Ironsmith QSM Toolkit

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This software has been developed for research purposes only and is not a clinical tool.

Description:

Ironsmith is a toolkit for creating and processing Quantitative Susceptibility Maps (QSM) and for extracting QSM based iron concentrations from subcortical and cortical brain regions.

Ironsmith can perform the following tasks in a fully automated pipeline:

a) Create QSM maps from GRE DICOM images using the MEDI toolbox **(see section 7 for details)** .
b) Align MPR/MEMPR T1 images to QSM maps and then segment them into 87 ROIs **(ROI list in section 8)** using freesurfer.
c) Filter outlier voxels from these ROIs, extract QSM based iron concentration, and format the output into easy to read tables.
d) Calculate SNR (magnitude image based) for each ROI as a measure of quality control for QSM in an easy to read table.
e) Warp QSM maps and aligned MPR/MEMPR to MNI152 1mm space for voxelwise QSM analyses.
f) Process single or multiple participants at a time (multiple instances and nohup supported).

1) Software requirements:

a) Operating system

Unix
Any linux distrubution that supports Signularity (see point c).

Ironsmith tested on:
Red Hat Enterprise Linux Workstation release 7.8 (Maipo)

Windows 10 WSL2
Ironsmith tested on:
Ubuntu 18.04 running on Windows 10 Subsystem for Linux V2 (WSL2)
Ubuntu 16.04 running on Windows 10 Subsystem for Linux V2 (WSL2)

b) MATLAB

Ironsmith requires Matlab to run MEDI Toolbox and supports versions R2017b to R2019b.
Matlab is not needed if MEDI is not required.

c) Singularity

Ironsmith tested on Singularity versions 3.5.2 and 3.5.3
Installation guide:
https://sylabs.io/guides/3.5/admin-guide/installation.html

d) Bash unix shell version 4.2.46(2) or later.

2) Installation:

a) Download Ironsmith QSM Toolkit

Option 1: download from github
https://github.com/vzachari/IronSmithQSM

Option 2: using git
```
git clone https://github.com/vzachari/IronSmithQSM.git && cd IronSmithQSM && git checkout v1.0
```

b) Download QSM_Container.simg (8.8GB) from:
https://drive.google.com/file/d/1wPdd2Xa0oLV2wwpHneXZ7nlIZB3XoKFb/view?usp=sharing
Or
https://tinyurl.com/QSMContainer

c) Place QSM_Container.simg in IronSmithQSM/Functions

d) Edit IronSmithQSM/Matlab_Config.txt with the path to the matlab executable on your system.
(e.g. /usr/local/MATLAB/R2019b/bin/matlab)
Supported versions R2017b to R2019b.

e) Add the IronSmithQSM directory to $PATH
Guide: https://opensource.com/article/17/6/set-path-linux

3) Syntax:

Ironsmith [MyInputFile] [absolute path to output folder]

Example: Ironsmith File.csv /home/data/MyAmazingExp/QSM_Analysis"

a) The output folder does not need to exist.

b) The output folder does not need to be empty but Ironsmith will skip any participant specified in MyInputFile that has a corresponding folder inside the output folder.

Ex. if S0001 is specified in MyInputFile and folder S0001 exists in output folder, S0001 will be skipped.

c) Freesurfer_Skip is a reserved folder name under output folder and may be used by Ironsmith. See section #5 on quality of life features below.

4) MyInputFile format:

a) MyInputFile has to be CSV formatted (entries separated by commas ',').

b) Each row corresponds to a different participant.

see Example_File.csv in IronSmithQSM folder:

If MEDI Toolbox is required to create QSM images/maps:

Column1 = Subj (nominal subject variable e.g. S0001 or 01 or Xanthar_The_Destroyer)
Column2 = MEDI_Yes <-- this is case sensitive
Column3 = Absolute path to directory with MPR/MEMPR files
(e.g. /home/subjecs/S01/MPR).

MPR/MEMPR files can be:

a) DICOMS

Only MPR/MEMPR DICOMS should be present in the MPR folder if you want Ironsmith to process DICOMS. If NIFTI files exist together with DICOMS, they will be selected instead (see "b" below).

b) Multiple .nii/.nii.gz files each corresponding to a different echo.

To make sure the correct files are selected, each NIFTI file needs to have _e# in the file name, where # is the echo number.
(e.g. S0001_MEMPR_e1.nii.gz, S0001_MEMPR_e2.nii.gz...)
This is the default **dcm2niix** output format for multiple echos.

c) Single .nii/nii.gz file with multiple timepoints, each corresponding to a different echo.
This single NIFTI file can have any name.

d) Single .nii/nii.gz file with a single echo/timepoint.
This can be rms/averaged across echos or just a single echo T1 MPRAGE.
This single NIFTI file can have any name.

Column4 = Absolute path to folder with QSM DICOM files
(e.g. /home/subjecs/S01/QSM_Dicom)
QSM DICOM folder must include DICOMS for both GRE magnitude and phase.

Preferably only QSM DICOMS should be present in the QSM_Dicom folder. However, Ironsmith can filter out the following filetypes .nii .json .txt .nii.gz .HEAD .BRIK .hdr .img

All 4 columns need to be provided, otherwise Ironsmith will exit with errors.

If QSM maps and GRE magnitude images are already available:

Column1 = Subj (nominal subject variable e.g. S0001 or 01 or Xanthar_The_Destroyer)
Column2 = MEDI_No <-- This is case sensitive
Column3 = Absolute path to directory with MPR/MEMPR files
(e.g. /home/subjecs/S01/MPR)

MPR/MEMPR files can be:

a) DICOMS

Only MPR/MEMPR DICOMS should be present in the MPR folder if you want Ironsmith to process DICOMS. If NIFTI files exist together with DICOMS, they will be selected instead (see "b" below).

b) Multiple .nii/.nii.gz files each corresponding to a different echo.

To make sure the correct files are selected, each NIFTI file needs to have _e# in the file name, where # is the echo number.
(e.g. S0001_MEMPR_e1.nii.gz, S0001_MEMPR_e2.nii.gz...)
This is the default **dcm2niix** output format for multiple echos.

c) Single .nii/nii.gz file with multiple timepoints, each corresponding to a different echo.
This single NIFTI file can have any name.

d) Single .nii/nii.gz file with a single echo/timepoint.
This can be rms/averaged across echos or just a single echo T1 MPRAGE.
This single NIFTI file can have any name.

Column4 = Absolute path including filename to QSM magnitude image
(e.g. /home/subjecs/S01/QSM/QSM_Magnitude.nii.gz)

Column5 = Absolute path including filename to QSM map
(e.g. /home/subjects/S01/QSM/QSM_Map.nii.gz)

All 5 columns need to be provided, otherwise Ironsmith will exit with errors

5) Quality of life features:

Skipping freesurfer segmentation

If a participant already has a completed freesurfer recon-all -all segmentation folder and you would like Ironsmith to skip the freesurfer segmentation step, do the following:

a) Copy the freesurfer recon-all folder (the one containing the *label*, *mri*, *scripts*, *stats*, *surf*... folders) into **/OutputFolder/Freesurfer_Skip**, where **OutputFolder** is the one specified/to be specified in the Ironsmith command.

You can create the /OutputFolder/Freesurfer_Skip folder or Ironsmith will create it for you if you have run it at least once previously for OutputFolder.

b) Rename the recon-all folder to **Subj_FreeSurfSeg_Skull**. Subj should match the one provided in MyInputFile and should correspond to the participant you want the segmentation step skipped.

Viewing output NIFTI files

If you do not have a NIFTI viewer, AFNI can be launched from within the QSM_Container.simg by using the *Ironsmith_AFNI* command. Just type *Ironsmith_AFNI* from within the folder you would like to view NIFTI files from.

AFNI viewer documentation:
https://afni.nimh.nih.gov/pub/dist/edu/latest/afni_handouts/afni03_interactive.pdf

6) Outputs:

Each participant processed by Ironsmith will have a corresponding folder in **OutputFolder**. For example, if "**/home/QSM_Analysis**" is the OutputFolder and "**S0001**" is one of the participants processed, then **/home/QSM_Analysis/S0001** will be created and populated with data.

a) All masks/ROIs are placed under:

S0001/QSM/Freesurf_QSM_Masks/Cort_Masks_AL_QSM_RS_Erx1
S0001/QSM/Freesurf_QSM_Masks/SubC_Masks_AL_QSM_RS_Erx1

b) All QSM maps/images created are placed under S0001/QSM/Freesurf_QSM_Masks and are labelled as:

Subj_QSM_Map_FSL.nii.gz <-- Default MEDI
Subj_QSM_Map_New_CSF_FSL.nii.gz <-- Lateral ventricles as the QSM reference structure
Subj_QSM_Map_New_WM_FSL.nii.gz <-- White matter as the QSM reference structure

c) All QSM maps warped to MNI space are placed under

S0001/QSM/Freesurf_QSM_Masks/MNI152_QSM

d) QSM per ROI means (87 ROIs) are under **/QSM_Analysis/Group** as follows:

Group_QSM_Mean.csv
Group_QSM_Mean_CSF.csv

Group_QSM_Mean_WM.csv
Group_QSM_ADJ_Mean.csv
Group_QSM_ADJ_Mean_CSF.csv
Group_QSM_ADJ_Mean_WM.csv
Group_QSM_SNR.csv

_Mean = Using only positive QSM voxels
_ADJ_Mean = Using only positive QSM voxels and adjusting for ROI size
_CSF = Lateral ventricles as the QSM reference structure
_WM = White matter as the QSM reference structure

SNR is calculated as follows:
mean signal intensity of magnitude image within an ROI / standard deviation of magnitude signal outside the head.

The outside the head mask can be found here:
/QSM_Analysis/S0001/QSM/Freesurf_QSM_Masks/Subj_QSM_Mag_FSL_rms_OH_Mask.nii.gz

7) Ironsmith uses the following software, provided in the form of a Singularity image:

AFNI

RW Cox. AFNI: Software for analysis and visualization of functional magnetic resonance neuroimages. Computers and Biomedical Research, 29:162-173, 1996.

RW Cox and JS Hyde. Software tools for analysis and visualization of FMRI Data. NMR in Biomedicine, 10:171-178, 1997.

S Gold, B Christian, S Arndt, G Zeien, T Cizadlo, DL Johnson, M Flaum, and NC Andreasen. Functional MRI statistical software packages: a comparative analysis. Human Brain Mapping, 6:73-84, 1998.

dcm2niix

Li, Xiangrui, et al. "The first step for neuroimaging data analysis: DICOM to NIFTI conversion." Journal of neuroscience methods 264 (2016): 47-56.

Freesurfer

Dale, A.M., Fischl, B., Sereno, M.I., 1999. Cortical surface-based analysis. I. Segmentation and surface reconstruction. Neuroimage 9, 179-194.

Dale, A.M., Sereno, M.I., 1993. Improved localization of cortical activity by combining EEG and MEG with MRI cortical surface reconstruction: a linear approach. J Cogn Neurosci 5, 162-176.

Desikan, R.S., Segonne, F., Fischl, B., Quinn, B.T., Dickerson, B.C., Blacker, D., Buckner, R.L., Dale, A.M., Maguire, R.P., Hyman, B.T., Albert, M.S., Killiany, R.J., 2006. An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest. Neuroimage 31, 968-980.

FSL

M.W. Woolrich, S. Jbabdi, B. Patenaude, M. Chappell, S. Makni, T. Behrens, C. Beckmann, M. Jenkinson, S.M. Smith. Bayesian analysis of neuroimaging data in FSL. NeuroImage, 45:S173-86, 2009

S.M. Smith, M. Jenkinson, M.W. Woolrich, C.F. Beckmann, T.E.J. Behrens, H. Johansen-Berg, P.R. Bannister, M. De Luca, I. Drobnjak, D.E. Flitney, R. Niazy, J. Saunders, J. Vickers, Y. Zhang, N. De Stefano, J.M. Brady, and P.M. Matthews. Advances in functional and structural MR image analysis and implementation as FSL. NeuroImage, 23(S1):208-19, 2004

M. Jenkinson, C.F. Beckmann, T.E. Behrens, M.W. Woolrich, S.M. Smith. FSL. NeuroImage, 62:782-90, 2012

MEDI Toolbox (outside Singularity, in IronSmithQSM/Functions folder)

de Rochefort, L., Liu, T., Kressler, B., Liu, J., Spincemaille, P., Lebon, V., … & Wang, Y. (2010). Quantitative susceptibility map reconstruction from MR phase data using bayesian regularization: validation and application to brain imaging. Magnetic Resonance in Medicine: An Official Journal of the International Society for Magnetic Resonance in Medicine, 63(1), 194-206.

Liu J, Liu T, De Rochefort L, Ledoux J, Khalidov I, Chen W, Tsiouris AJ, Wisnieff C, Spincemaille P, Prince MR, Wang Y (2012)
Morphology enabled dipole inversion for quantitative susceptibility mapping using structural consistency between
the magnitude image and the susceptibility map. Neuroimage 59, 2560-2568.

http://pre.weill.cornell.edu/mri/pages/qsm.html

8) ROI List:

LR_Frontal_Lobe_GM
LR_Parietal_Lobe_GM
LR_Occipital_Lobe_GM
LR_Temporal_Lobe_GM
L_CaudalAnteriorCingulate_GM
L_CaudalMiddleFrontal_GM
L_Cuneus_GM
L_DLPFC_GM
L_Entorhinal_GM
L_Frontal_GM
L_Fusiform_GM
L_InferiorParietal_GM
L_InferiorTemporal_GM
L_Insula_GM
L_IsthmusCingulate_GM
L_LateralOccipital_GM
L_LateralOrbitofrontal_GM
L_Lingual_GM
L_MedialOrbitofrontal_GM
L_MiddleTemporal_GM
L_Occipital_GM_Mask
L_Parietal_GM_Mask
L_Temporal_GM_Mask
L_Parahippocampal_GM
L_Pericalcarine_GM
L_Postcentral_GM
L_PosteriorCingulate_GM
L_Precentral_GM
L_Precuneus_GM
L_RostalMiddleFrontal_GM

L_RostralAnteriorCingulate_GM
L_SuperiorFrontal_GM
L_SuperiorParietal_GM
L_SuperiorTemporal_GM
L_TransverseTemporal_GM
R_CaudalAnteriorCingulate_GM
R_CaudalMiddleFrontal_GM
R_Cuneus_GM
R_DLPFC_GM
R_Entorhinal_GM
R_Frontal_GM_Mask
R_Fusiform_GM
R_InferiorParietal_GM
R_InferiorTemporal_GM
R_Insula_GM
R_IsthmusCingulate_GM
R_LateralOccipital_GM
R_LateralOrbitofrontal_GM
R_Lingual_GM
R_MedialOrbitofrontal_GM
R_MiddleTemporal_GM
R_Occipital_GM_Mask
R_Parietal_GM_Mask
R_Temporal_GM_Mask
R_Parahippocampal_GM
R_Pericalcarine_GM
R_Postcentral_GM
R_PosteriorCingulate_GM
R_Precentral_GM
R_Precuneus_GM
R_RostalMiddleFrontal_GM
R_RostralAnteriorCingulate_GM
R_SuperiorFrontal_GM
R_SuperiorParietal_GM
R_SuperiorTemporal_GM
R_TransverseTemporal_GM
LR_Accumbens_area
LR_Amygdala
LR_Caudate
LR_Hipp
LR_Pallidum
LR_Putamen
LR_Thalamus_Proper
L_Accumbens_area
L_Amygdala
L_Caudate
L_Hipp
L_Pallidum
L_Putamen
L_Thalamus_Proper
R_Accumbens_area
R_Amygdala
R_Caudate
R_Hipp
R_Pallidum
R_Putamen
R_Thalamus_Proper