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Dual-Perspective Brain MRI AI: Clinical Tumor Segmentation and Structural Biomarker Analysis

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Abstract*— This work describes a dual-perspective pipeline for the analysis of brain MRI that couples automated tumor segmentation with research-oriented structural biomarker extraction. The system processes four MRI modalities (T1, T1CE, T2, FLAIR) using a pretrained 3D U-Net model, localizing and quantifying tumor regions, and further performs tissue-based volumetry and hemispheric asymmetry on T1 scans to estimate gray matter, white matter, and cerebrospinal fluid volumes. The complete workflow was implemented as an automated Google Colab environment, creating visual overlays, volumetric metrics, and a structured PDF output. It is designed for use in medical education, clinical AI exploration, and neuroscience research, while it has been deliberately designed not to be diagnostic for structural biomarkers.

Index Terms*— ANTs, Brain Tumor Segmentation, Biomarkers, MRI.

I. INTRODUCTION

MRI is a core modality in neuro-oncology because of its excellent soft-tissue contrast, multiplanar imaging capability, and its ability to visualize tumor subregions such as edema, necrosis, and enhancing cores. Early progress in automated tumor segmentation was rooted in standardized benchmarks like the Multimodal Brain Tumor Segmentation dataset (BraTS) that furnished aligned T1, T1CE, T2, and FLAIR sequences with expert-labeled tumor masks [1]. The availability of curated MRI cohorts catalyzed a transition from manual segmentation toward fully automated deep learning-based methodologies.

Deep learning architectures led to a rapid improvement in segmentation performance. The self-configuring preprocessing, model structure, and training strategies of the nnU-Net framework for any medical imaging task got rid of manual tuning and outperformed all handcrafted architectures [2]. Further improvements in 3D tumor delineation were done by embedding autoencoder-based regularization into U-Net, contributing to the reduction of overfitting on limited datasets and the stabilization of volumetric reconstruction [3]. Complementary to these contributions, in-depth analyses of multimodal MRI have shown that different tumor signatures arise. For instance, T1CE emphasizes the enhancing region, FLAIR captures peritumoral edema, and T2 resolves heterogeneous non-enhancing tissues, all forming the basis for reliable segmentation pipelines [4].

Advances in transformer-based medical segmentation extended this paradigm. Swin-UNETR proposed hierarchical self-attention for volumetric MRI, thus allowing long-range contextual reasoning that is hard to be captured by traditional CNNs [5]. Apart from lesion masking, MRI also allows the structural mapping of a healthy brain. FreeSurfer is a well-established suite for cortical reconstruction, anatomical parcellation, and volumetric measurements often used in dementia, aging, or psychiatric studies [6]. The ANTsX ecosystem is another alternative stack that puts an emphasis on reproducible registration, preprocessing, and statistical tissue modeling suitable for neuroimaging population studies [7]. Robust diffeomorphic registration via the ANTs framework provides an anatomically consistent template alignment across subjects, improving downstream accuracy and comparability of biomarker analysis [8]. For instance, multi-tissue segmentation using Atropos further enables probabilistic classification into gray matter (GM), white matter (WM), and CSF compartments foundational in structural biomarker computation [9].

Although volumetric MRI features are widely used in research, their diagnostic specificity remains limited. Woo et al. highlight that most structural biomarkers fail to translate reliably into clinical psychiatry, because the same volumetric changes can reflect aging, trauma, stress, or unrelated comorbidities [10]. Nevertheless, MRI segmentation research continues to expand beyond tumor-only models. Hybrid CNN autoencoders have been used for 3D structural MRI segmentation of brain tissue and tumor subregions, demonstrating improved representation learning [11]. Other approaches incorporate anatomical priors; multimodal tumor segmentation has been boosted by normal-brain image references, significantly enhancing robustness under real-world patient variability [12]. Multi-stage U-Net architectures have also been explored, combining deep encoders with tailored skip pathways to refine lesion

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boundaries on multimodal MRI data [13]. Non-deep learning methods remain active as well—segmentation using the EMAP algorithm leverages adaptive clustering to detect tumors without training requirements [14].

Recent deep learning pipelines harness architectural diversity. Multi-encoder U-Net models process individual modalities via separate feature extractors before fusing latent representations, thereby providing superior performance on multimodal datasets [15]. CNN-based multi-label segmentation systems have been designed to classify voxels into multiple tumor compartments simultaneously, therefore enabling interpretable tumor habitat differentiation [16]. Web-based AI systems further democratize access by packaging inference into browser-accessible platforms for rapid tumor identification [17]. More recently, explainability-oriented MRI models have emerged to increase clinical trust and strive toward making algorithmic segmentation decisions transparent and auditable for practitioners [18].

Despite this progress, such pipelines remain siloed in their scope. Tumor segmentation models emphasize lesion localization, while volumetric neuroimaging pipelines focus on tissue quantification and morphometric biomarkers. These tools typically require separate installations, GPU configurations, dependencies, and expertise. Furthermore, clinical users need tumor masks, whereas research users are interested in statistical brain metrics—no unified solution bridges the two perspectives. To address this gap, we propose the first integrated dual-perspective MRI pipeline, which combines pretrained tumor segmentation with ANTs-based structural biomarker extraction and can be deployed fully in Google Colab without any local setup. This enables one workflow to provide clinical visualization, quantitative research analysis, and educational exploration in neuroimaging.

II. RELATED WORK

The automated analysis of brain MRI has evolved along two major research lines: lesion segmentation and structural neuroimaging. Though each domain has established mature methodologies independently, integration remains largely underexplored. The section provides a critical review of the relevant works for the proposed dual-perspective framework.

A. Deep Learning Models for Tumor Segmentation

It introduced, for the first time, a standardized multi-institutional data set comprising multi-modal MRI volumes and expert-annotated tumor masks; this provided a seminal point upon which reproducible algorithmic development could base itself [1]. The competing methods that were built around BraTS rapidly converged toward convolutional encoder–decoder architectures. 3D U-Net derivatives became the dominant backbone owing to their localized receptive fields and the spatial resolution preserved through skip connections.

A big step forward was made from the nnU-Net system, which demonstrated that model performance is less dependent on novel architectures than on automated configuration of patch sizes, normalization, and post-processing heuristics [2]. This shifted the focus in research away from manually crafted design towards reproducible and data-driven pipeline optimization. In a similar direction, Myronenko proposed a regularized 3D U-Net with a VAE reconstruction branch, enhancing feature robustness and segmentation stability in low-data scenarios [3]. Similar autoencoder-regularized models have achieved consistent improvements in pathological brain segmentation tasks where lesion boundaries are ambiguous.

Multi-modal fusion remains essential in clinical MRI. T1 captures anatomical layout, T1CE highlights enhancing tumor regions, T2 reflects infiltrative edema, and FLAIR isolates peritumoral hyperintensities. Combining these signals within a joint inference model often yields superior delineation of tumor compartments [4]. Transformer-augmented segmentation has further improved contextual sensitivity. Swin-UNETR incorporates hierarchical self-attention, enabling long-range 3D relationships that CNNs struggle to encode [5]. These developments toward hybrid CNN–Transformer architectures represent the current frontier of BraTS-style medical image segmentation.

B. Structural MRI and Tissue Volumetry

In contrast with lesion-focused pipelines, structural MRI research attempts to quantify tissue composition and anatomical variation. FreeSurfer remains the most commonly used plat-form for neuroanatomical reconstruction, supporting cortical thickness measurement, automated parcellation, and GM/WM segmentation [6]. Despite scientific impact, FreeSurfer is computationally expensive and sensitive to preprocessing artifacts; it is therefore ill-suited for rapid prototyping or educational workflows.

The ANTs/ANTsX ecosystem offers a more modular and reproducible alternative that combines diffeomorphic registration, robust skull-stripping, and probabilistic tissue labeling [7]. Its core registration method has demonstrated strong reproducibility in benchmarking studies, outperforming traditional affine and B-spline techniques [8]. Atropos segmentation using Markov random fields performs probabilistic classification of voxels into tissue classes, therefore allowing for stable gray/white/CSF volumetry even in very heterogeneous datasets [9]. Such structural biomarkers support large-scale studies of cognitive aging, brain development, and neurodegeneration.

Yet, psychiatric diagnostic reliability remains limited. Woo et al. emphasize that volumetric features lack disorder-specific signatures and are therefore incapable of serving as clinical predictors in the absence of complementary behavioral or genetic context [10]. This is in line with the orientation of our pipeline: volumetry is offered as a

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research-oriented neuroimaging tool and not as a diagnostic system.

C. Hybrid and Complementary Segmentation Strategies

A number of works investigate alternatives to pure CNN models. Farzana et al. coupled a U-Net autoencoder with semantic regularization to enhance stability in tumor boundary learning in volume segmentation [11]. Liu et al. suggested the inclusion of healthy MRI priors and demonstrated that models jointly trained on normal and pathological brains generalize better across unseen locations [12]. Other lighter-weight convolutional approaches include volumetric CNN classifiers specifically tailored for segmentation, showing practical performance given memory constraints [13]. At the other end of the methodological spectrum lie probabilistic clustering algorithms such as EMAP, which eschew deep supervision and instead segment lesion regions based on statistical appearance patterns [14]. These approaches remain valuable in low-data regimes.

D. Gaps in Existing Research

While sophisticated, segmentation and neuroimaging pipelines remain siloed. Tumor models output voxel-wise lesion maps but give no structural brain metrics. Volumetric frameworks quantify en masse the GM/WM/CSF distributions but pay no attention to the disease-specific morphology. Each of these systems requires a different toolchain, GPU/CPU configuration, and domain expertise-inaccessible to any student or clinician. Therefore, the proposed system resolves this gap in the literature by incorporating BraTS-like tumor segmentation and ANTs-based volumetry into one cohesive workflow; thus, both lesion visualization and the computation of various anatomical biomarkers will be provided from one MRI acquisition.

III. PROPOSED METHODOLOGY

The proposed dual-perspective brain MRI pipeline unifies clinical tumor segmentation with research-oriented computation of structural biomarkers. The pipeline converts raw MRI inputs into voxel-level tumor predictions and volumetric neuroanatomical metrics suitable for exploratory research without requiring multiple independent toolchains.

A. System Overview

Given a single MRI exam, the system performs:

1. Automated preprocessing and spatial alignment of modalities,
2. Deep learning-based clinical tumor segmentation,
3. Structural biomarker extraction from T1-weighted MRI,
4. Automatic visualization and report generation.

All components are hosted on Google Colab to enable reproducibility, availability of a GPU, and avoid workstation dependent installation hassles or incompatible dependencies.

B. Module 1: Clinical Tumor Analysis

This module processes four complementary MRI modalities: T1, T1CE, T2, and FLAIR. Each modality encodes distinct diagnostic cues: T1 captures the anatomical layout, T1CE enhances the actively vascularized tumor core, T2 highlights fluid-rich regions, and FLAIR suppresses cerebrospinal fluid to reveal edema. [4].

These modalities are combined into a unified multi-channel 4D tensor. This numerically encodes their complementary contrast patterns, consistent with BraTS-style pipelines [1],[3], [4]. The output is a voxel-wise tumor segmentation mask and quantitative tumor volume in milliliters.

Sliding-window inference is used to handle large 3D volumes under GPU constraints [2]. The raw probability map is post-processed with argmax masking, filtering of connected components, and morphological smoothing to stabilize discontinuities and remove isolated false positives.

C. Module 2: Structural Biomarker Analysis

This module focuses only on tissue-level anatomical features using a single T1-weighted MRI. Following skull stripping and intensity correction, probabilistic tissue classification is generated through ANTs/Atropos, a robust segmentation approach commonly adopted in multi-site neuroimaging studies [7], [9].

The outputs of segmentation are the voxel-wise gray matter

(GM), white matter (WM), and cerebrospinal fluid (CSF) labels, from which:

1) Intracranial volume (ICV),
2) Tissue volumes (in ml),
3) The hemispheric asymmetry index

are computed:

$$AI = \frac{R - L}{R + L}$$

where R and L are right and left hemisphere volumes. Asymmetry metrics are used in research contexts across aging and developmental studies [6], [10], but remain non-diagnostic, especially in psychiatric applications [10].

D. Automation and User Interaction

The pipeline is designed to reduce user burden by allowing single click execution:

1) Raw NIfTI MRI files are uploaded directly,
2) The pipeline executes preprocessing → segmentation → volumetry,
3) Outputs include segmentation masks and volumetric tables,
4) A structured PDF report is generated with metrics and overlays.

This approach democratizes complex neuroimaging workflows for clinical education, early AI adopters, and non-expert researchers.

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E. Advantages of the Integrated Design

Unlike previous systems where segmentation and volumetry were disjoint processes, the proposed pipeline:

- Provides lesion analysis and structural biomarkers simul-taneously,
- Uses pretrained models with no retraining requirement,
- Runs on cloud GPUs with no software installation,
- Produces overlay visualizations and interpretable metrics.

The integration bridges radiological lesion interpretation with neuroscientific structural analysis, something rarely offered within one execution environment.

F. Preprocessing Pipeline

Preprocessing is important in normalizing the distribution of MRI inputs and enhancing model robustness.

1) N4 Bias Field Correction: Removes smooth intensity inhomogeneity from coils using N4, considered state-of-the-art for MRI normalization [7].
2) Skull Stripping: Non-brain tissues are removed in order to isolate cerebral parenchyma. In volumetric pipelines such as FreeSurfer, skull stripping directly affects downstream anatomical estimation [6].
3) Multi-Modal Registration: T1CE, T2, and FLAIR are rigidly or nonlinearly aligned to the T1 framework using ANTs registration [8]. Consistent alignment significantly improves tumor boundary localization in multi-modal fusion [3].
4) Intensity Standardization: Voxel intensities are normalized to reduce scanner-dependent variation, a critical strategy for multi-scanner MRI datasets like BraTS [1].

G. Segmentation Model

Segmentation is performed using a pre-trained BraTS-derived 3D U-Net from the MONAI Model Zoo. An encoder-decoder network architecture with skip-connections will maintain anatomical boundaries while extracting contextually relevant semantic features [2]. Sliding-window inference maintains memory efficiency during volumetric prediction.

The output segmentation is further post-processed into connected components, and tumor volume estimation is computed using voxel spacing metadata from NIfTI headers.

H. Biomarker Computation

ANTs/Atropos uses a Markov random field formulation to estimate the probabilities of tissue classes [9]. The technique provides homogeneous GM/WM/CSF classification across heterogeneous data. Hemispheric volumes are obtained following deformable normalization, ensuring biomarker estimates that are stable yet strictly research oriented [10].

IV. EXPERIMENTAL SETUP

In this work, the proposed dual-perspective MRI analysis system was implemented in its entirety in a cloud-based setting to ensure reproducibility and accessibility. All experiments were conducted within a Google Colab environment with one NVIDIA Tesla T4 GPU, 16 GB system memory, and Python 3.10 runtime. Major components of the pipeline were developed based on MONAI and PyTorch for segmentation, and ANTsPy/ANTsX for neuroimaging and volumetric processing, building upon their established dependability in medical image analysis platforms [7]–[9].

A. Datasets

Two MRI datasets, publicly available, were used:

1) BraTS Dataset: The Brain Tumor Segmentation Challenge dataset includes expert annotations of tumors on high-quality, multimodal MRI volumes in T1, T1CE, T2, FLAIR,which is generally recognized benchmark data for lesiondetection [1], [4]. Thus far, BraTS has granted a fair comparison between segmentation methods by enforcing standard acquisition, voxel alignment, and region-of-interest definitions.
2) IXI Dataset: This IXI dataset consists of normal T1-weighted MRI scans gathered from several sites and scanner vendors; thus, it is highly suitable for the evaluation of structural biomarker stability due to normal anatomical variability [6]. Unlike BraTS, IXI does not provide tumor annotation; therefore,it focuses only on brain volumetry, tissue segmentation, and hemisphere asymmetry.

A representative subset of each dataset was selected to remain compatible with the Colab resources while covering various anatomical variations without exceeding the GPU constraints.

B. Preprocessing and Inference Parameters

All MRI scans were preprocessed before any clinical inference or volumetric analysis was performed.

Bias Field Correction: N4 correction was performed to decrease low-frequency intensity inhomogeneities and grant robustness to downstream tissue classification [7]. This is indeed the standard in most structural MRI workflows, as this method yields very stable results across vendors and coil geometries.

Multi-Modal Spatial Registration: For tumor segmentation, T1CE, T2, and FLAIR images were all rigidly registered to the T1 anatomical reference using ANTs registration [8]. The nonlinear SyN deformation due to its superior anatomical fidelity was applied especially when dealing with complex cortical interfaces in selected experiments due to its superior anatomical fidelity.

Model Inference: For lesion segmentation, the pre-trained MONAI 3D U-Net was used, and sliding window inference was performed in order to overcome limitations of GPU

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memory [2]. Inference parameters:

- ROI window: 128 × 128 × 128
- Overlap ratio: 0.5
- Batch size: 1

Inference runtime was recorded to compare registration strategies: no alignment versus rigid versus SyN.

Volumetric Biomarker Extraction: ANTs/Atropos probabilistic segmentation was applied to the T1-weighted scans to generate gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) labels [9]. Tissue compartment volumes (in ml) were calculated by multiplying voxel counts with the NIfTI header voxel spacing. Intracranial volume was defined as the union of GM + WM + CSF.

C. Evaluation Metrics

Performance of tumor segmentation was evaluated using standard metrics.

1) Dice Similarity Coefficient

$$Dice = \frac{2|P \cap G|}{|P| + |G|}$$

where P and G represent predicted and ground-truth tumor voxel sets, respectively. DSC remains the dominant accuracy metric in BraTS challenge evaluations due to its sensitivity to boundary overlap and lesion size variability [4], [5].

2) Sensitivity

$$Sensitivity = \frac{TP}{TP + FN}$$

This metric reflects the ratio of correctly identified tumor voxels, with a greater emphasis on under-segmentation risk, especially within enhancing tumor core regions. [1].

3) Structural Volumetric Metrics Research-oriented analysis was conducted using:

- Percentage variation in tissue volumes across preprocessing pipelines
- Hemispheric asymmetry index:

$$AI = \frac{R - L}{R + L}$$

where R and L represent right and left hemisphere volumes. Asymmetry has been studied as a macro-level indicator of anatomical organization, aging, and developmental variation, though it is not diagnostic of psychiatric disorders [10].

D. Report Generation

All segmentation masks, volumetric results, slice overlays, and computed metrics have been compiled in a structured PDF report. The report includes the following:

1) Tumor probability slices and binary masks
2) Tumor volume summary (ml)
3) GM/WM/CSF volumetry table
4) Hemispheric asymmetry results

This automated reporting demonstrates the feasibility of the system as a user-friendly AI toolbox in the support of clinical education, research pipelines, and rapid prototyping of imaging models.

V. RESULTS

The proposed dual-perspective pipeline was evaluated on multimodal tumor segmentation and single-modality structural volumetry. The performance metrics have three components: (i) segmentation accuracy, (ii) volumetric biomarker stability, and (iii) comparative analysis against existing neuroimaging pipelines.

A. Tumor Segmentation Performance

Table 1 reports segmentation accuracy on representative BraTS subjects. The pretrained 3D U-Net was a strong baseline, while the spatial registration of input modalities significantly improved the tumor localization.

Table 1. Tumor Segmentation Performance on Brats Samples

Method	Dice	Sensitivity	Time(s)
No Registration	0.84	0.89	60
Rigid Registration	0.88	0.92	120
SyN Registration	0.89	0.93	360

Experiments demonstrate that multi-modality alignment decreases the inconsistency in tumor boundaries, brought about by scanner geometry or patient motion. Rigid registration offered a good balance between the inference speed and quality.

SyN non-linear registration achieved the highest quality of segmentation but at the cost of a 3× increased runtime due to deformable field optimization.

Qualitatively, tumour masks kept coherent lesion boundaries across enhancing and non-enhancing compartments. Overlay visualizations generated with the system helped users and educators visually validate the quality of the segmentation.

The automated PDF reports confirm that combined segmentation, tissue volumes, and asymmetry metrics can be compiled without manual post-processing or external tools.

Table 2. Volumetric Tissue Measurements From IXI MRI Subjects

Subject	GM(ml)	WM(ml)	CSF(ml)	Asymmetry Index
1	715	518	254	0.012
2	702	525	261	0.009
3	721	510	248	0.015

B. Volumetric Biomarker Analysis

The biomarker consistency was evaluated for the structural module using ANTs-based tissue segmentation of healthy IXI scans.

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Gray matter volumes were consistently higher than white matter volumes, according to well-known neuroanatomical proportions in young adults. The low asymmetry values ($|AI| < 0.03$) point to the normal variability between hemi- spheres and thus reflect stable segmentation performance. These metrics do not indicate psychiatric or pathological conditions but instead provide quantitative neuroanatomical references suitable for structural research.

C. Comparative Analysis

A qualitative comparison of performance characteristics is summarized below:

- Segmentation Accuracy: Registration improves the spatial coherence and tumor core localization; multi-modal intensity profiles are tighter in their alignment.
- Computational Trade-off: SyN registration results in marginally higher Dice scores but increases inference time by up to 6× compared to unaligned scans.
- Volumetric Robustness: Tissue volume estimates remain stable under preprocessing variations, which provides an indication that the ANTs-based segmentation is resilient to bias-field and linear alignment effects.

The integrated nature of the system—tumor and structural analysis within the same pipeline—contrasts with the existing neuroimaging frameworks. Table 3 compares representative approaches from prior literature.

Table 3. Comparison with Representative MRI Analysis Approaches

Method	Tumor	Vol.	Platform	Limitation
BraTS U-Net [3]	Yes	No	GPU	Tumor-Only
FreeSurfer [9]	No	Yes	CPU/HPU	Slow, no lesions
ANTsX [7]	No	Yes	CPU/GPU	No tumor logic
Swin-UNETR [4]	Yes	No	GPU	No biomarkers
Proposed	**Yes**	**Yes**	**Colab**	**Research-only volumetry**

The proposed pipeline uniquely unites clinical segmentation and research volumetry within a single executable environment, which enables accessible experimentation without the need for either HPC clusters or multi-tool workflows.

VI. CONCLUSION

This work described a unified AI-driven framework for the analysis of brain MRI that incorporates clinical tumor segmentation with research-oriented structural biomarker extraction. By combining a BraTS-derived pre-trained 3D U-Net with ANTs-based volumetry, the system automates lesion localization, tumor volume quantification, and gray-white-CSF tissue analyses in one pipeline. Experimental results have shown that spatial registration improves segmentation accuracy, and volumetric outputs for healthy subjects are consistent. Pipeline execution in Google Colab offers ease of access without dedicated hardware and is appropriate for medical imaging education, rapid prototyping, and early-stage clinical AI investigations. The derived structural biomarkers, though highly quantitative for neuroscience and psychiatric research, are rigorously nondiagnostic. Future extensions will be added for brain-age modeling, longitudinal tumor monitoring, and explainability modules that increase adaptability and build clinical trust.

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