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## MRI\_preprocessing\_protocol

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**Protocol status:** Working

**We use this protocol and it's working**

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## Abstract

Preprocessing protocol for structural, DWI and T2\* MRI acquisitions



## Structural T1w (MP-RAGE acquisition)

- 1 Data transformation from DICOM to NIFTI standard (software: dcm2niix)
- 2 Field of view optimization (command: fslreorient2std; software: FSL)
- 3 Bias field correction (command: N4BiasFieldCorrection; software: ANTs)
- 4 Non-brain tissue removal (command: bet; software: FSL)
- 5 Deep-brain nuclei segmentation (command: run\_first\_all; software: FSL)
- 6 CSF, GM and WM tissue segmentation (command: fast; software: FSL)
- 7 Diffeomorphic registration to MNI152 2009c sym template (command: antsRegistrationSyN.sh; software: ANTs)

## T2\* (multi-echo gradient echo acquisition)

- 8 Data transformation from DICOM to NIFTI standard (software: dcm2niix)
- 9 Affine registration to structural T1w using the first volume as reference (command: antsRegistration; software ANTs)

## Single-shell DWI (single-shot 2D spin-echo, b=1000)

- 10 Data transformation from DICOM to NIFTI standard (software: dcm2niix)
- 11 B0 pair isolation (AP and PA)



- 12 Image denoising using the overcomplete local PCA approach (MATLAB)
- 13 Geometric distortions and magnetic field inhomogeneities corrections (command: topup; software: FSL)
- 14 Eddy current-induced distortion corrections (command: eddy; software: FSL)
- 15 Bias field correction (command: N4BiasFieldCorrection; software: ANTs)
- 16 Affine registration to structural T1w using the first volume (B0) as reference (command: antsRegistration; software ANTs)