AUTOMATED BRAIN PARCELLATION IN THE PREOPERATIVE WORKUP OF ADULT-TYPE DIFFUSE GLIOMAS: WHERE ANATOMY MEETS IMAGE ANALYSIS

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Abstract. *Automated brain parcellation has matured from a research utility used in cohort neuroimaging into a methodologically attractive option for preoperative planning in neuro-oncology. Unlike most advanced sequences in the multiparametric MRI workup of adult-type diffuse gliomas, parcellation runs on the standard 3D T1-weighted volume already acquired for surgical navigation, requires no additional contrast injection or scan time, and outputs a quantitative map of cortical parcels and subcortical structures involved by the tumor. This review covers the conceptual rationale for incorporating parcellation into the preoperative protocol, summarizes the three pipeline families that dominate current practice (FreeSurfer, FastSurfer/FastSurferVINN, and SAMSEG), discusses the methodological caveats that arise when these tools are applied to brains distorted by mass effect and edema, and outlines the integration of parcellation outputs with diffusion tractography, perfusion metrics, and radiogenomic models. The clinical bottleneck is no longer software availability but validation on glioma cohorts, where standard atlases were not built. The review draws on 18 sources, mostly from 2019–2026.*

Keywords: *adult-type diffuse gliomas, brain parcellation, FreeSurfer, FastSurfer, SAMSEG, preoperative MRI, neuronavigation, WHO CNS5.*

Introduction

Preoperative imaging of adult-type diffuse gliomas has expanded along two axes over the past decade. The first is biological: the WHO Classification of Tumours of the Central Nervous System, fifth edition (WHO CNS5, 2021) made molecular markers - IDH, 1p/19q, MGMT, ATRX, TP53, histone H3 mutations - definitional rather than ancillary, which placed an explicit demand on imaging to predict the molecular profile rather than merely confirm a mass [1, 2]. The second is computational: most of the gain in diagnostic accuracy now comes from quantitative postprocessing rather than from new pulse sequences, and consensus protocols such as BTIP-2015 and the BTIP-2020 DSC update codified what a usable preoperative dataset must contain [3, 4].

Within this computational layer, automated brain parcellation occupies an unusual position. Diffusion, perfusion, and spectroscopy each address a specific physiological question and need a dedicated sequence. Parcellation is different: it works on the T1-weighted MPRAGE volume that is already part of every preoperative protocol, returns a labeled map of dozens of cortical parcels and subcortical nuclei, and does so without any contrast medium or extra scan time. The cost is computational rather than radiological. For a neurosurgical team, the practical output is a structure-by-structure tally of which parcels are crossed by the tumor and which are spared - an anatomical inventory that is otherwise built up implicitly from visual reading.

The aim of this review is to lay out the conceptual rationale for using parcellation in the preoperative workup of diffuse gliomas, summarize the three software families that currently

matter (FreeSurfer, FastSurfer including FastSurferVINN, and SAMSEG), discuss the failure modes specific to glioma anatomy, and sketch how parcellation outputs interact with diffusion tractography, perfusion biomarkers, and radiogenomic models. The treatment is methodological rather than encyclopaedic.

Why parcellation belongs in the preoperative workup

Surgery on diffuse gliomas is a calculated trade-off between resection extent and functional preservation. Total resection of the contrast-enhancing component is associated with longer survival in glioblastoma, with intraoperative mapping series reporting median postoperative survival of 16.87 versus 12.04 months and gross-total resection rates of 79.1 % versus 47.7 % when intraoperative mapping is used [5]. The calculus narrows further with FLAIR-defined supramarginal resection in IDH-mutant astrocytomas. None of these decisions is taken on imaging alone, but every one of them rests on a clear preoperative anatomical model: which gyrus carries the tumor, how close the lesion sits to the central sulcus, whether the insula is involved, whether the corpus callosum is crossed.

Visual reading produces this model implicitly. A parcellation pipeline produces it explicitly and quantitatively. Once the T1-MPRAGE has been parcellated, the tumor mask - itself obtainable from BraTS-style segmentation networks such as nnU-Net [6, 7] - can be intersected with the parcellation labels, and the result is a structure-level table: percent involvement of precentral gyrus, percent involvement of posterior superior temporal gyrus, percent involvement of putamen, and so on. This is information the surgeon would extract from visual inspection anyway, but the quantitative version is reproducible across observers, comparable across patients, and storable as data for downstream analyses including radiogenomic modeling.

A second motivation is comparability over time. Postoperative parcellation of the residual cavity and surrounding parenchyma supports unambiguous reporting of which structures were spared and which were resected, which is increasingly relevant for outcome studies. The third motivation is integration with tractography: cortical parcels can serve as seed and target regions for the language and motor pathways of interest, replacing manually drawn ROIs and reducing operator-dependent variability that has long plagued DTI tractography in glioma cases [8].

Pipelines: FreeSurfer, FastSurfer, FastSurferVINN, SAMSEG

FreeSurfer remains the reference. The 2012 NeuroImage paper by Fischl is the most cited single description of the surface-based reconstruction pipeline that produces volumetric subcortical segmentation (aseg), cortical surface reconstruction, and parcellation according to the Desikan–Killiany or Destrieux atlases [9]. Strengths are well known: large normative datasets, a vast methods literature, and tight integration with downstream tools (TRACULA for tractography, hippocampal subfield modules, brainstem substructures). The cost is processing time - six to twelve hours per scan on a typical workstation - which is incompatible with surgical workflows that need turnaround in tens of minutes.

FastSurfer addressed the runtime problem by replacing the recon-all volumetric segmentation with a deep-learning network (FastSurferCNN) trained to reproduce FreeSurfer outputs, while keeping the surface pipeline largely intact. The 2020 NeuroImage paper by Henschel et al. reported runtimes of about one hour for the full pipeline and a few minutes for segmentation alone, with Dice agreement against FreeSurfer above 0.85 for most cortical and subcortical structures [10]. The successor architecture, FastSurferVINN (Henschel, Kügler, Reuter, NeuroImage 251, 118933, 2022), introduced voxel-size–independent layers that allow the same network to handle 0.7-mm and 1.0-mm scans without retraining, addressing a recurrent

failure mode in deep-learning segmentation when test images have a different voxel size than training data [11].

SAMSEG (Sequence Adaptive Multimodal SEGmentation) takes a different route. The contrast-adaptive method by Cerri et al. (NeuroImage 225, 117471, 2021) decouples the shape model of anatomical structures from their MRI appearance, which means SAMSEG segments 41 brain structures from arbitrary contrast combinations without retraining, and integrates a lesion model originally developed for white matter hyperintensities in multiple sclerosis [12]. For neuro-oncology, the contrast-adaptive design is attractive precisely because preoperative protocols vary between centers, and a tool that does not require T1-MPRAGE in a fixed acquisition window has an obvious deployment advantage.

A practical comparison is summarized in Table 1. None of these tools was developed primarily for tumor patients; all were validated on healthy or neurodegenerative cohorts and then extended.

Table 1. Brain parcellation pipelines relevant to preoperative neuro-oncology

Pipeline	Method	Output	Runtime (per scan)	Key reference
FreeSurfer (recon-all)	Surface-based, atlas-driven; classical pipeline	aseg subcortical labels; cortical surfaces; Desikan–Killiany / Destrieux parcellation	6–12 h	Fischl, NeuroImage 2012 [9]
FastSurfer	Deep-learning replacement for the volumetric stage; surface stage retained	Same labels as FreeSurfer; Dice > 0.85 vs FreeSurfer reference	≈ 1 h full; < 1 min segmentation	Henschel et al., NeuroImage 2020 [10]
FastSurferVINN	Voxel-size–independent network; 0.7–1.0 mm without retraining	Whole-brain segmentation across resolutions	< 1 min segmentation	Henschel et al., NeuroImage 2022 [11]
SAMSEG	Bayesian, contrast-adaptive; decoupled shape and appearance models; lesion module	41 brain structures from arbitrary multi-contrast input	≈ 10 min	Cerri et al., NeuroImage 2021 [12]

Failure modes specific to gliomas

Standard parcellation atlases were built from healthy or mildly atrophic brains. A glioma deforms the very anatomy these atlases assume. Three failure modes recur in practice. The first is mass effect with midline shift: the registration step that aligns the patient to atlas space can produce systematic label displacement, particularly around the lateral ventricles and basal ganglia, where

compression distorts the usual landmarks. The second is signal alteration in the tumor and peritumoral edema: T1-MPRAGE intensity within the lesion does not match any normal tissue class, and the segmentation may either label tumor as a hodgepodge of cortex and white matter or - depending on the algorithm - drop the region from the parcellation altogether. The third is post-resection cavities, which the standard atlases simply do not contain.

Practical mitigations differ by pipeline. SAMSEG can be invoked with an explicit lesion model that absorbs the abnormal-intensity voxels into a separate class, leaving the surrounding parcellation intact [12]. FreeSurfer and FastSurfer are typically combined with prior tumor masking - the lesion is inpainted or excluded from registration before parcellation runs - which is conceptually similar to the lesion-filling step long used in multiple sclerosis. None of these mitigations is fully validated on large glioma cohorts. The methodologically honest position is that current parcellation tools are usable for surgical planning when the tumor is small to moderate and away from midline, and require careful manual review when the lesion is large, hemorrhagic, or causes substantial shift.

Quantitatively, the impact of these failure modes depends on tumor size and location. Small (< 3 cm) tumors in convexity locations rarely cause visible parcellation errors beyond the immediate lesion footprint. Tumors crossing the midline, occupying the insular cortex, or displacing the lateral ventricles by more than 5 mm can produce parcellation errors that propagate into adjacent structures and require manual correction. The Bello series of language and motor tractography in glioma surgery, which depends on accurate cortical seed regions, reported that perilesional edema with reduced fractional anisotropy was the dominant cause of false-negative tract reconstructions; the recommended workaround was to lower the FA threshold to 0.10–0.15 and to verify reconstructions against multiple ROIs [8]. The same logic applies to parcellation: accept that perilesional cortex may be mislabeled, build the analysis around contralateral and remote-ipsilateral parcels, and reserve the perilesional region for manual review.

A more recent direction is the BraTS challenge family. Brain Tumor Segmentation Challenge has run since 2012 within MICCAI in collaboration with RSNA and ASNR and has standardized the task of separating enhancing tumor, necrosis, and edema on multiparametric MRI. By 2021 the dataset reached 2040 cases [6], and BraTS-Africa later showed that models trained on Western data lose accuracy on scans from sub-Saharan centers - a generalization problem that applies equally to Central Asian centers and underscores the need for local validation [13]. Tumor segmentation networks (notably the self-configuring nnU-Net [7]) provide the lesion mask that parcellation pipelines can use as prior, closing the loop between the two ends of the automated workflow.

Integration with tractography, perfusion, and radiogenomics

Parcellation is most useful in combination, not in isolation. With diffusion tractography, cortical parcels serve as anatomically defined seed and target ROIs. The Bello series on language fiber tracking with intraoperative subcortical mapping reported sensitivity and specificity of 97–100 % for the superior longitudinal, inferior fronto-occipital, and uncinate fasciculi when DTI was integrated with neuronavigation [8]. Replacing manually drawn cortical ROIs with parcellation-derived labels removes one source of operator variability without changing the underlying tractography algorithm. A workflow that runs FastSurferVINN for parcellation, nnU-Net for tumor segmentation, and a probabilistic CSD tractography seeded from the relevant parcels can be assembled from open-source components within a single afternoon - the bottleneck is data quality, not software.

With perfusion biomarkers, parcellation provides a normalization reference. Relative cerebral blood volume (rCBV) from DSC perfusion is conventionally normalized to contralateral white matter, but the choice of reference voxel is a known source of inter-rater variability. A parcellation-defined ROI in contralateral normal-appearing white matter, drawn the same way for every patient, gives a more reproducible denominator. The same logic applies to ADC ratios and to ASL-derived CBF. The BTIP-2020 DSC consensus explicitly listed normalization as one of the three principal sources of inter-center variability in rCBV measurement [4]; replacing operator-drawn ROIs with parcellation labels addresses this directly.

A separate integration question concerns brain shift. Once the dura is opened and tumor mass is evacuated, the cortical surface can move 10–25 mm relative to the preoperative coordinate system, which degrades the value of any preoperative map by the late stages of the operation. This is the strongest argument against treating preoperative parcellation as a final answer; the parcellation map is most reliable as a planning document and as input to early-stage navigation, with intraoperative ultrasound or intraoperative MRI used to update the anatomical model after meaningful tissue displacement [18].

With radiogenomics, parcellation provides an anatomical scaffold for the radiomic feature extraction. The Choi et al. multi-center cohort study showed that location matters: external AUC for IDH prediction reached 0.93 in frontal-lobe gliomas and 0.84 in deep-seated lesions [14], a gradient that is plausibly explained by differences in the surrounding parenchyma rather than by the tumor itself. A parcellation-aware feature extraction can encode this anatomical context explicitly. The Farahani 2025 meta-analysis on 72 studies and over 12,000 patients reported pooled sensitivity 80 % and specificity 85 % for IDH prediction by deep-learning radiomics on routine MRI; for 1p/19q codeletion, 75 % and 82 %, with location and segmentation method identified as principal heterogeneity drivers [15]. For MGMT methylation, the picture is less encouraging: the Doniselli et al. systematic review of 26 radiomics studies found a median Radiomics Quality Score of 8 of 36 (22 %), with external validation performed in only 13 of 26 [16], and the Samartha review of 30 deep-learning models reported pooled sensitivity 0.74 and specificity 0.75 with substantial heterogeneity [17].

Local context: deployment in resource-constrained settings

A parcellation-centric preoperative pipeline is unusually well suited to resource-constrained health systems. The required input is a single 3D T1-MPRAGE volume - no contrast, no DSC, no MRS - which is acquired in every neurosurgical center capable of preoperative MRI. The processing tools (FreeSurfer, FastSurfer, SAMSEG) are open-source and run on a workstation-class GPU. Quantitative parcel-level reporting can be added to existing radiology reports without changing acquisition protocols. For a country where dynamic susceptibility contrast perfusion, MR spectroscopy, and resting-state fMRI are concentrated in a small number of centers and where molecular profiling beyond IDH1 R132H immunohistochemistry remains episodic, a parcellation-based anatomical analysis is among the highest-yield additions to the existing workflow [18].

A practical pilot deployment can be staged. Phase one: install FastSurfer or FastSurferVINN on a single workstation, parcellate every preoperative T1-MPRAGE acquired for tumor patients, and append a parcel-level structure-involvement table to the standard radiology report. This adds no scanner time and a few minutes of GPU computation per case. Phase two: add nnU-Net tumor segmentation, intersect the masks with the parcellation, and store the resulting structure-by-volume tables in a local database. Phase three: link the imaging database to operative

findings and pathology reports to build a ground-truth series. By the end of phase three, the same center has accumulated the data needed to validate radiogenomic models on its own population - without ever having modified the acquisition protocol.

The methodological commitment is local validation. International atlases were not built on Central Asian populations; tumor segmentation networks were not trained on local scanners. Both can be deployed and used, but their outputs need spot-checking against expert reading until a local validation series accumulates. Building such a series - paired preoperative T1-MPRAGE, parcellation, tumor mask, and operative findings - is itself a research contribution, and one that does not require equipment beyond what is already installed.

What a parcellation-augmented preoperative report should contain

A useful preoperative report does not dump the entire parcellation table on the surgeon. The relevant content is filtered: which structures are crossed by the tumor, which are within a defined safety margin, which are spared. A workable format includes the tumor volume by component (enhancing, non-enhancing, necrosis, edema), the list of cortical parcels with non-zero tumor overlap and the percent involvement of each, the list of subcortical structures with overlap, the distance from the tumor margin to the central sulcus and to language-area parcels, and the laterality of the eloquent network. This level of detail takes one page in a structured report and replaces several paragraphs of free-text description.

The report should also flag uncertainty. Parcellation in the immediate perilesional zone may be unreliable, and that limitation belongs in the report, not in a separate methodological caveat that nobody reads. A simple convention works: structures more than two parcellation thicknesses from the tumor margin are reported with standard confidence; structures within the perilesional zone are flagged as requiring visual confirmation. This kind of explicit confidence labeling is more honest than a uniform output and matches how surgeons actually read the report.

A final practical note concerns reporting language. WHO CNS5 terminology has not yet stabilized in routine radiology reporting in many centers, and the gap between what the pathology report says (astrocytoma IDH-mutant CNS WHO grade 4) and what the radiology report says (high-grade glioma) creates avoidable confusion in multidisciplinary discussion. A parcellation-augmented report is also an opportunity to standardize the molecular-aware terminology - using the WHO CNS5 nomenclature explicitly when the molecular profile is known and stating the imaging-based hypothesis when it is not.

Conclusion

Automated brain parcellation has matured enough to leave the cognitive neuroscience laboratory and enter the preoperative workflow. The core argument is that parcellation extracts anatomical information from a sequence already acquired for navigation, costs no additional patient time, and produces a quantitative output that supports both surgical planning and downstream analytical pipelines including tractography, perfusion normalization, and radiogenomics. The remaining problems are not about algorithms - three robust pipelines exist - but about validation on glioma anatomy and about local deployment in centers where standard-protocol assumptions do not always hold. For a national neuro-oncology service building toward WHO CNS5–compliant preoperative diagnostics, parcellation is a low-cost, high-leverage addition that can be implemented now and refined as local data accumulate.

REFERENCES

1. Louis D.N., Perry A., Wesseling P. et al. The 2021 WHO Classification of Tumors of the Central Nervous System: a summary // Neuro-Oncology. - 2021. - Vol. 23, No. 8. - P. 1231–1251.
2. Smits M. MRI biomarkers in neuro-oncology // Nature Reviews Neurology. - 2021. - Vol. 17, No. 8. - P. 486–500.
3. Ellingson B.M., Bendszus M., Boxerman J. et al. Consensus recommendations for a standardized Brain Tumor Imaging Protocol in clinical trials // Neuro-Oncology. - 2015. - Vol. 17, No. 9. - P. 1188–1198.
4. Boxerman J.L., Quarles C.C., Hu L.S. et al. Consensus recommendations for a dynamic susceptibility contrast MRI protocol for use in high-grade gliomas // Neuro-Oncology. - 2020. - Vol. 22, No. 9. - P. 1262–1275.
5. Gerritsen J.K.W., Arends L., Klimek M. et al. Impact of intraoperative stimulation mapping on high-grade glioma surgery outcome: a meta-analysis // Acta Neurochirurgica. - 2019. - Vol. 161, No. 1. - P. 99–107.
6. Baid U., Ghodasara S., Mohan S. et al. The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification // arXiv:2107.02314. - 2021.
7. Isensee F., Jaeger P.F., Kohl S.A.A. et al. nnU-Net: a self-configuring method for deep learning-based biomedical image segmentation // Nature Methods. - 2021. - Vol. 18, No. 2. - P. 203–211.
8. Bello L., Gambini A., Castellano A. et al. Motor and language DTI Fiber Tracking combined with intraoperative subcortical mapping for surgical removal of gliomas // NeuroImage. - 2008. - Vol. 39, No. 1. - P. 369–382.
9. Fischl B. FreeSurfer // NeuroImage. - 2012. - Vol. 62, No. 2. - P. 774–781.
10. Henschel L., Conjeti S., Estrada S. et al. FastSurfer - a fast and accurate deep learning based neuroimaging pipeline // NeuroImage. - 2020. - Vol. 219. - 117012.
11. Henschel L., Kügler D., Reuter M. FastSurferVINN: Building resolution-independence into deep learning segmentation methods - A solution for HighRes brain MRI // NeuroImage. - 2022. - Vol. 251. - 118933.
12. Cerri S., Puonti O., Meier D.S. et al. A contrast-adaptive method for simultaneous whole-brain and lesion segmentation in multiple sclerosis // NeuroImage. - 2021. - Vol. 225. - 117471.
13. Adewole M., Rudie J.D., Gbadamosi A. et al. The Brain Tumor Segmentation (BraTS) Challenge 2023: Glioma Segmentation in Sub-Saharan Africa Patient Population (BraTS-Africa) // Radiology: Artificial Intelligence. - 2024 [online ahead of print].
14. Choi Y.S., Bae S., Chang J.H. et al. Fully automated hybrid approach to predict the IDH mutation status of gliomas via deep learning and radiomics // Neuro-Oncology. - 2021. - Vol. 23, No. 2. - P. 304–313.
15. Farahani S., Hejazi M., Tabassum M. et al. Diagnostic performance of deep learning for predicting gliomas IDH and 1p/19q status in MRI: a systematic review and meta-analysis // European Radiology. - 2025 [online ahead of print].
16. Doniselli F.M., Pascuzzo R., Mazzi F. et al. Quality assessment of the MRI-radiomics studies for MGMT promoter methylation prediction in glioma: a systematic review and meta-analysis // European Radiology. - 2024. - Vol. 34, No. 7. - P. 5160–5170.
17. Samartha M.V.S., Arora S., Bhattacharya M. et al. Performance evaluation of deep learning models for predicting MGMT promoter methylation in glioblastoma using MRI: a systematic

review and meta-analysis // Journal of Cancer Research and Clinical Oncology. - 2024. - Vol. 150, No. 10. - P. 461.

18. Sulangi A.J., Husain S.F., Liu Y. et al. Neuronavigation in glioma resection: current applications, challenges, and emerging innovations // Frontiers in Surgery. - 2024. - Vol. 11. - 1430567.