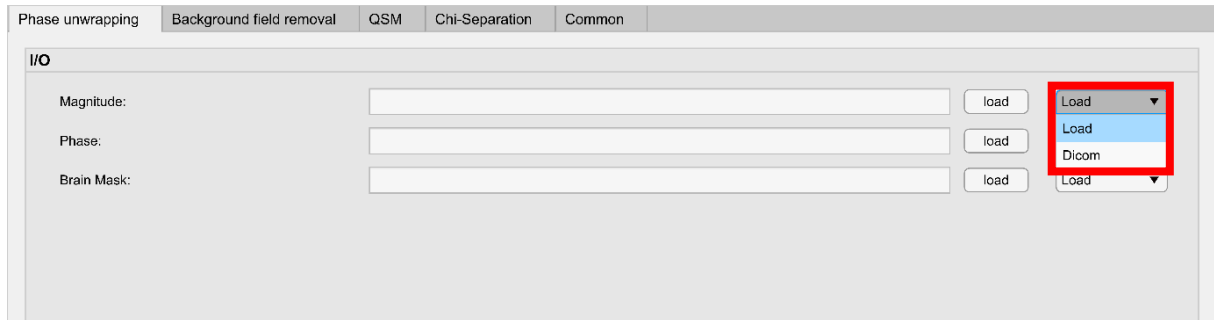
- Phase unwrapping: Laplacian-based method (STI Suite)
- Background field removal: V-SHARP
- QSM: iLSQR or QSMnet
- χ -separation: χ -separation or χ -sepnet

① Execute χ -sep toolbox GUI.

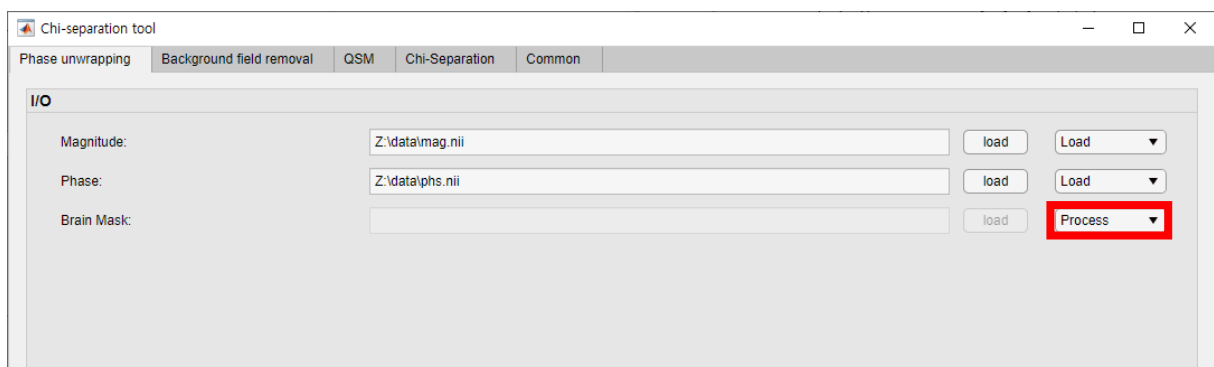
- Type “Chisep” in MATLAB command.
- Click “GUI for chi-separation” button.

② Load input data.

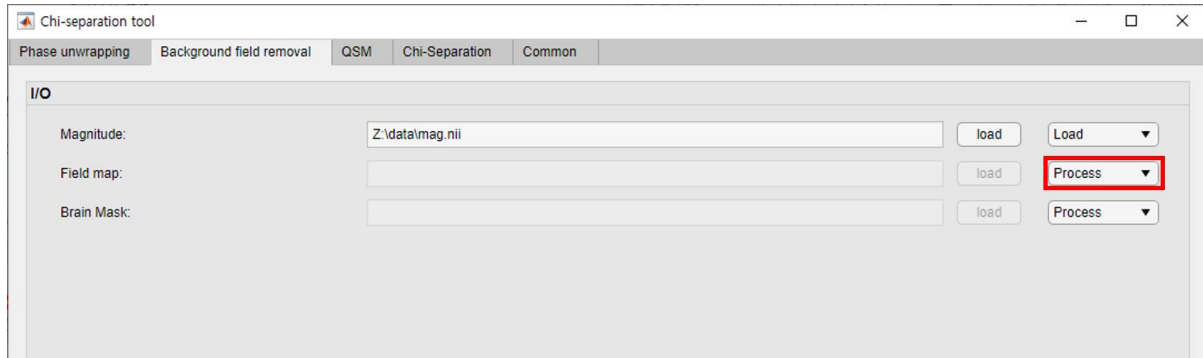
- Set the dropbox to 'Load' if the magnitude and phase are NIfTI or MAT files, or 'Dicom' if they are DICOM in Phase unwrapping tab.
- Then press the load button to select a NIfTI or MAT file or a Dicom directory to load the data.



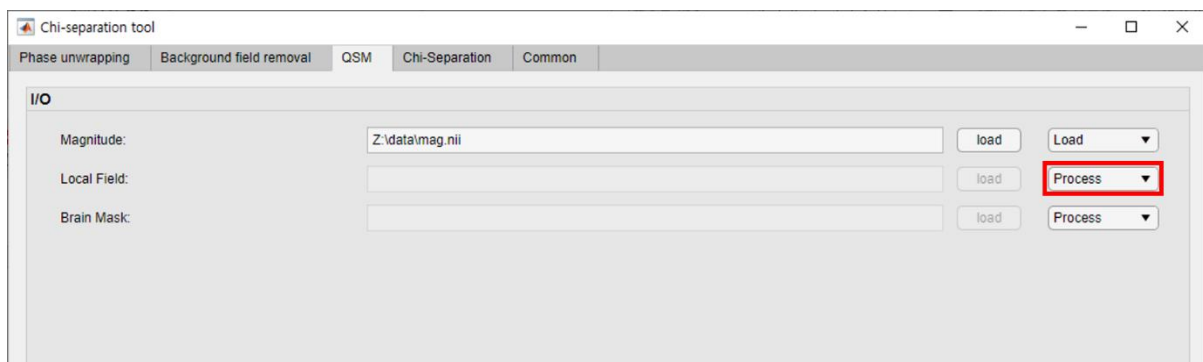
- Set dropbox of Brain Mask to 'Process' in Phase unwrapping tab.



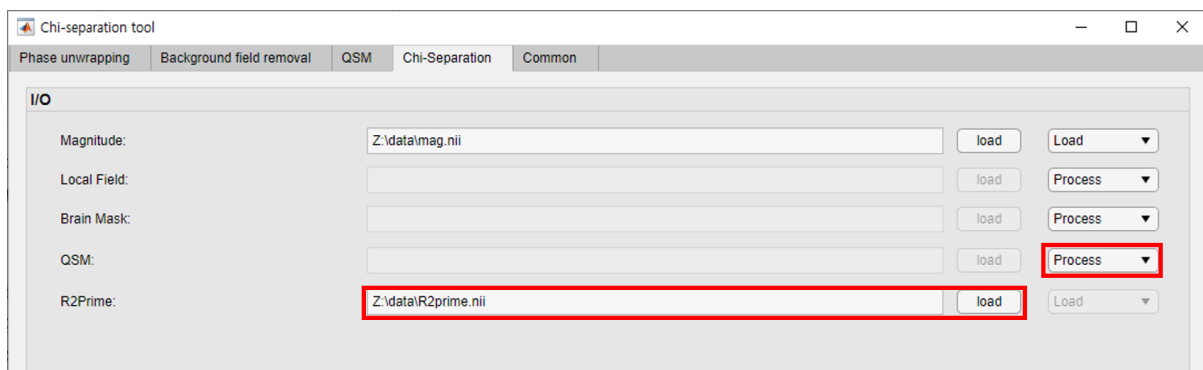
- Set dropbox of Field map to 'Process' in Background field removal tab.




- Set dropbox of Local field to 'Process' in QSM unwrapping tab.



- Set dropbox of QSM to 'Process' and load R2' in χ -separation tab.

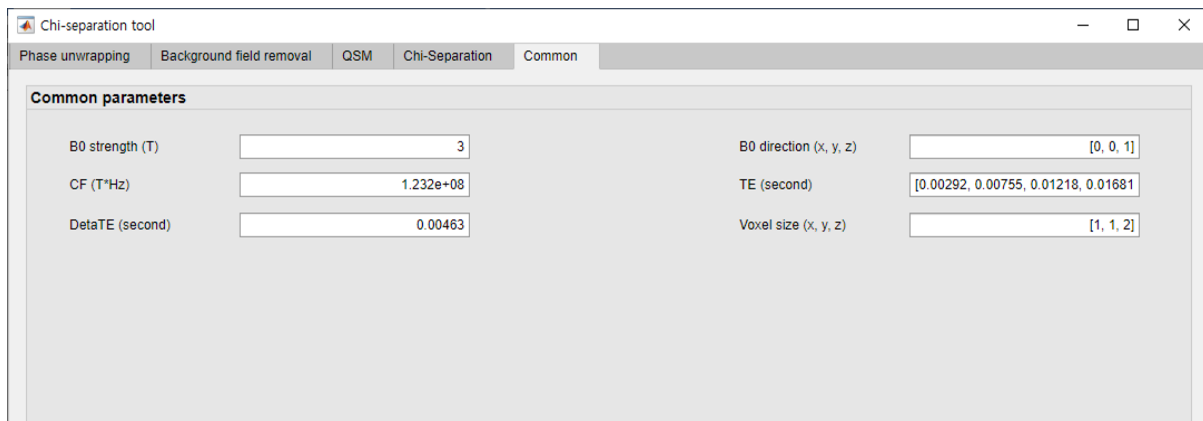


③ Set dropbox of output directory to 'NIFTI' and load output directory.



A screenshot of a software interface showing the 'Output Directory' field. The field contains the text 'Z:\results'. To the right of the field is a 'load' button and a dropdown menu currently set to 'NIFTI'. A red rectangular box highlights the 'Output Directory' field and the 'load' button.

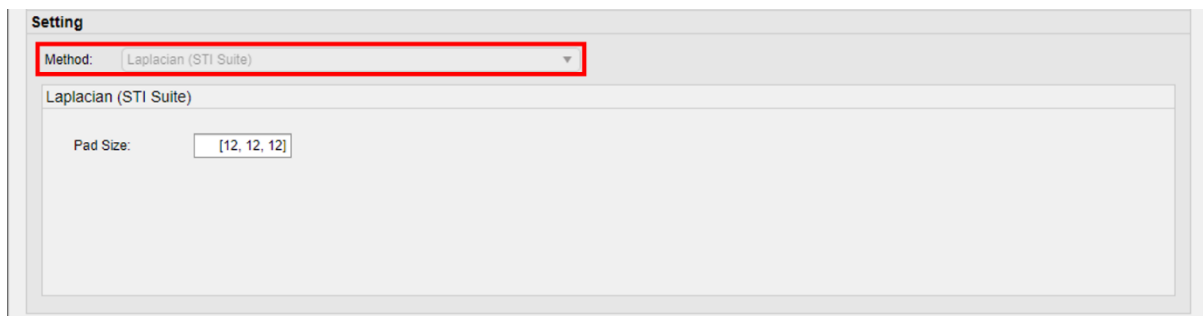
④ Put common parameters of your data.



A screenshot of the 'Chi-separation tool' window. The 'Common' tab is selected. The 'Common parameters' section contains several input fields: 'B0 strength (T)' with value '3', 'CF (T*Hz)' with value '1.232e+08', 'DeltaTE (second)' with value '0.00463', 'B0 direction (x, y, z)' with value '[0, 0, 1]', 'TE (second)' with value '[0.00292, 0.00755, 0.01218, 0.01681]', and 'Voxel size (x, y, z)' with value '[1, 1, 2]'. The window title bar shows 'Chi-separation tool' and standard window controls.

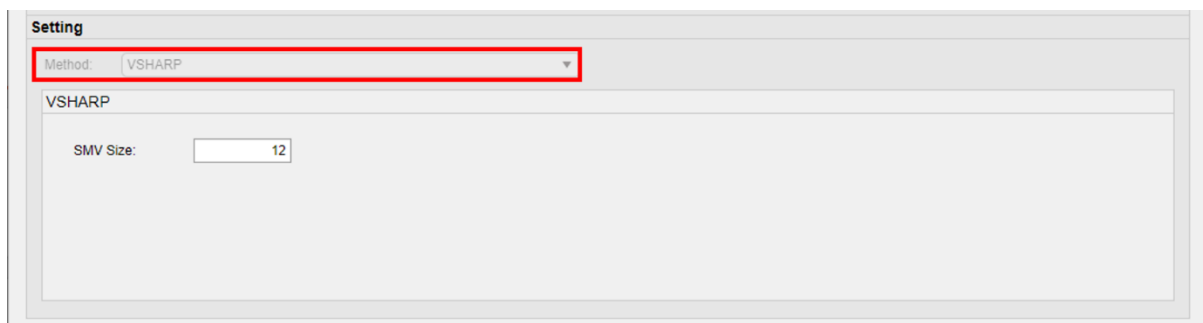
⑤ Set method of each process.

- Keep the Laplacian method in Phase unwrapping tab.



A screenshot of the 'Setting' dialog box. The 'Method' dropdown is set to 'Laplacian (STI Suite)'. Below it, the 'Laplacian (STI Suite)' section is expanded, showing a 'Pad Size' input field with the value '[12, 12, 12]'. A red rectangular box highlights the 'Method' dropdown menu.

- Keep the V-SHARP method in Background field removal tab.



A screenshot of the 'Setting' dialog box. The 'Method' dropdown is set to 'VSHARP'. Below it, the 'VSHARP' section is expanded, showing an 'SMV Size' input field with the value '12'. A red rectangular box highlights the 'Method' dropdown menu.

- On the QSM tab, select either the iLSQR method or the QSMnet method.

Setting

Method: iLSQR

iLSQR

QSMnet

Pad Size: [12, 12, 12]

- On the χ -separation tab, select either the L1, SA or χ -sepnet method.

Setting

Method: L1 norm-regularization

L1 norm-re

Streaking artifact-suppression

Using R: Chi-sep net

Nominal Value: 0

load Process

Set Chi-Sep L1 Norm Parameters Load Chi-Sep L1 Norm Data

⑥ Run processing

- Check all processes in start panel.
- Press the start button.

Processing

☒ Phase unwrapping

☒ Background field removal

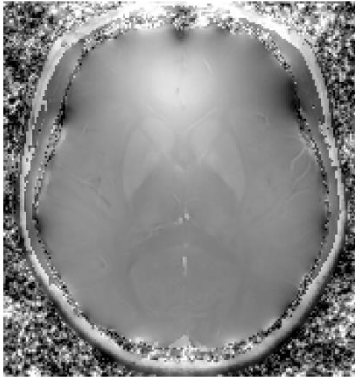
☒ QSM

☒ Chi-Separation

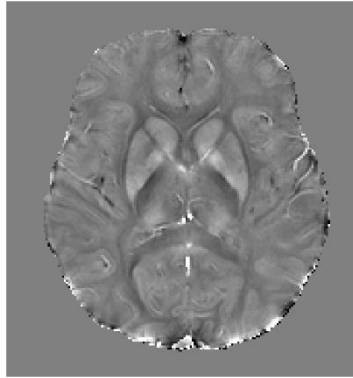
Start

- When all processes are finished, the results are saved to the output directory.

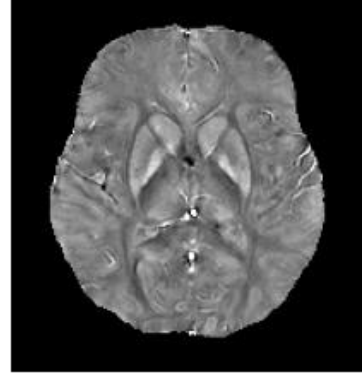
Total field



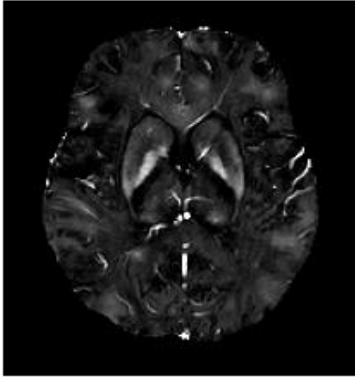
Local field



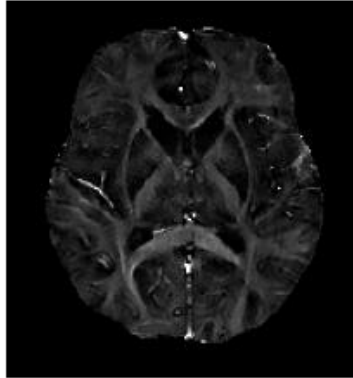
QSM



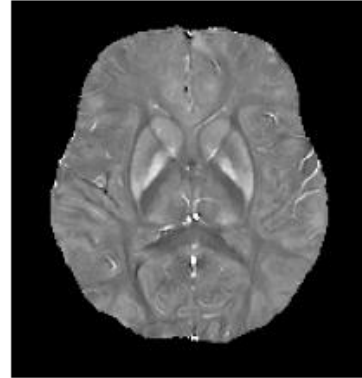
$\chi_{positive}$



$\chi_{negative}$



χ_{total}



2. For whole processing from phase processing to χ -separation (R2* version)

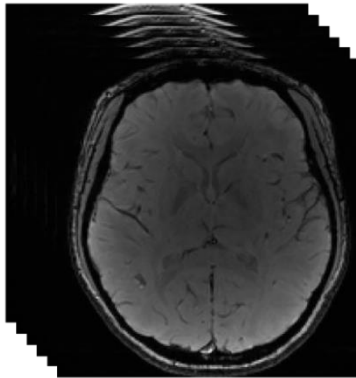
Exercise

- Perform whole processing implemented in the tool with one run from phase processing to χ -separation.
(MEDI toolbox and STI Suite are required for full processing.)

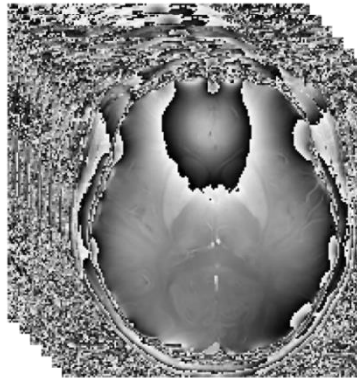
Input data

- Multi-echo GRE magnitude (4D: x, y, z, echo time)
- Multi-echo GRE phase (4D: x, y, z, echo time)

Magnitude



Phase



- Perform all processes implemented in the tool with one run using only multi-echo gre data.

Processes

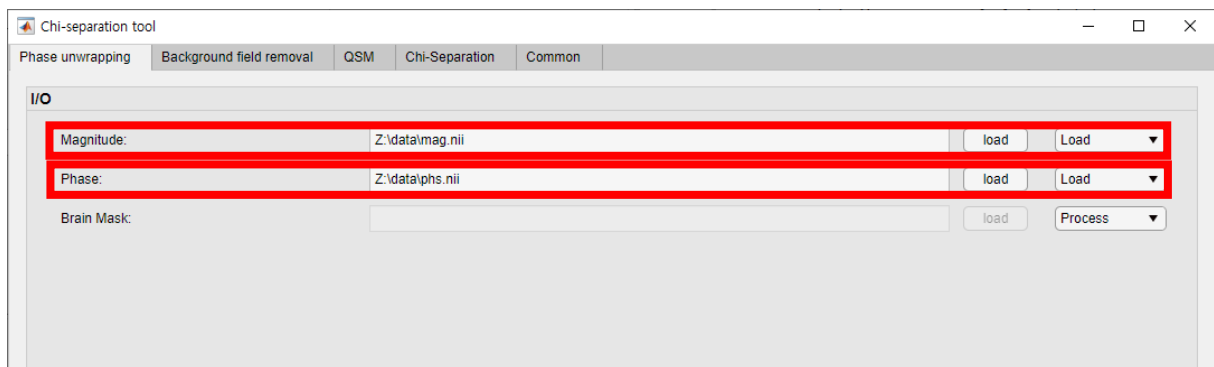
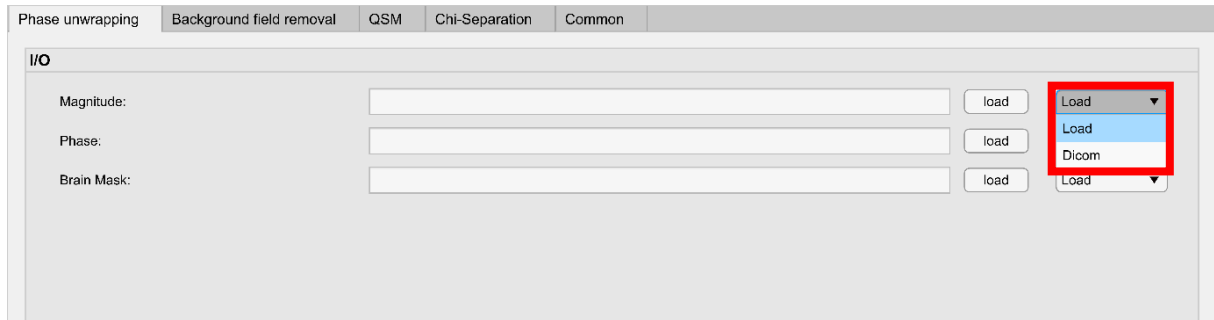
- Phase unwrapping: Laplacian-based method (STI Suite)
- Background field removal: V-SHARP
- QSM: iLSQR or QSMnet
- χ -separation: χ -separation or χ -sepnet

① Execute χ -sep toolbox GUI.

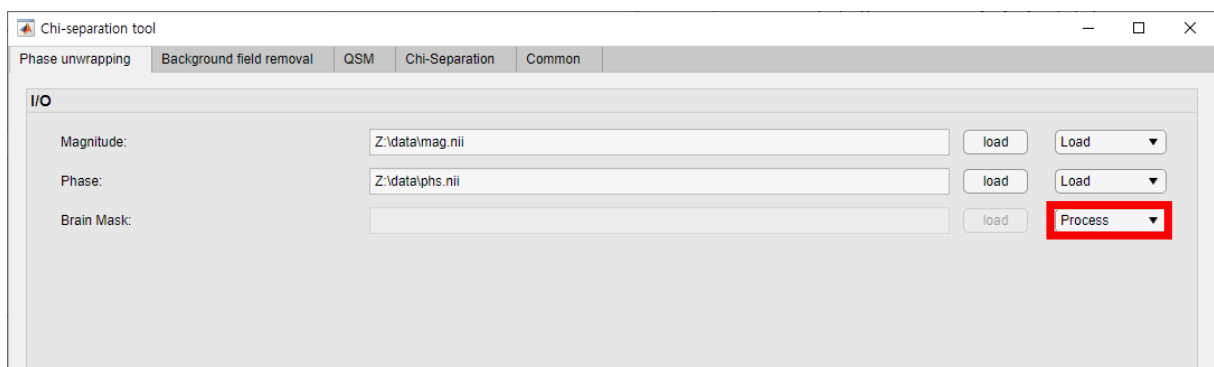
- Type "Chisep" in MATLAB command.
- Click "GUI for chi-separation" button.

② Load input data.

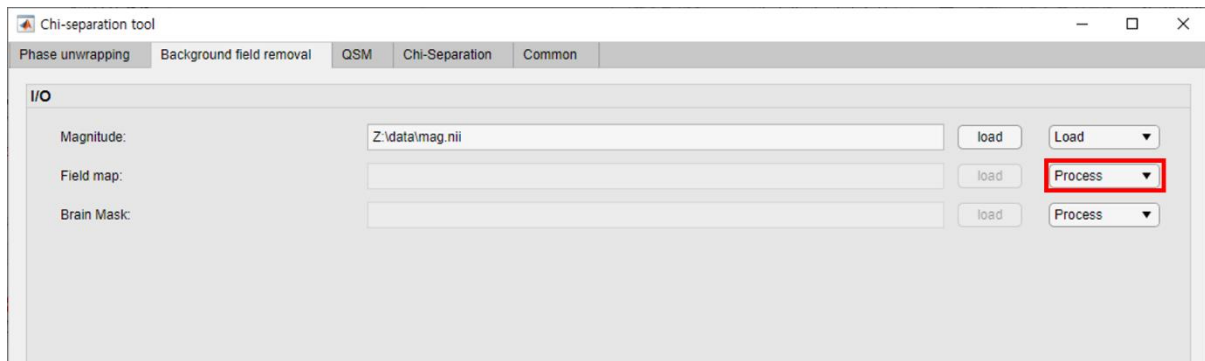
- Set the dropbox to 'Load' if the magnitude and phase are NIfTI or MAT files, or 'Dicom' if they are DICOM in Phase unwrapping tab.
- Then press the load button to select a NIfTI or MAT file or a Dicom directory to load the data.



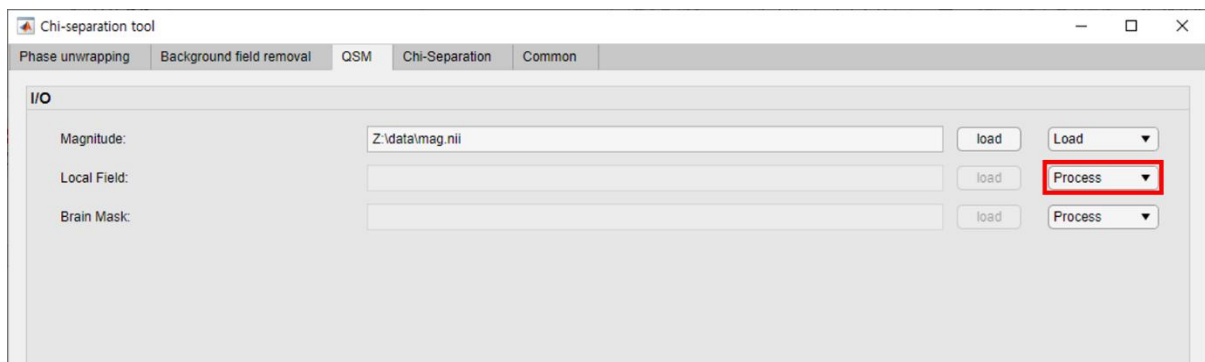
- Set dropbox of Brain Mask to 'Process' in Phase unwrapping tab.



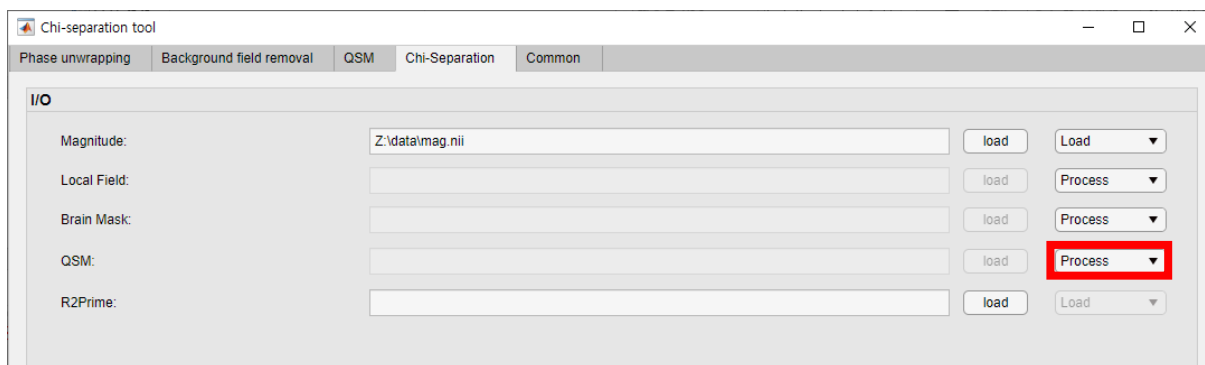
- Set dropbox of Field map to 'Process' in Background field removal tab.



- Set dropbox of Local field to 'Process' in QSM unwrapping tab.



- Set dropbox of QSM to 'Process' in χ -separation tab.

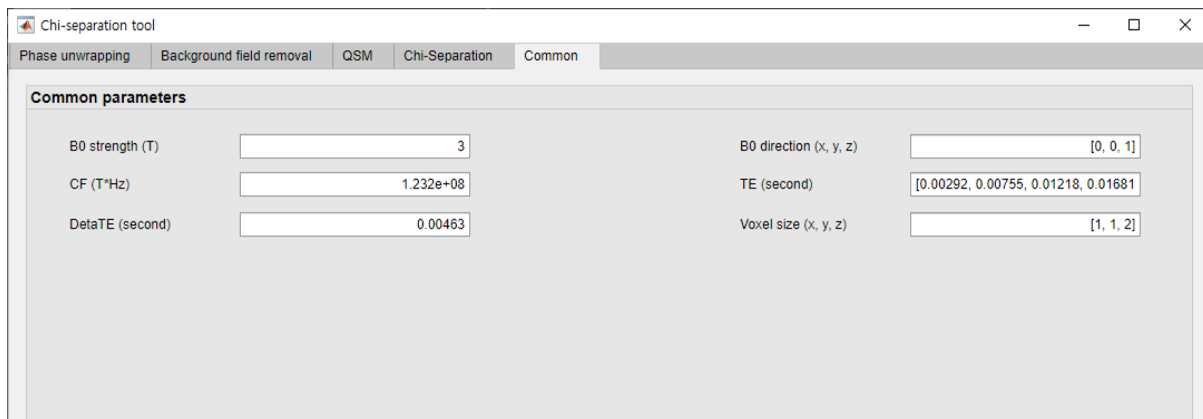


③ Set dropbox of output directory to 'NIFTI' and load output directory.



A screenshot of the 'Output Directory' field in the Chi-separation tool. The field contains the text 'Z:\results'. To the right of the field is a 'load' button and a dropdown menu currently showing 'NIFTI'. The entire field and button area are enclosed in a red rectangular box.

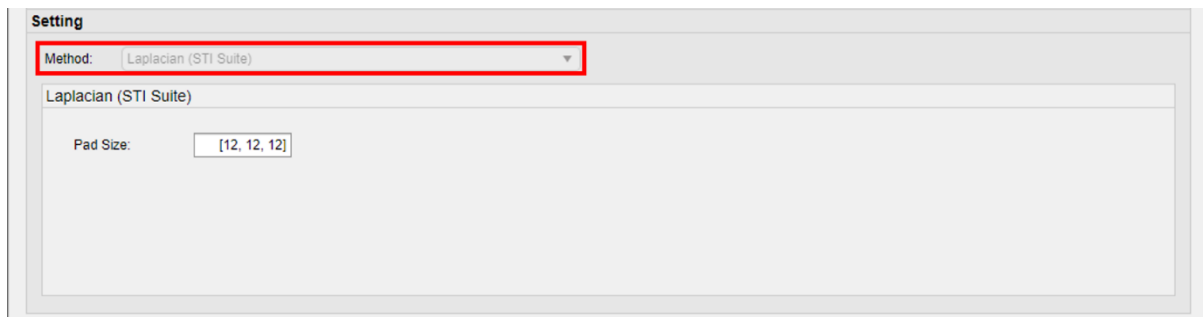
④ Put common parameters of your data.



A screenshot of the 'Common parameters' tab in the Chi-separation tool. The window title is 'Chi-separation tool'. The tabs are 'Phase unwrapping', 'Background field removal', 'QSM', 'Chi-Separation', and 'Common'. The 'Common' tab is active. It contains several input fields: 'B0 strength (T)' with value '3', 'CF (T*Hz)' with value '1.232e+08', 'DeltaTE (second)' with value '0.00463', 'B0 direction (x, y, z)' with value '[0, 0, 1]', 'TE (second)' with value '[0.00292, 0.00755, 0.01218, 0.01681]', and 'Voxel size (x, y, z)' with value '[1, 1, 2]'. The fields are arranged in two columns.

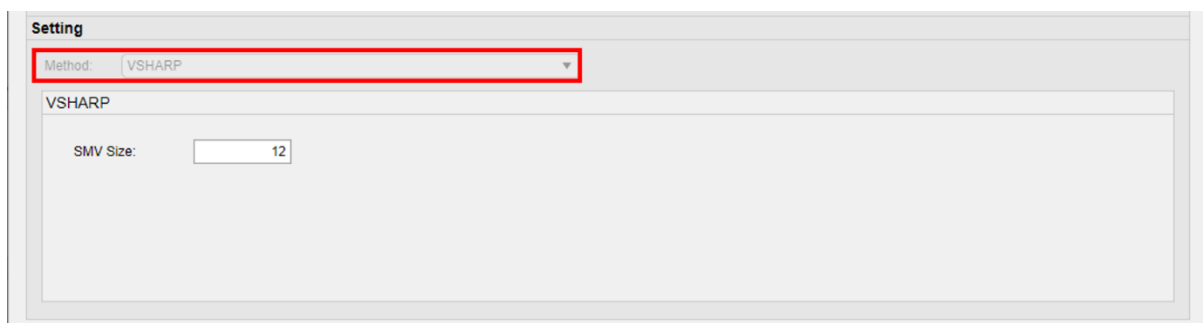
⑤ Set method of each process.

- Keep the Laplacian method in Phase unwrapping tab.



A screenshot of the 'Setting' dialog box for the 'Laplacian (STI Suite)' method. The 'Method:' dropdown is set to 'Laplacian (STI Suite)'. Below it, the 'Pad Size:' field is set to '[12, 12, 12]'. The entire dialog box is highlighted with a red border.

- Keep the V-SHARP method in Background field removal tab.



A screenshot of the 'Setting' dialog box for the 'VSHARP' method. The 'Method:' dropdown is set to 'VSHARP'. Below it, the 'SMV Size:' field is set to '12'. The entire dialog box is highlighted with a red border.

- On the QSM tab, select either the iLSQR method or the QSMnet method.

Setting

Method: iLSQR

iLSQR

QSMnet

Pad Size: [12, 12, 12]

- On the χ -separation tab, select either the L1, SA or χ -sepnet method.
- Check Using R2Star (at the same time, dropbox of R2prime is set to 'None').
- If you selected the L1 or SA method, enter a nominal value for the pseudo R2 map, and if you selected χ -sepnet, enter a relaxation metric value in Dr blank. (default: 137).
- Set dropbox of R2Star to 'Process' (available if multi-echo magnitude is given).

R2Prime: [None] load

Output Directory: Z:\results load NIFTI

Setting

Method: Chi-sep net

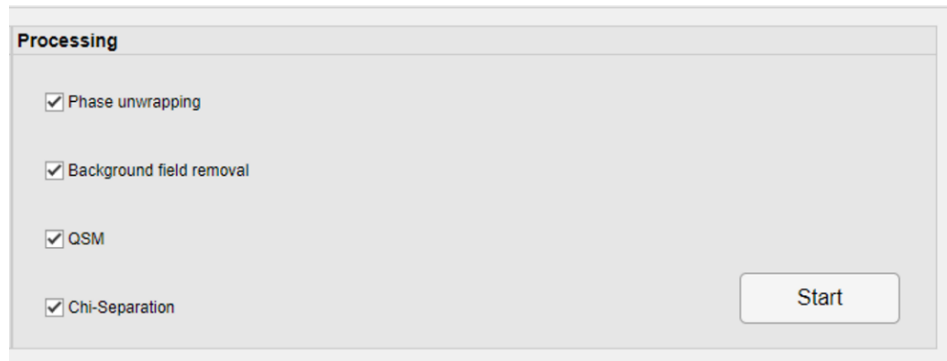
Chi-sep net

Using R2Star: ☒ R2Star: [Process] load

Dr: 137

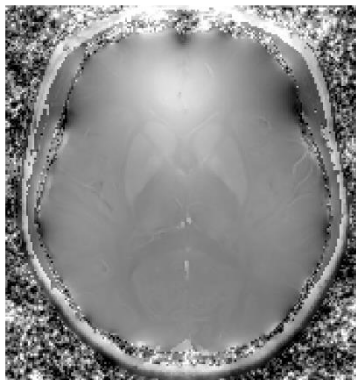
⑥ Run processing

- Check all processes in start panel.
- Press the start button.

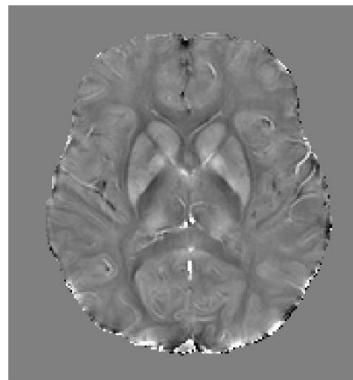


- When all processes are finished, the results are saved to the output directory.

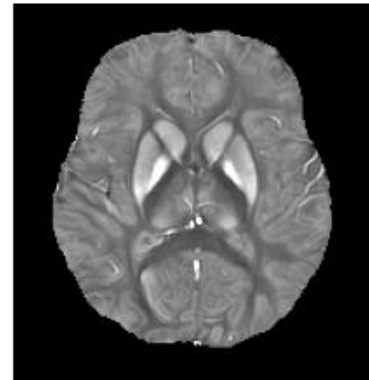
Total field



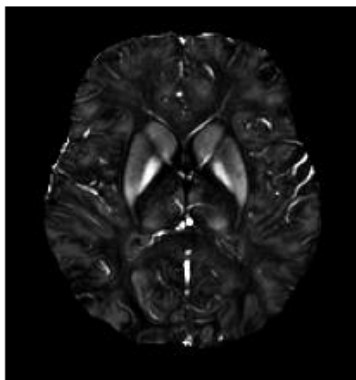
Local field



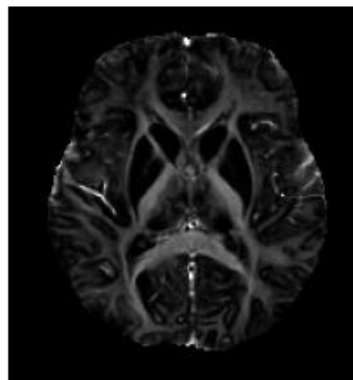
QSM



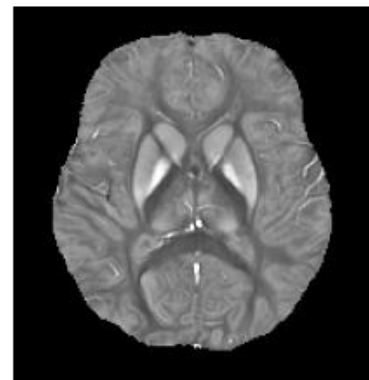
$\chi_{positive}$



$\chi_{negative}$



χ_{total}



3. For phase processing

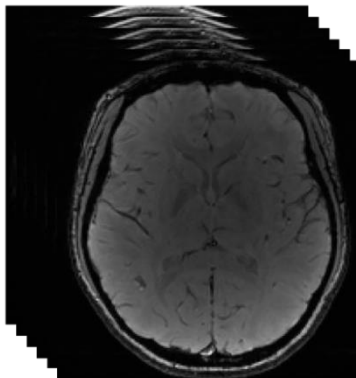
Exercise

- Perform phase processing from phase to local field map. (MEDI toolbox and STI Suite are required for processing.)

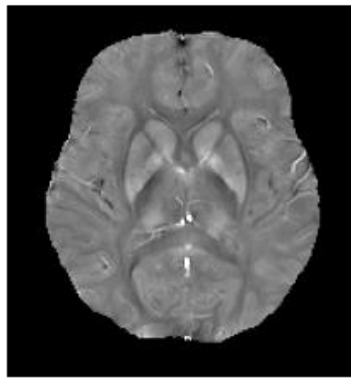
Input data

- Multi-echo GRE magnitude (4D: x, y, z, echo time)
- Multi-echo GRE phase (4D: x, y, z, echo time)

Magnitude



Local field



Processes

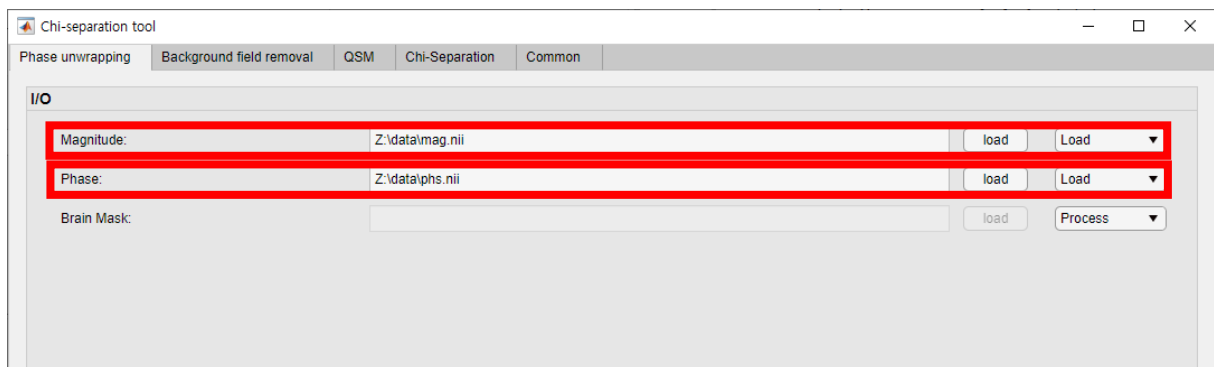
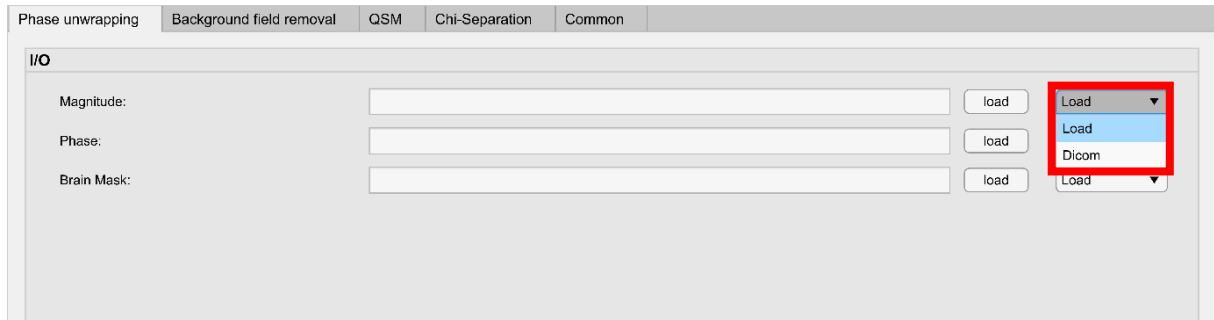
- Phase unwrapping: Laplacian-based method (STI Suite)
- Background field removal: V-SHARP

① Execute χ -sep toolbox GUI.

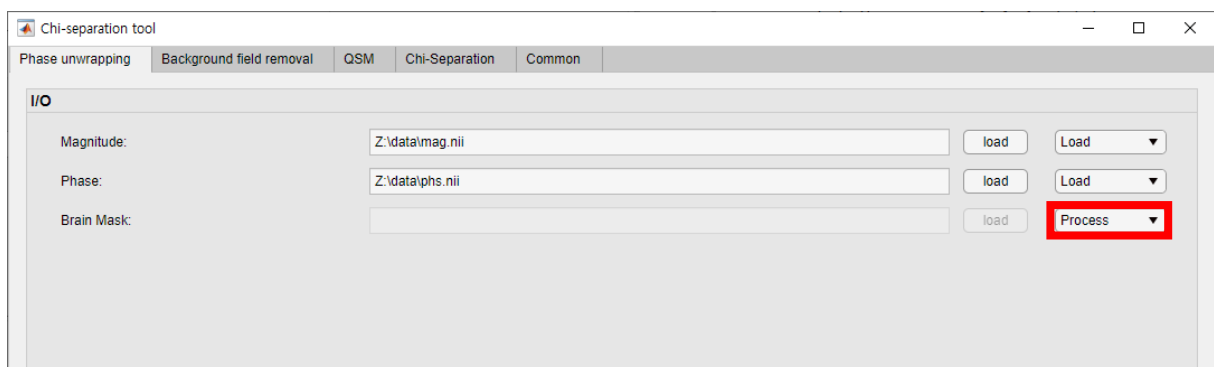
- Type “Chisep” in MATLAB command.
- Click “GUI for chi-separation” button.

② Load input data.

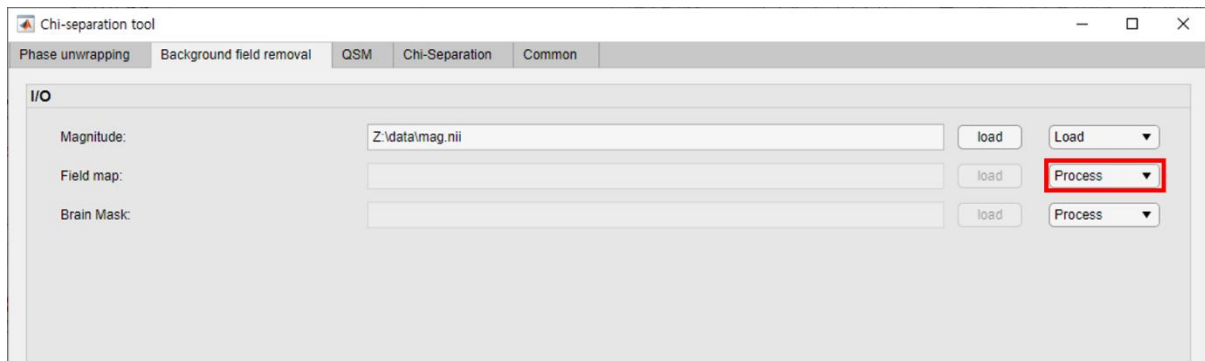
- Set the dropbox to 'Load' if the magnitude and phase are NIfTI or MAT files, or 'Dicom' if they are DICOM in Phase unwrapping tab.
- Then press the load button to select a NIfTI or MAT file or a Dicom directory to load the data.



- Set dropbox of Brain Mask to 'Process' in Phase unwrapping tab.



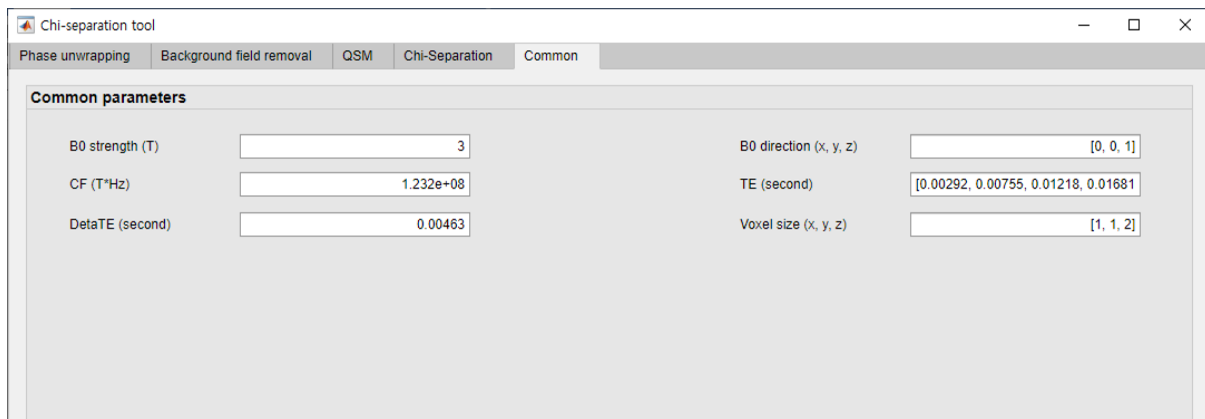
- Set dropbox of Field map to 'Process' in Background field removal tab.



- ③ Set dropbox of output directory to 'NIFTI' and load output directory.

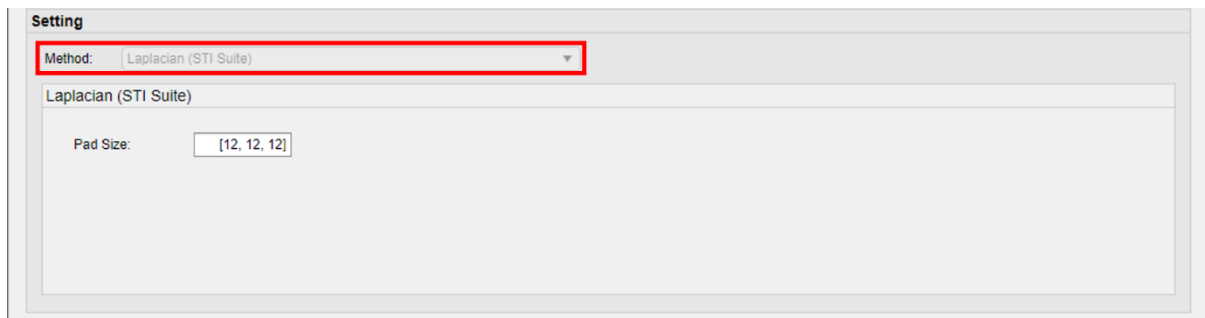


- ④ Put common parameters of your data.

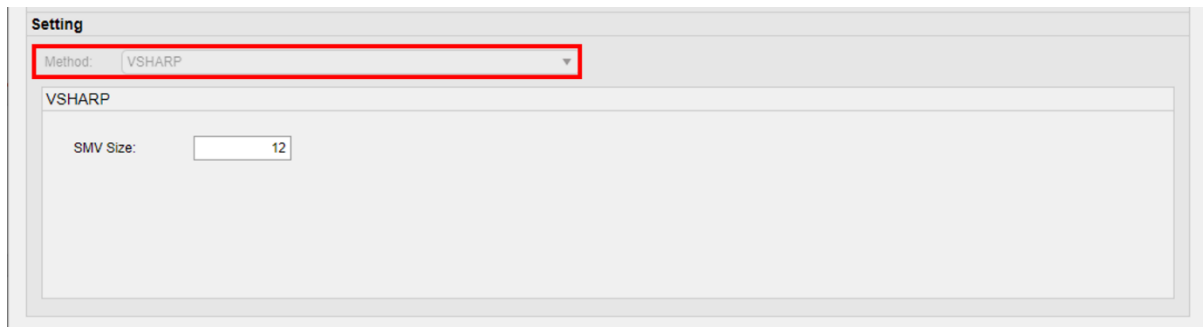


- ⑤ Set method of each process.

- Keep the Laplacian method in Phase unwrapping tab.

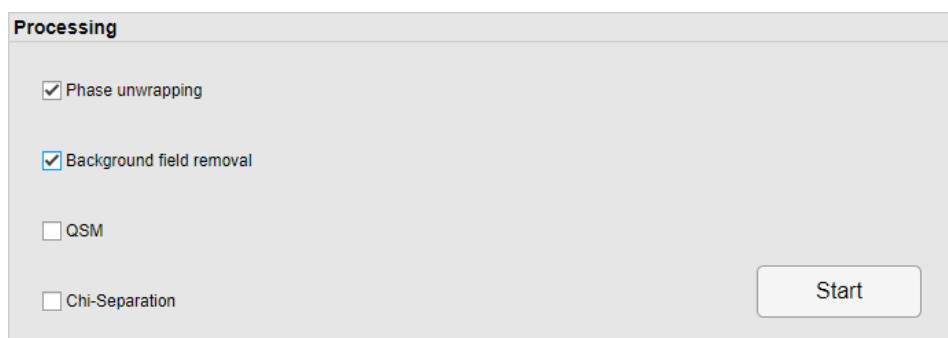


- Keep the V-SHARP method in Background field removal tab.



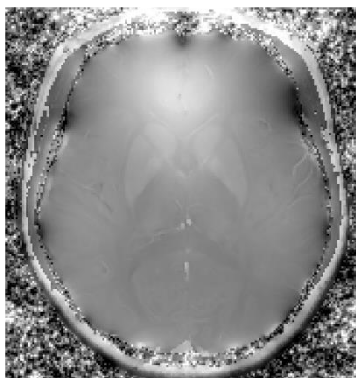
⑥ Run processing

- Check Phase unwrapping and Background field removal in start panel.
- Press the start button.

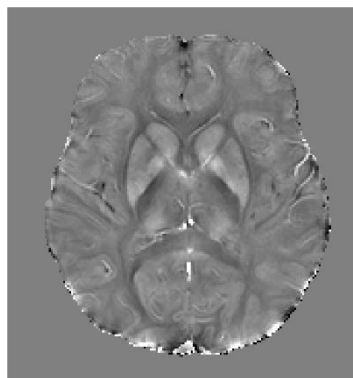


- When all processes are finished, the results are saved to the output directory.

Total field



Local field



4. For QSMnet and χ -separation (R2' version)

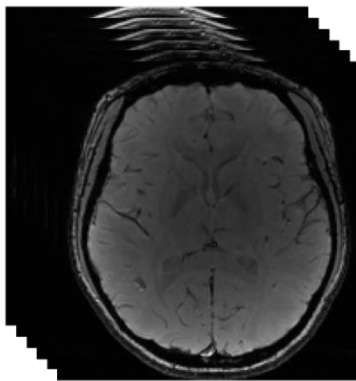
Exercise

- Perform to χ -separation (R2' version).
(Because it only uses QSMnet and x-separation, you don't need the MEDI Toolbox and STI Suite.)

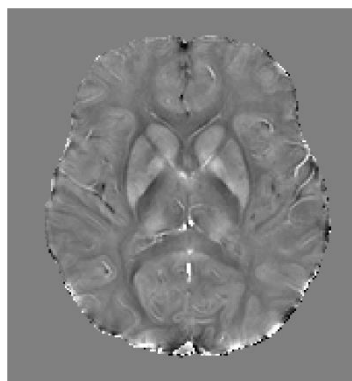
Input data

- Multi-echo GRE magnitude (4D: x, y, z, echo time)
- Local field map (3D)
- R2prime (3D)
- Brain mask (3D)

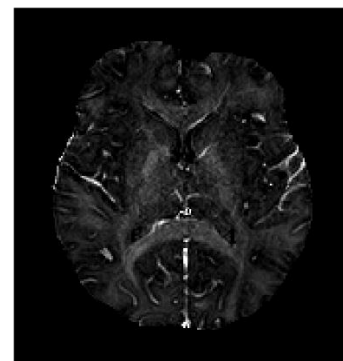
Magnitude



Local field



R2prime



Processes

- QSM: QSMnet
- χ -separation: χ -separation or χ -sepnet

① Execute χ -sep toolbox GUI.

- Type "Chisep" in MATLAB command.
- Click "GUI for chi-separation" button.

② Load input data.

- Set the dropbox to 'Load' if the magnitude is NIfTI or MAT files, or 'Dicom' if they are DICOM in QSM tab.
- Then press the load button to select a NIfTI or MAT file or a Dicom directory to load the data.

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: load Load ▾

Local Field: load Load ▾

Brain Mask: load Load ▾

- Set the dropbox for local field map to 'Load', then press the Load button to select the NIfTI or MAT file you want to load data from.

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: load Load ▾

Local Field: load Load ▾

Brain Mask: load Load ▾

- Set the dropbox for brain mask to 'Load', then press the Load button to select the NIfTI or MAT file you want to load data from.

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: load Load ▾

Local Field: load Load ▾

Brain Mask: load Load ▾

- Set dropbox of QSM to 'Process' and load R2' in χ -separation tab.

Chi-separation tool

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: Z:\data\mag.nii load Load ▾

Local Field: load Process ▾

Brain Mask: load Process ▾

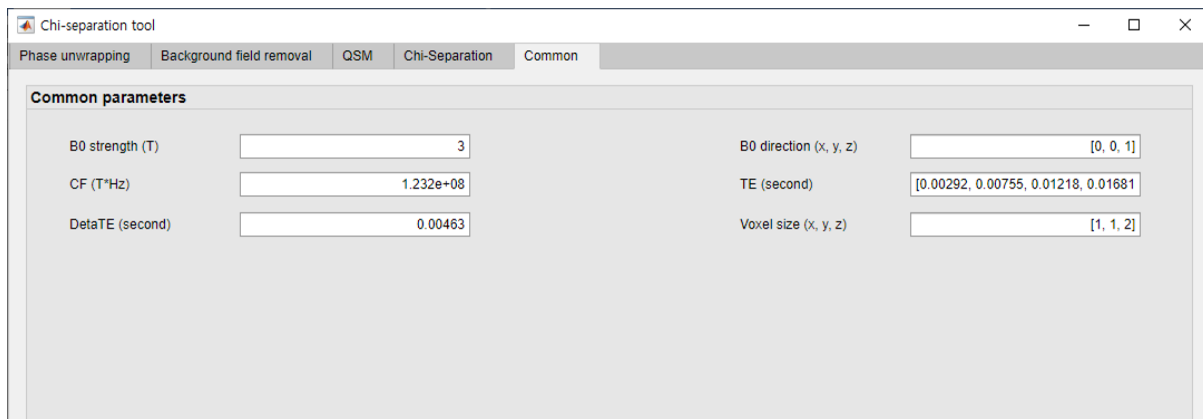
QSM: load Process ▾

R2Prime: Z:\data\R2prime.nii load Load ▾

③ Set dropbox of output directory to 'NIFTI' and load output directory.

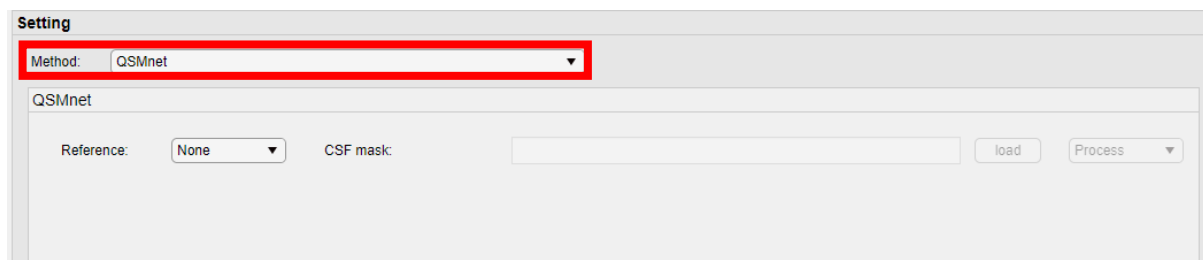


④ Put common parameters of your data.

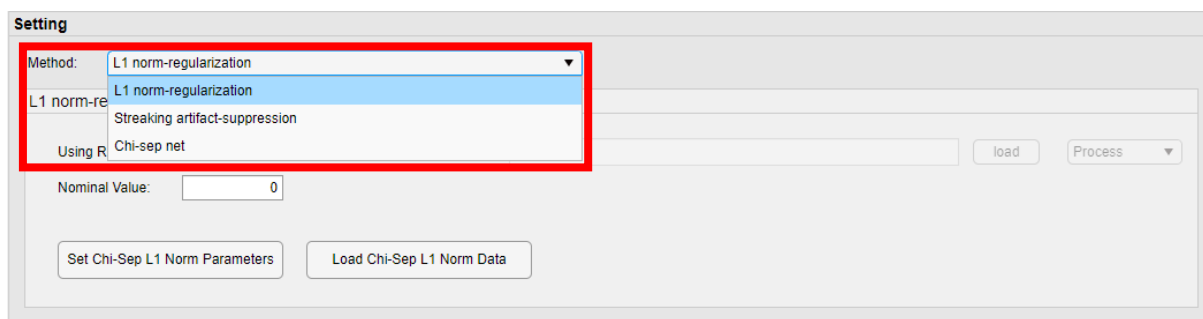


⑤ Set method of each process.

- On the QSM tab, select the QSMnet method.

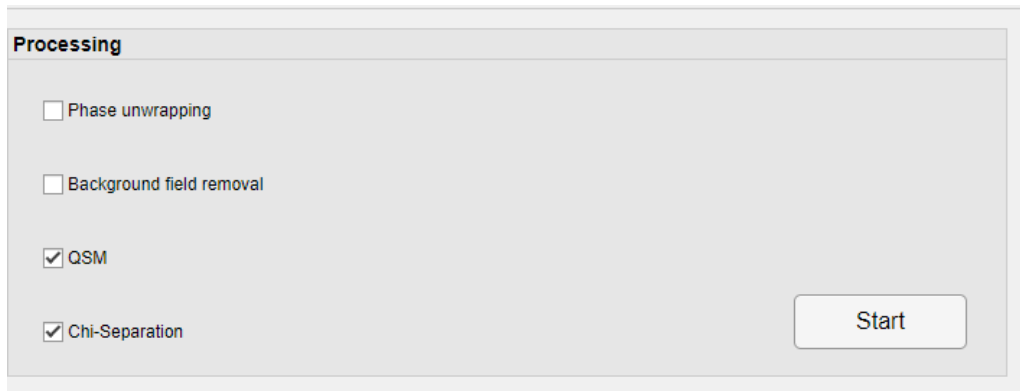


- On the χ -separation tab, select either the L1, SA or χ -sepnet method.



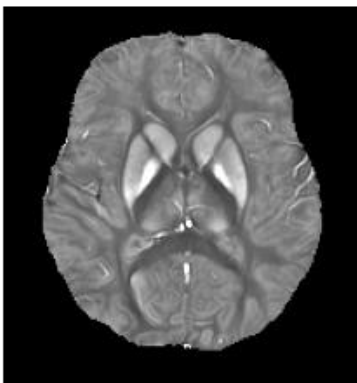
⑥ Run processing

- Check QSM and Chi-separation in start panel.
- Press the start button.

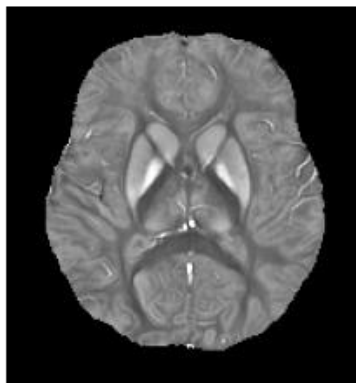


- When all processes are finished, the results are saved to the output directory.

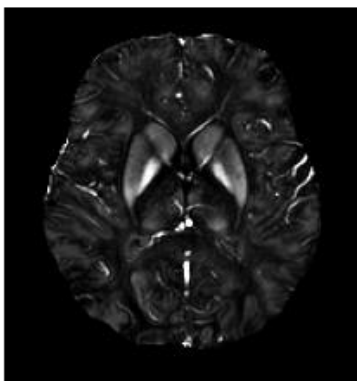
QSM



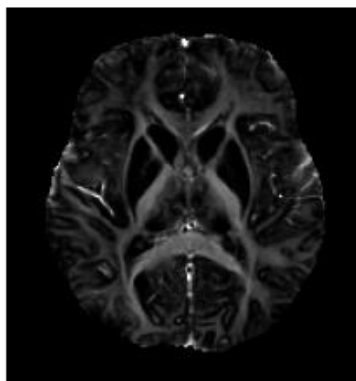
χ_{total}



$\chi_{positive}$



$\chi_{negative}$



5. For QSMnet and χ -separation (R2* version)

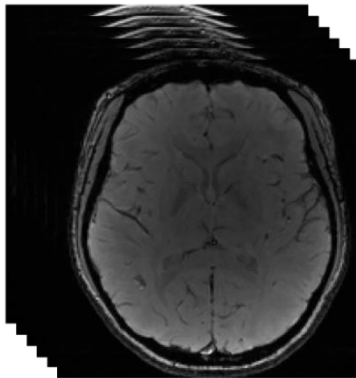
Exercise

- Perform to χ -separation (R2* version).
(Because it only uses QSMnet and x-separation, you don't need the MEDI Toolbox and STI Suite.)

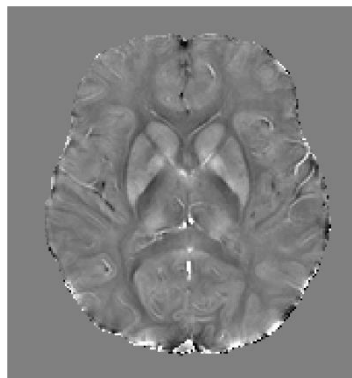
Input data

- Multi-echo GRE magnitude (4D: x, y, z, echo time)
- Local field map (3D)
- Brain mask (3D)

Magnitude



Local field



Processes

- QSM: QSMnet
- χ -separation: χ -separation or χ -sepnet

① **Execute χ -sep toolbox GUI.**

- Type “Chisep” in MATLAB command.
- Click “GUI for chi-separation” button.

② Load input data.

- Set the dropbox to 'Load' if the magnitude is NIfTI or MAT files, or 'Dicom' if they are DICOM in QSM tab.
- Then press the load button to select a NIfTI or MAT file or a Dicom directory to load the data.

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: load Load ▾

Local Field: load Load ▾

Brain Mask: load Load ▾

- Set the dropbox for local field map to 'Load', then press the Load button to select the NIfTI or MAT file you want to load data from.

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: load Load ▾

Local Field: load Load ▾

Brain Mask: load Load ▾

- Set the dropbox for brain mask to 'Load', then press the Load button to select the NIfTI or MAT file you want to load data from.

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: load Load ▾

Local Field: load Load ▾

Brain Mask: load Load ▾

- Set dropbox of QSM to 'Process' in χ -separation tab.

Chi-separation tool

Phase unwrapping Background field removal QSM Chi-Separation Common

I/O

Magnitude: Z:\data\mag.nii load Load ▾

Local Field: load Process ▾

Brain Mask: load Process ▾

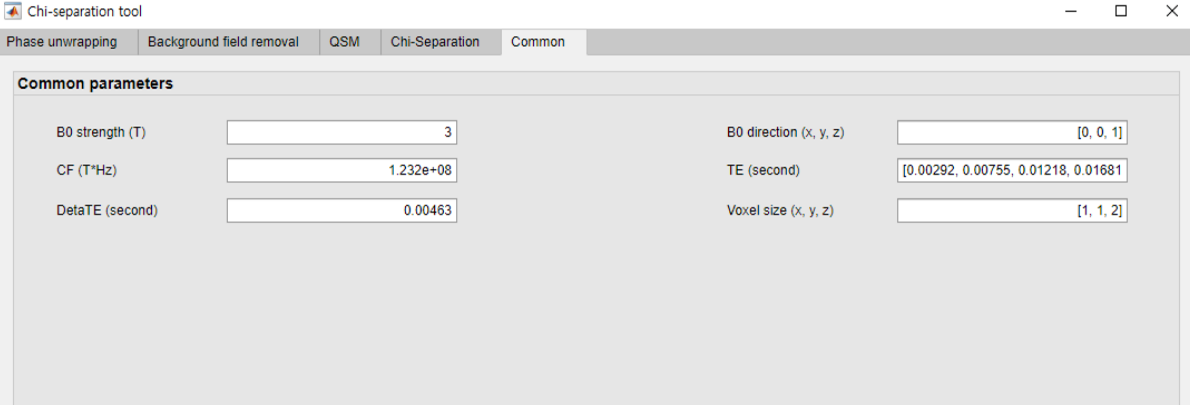
QSM: load Process ▾

R2Prime: load Load ▾

③ Set dropbox of output directory to 'NIFTI' and load output directory.

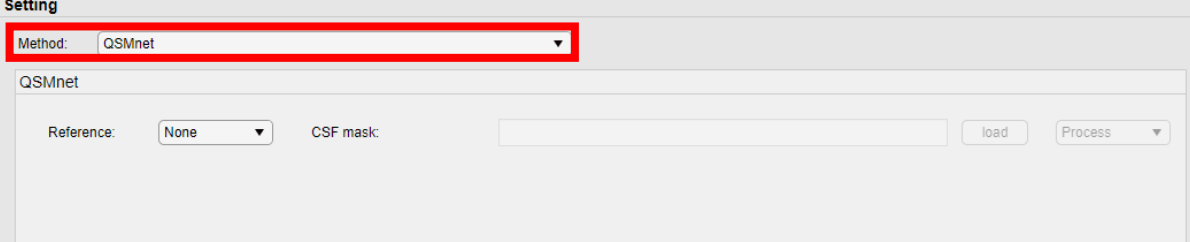


④ Put common parameters of your data.

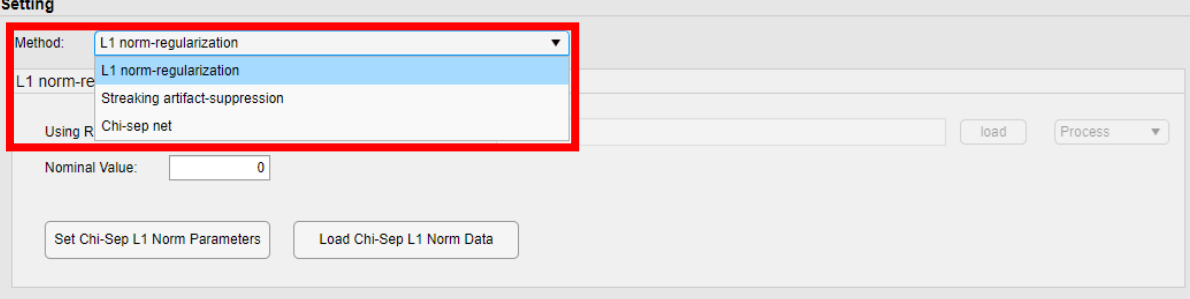


⑤ Set method of each process.

- On the QSM tab, select the QSMnet method.



- On the χ -separation tab, select either the L1, SA or χ -sepnet method.



- On the χ -separation tab, select either the L1, SA or χ -sepnet method.
- Check Using R2Star (at the same time, dropbox of R2prime is set to 'None').
- If you selected the L1 or SA method, enter a nominal value for the pseudo R2 map, and if you selected χ -sepnet, enter a relaxation metric value in Dr blank. (default: 137).
- Set dropbox of R2Star to 'Process' (available if multi-echo magnitude is given).

The screenshot shows the 'Setting' panel of the software. At the top, the 'R2Prime' dropdown is set to 'None'. Below it, the 'Output Directory' is 'Z:\results'. In the 'Setting' section, the 'Method' dropdown is set to 'Chi-sep net'. Under the 'Chi-sep net' sub-section, the 'Using R2Star' checkbox is checked, and the 'Dr.' field contains the value '137'. To the right, the 'R2Star' dropdown is set to 'Process'.

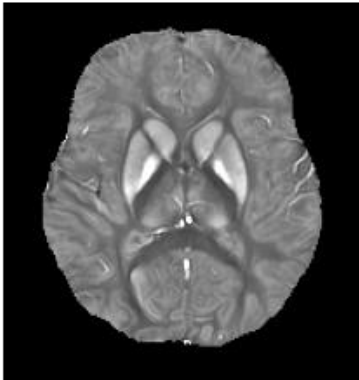
⑥ Run processing

- Check QSM and Chi-separation in start panel.
- Press the start button.

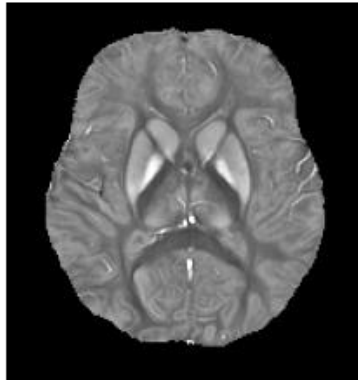
The screenshot shows the 'Processing' panel. It contains four checkboxes: 'Phase unwrapping' (unchecked), 'Background field removal' (unchecked), 'QSM' (checked), and 'Chi-Separation' (checked). A 'Start' button is located at the bottom right of the panel.

- When all processes are finished, the results are saved to the output directory.

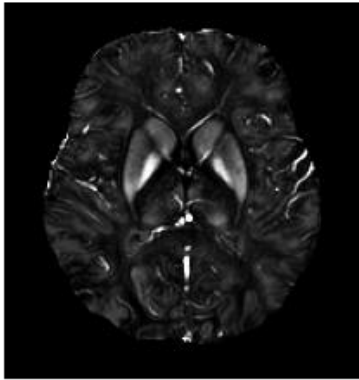
QSM



χ_{total}



$\chi_{positive}$



$\chi_{negative}$

