

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

MGA - Multimodal Glioma Analysis

RRID:SCR_014122

Type: Tool

Proper Citation

MGA - Multimodal Glioma Analysis (RRID:SCR_014122)

Resource Information

URL: <http://www.nitrc.org/projects/hof/>

Proper Citation: MGA - Multimodal Glioma Analysis (RRID:SCR_014122)

Description: An MRI preprocessing pipeline built with HOF (Heterogeneous Optimization Framework) methodology. MGA prepares neuro-oncology clinical imaging studies for scientific analysis in both longitudinal and cross-sectional studies. It works on DICOM images from a single MRI study and includes perfusion (DSC sequence based) analysis and DTI analysis. MGA spatially co-registers all study images to an atlas template and to a template image within the study.

Abbreviations: MGA

Synonyms: Multimodal Glioma Analysis

Resource Type: data processing software, image analysis software, software application, software resource, standalone software, workflow software

Keywords: image analysis, workflow software, standalone, pipeline, mri, heterogeneous optimization framework, clinical image study, image

Availability: Available to the research community

Resource Name: MGA - Multimodal Glioma Analysis

Resource ID: SCR_014122

License: BSD License

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260905T132743+0000

Ratings and Alerts

No rating or validation information has been found for MGA - Multimodal Glioma Analysis.

No alerts have been found for MGA - Multimodal Glioma Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Milchenko M, et al. (2016) Heterogeneous Optimization Framework: Reproducible Preprocessing of Multi-Spectral Clinical MRI for Neuro-Oncology Imaging Research. Neuroinformatics, 14(3), 305.