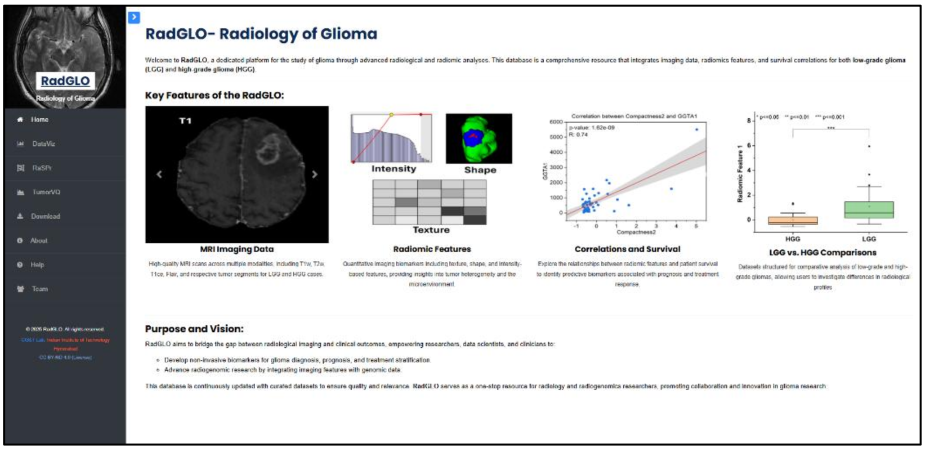
Overall architecture and implementation of RadGLO

RadGLO, a dedicated platform for the study of glioma through advanced radiological and radiomic analyses. This database is a comprehensive resource that integrates imaging data, radiomics features, and survival correlations for both low-grade glioma (LGG) and high-grade glioma (HGG). RadGLO aims to bridge the gap between radiological imaging and clinical outcomes, empowering researchers, data scientists, and clinicians to, (1) Develop non-invasive biomarkers for glioma diagnosis, prognosis, and treatment stratification. (2) Advance radiogenomic research by integrating imaging features with genomic data. This database is continuously updated with curated datasets to ensure quality and relevance. RadGLO serves as a one-stop resource for radiology and radiogenomics researchers, promoting collaboration and innovation in glioma research. Figure 1 represents home page of RadGLO.



RadGLO- Radiology of Glioma

Welcome to **RadGLO**, a dedicated platform for the study of glioma through advanced radiological and radiomic analyses. This database is a comprehensive resource that integrates imaging data, radiomics features, and survival correlations for both **low-grade glioma (LGG)** and **high-grade glioma (HGG)**.

Key Features of the RadGLO:

MRI Imaging Data

High-quality MRI scans across multiple modalities, including T1w, T2w, T1ce, Flair, and respective tumor segments for LGG and HGG cases.

Radiomic Features

Quantitative imaging biomarkers including texture, shape, and intensity-based features, providing insights into tumor heterogeneity and the microenvironment.

Correlations and Survival

Explore the relationships between radiomic features and patient survival to identify predictive biomarkers associated with prognosis and treatment response.

LGG vs. HGG Comparisons

Datasets structured for comparative analysis of low-grade and high-grade gliomas, allowing users to investigate differences in radiological profiles.

Purpose and Vision:

RadGLO aims to bridge the gap between radiological imaging and clinical outcomes, empowering researchers, data scientists, and clinicians to:

- Develop non-invasive biomarkers for glioma diagnosis, prognosis, and treatment stratification.
- Advance radiogenomic research by integrating imaging features with genomic data.

This database is continuously updated with curated datasets to ensure quality and relevance. RadGLO serves as a one-stop resource for radiology and radiogenomics researchers, promoting collaboration and innovation in glioma research.

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Figure 1: Home page interface of RadGLO .

Platform Overview

RadGLO is hosted on a Linux-based Apache HTTP Server (v2.4). The front-end is built with HTML5, CSS3, JavaScript, jQuery, and D3.js for dynamic visualizations. Backend processing is handled via Python and R scripts executed through PHP files, which are called directly from the front-end. Data is fetched directly from CSV files stored on the server without using a database. The platform is compatible with modern browsers and supports responsive design across desktop and mobile devices.

1. DataViz

The DataViz module provides four interactive tools for exploring radiomic features:

1.1 Survival Analysis: Users can assess the prognostic impact of radiomic features using Kaplan-Meier plots with selectable cutoff methods (median, mean, or optimal) to stratify patients (Group0: above cutoff, Group1: below cutoff), displaying p-values for significance (Figure 2a).

1.2 Statistical Comparison: Users can compare radiomic feature distributions across tumor grades (LGG vs GBM), datasets, and methylation status (Meth vs UnMeth) in TCGA, UCSF, and UPENN cohorts, generating five comparative plots (Figure 2b).

1.3 Correlation Analysis: Users can visualize the relationship between radiomic features and gene expression data by selecting a feature and gene to plot scatterplots with Spearman correlation coefficients and p-values (Figure 2c).

1.4 Feature Distribution Heatmap: Users can view feature distributions as a complex heatmap with hierarchical clustering of both rows and columns (Figure 2d).

This module supports HTML and user-uploaded CSV files containing radiomic, clinical, and genomic data. Interactive visualizations are implemented using Plotly.js and D3.js for filtering and export.

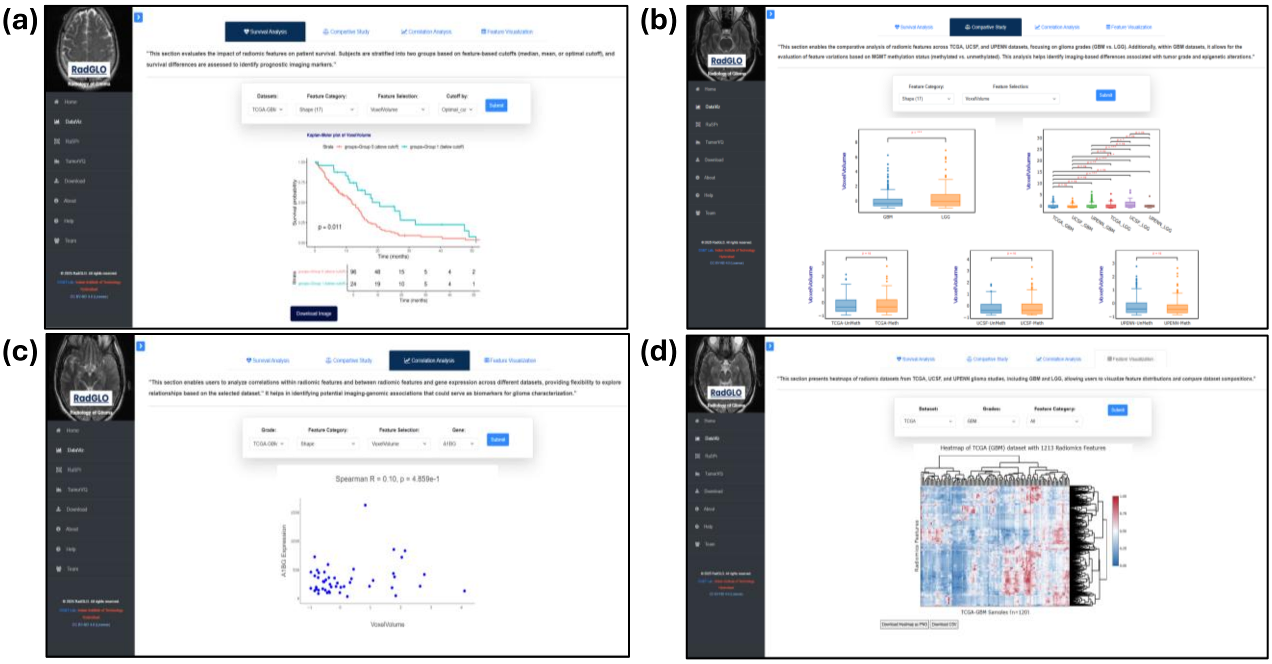
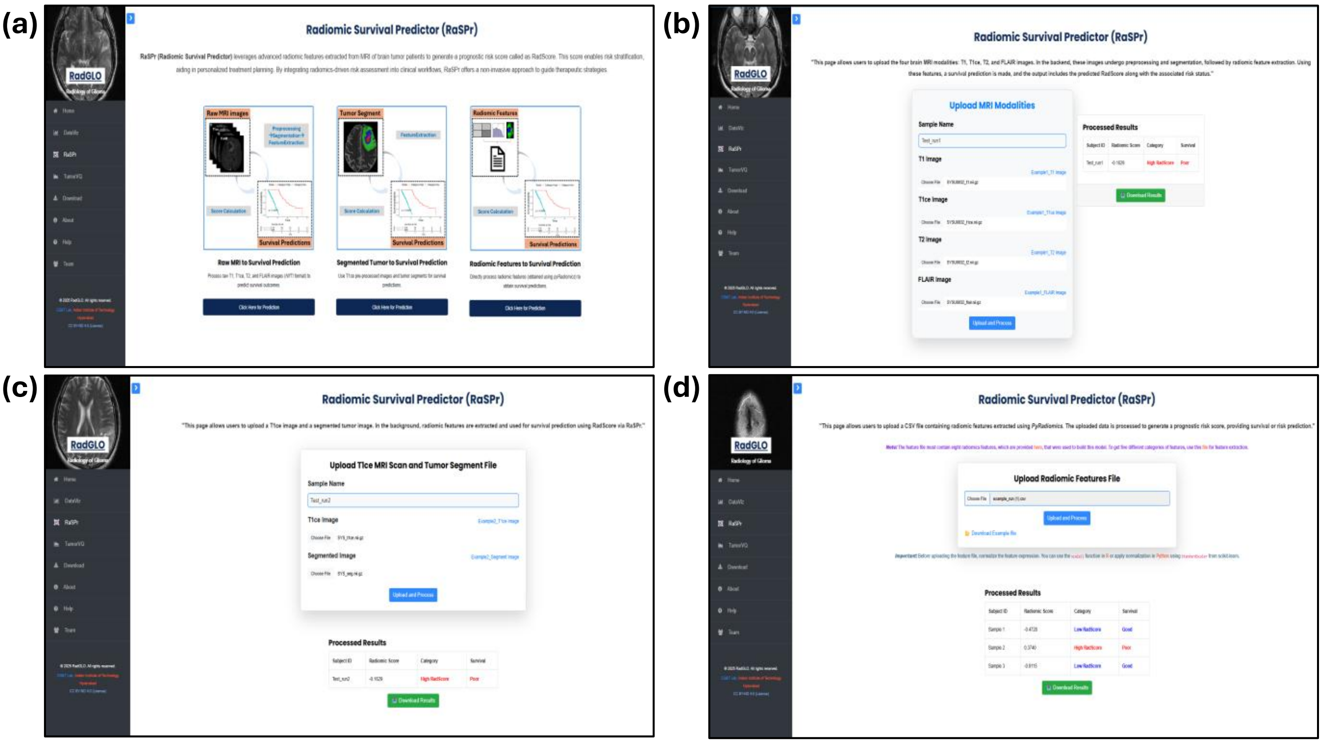


Figure 2: (a) Kaplan-Meier survival analysis for radiomic features, enabling users to evaluate feature-based survival impact. (b) Statistical comparison of radiomic feature distributions between LGG and GBM, different datasets, and methylation subtypes. (c) Correlation analysis between selected radiomic features and gene expression profiles. (d) Heatmap of radiomic feature distributions across samples, visualizing clustering patterns within the dataset.

2. Radiomic Survival Predictor (RaSPr)

RaSPr is an in-house developed prognostic tool tailored for glioblastoma survival prediction using radiomic features. It calculates a risk score, termed the **RadScore**, from a model built on eight key radiomic features. The tool offers three flexible pipelines for survival risk prediction (Figure 3a).


Radiomic Survival Predictor (RaSPr)

RaSPr (Radiomic Survival Predictor) leverages advanced radiomic features extracted from MRI of brain tumor patients to generate a prognostic risk score called as RadScore. This score enables risk stratification, aiding in personalized treatment planning. By integrating radiomics-driven risk assessment into clinical workflows, RaSPr offers a non-invasive approach to guide therapeutic strategies.

"This page allows users to upload a T1ce image and a segmented tumor image. In the background, radiomic features are extracted and used for survival prediction using RadScore via RaSPr."

Figure 3: (a) User interface of RaSPr, showcasing its three approaches for risk prediction. (b) Approach I involve uploading four MRI modalities for full preprocessing and feature extraction. (c) Approach II requires only the segmented mask and T1ce image. (d) Approach III uses directly uploaded radiomic features in CSV format to predict patient risk and survival outcome.

2.1 In the first approach, users upload raw GBM MRI data containing all four modalities (T1, T1ce, T2, and FLAIR) with the strict "*.nii.gz" extension and a naming convention specifying the modality (e.g., "Sample1_t1.nii.gz"). Upon submission, a backend bash script runs the BraTS pre-processing pipeline, involving image re-orientation to LPS or RAI coordinates, N4 bias field correction to reduce intensity non-uniformities, and rigid registration to align all modalities to T1ce. T1ce images are then registered to the SRI-24 standard brain atlas, and atlas-based skull-stripping is performed to remove non-brain tissues. Tumor segmentation is conducted using EnsembleUNets, a CNN-based benchmarked method, followed by radiomic feature extraction with PyRadiomics. The selected eight features are used to calculate the RadScore and predict patient survival risk, as illustrated in Figure 3b.

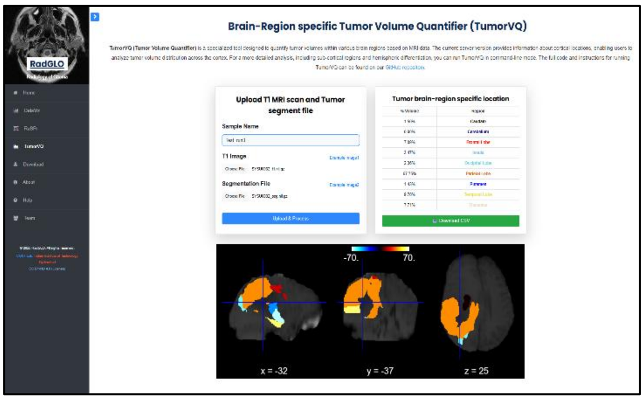
2.2 The second approach allows users to upload pre-segmented tumor images in "XYZ_seg.nii.gz" format alongside the T1 MRI scans. In this case, the backend directly performs feature extraction, selection of the eight features, and RadScore estimation for risk prediction (Figure 3c).

2.3 The third approach enables users to upload radiomic feature files in CSV format, provided these features are extracted using PyRadiomics and normalized using either the "scale" function in R or "StandardScaler" in Python (Figure 3d).

For all three approaches, the output includes Subject ID, RadScore, assigned risk category, and predicted survival outcome, presented in a downloadable tabular format for user convenience.

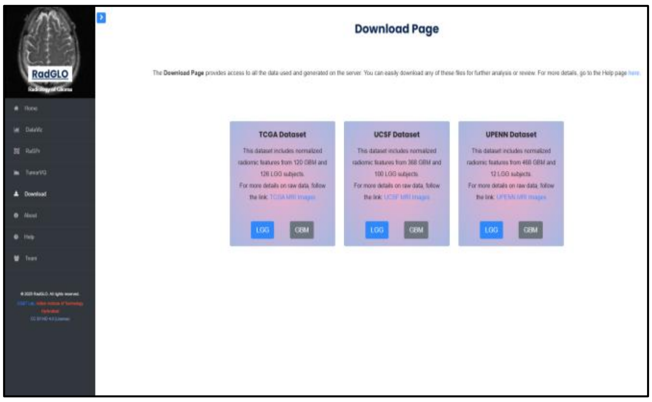
3. Tumor Volume Quantifier (TumorVQ)

TumorVQ is another in-house developed tool that estimates tumor volume within specific brain regions using segmentation maps and atlas-based localization. Users upload tumor-segmented masks along with corresponding MRI images. In the backend, these images are registered and transformed to the MNI152 standard brain template. Tumor volumes are then quantified based on the MNI cortical atlas, and results are visualized through interactive charts for intuitive interpretation (Figure 4).



TumorVQ (Tumor Volume Quantifier) is a specialized tool designed to quantify tumor volumes within various brain regions based on MRI data. The current server version provides information about cortical locations, enabling users to analyze tumor volume distribution across the cortex. For a more detailed analysis, including sub-cortical regions and hemispheric differentiation, you can run TumorVQ in command-line mode. The full code and instructions for running TumorVQ can be found on our GitHub repository.

Figure 4: Interface of TumorVQ



The **Download Page** provides access to all the data used and generated on the server. You can easily download any of these files for further analysis or review. For more details, go to the Help page here.

TCGA Dataset

This dataset includes normalized radiomic features from 120 GBM and 126 LGG subjects.
For more details on raw data, follow the link: TCGA MRI images

UCSF Dataset

This dataset includes normalized radiomic features from 368 GBM and 100 LGG subjects.
For more details on raw data, follow the link: UCSF MRI images

UPENN Dataset

This dataset includes normalized radiomic features from 468 GBM and 12 LGG subjects.
For more details on raw data, follow the link: UPENN MRI images

Figure 5: Interface of Download Page

4. Download

This section provides access to complete sets of normalized radiomics features for each dataset and tumor grade (LGG and GBM), accompanied by brief descriptions to guide users in selecting the relevant data (Figure 5).

5. About

The About section offers comprehensive information on the datasets used in RadGLO, the data processing pipelines, and detailed explanations of the different analysis tools. Users can explore this section to understand the platform's methodology and data sources more deeply.

6. Help

This module serves as a complete navigation guide for the RadGLO platform. It offers concise descriptions of each section and their functionalities to ensure a smooth user experience.

7. Team

The Team section introduces the members behind RadGLO and provides contact information for any queries or collaborations.