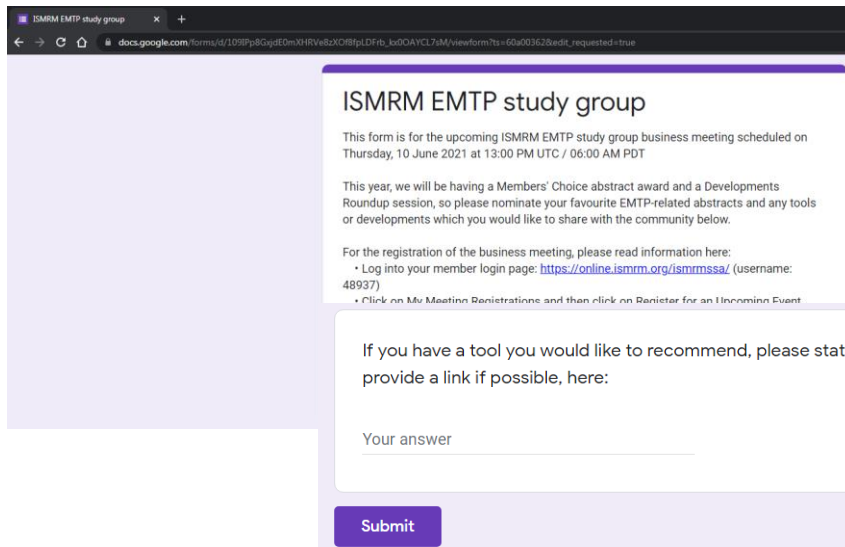


Tools Roundup



The screenshot shows a web browser window with a Google Forms survey. The browser's address bar shows the URL: docs.google.com/forms/d/1D98Pp8GygdEmX1RyVell2X089pLDFrb_kuDOAYC17uM/viewform?ts=60a03628&edit_requested=true. The form title is "ISMRM EMTP study group". The text on the form reads: "This form is for the upcoming ISMRM EMTP study group business meeting scheduled on Thursday, 10 June 2021 at 13:00 PM UTC / 06:00 AM PDT". It continues: "This year, we will be having a Members' Choice abstract award and a Developments Roundup session, so please nominate your favourite EMTP-related abstracts and any tools or developments which you would like to share with the community below." It then provides registration information: "For the registration of the business meeting, please read information here: • Log into your member login page: [https://online.ismrm.org/ismrmssa/](\"https://online.ismrm.org/ismrmssa/\") (username: 48937) • Click on My Meeting Registrations and then click on Register for an Incoming Event". Below this is a text input field with the prompt: "If you have a tool you would like to recommend, please state what it does and provide a link if possible, here:". The input field contains the placeholder text "Your answer". At the bottom right of the form is a blue "Submit" button.

New feature: tools roundup

These are Study Group requests in answer to the questionnaire which Jongho sent to the SG mailing list near the end of May 2021.

We received 14 methods recommendations.

Tools Roundup

Acquisition

- 3D-EPI Siemens WIP 1043A
- ASPIRE online coil combination for Siemens (C2P)

Pre-processing

- SEGUE phase unwrapping
- ROMEO phase unwrapping

SWI

- CLEAR-SWI

QSM

- SMWI (for nigrosome 1), QSMnet, QSMnet+
- AutoQSM & MoDL-QSM
- FANSI
- TKD etc
- QSMxT
- LPCNN - DL QSM for arbitrary magnetic direction
- SEPIA

Conductivity:

- UCL
- EPTlib

These are the tools we will be looking at, arranged into Acquisition, Pre-processing, SWI, QSM and ETP-related.

An abbreviated version of the authors' text appears with each slide.

Acquisition methods: 3D-EPI WIP from Siemens Australia and UQ, on-console coil combination with ASPIRE

Phase unwrapping with SEGUE from UCL, ROMEO from the Medical University of Vienna

CLEAR-SWI, a multi-echo SWI method for UHF from the Medical University of Vienna
Susceptibility Map Weighted Imaging, QSMnet and QSMnet+ from Seoul National University

AutoQSM from Shanghai Jiao Tong University

Fansi from Carlos Milovic

TKD methods from UCL

QSMxT from the University of Queensland

LPCNN QSM tool for arbitrary magnetic field direction from Johns Hopkins and the meta QSM tool

SEPIA from Kwok-shing Chan and Jose Marques from Radboud University Nijmegen

And we finish with conductivity tools from Anita Karsa and Karin Shmueli

And EPTlib from Alessandro Arduino and Ulrich Katscher

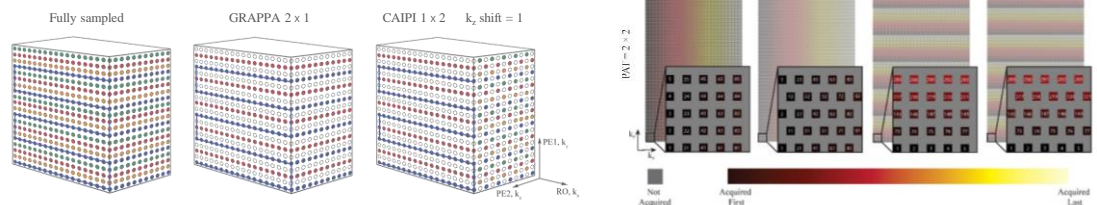
Multi-shot 3D EPI with CAIPIRINHA acceleration

Siemens' WIP1043A

J. Jin, M. Tourell, P. Sati, S. Patil, K. Liu, J. Derbyshire, F. Han, J. Pfeuffer, S. Bollmann, S. Robinson, S. Bollmann, M. Barth, K. O'Brien

Features

- VE11C and VE11E released; VE12U in testing
- Navigators for each shot
- Two reordering schemes
- GRAPPA /CAIPI acceleration
- Option to limit CAIPI patterns such that k-space center is always sampled
- Binomial water excitation pulses using 180 or 540 degree phase evolution
- Bi-polar binomial water excitation pulses
- Improved bi-polar water excitation at ends of slab through optional slab scaling and slice oversampling



We're going to begin with Siemens' WIP1043A for 3D EPI. This enables a flexible combination of single- and multi-shot 3DEPI schemes, image resolution, in-plane segmentation, echo-train length and partial Fourier factors.

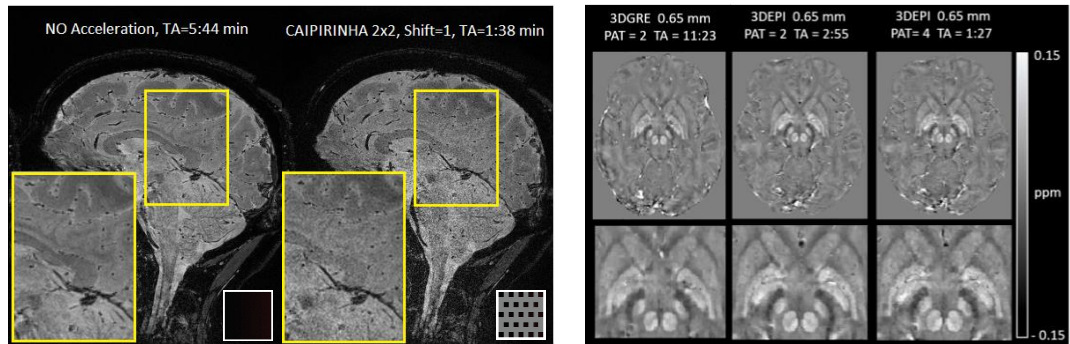
CAIPIRINHA and GRAPPA acceleration are achieved through skipping appropriate partitions and shots. Image reconstruction is improved by implementation of navigators for each shot.

The WIP is currently available for VE11C and VE11E, with a VE12U release for 7T currently in testing.

Multi-shot 3D EPI with CAIPIRINHA acceleration

Siemens' WIP1043A

Fast, whole-brain sub-millimeter anatomical and susceptibility-based imaging with minimal distortion



Links:

ISMRM abstract #4190

ISMRM abstract #787

For further information contact Jin Jin: jin.jin@siemens-healthineers.com

SIEMENS
Healthineers

Cleveland Clinic

THE UNIVERSITY
OF QUEENSLAND
AUSTRALIA

Cedars
Sinai



Centre for Innovation in
Biomedical Imaging Technology
McGill Graduate Program in Biomedical Engineering



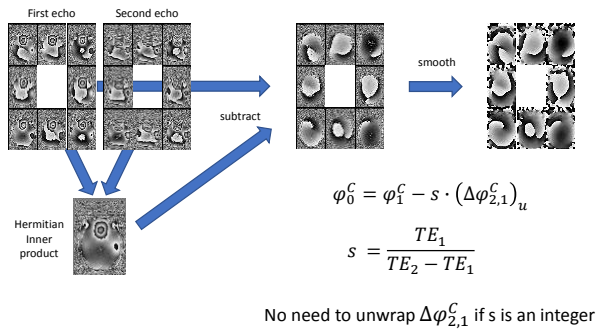
National Institutes of Health
Turning Discovery Into Health

Susceptibility maps obtained from 3D EPI phase images acquired on a Prisma scanner are shown on the right. The susceptibility values produced compared well with the standard 3D GRE scan and were achieved in a fraction of the time.

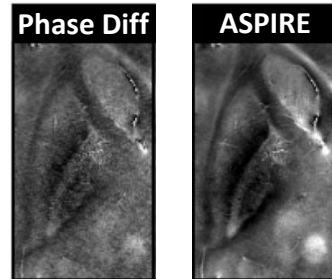
For further information on the WIP please contact Jin Jin at Siemens Healthineers, Brisbane, Australia.

Computationally Efficient Combination of Multi-channel Phase Data From Multi-echo Acquisitions (ASPIRE)

Korbinian Eckstein, Simon Robinson



e.g. $S = 1; TE_2 = 2 \cdot TE_1$



- Removes physical phase offsets
- Higher CNR than phase difference (HIP)
- No unwrapping, fast
- Runs on the MRIR

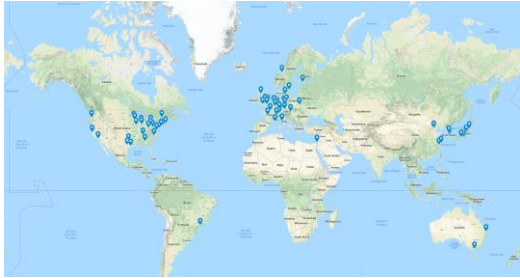
Not such a new one here, I hasten to say that this is a request rather than a self-dedication.

ASPIRE is a coil combination method for multi-echo acquisitions, particularly for ultra-high field systems, which don't have a body coil.

The phase offsets for each coil can be calculated by subtracting, from the first echo phase, the scaled difference between the phase measured at two echo times. Generally we would have to unwrap that phase difference, but we don't have to if the scaling factor is an integer, for instance if the second echo time is twice the first – that's essentially the basis of the ASPIRE method.

It removes **real** phase offsets rather than **relative** phase offsets, so removes all sources of phase which are unrelated to B0, and yields a higher CNR result than phase difference approaches.

ASPIRE



~ 80 Systems (2019),
~ 60 Siemens,
32 sites using ASPIRE



<https://layerfmri.com/2018/01/04/high-field-mri-scanners/#more-209>

Eckstein K, Dymerska B, Bachrata B, Bogner W, Poljanc K, Trattnig S, Robinson SD. Computationally Efficient Combination of Multi-channel Phase Data From Multi-echo Acquisitions (ASPIRE). *Magn Reson Med*. 2018 Jun;79(6):2996-3006. doi: 10.1002/mrm.26963. Epub 2017 Oct 16. PMID: 29034511.

Links:

Available for Siemens (VB17, VE11, VE12U) via C2P; contact simon.robinson@meduniwien.ac.at

<https://github.com/korbinian90/ASPIRE>

<https://onlinelibrary.wiley.com/doi/epdf/10.1002/mrm.26963>

ASPIRE is in use at 32 UHF sites. It's available via C2P for VB17, VE11C and VE12U. Just send me an email if you'd like to try it and I'll send you the C2P form.

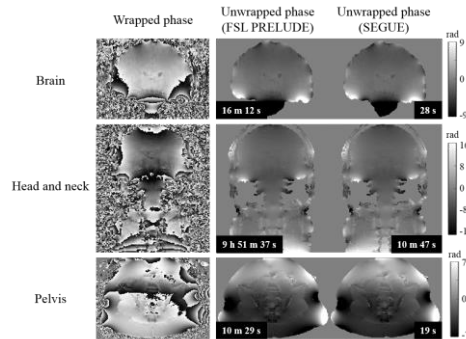
SEGUE: A Speedy rEgion-Growing Algorithm for Unwrapping Estimated Phase

Author: Anita Karsa, PhD and Karin Shmueli, PhD.

Department of Medical Physics and Biomedical Engineering, University College London, UK

Matlab software designed to quickly unwrap 3D MRI phase images without affecting the total magnetic field distribution.

SEGUE has been shown to perform up to 80 times faster than FSL PRELUDE and with equivalent accuracy.



Links: <https://xip.uclb.com/product/SEGUE> Contact: segueUCL@gmail.com
IEEE TMI paper DOI: 10.1109/TMI.2018.2884093

Moving onto 2 phase unwrapping methods now.

The first was developed by Anita Karsa at University College London, SEGUE is a Speedy Region Growing algorithm for Unwrapping Estimated Phase data.

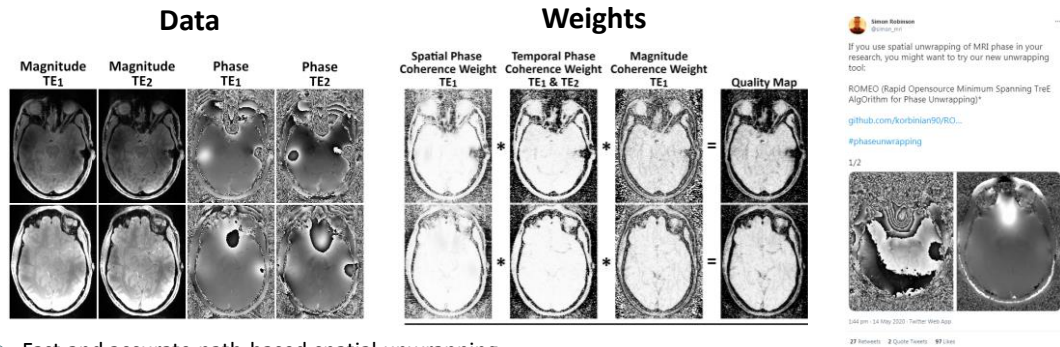
Implemented in Matlab, SEGUE is designed to quickly unwrap 3D phase images without affecting the total magnetic field distribution. This means that the resulting unwrapped phase images can be used for distortion correction and as an input for EMTP applications like QSM.

SEGUE has been shown to perform up to 80 times faster than FSL PRELUDE and with equivalent accuracy in MRI phase images of the brain, head-and-neck region, and pelvis.

To register your interest in a python version, please email segueUCL@gmail.com

Rapid Opensource Minimum Spanning TreE AlgOrithm for Phase Unwrapping (ROMEo)

Barbara Dymerska (UCL), Korbinian Eckstein (MU Vienna), Simon Robinson (MU Vienna)

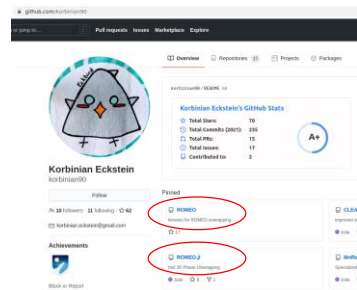


- Fast and accurate path-based spatial unwrapping
- Single-step for multi-echo, multi timepoint data
- New features, calculate B_0 “-B”, remove phase offsets “--phase-offset-correction”, write quality maps “-q,-Q”

The second phase unwrapping method is ROMEo: is a **Rapid Opensource Minimum Spanning TreE AlgOrithm for Phase Unwrapping**.

It’s a fast and accurate path-based spatial unwrapping method which defines unwrapping paths through the object using up to 3 weights: a Spatial phase coherence weight, a Temporal phase coherence weight if we’re dealing with multi-echo data and a Magnitude coherence weight if magnitude data is available.

ROMEO



Dymerska B, Eckstein K, Bachrata B, Siow B, Trattng S, Shmueli K, Robinson SD. Phase unwrapping with a rapid opensource minimum spanning tree algorithm (ROMEO). Magn Reson Med. 2021 Apr;85(4):2294-2308.

Links:

<https://github.com/korbinian90/ROMEO>

<https://github.com/korbinian90/ROMEO.jl>

Harvard Dataverse. <https://dataverse.harvard.edu/dataverse/ROMEO>

<https://onlinelibrary.wiley.com/doi/full/10.1002/mrm.28563>

ROMEO was an MRM Reproducible Research Editor's pick in April this year.

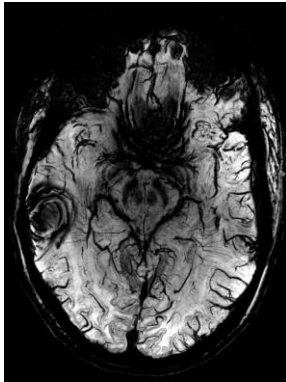
It's written in Julia, it's open source and is available in both Julia and compiled versions for Windows, Mac and Linux.

We have an alpha implementation of this in ICE (you'll find it in the special card in the ASPIRE C2P) and we're talking to Kwok-shing about how best to integrate ROMEO into SEPIA.

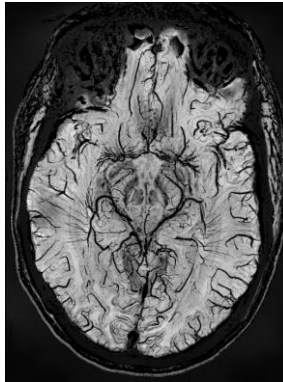
CLEAR-SWI: Susceptibility Weighted Imaging at 7T using bipolar multi-echo acquisition and optimized processing of phase and magnitude

Korbinian Eckstein, Simon Robinson

Standard SWI



CLEAR-SWI



- reduced signal dropouts
- no phase wrap artefacts
- improved contrast
- improved homogeneity

Moving on to SWI,

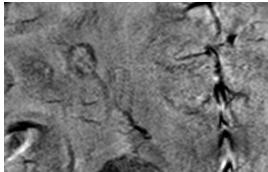
CLEAR-SWI is a method for susceptibility-weighted imaging at ultra-high field, which has been developed with a view to online implementation. It uses both existing and new solutions to the problems of SWI at ultra-high field.

- Optimized weighting of phase and magnitude in multi-echo acquisitions reduces signal dropouts compared to standard, single-echo SWI
- Coil combination is performed with ASPIRE and phase images are unwrapped with Laplacian unwrapping rather than Homodyne Filtering, and it includes
- An inhomogeneity correction

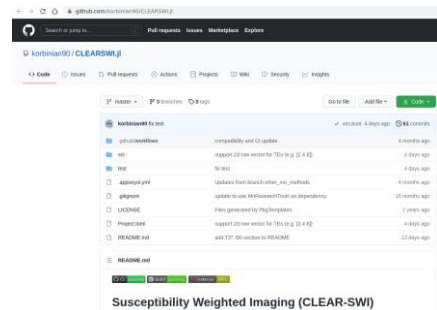
CLEAR-SWI

Example: peripheral enhancing rim lesion in multiple sclerosis

Standard SWI



CLEAR-SWI



Eckstein K, Bachrata B, Hangel G, Widhalm G, Enzinger C, Barth M, Trattng S, Robinson SD. Improved susceptibility weighted imaging at ultra-high field using bipolar multi-echo acquisition and optimized image processing: CLEAR-SWI. Neuroimage. 2021 May 15;237:118175.

Links:

<https://github.com/korbinian90/CLEARSWI.jl>

Harvard Dataverse. <https://doi.org/10.7910/DVN/4ZUFTH>

<https://www.sciencedirect.com/science/article/pii/S1053811921004523>

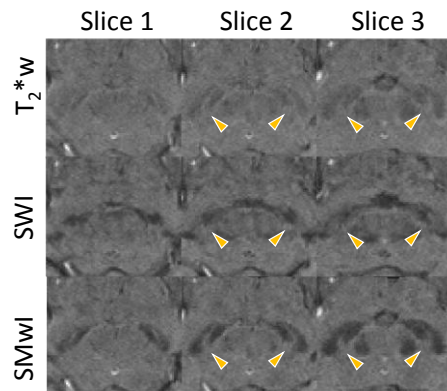
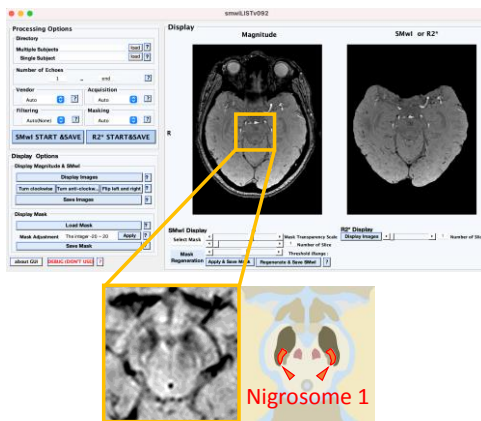
Here's an example in a patient with multiple sclerosis, where this lesion with an enhancing rim and a central vein is more clearly visible on CLEAR-SWI than on standard, single-echo SWI.

CLEAR-SWI appeared in NeuroImage in May and is available free and open source in Julia on github.

We're working on implementing this in ICE and bundling this with ASPIRE, probably around the end of the year.

Susceptibility Map-weighted Imaging (SMWI)

Authors: Hyeong-Geol Shin @ Seoul National University



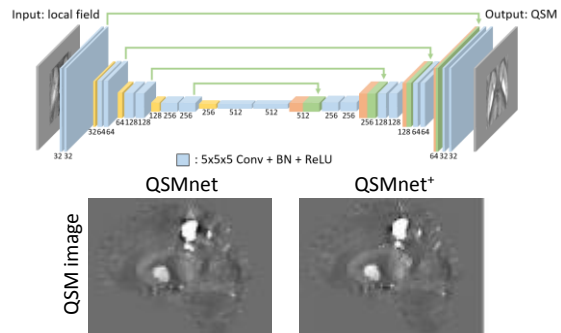
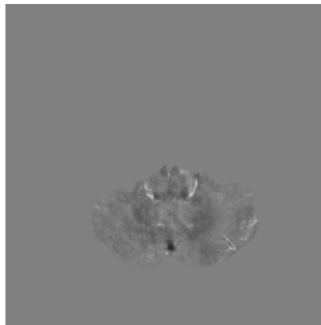
CNR enhanced by $\times 1.4$

Link of software: <http://list.snu.ac.kr/index.php/software/>
Paper: Yoonho Nam, JMRI, 2017

We're moving onto the QSM section now, with two methods from Seoul National University. The first one is Susceptibility Map-Weighted Imaging or SMWI, which combines the multi-echo magnitude images with a QSM generated mask. This method is utilized to visualize so-called swallow-tail or nigrosome 1 in substantia nigra for Parkinson's disease. As compared to a T₂* weighted image or an SWI image, an SMWI image provides 1.4 times higher CNR, enabling reliable detection of the swallow-tail structure at 3T.

QSMnet, QSMnet⁺ and multiorientation QSM data

Authors: Woojin Jung @ Seoul National University



Link of software: <https://github.com/SNU-LIST/QSMnet>

Paper: Jae Yeon Yoon, Neuroimage, 2018

Woojin Jung, Neuroimage, 2020

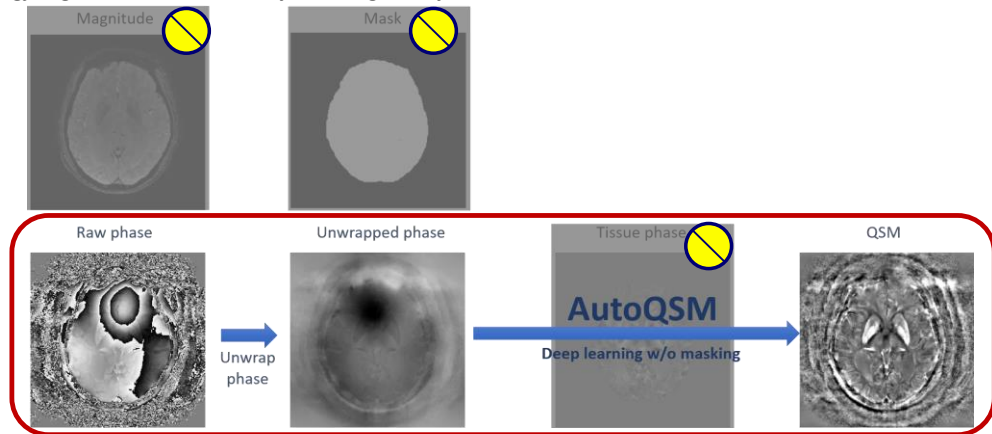
Data available: 6 orientation datasets from 12 subjects

email: snu.list.software@gmail.com

The next tool is QSMnet which performs dipole deconvolution using a deep neural network. The network provide a COSMOS quality susceptibility map for a single head orientation data input. QSMnet⁺ is a generalized version of QSMnet for larger susceptibility ranges. Both pretrained networks and multiorientation data for network training are available for sharing.

AutoQSM: Learning-based single-step quantitative susceptibility mapping reconstruction without brain extraction

Hongjiang Wei , Steven Cao, Yuyao Zhang , Xiaojun Guan , Fuhua Yan , Kristen W. Yeom , Chunlei Liu



The next method is AutoQSM, which was developed by Prof. Hongjiang Wei, et al. It uses a simple U-Net structure as the backbone and was trained using a large dataset across 1-80 y/o subjects. It takes the unwrapped phase as the input and directly predicts high quality QSM.

AutoQSM: Learning-based single-step quantitative susceptibility mapping reconstruction without brain extraction

Our contributions:

- Without skull removal;
- No parameter tuning;
- Full FOV QSM with perserved cortical tissues, e.g., cortical vessels;
- Ultra-fast QSM reconstruction within a few seconds

Links:

download link: <https://github.com/AMRI-Lab/AutoQSM>

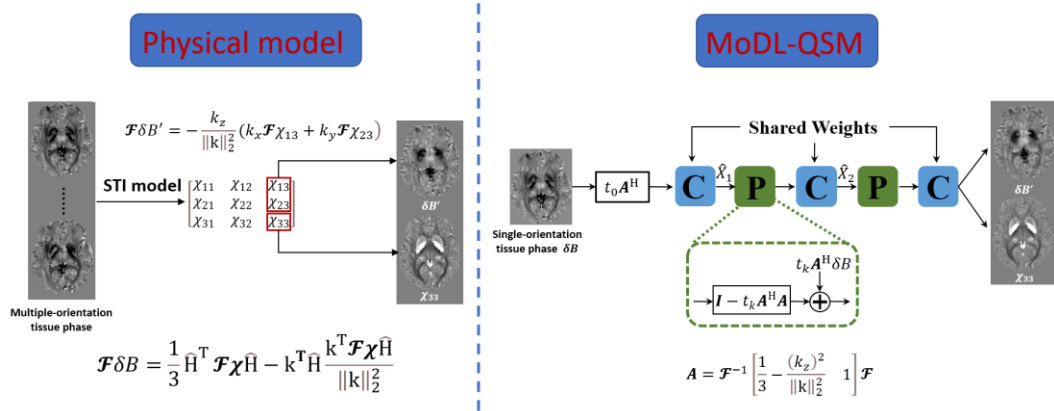
publication links: <https://www.sciencedirect.com/science/article/pii/S1053811919306469>

Wei et al. NIMG, 2019

The advantages of AutoQSM are: no skull removal, no background phase removal, full FOV QSM with cortical tissue. The source codes and trained networks ready for testing can be download at: <https://github.com/AMRI-Lab/AutoQSM>. The original paper has been published in NIMG 2019 at: <https://www.sciencedirect.com/science/article/pii/S1053811919306469>

MoDL-QSM: Model-based Deep Learning for Quantitative Susceptibility Mapping

Ruimin Feng, Jiayi Zhao, Chunlei Liu, Yuyao Zhang, Hongjiang Wei



MoDL-QSM was also developed by Prof. Hongjiang Wei's group. It incorporates the physical Susceptibility Tensor model into convolutional neural networks. MoDL-QSM reconstructs a high quality STI component χ_{33} map and the field induced by χ_{13} and χ_{23} terms from the tissue phase.

MoDL-QSM: Model-based Deep Learning for Quantitative Susceptibility Mapping

Our contributions:

- STI (Susceptibility tensor imaging) model-based deep learning;
- Provide a more realistic susceptibility reference for single-orientation QSM;
- Simultaneously predict χ_{33} and the field induced by χ_{13} and χ_{23} terms;

Links:

download link: <https://github.com/AMRI-Lab/MoDL-QSM>

publication links: <https://arxiv.org/abs/2101.08413>

Feng et al. NIMG, under review

The advantages of MoDL-QSM are that it is STI model-based, it preserves susceptibility anisotropy, and simultaneously predicts χ_{33} and the field induced by χ_{13} and χ_{23} terms.

MoDL-QSM provides a more realistic reference for single-orientation QSM.

FANSI Toolbox

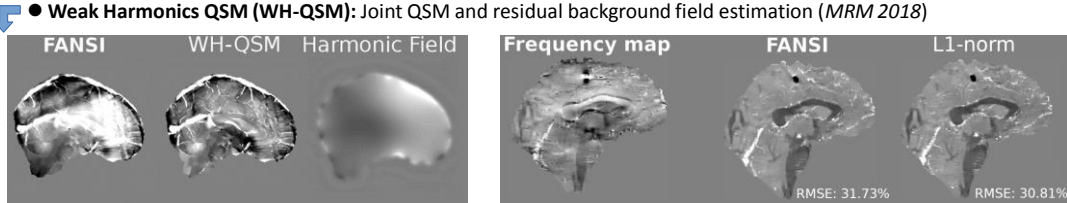
Author: Carlos Milovic

Toolbox developed at Pontificia Universidad Catolica de Chile, Chile and University College London, UK

Matlab toolbox for Quantitative Susceptibility Mapping and Phase processing

Dipole inversion:

- **Closed form solvers:** TKD, direct Tikhonov, L2-norm (gradient penalty)
- **FANSI:** Linear and nonlinear - TV and TGV regularized QSM (*MRM 2018*)
- **Weak Harmonics QSM (WH-QSM):** Joint QSM and residual background field estimation (*MRM 2018*)



- **L1-norm QSM:** L1-norm **data fidelity** terms to suppress streaking artifacts (*ISMRM 2020 3257*).
- **Early Stopping Nonlinear Dipole Inversion (NDI):** fast conjugate gradient solver for parameter-free QSM (*ISMRM 2021 3982*)

The FANSI Toolbox was written by Carlos Milovic, in MATLAB.

FANSI focuses on state-of-the-art dipole inversion algorithms,

Including:

Closed form solvers such as TKD, direct Tikhonov, and a L2-norm gradient penalty.

FASt Nonlinear Susceptibility Inversion

Weak Harmonics QSM, L1-norm QSM

And finally, a reimplementaion of the Nonlinear Dipole Inversion (NDI) using a fast Conjugate Gradient descent solver

FANSI Toolbox

Phase processing tools:

- **Unwrapping:** Laplacian-based algorithms (with different data consistency formulations)
- **Multi-echo Combination:** Regularized nonlinear fitting
- **Background Field Removal:** Multiscale Spherical Mean Value (MSMV, *ISMRM 2019 4940*) and Nonlinear PDF (*ISMRM 2018 2203*)

Relaxometry: Regularized $R2^*$ mapping tools (Tikhonov, TV and TGV)

Experiment design and evaluation tools:

- Numerical Phantom data (based on Wisnieff NeuroImage 2014 and Langkammer MRM 2017)
- Analytic Models: Spheres and cylinders plus Intravoxel effects
- Error metrics: RMSE, SSIM, XSIM (SSIM metric redesigned for QSM), HFEN, Mutual Information, Correlation Coefficient, Mean Absolute Difference, Gradient domain errors

Parameter optimization tools: L-curve and Fourier-based analysis (*MRM 2021*)

Many sample scripts!

Links: <http://gitlab.com/cmilovic/FANSI-Toolbox> Contact: c.milovic@ucl.ac.uk

The authors have included code to perform tasks throughout the QSM pipeline, including Laplacian-based unwrapping algorithms, multiecho combination and background field removal as well as nonlinear $R2^*$ mapping tools.

To facilitate evaluation of QSM tools, they include synthetic brain phantom datasets.

Lastly, the FANSI toolbox includes tools to calculate and display L-curves, and to analyze the Fourier coefficients of the solutions, which can help you find optimal QSM reconstruction parameters.

QSM: Susceptibility Calculation Methods

Authors: Anita Karsa, Karin Shmueli

Department of Medical Physics and Biomedical Engineering, University College London, United Kingdom

- Toolbox for MRI susceptibility (χ) calculation step written in both [MATLAB](#) and [Python](#)
- Three χ calculation techniques:

- Truncated k-space division (**TKD**)¹
- Closed-form k-space inversion with Tikhonov regularisation (**dirTik**)²
- **Iterative fitting with Tikhonov regularisation (iterTik)**²

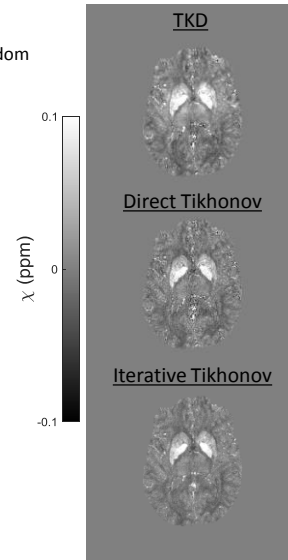
$$\arg \min_{\chi} \|MW(B_{local} - B_0(d * \chi))\|_2^2 + \alpha \|M\chi\|_2^2$$

Binary tissue mask

Weighting term accounting for spatially varying noise

Regularisation term (default $\alpha = 0.05$)

- Note all three methods have default PSF-based correction for χ underestimation³



- The next tool is a set of three susceptibility calculation methods from Anita Karsa and Karin Shmueli, written in both MATLAB and Python.
- The methods include TKD, k-space inversion with Tikhonov regularisation also known as Direct Tikhonov, and iterative fitting with Tikhonov regularisation.
- This last method is explained in Anita's paper on Optimised QSM for the Head and Neck.

QSM: Susceptibility Calculation Methods

How to access:

- Request download as either:

Free Academic licence: 24 month term

Other use licence: Negotiable

Example use (MATLAB):

```
Parameters.FieldMap = FieldMap;  
Parameters.Noise = NoiseMap; ←  
Parameters.Mask = Mask;  
Parameters.Resolution = [1 1 1];  
Parameters.B0direction = [0 0 1];  
Parameters.Alpha = 0.05;
```

```
QSM = iterTik(Parameters);
```

From N_std output of
Fit_ppm_complex.m
or
Fit_ppm_complex_TE.m
from MEDI Toolbox

Download: https://xip.uclb.com/product/mri_qsm_tkd

[1]: Shmueli, K et al. (2009). Magnetic susceptibility mapping of brain tissue in vivo using MRI phase data, Magnetic Resonance in Medicine vol 62 issue 6, 1510-1522

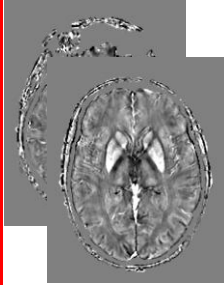
[2]: Karsa, A., Punwani, S., & Shmueli, K. (2020). An optimized and highly repeatable MRI acquisition and processing pipeline for quantitative susceptibility mapping in the head-and-neck region. Magnetic Resonance in Medicine, 84(6), 3206-3222

[3]: Schweser, F et al. (2013). Toward online reconstruction of quantitative susceptibility maps: superfast dipole inversion, Magnetic Resonance in Medicine vol 69 issue 6, 1581-1593

- To download this toolbox simply request a download and provide an academic email address for the academic licence, or the authors would be happy to negotiate a licence for non-academic or commercial use.
- An example use of the iterTik function in MATLAB is shown here, where the Noise input to the Parameter struct is obtained from one of the Fit_ppm_complex functions in the MEDI toolbox.

QSMxT: End-to-end QSM in a Container

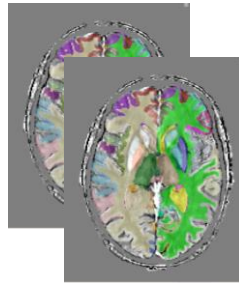
Ashley Stewart, Thomas Shaw, Steffen Bollmann



QSM reconstruction



Template space
construction



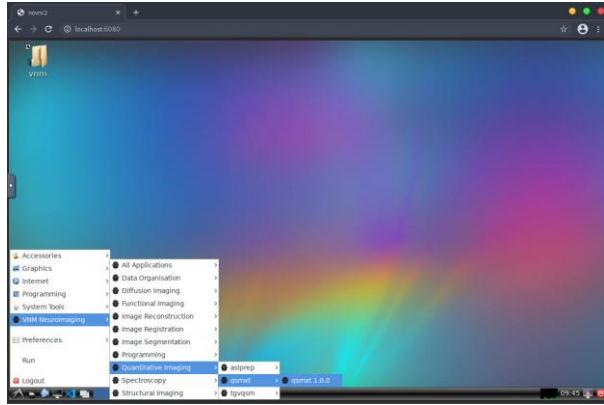
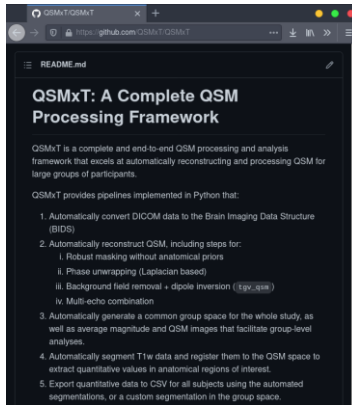
Segmentation

| ROI | Y | num_voxels | min Y | max Y | median Y | mean Y | std Y |
|-----|---|------------|-------|-------|----------|--------|-------|
| 0 | | 1023879 | -0.12 | 0.1 | 0 | 0 | 0.01 |
| 2 | | 227818 | -0.02 | 0.02 | 0 | 0 | 0 |
| 3 | | 214231 | -0.06 | 0.06 | 0 | -0 | 0 |
| 4 | | 16952 | -0.04 | 0.02 | 0 | 0 | 0 |
| 5 | | 636 | -0.01 | 0.01 | 0 | 0 | 0 |
| 7 | | 14586 | -0.01 | 0.01 | -0 | -0 | 0 |
| 8 | | 50564 | -0.04 | 0.02 | -0 | 0 | 0 |
| 10 | | 6214 | -0.03 | 0.03 | 0 | -0 | 0 |
| 11 | | 3476 | -0.02 | 0.02 | 0 | -0 | 0 |
| 12 | | 4924 | -0.02 | 0.01 | 0 | 0 | 0 |
| 13 | | 1811 | -0.01 | 0.01 | 0 | 0 | 0 |
| 14 | | 1902 | -0.02 | 0.01 | 0 | 0 | 0 |

Susceptibility by participant and ROI

The next QSM method is from Steffen Bollmann's group at the University of Queensland. QSMxT is an automated, end-to-end QSM pipeline with straightforward scripts for QSM reconstruction, template space construction for group-level analysis, automated segmentations in the QSM space and the export of susceptibility values by participant and region of interest.

QSMxT: End-to-end QSM in a Container



Links:

GitHub: <https://github.com/QSMxT/QSMxT>

bioRxiv: <https://doi.org/10.1101/2021.05.05.442850>

QSMxT is open-source and freely available on GitHub.

It is distributed as a single software container with all dependencies installed, enabling a simple setup.

The easiest way to get QSMxT is to use the Virtual Neuroimaging Machine from the Neurodesk project. You can see here that it is available there through the applications menu.

One of QSMxT's major features is that it can process multiple subjects and processing steps in parallel using multiple threads, and can also utilise cluster computing systems including PBS.

QSMxT is in a rapid development cycle and the authors would like to hear of user experiences and receive feature requests.

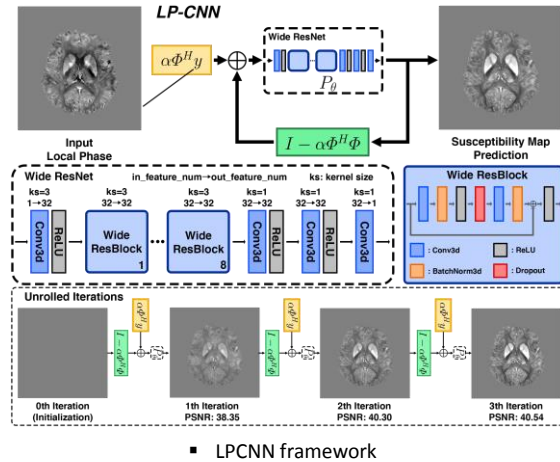
LPCNN QSM Tool for Arbitrary Orientation Dipole Inversion

Authors

Kuo-Wei Lai, Manisha Aggarwal, Peter van Zijl, Xu Li, Jeremias Sulam

Learned Proximal Convolutional Neural Network (LPCNN)

- Solves field-to-susceptibility dipole inversion with data-driven restoration priors (neural network) + iterative solver (proximal gradient descent) according to the dipole model
- Handles dipole inversion with arbitrary orientation (oblique acquisition) and can-do multiple-orientation QSM
- Implemented in PyTorch



Learned Proximal Convolutional Neural Network is a QSM tool for arbitrary magnetic field direction from Johns Hopkins

It combines the data-driven restoration priors and the iterative solver based on the forward dipole-model. The neural network serves as a data-driven regularizer. Because the learned parameters in the neural network are separated from the forward operator, LPCNN can solve arbitrary orientation dipole inversion and can do multiple orientation QSM without retraining or model modification.

LPCNN QSM Tool for Arbitrary Orientation Dipole Inversion

LPCNN tool includes

- **Multiple orientation QSM dataset (n=8)**
- **Scripts** used for preprocessing, training, validation and testing
- **Trained model weight** for immediate testing on your own data
- Need input of preprocessed local field map and pre-calculated dipole kernel



- Multiple orientation QSM

Links:

[Github/Download link]

<https://github.com/Sulam-Group/LPCNN>

[Publication link]

Kuo-Wei Lai, Manisha Aggarwal, Peter van Zijl, Xu Li, Jeremias Sulam. Learned proximal networks for quantitative susceptibility mapping. InternationalConference on Medical Image Computing and Computer-Assisted Intervention. pp. 125–135. Springer 2020.

https://link.springer.com/chapter/10.1007/978-3-030-59713-9_13

The authors provide the QSM dataset they used in the publication on github with the script used for preprocessing, training, validation and testing, as well as a trained LPCNN model weight for direct testing on your own data.

SEPIA – A Pipeline Processing Tool for QSM

Kwok-Shing Chan and José P. Marques

SEPIA is a tool to bring various phase processing methods together for better QSM

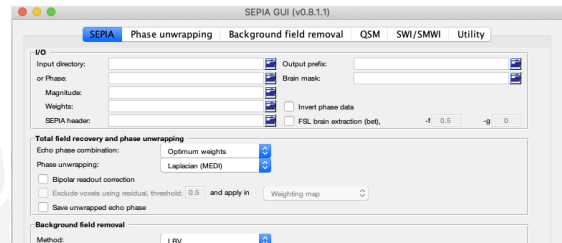
New to QSM? No problem!

- Intuitive graphical-based operations
- Mix-and-match methods across various toolboxes
- Extra utilities to further improve QSM results
- Output with pre-defined units
- Comprehensive documentation & tutorials online

Experienced researcher? Even better!

- Well-organised pipeline structure
- Straightforward adaptation to batch processing
- Config file for reproducible research

*Well-structured pipeline script
with all algorithm settings→*



SEPIA graphical user interface↑

```
19 % Total field recovery algorithm parameters
20 -
21 -
22 -
23 -
24 % Background field removal algorithm parameters
25 -
26 -
27 -
28 -
29 -
30 -
31 -
32 % QSM algorithm parameters
33 -
34 -
35 -
36 -
37 -
```

The last tool in the QSM section is the meta-toolbox SEPIA, a QSM pipeline processing tool to connect various toolboxes, such as MEDI, FANSI, STI Suite and SEGUE, in a single framework.

Its graphical user interface provides an intuitive way to build a pipeline, with the ability to combine methods across toolboxes.

SEPIA uses standard units for its outputs to facilitate communication across multiple toolboxes. Full documentation is available online, including detailed explanations of the interface, as well as tutorials to help you building your first QSM pipeline.

****Click for animation****

SEPIA can also be run entirely by script and the pipeline configuration file provides a clean overview of how the pipeline is set up.

SEPIA – A Pipeline Processing Tool for QSM

Use SEPIA to share your method!

Be part of the solution

- and benefit from other existing tools

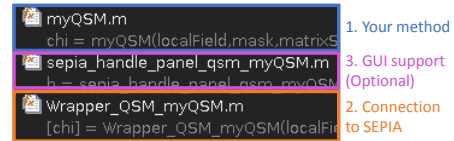
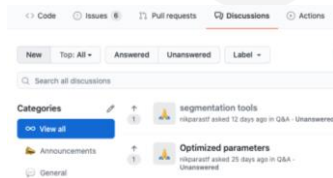
Your method, Your way

- develop in your favourite way: all you need is a wrapper to communicate with SEPIA

Easy Integration

- plug-in to SEPIA with 3 simple scripts (+1 for GUI), put them together with SEPIA and you are all set 😊

Let's make SEPIA better together



↑ Example of new SEPIA add-on
More info on SEPIA documentation website



SEPIA GitHub



Documentation

Links:

Download: github.com/kschan0214/sepia

Documentation: sepia-documentation.readthedocs.io/en/latest/

Publication: Chan, K.-S., Marques, J.P., 2021. SEPIA—Susceptibility mapping pipeline tool for phase images. Neuroimage 227, 117611.

The community is encouraged to use SEPIA as a platform to share their latest developments with the MR community.

Adding a new method in SEPIA is easy: just create a wrapper function for your method to get the input data from SEPIA and send back the result when the process is finished. Then copy everything to the SEPIA add-on folder and the integration is done!

****Click for animation****

Tools Roundup



emtphub.org

I'd like to thank all the authors who contributed their slides and methods. With their permission, we'll be including these slides in the software section of the emtphub.org website