

Recommended Implementation of Quantitative Susceptibility Mapping for Clinical Research in The Brain: A Consensus of the ISMRM Electro-Magnetic Tissue Properties Study Group - Supplementary Materials: Example Data and Code

Full data, results and processing scripts are available on Zenodo:
<https://doi.org/10.5281/zenodo.7410455>

Data availability

Data are available from three vendors: GE, Siemens and Philips, using the recommended acquisition in the main text. For each vendor, both monopolar and bipolar readout strategies were used to acquire the data. The data from GE and Siemens are not pre-scan normalized, while the Philips data have two normalization methods applied.

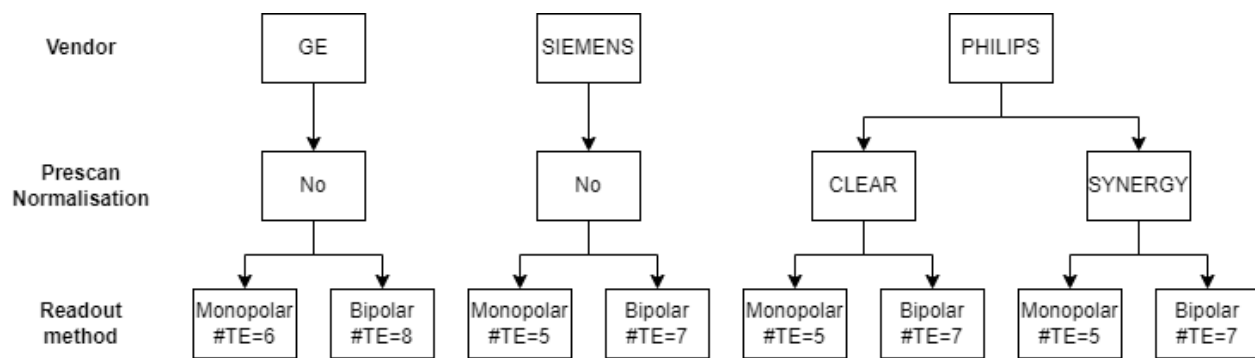


Figure S1: An illustration of data availability.

Data preparation and organization

Data preparation

Remark: The following steps for Data preparation are only required if you want to start the processing using the 'QSM_CONSENSIS_DATA.zip' file from a clean directory.

Step 1: Unzip the received data and reformat the directory structure

Scripts:

- Preparation_01_rename_received_data.sh

Step 2: Convert DICOM images into NIfTI format

Dependency: dcm2niix (version 1.0.20220720)

Scripts:

- Preparation_02_convert_dicom2nii.sh

Step 3: Rename the NIfTI files according to the BIDS format

Dependency: Matlab R2016b onwards

The naming strategy as follows:

- Vendors are identified using the session tag: **ses-<GE|PHILIPS|SIEMENS>**
- For **GE** and **SIEMENS**, different readout methods are identified using the acquisition tag: **acq-<Bipolar|Monopolar>**;
- For **PHILIPS**, the normalisation method is also printed on the acquisition tag, i.e., **acq-<BipolarCLEAR|BipolarSYNERGY|MonopolarCLEAR|MonopolarSYNERGY>**

Script:

- Preparation_03_rename_to_bids_format.m

Step 4: Prepare NIfTI data for SEPIA

Dependency: (1) Matlab R2016b onwards, (2) SEPIA v1.2.1

Involves the following operation:

- Combining individual multi-echo 3D volumes into a single 4D volume with TE in the 4th dimension;
- Obtaining header info (e.g., B₀ direction and TE) from NIfTI header and JSON sidecar files and saving as SEPIA's header format;
- (GE only) Correcting inter-slice opposite polarity on real and imaginary images and exporting phase images from the corrected real/imaginary data

Script:

- Preparation_04_prepare_for_sepia.m

Data organization

```
QSM_consensus_paper/
|-- QSM_CONSENSUS_DATA.zip          % Zip file containing all DICOM images
|-- protocols                      % Protocol text files
|-- QSM_Consensus_Paper_Example_Code % Containing all the scripts
|   |-- From_DICOM_zip_file_to_SEPIA_ready % Scripts for preparing QSM_CONSENSUS_DATA.zip
|   |-- SEPIA_Standard_Pipeline          % SEPIA pipeline config files for Standard
|   |-- SEPIA_Alternative1_Pipeline      % SEPIA pipeline config files for Alternative 1 (MEDI)
|   |-- SEPIA_Alternative2_Pipeline      % SEPIA pipeline config files for Alternative 2 (FANSI)
|-- raw                             % DICOM images
|-- converted                       % dcm2niix output
|   |-- GE
|   |   |-- Bipolar                  % Bipolar readout acquisition
|   |   |-- Monopolar                % Monopolar readout acquisition
|   |-- PHILIPS
|   |   |-- Bipolar_CLEAR            % with CLEAR normalisation
|   |   |-- Bipolar_SYNERGY          % with SYNERGY normalisation
|   |   |-- Monopolar_CLEAR
|   |   |-- Monopolar_SYNERGY
|   |-- SIEMENS
|   |   |-- Bipolar
|   |   |-- Monopolar
|-- derivatives                     % directory contains all derived output
    |-- SEPIA                      % SEPIA output
        |-- GE
            |-- Bipolar
            |   |-- GRE
            |   |-- Pipeline_Standard % Standard reconstruction output
            |   |-- Pipeline_Alternative1 % Dipole inversion Alternative 1 output
            |   |-- Pipeline_Alternative2 % Dipole inversion Alternative 2 output
```

```
|  `-- Monopolar
|  |-- PHILIPS
|  |-- SIEMENS
```

QSM reconstruction pipeline

This section describes all the QSM reconstruction processing steps performed in SEPIA. All the processing steps are specified in the SEPIA pipeline configuration files, which are in the sub-directories of the script directory:

'QSM_Consensus_Paper_Example_Code/SEPIA_Standard_Pipeline/',
'QSM_Consensus_Paper_Example_Code /SEPIA_Alternative1_Pipeline/' and
'QSM_Consensus_Paper_Example_Code /SEPIA_Alternative2_pipeline/', corresponding to the three processing pipelines demonstrated as follows.

Environment and dependencies

The data were processed using the following set-up

Operating system

- Linux CentOS 7

Environment

- Matlab R2021a (but the scripts are backwards compatible to early Matlab version from R2016b onwards)

Dependencies

- SEPIA v1.2.1 [<https://github.com/kschan0214/sepia/releases/tag/v1.2.1>]
- MRITools v3.5.6 [<https://github.com/korbinian90/CompileMRI.jl/releases/tag/v3.5.6>]
- MRI susceptibility calculation methods (accessed 12 September 2019) [https://xip.uclb.com/product/mri_qsm_tkd]
- MEDI toolbox (release: 15th January 2020) [<http://pre.weill.cornell.edu/mri/pages/qsm.html>]
- (FANSI toolbox [v3]) [<https://gitlab.com/cmilovic/FANSI-toolbox>]

Processing steps

Step 1: Preparation

- (GE only) Phase data are inverted before processing (i.e., phase = -phase), so that paramagnetic susceptibility gives a positive value while diamagnetic susceptibility gives a negative value, same as the data from other vendors
- Brain mask is obtained by using MEDI toolbox implementation of FSL's BET on the 1st echo magnitude image, using default setting -f 0.5 -g 0
- (Bipolar readout data only) Bipolar readout correction based on (Li et al., 2015) using the implementation provided with SEPIA.

Step 2: Total field estimation and echo combination

Table S1: Algorithm parameters for total field estimation and echo combination.

Parameters	Values	Remark
Echo phase combination	ROMEO total field calculation	(Dymerska et al., 2021)

MCPC-3D-S phase offset correction	On	
Mask for unwrapping	SEPIA mask	FSL's BET mask
Using ROMEO Mask in SEPIA	Off	
Exclude voxel using relative residual with threshold	0.3 (applied on weighting map)	See https://sepia-documentation.readthedocs.io/en/latest/method/weightings.html

Step 3: Background field removal

Table S2: Algorithm parameters for background field removal.

Parameters	Values	Remark
Method	VSHARP	(Li et al., 2011)
Spherical mean value filtering size	12	Unit: mm
Remove residual B1 field	No	
Erode brain mask before BFR	1	Unit: voxel
Erode brain mask after BFR	0	

Step 4: Dipole inversion (corresponding to “Standard” pipeline)

Table S3: Algorithm parameters for dipole field inversion using ‘Standard’ pipeline.

Parameters	Values	Remark
Method	Iterative Tikhonov	(Karsa et al., 2020; Schweser et al., 2013)
Regularisation parameter (lambda)	0.1	
Conjugate gradient tolerance	0.03	
Reference tissue	Brain mask	

Alternative dipole inversion methods: (MEDI and FANSI)

Step 4 (Alternative 1): Dipole inversion

Table S4: Algorithm parameters for dipole field inversion using ‘Alternative 1’ pipeline.

Parameters	Values	Remark
Method	MEDI	(Liu et al., 2011)
Regularisation parameter (lambda)	2000	
Method of data weighting	1	SNR weighting

Percentage of voxels considered to be edges	90	
Array size for zero padding	[0 0 0]	
Performing spherical mean value operator	On	
Radius of the spherical mean value operation	5	Unit: voxels
Performing modal error reduction through iterative tuning (MERIT)	On	
Performing automatic zero reference (MEDI+0)	Off	
Reference tissue	Brain mask	

P.S. Output from the ‘standard’ pipeline is required. The scripts are in ‘QSM_Consensus_Paper_Example_Code/SEPIA_Alternative1_Pipeline’.

Step 4 (Alternative 2): Dipole inversion

Table S4: Algorithm parameters for dipole field inversion using ‘Alternative 2’ pipeline.

Parameters	Values	Remark
Method	FANSI	(Milovic et al., 2019, 2018)
Iteration tolerance	0.1	
Maximum number of iterations	400	
Gradient L1 penalty, regularisation weight	0.0005	
Gradient consistency weight	0.05	
Fidelity consistency weight	1	
Solver	Non-linear	
Constraint	TV	
Method for regularisation spatially variable weight	Vector field	
Using weak harmonic regularisation	On	
Harmonic constraint weight	150	
Harmonic consistency weight	3	
Reference tissue	Brain mask	

P.S. Output from the 'standard' pipeline is required. The scripts are in 'QSM_Consensus_Paper_Example_Code/SEPIA_Alternative2_Pipeline/'.

Re-run the scripts

To re-run the processing scripts, including the preparation shell scripts and the SEPIA pipeline configuration scripts, you may need to adapt the file and/or directory paths on the scripts to the correct paths of the files/directories stored in your (local) computer.

Example results

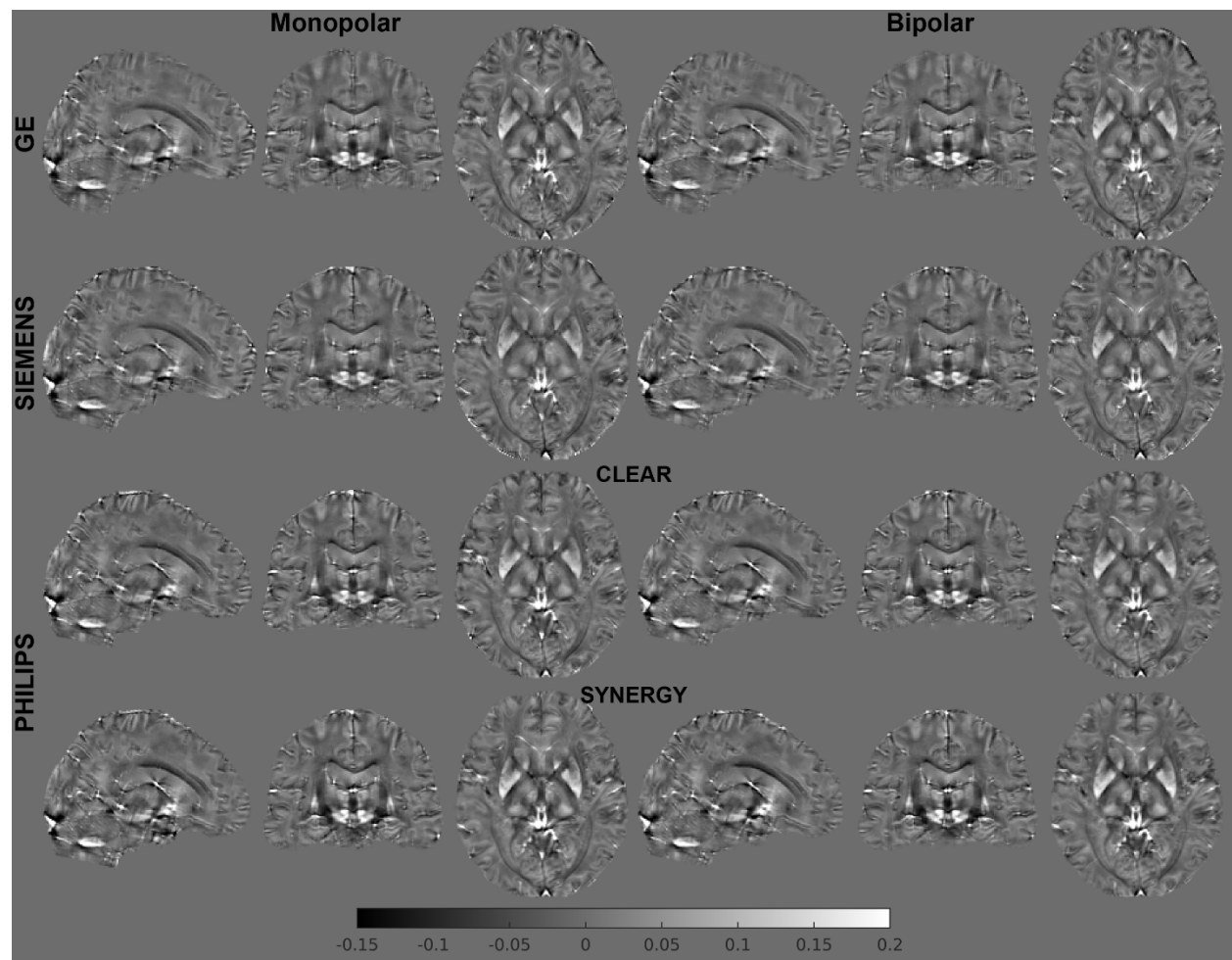


Figure S2: Susceptibility maps derived using the 'Standard' processing pipeline.

References

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