Automated MRI Data Preprocessing Pipeline

CBI Town Hall 9/16/2025



Automated MRI Data Preprocessing Pipeline

We developed this pipeline for Dr. Lisa McTeague's DARPA RECOVERS study to streamline data preparation and automate repetitive tasks:

- Data retrieval (from CBI Home or from local folder)
- DICOM extraction and NIfTI conversion
- Metadata extraction
- Data validation
- Conversion to BIDS format
- De-identification and defacing
- Upload to Box

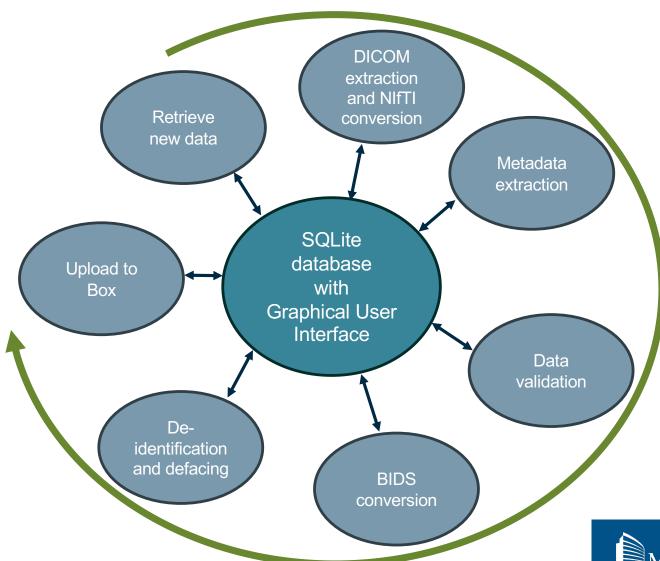
The pipeline can be easily adapted to other studies by modifying the configuration files

The software is freely available on GitHub:

https://github.com/finetto/musc-automated-imaging-pipeline



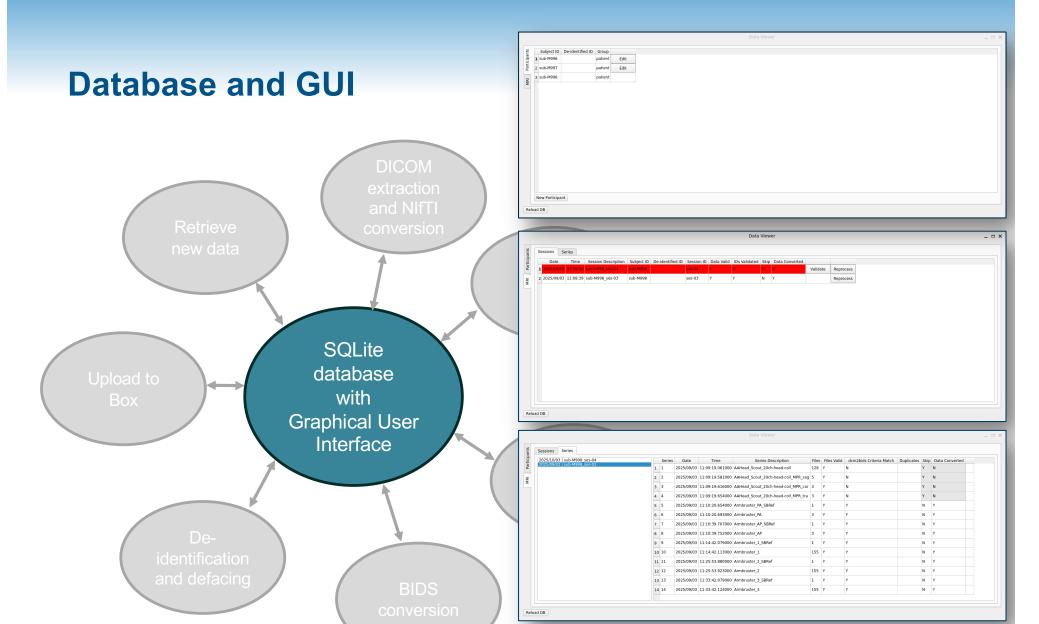
Automated MRI Data Preprocessing Pipeline



- Can be run manually or on a schedule
- Modular design (steps can be enabled or disabled)
- Fully local (except data download and upload)
- Database stores information on each participant, session and series
- Database stores current processing state for each session

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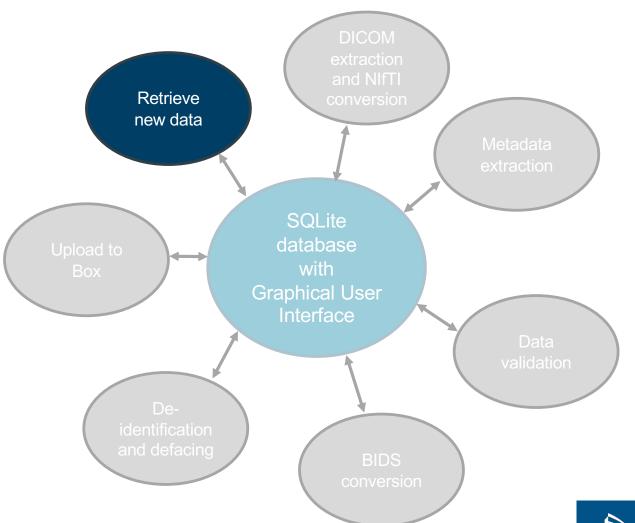
of South Carolina





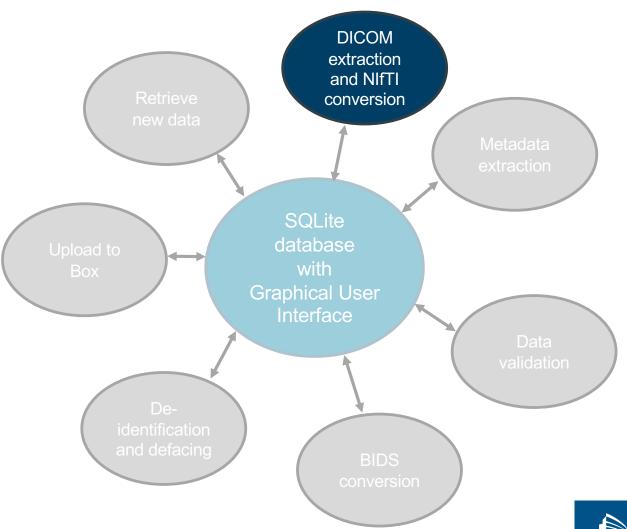
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Data Retrieval



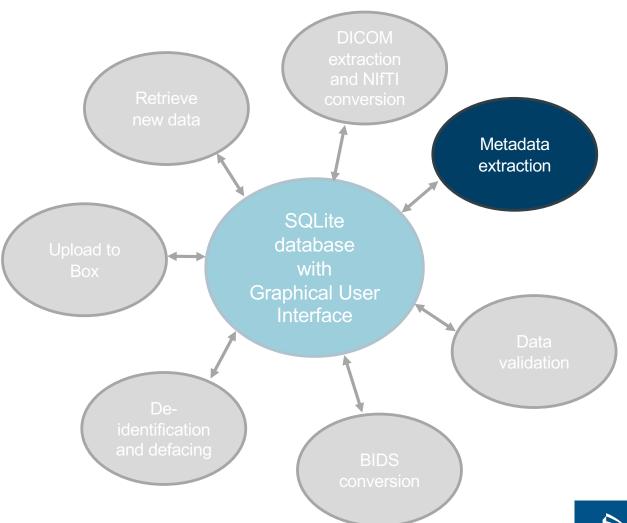
- Scans the study folder on CBI home, or a local folder
- If a new session is found, the data is downloaded
- New sessions are added to the database, initiating all following steps

DICOM extraction and NIfTI conversion



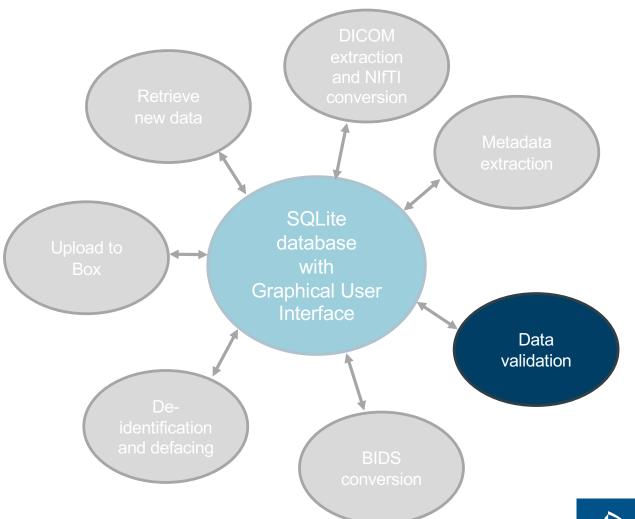
- Extract the downloaded zip file
- Use <u>dcm2niix</u> [1] to convert to NIfTI
- Get all series for the session and add them to the database

Metadata extraction



- Extract timestamp, subject ID and session ID from data file name
- Extract series information from sidecar file

Data validation

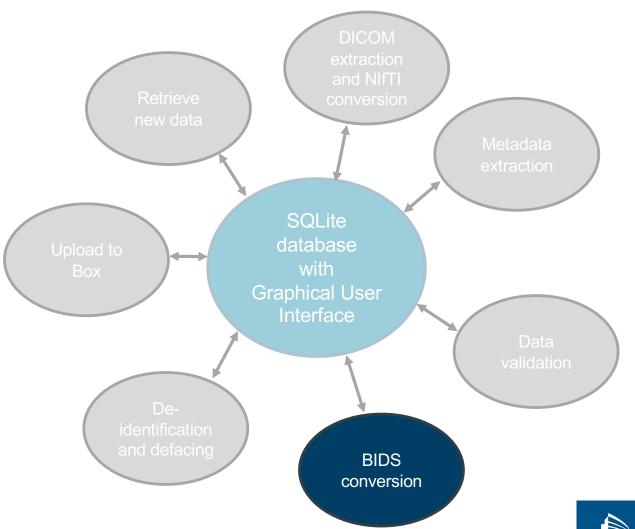


- Make sure files were extracted correctly
- Match dcm2bids criteria to each series
- Identify duplicate series (only one will be processed)
- Make sure the extracted series match the CBI Summary file (if available)
- Ask user to confirm subject ID and session ID
- User can mark sessions or series to skip



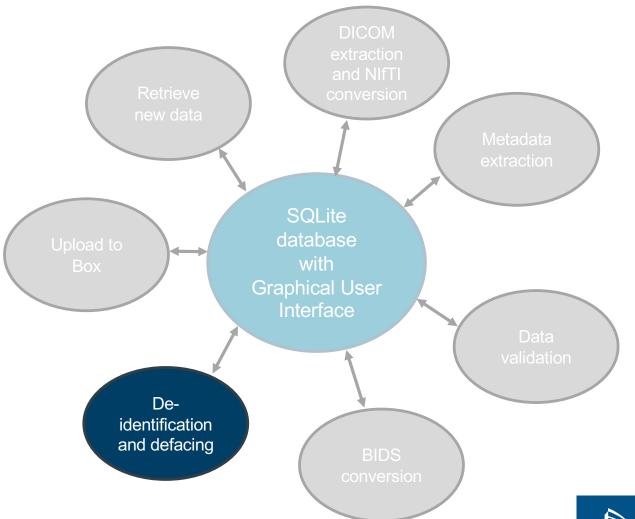
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BIDS conversion



- Sessions that passed data validation will be converted to BIDS format
- NIfTI files are converted using dcm2bids [2]
- User needs to define a dcm2bids configuration file

De-identification and defacing



- Optional step
- De-identified IDs are either assigned to subject or automatically generated
- All files are renamed using de-identified subject IDs
- Anatomical images are defaced using <u>FSL</u>
 [3] and <u>pydeface</u> [4]
- De-identified data is stored in separate folder structure

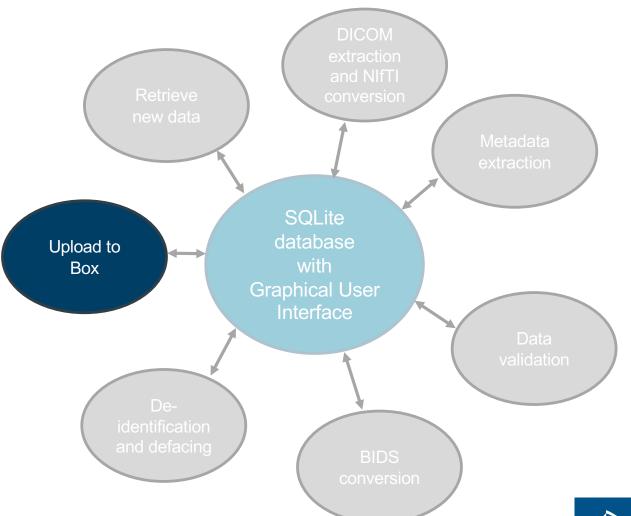
[3] https://fsl.fmrib.ox.ac.uk/fsl

[4] https://github.com/poldracklab/pydeface



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Data upload to Box



- Optional step
- Data is uploaded to Box using <u>Box SDK [5]</u>
- Source data, converted data and de-identified data are uploaded to separate folders
- For each file, the upload is verified and repeated if necessary
- Database and config files are backed up to Box as well

Installation and configuration

Installation

- Tested on Ubuntu and WSL2
- Instructions provided in the repository *README* file
- To install, download/clone the repository and run the install.sh script

Configuration

- There are several configuration files that need to be added and/or modified
 - Database configuration
 - Data download configuration (CBI Home or local folder)
 - Study configuration (e.g. study name, format of IDs,...)
 - Processing configuration (e.g. destination folders)
 - Box configuration
 - Notifications
- If synchronizing from CBI Home, one needs to create a credentials file
- A dcm2bids configuration file is necessary for the BIDS conversion



Running the pipeline

- The pipeline can be run on a schedule (e.g. every hour). This is configured automatically when running the installation script
- The pipeline can also be run manually with the run_mri_pipeline.sh script
- To launch the Data Viewer GUI, one can use the run_data_viewer.sh script



Software demo

