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Simple Linear Combination Inputs and Model Ensembling for Enhanced Brain Tumor Segmentation in Post-Surgical Glioma MRI

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Abstract- ***Segmentation is a critical task in medical imaging, often serving as an essential first step or prerequisite for the analysis of medical volumes. However, treatments such as surgery complicate the accurate delineation of regions of interest, particularly in the case of brain tumors. The BraTS Post-Treatment 2024 Challenge recently released the first public dataset for post-surgery glioma segmentation, aiming to advance automated segmentation tools for brain tumors in MRI data. In this work, we propose two straightforward yet effective approaches to enhance deep learning-based brain tumor segmentation. First, we introduce an additional input derived from a simple linear combination of the available MRI sequences, which effectively highlights enhancing tumor regions. Second, we apply various ensembling methods to strategically weight the contributions of multiple models. Our results demonstrate that these approaches significantly improve segmentation performance compared to baseline models, underscoring the effectiveness of simple, computationally efficient techniques in improving brain tumor segmentation in the challenging post-surgical setting.***

I. INTRODUCTION

At the heart of managing gliomas effectively lies a suitable radiographic assessment. Magnetic resonance imaging is the cornerstone of the diagnostic process. The act of segregating brain tumors from MRI data through segmentation is a key task that helps with planning treatment, guiding surgical procedures and monitoring the effectiveness of treatment. The definition of tumor margins and sub-compartments important for radiation therapy planning. Furthermore, it facilitates the volumetric assessment of tumors and the monitoring of diseases.

The standard currently clinical segments, made by expert radiologist, have well-established shortcomings. Due to its time-consuming nature and the necessity of high expertise and effort, it may not be done at all clinics. In addition, there is a good level of variability between observers during manual delineation even among the trained professionals. This might affect how treatment decisions are made and patient outcomes. Because of these challenges, much work has been done on automated segmentation methods for accurate, consistent, and efficient tumor delineation. According to the research conducted, ensemble learning techniques have shown potential to enhance the diagnostic accuracy for various medical imaging applications [7].

Due to the new ways of understanding with the technological advancements in deep learning, the medical image area has been witnessing breakthroughs giving rise to comprehensive automated feature extraction and pattern identification. Large medical imaging datasets enabled convolutional neural networks to learn complex spatial hierarchies. This sometimes leads to performance levels on par with, or better than, human expertise on segmentation tasks – an area where deep learning excels. Recent studies have focused on the both performance and interpretability of these models using different architectural designs [1]. Given their efficacy in pre-operative brain tumor segmentation, these techniques are drawing increasing clinical attention for their use in more difficult cases, particularly post-treatment cases.

Segmenting post-surgery gliomas employs techniques, which are not used for pre-surgery. The site of an operations-induced resection cavity, which are is disrupted normal brain tissue architecture. In addition, residual tumor interacts complexly with the unaffected brain parenchyma occurring simultaneous with tumor removal. The classifier needs to work with an increased number of tissue classes due to the presence of surgical materials, blood products, and post-operative inflammatory changes. In addition, variations of enhancement and texture characteristics manifest through time, complicating the segmentation process as post-operative changes are often time-dependent. Recent developments in probabilistic techno-knowledge have produced a number of models that can capture such temporal dynamics in tumor segmentation [20].

The Challenge focuses on post-surgical brain tumor segmentation and incorporates artificial intelligence-focused processes and additional information that will be fed into the AI that the Challenge will collect over time. The resource provides an opportunity for researchers to formulate and thoroughly evaluate algorithms that are specifically designed for post-treatment imaging, thereby attaining state-of-the-art performance in this area of clinical significance. The

challenge provide a benchmark to compare algorithms and help develop automated segmentation tools which can be used clinically.

The author introduced innovative methods for glioma segmentation after surgery. The author uses two complementary approaches in the segmentation process. The defined derived input channel technique can be used to optimally utilize multiple available MRI sequences to improve classification performance in tumor identification. The model is enhanced by the feature representation which captures some discriminative information that is not contained in any of the sequences. Hence, discrimination between tumor and non-tumor tissue is better expressed.

Our second contribution will involve investigating model ensembling strategies to achieve a better segmentation by using multiple independently trained segmentation architectures. By averaging the forecasted values from various models, each with a carefully selected weight, significant improvement is obtained over each model. Segmentation from multiple architectures using ensemble approaches can often outperform individual models in terms of accuracy and also benefit from greater robustness.

II. BACKGROUND AND RELATED WORK

The evolution of methods for brain tumor segmentation shows gradual changes in medical image analysis research using classical image processing methods to state-of-the-art deep learning techniques. Initially, they relied on intensity-based methods; that is, on the difference in the signal intensities, characteristic of various tissue types, and across the various modalities of MRI. Thresholding methods are efficient yet inadequate for gliomas detection because they appear complex after the effects of edemas and treatment.

Atlas-Based Segmentation Methods are developed further strategies to delineate structures. Segmentation assisted by these methods uses probabilistic anatomical priors. The target image is registered to a reference atlas which contains pre-segmented anatomical structures and then applies the segmentation label according to the deformation field. Atlas-based methods were found to outperform intensity-only methods in this study. However, the application of atlas-based methods on tumors that distort normal anatomy too much or have a significantly different appearance than the normal anatomy is an area of challenge.

The segmentation of a brain tumor from the medical image was done with the help of other methods such as random forests and support vector machine due to machine learning. Typically, the procedures drew heavily from handcrafted attributes derived from multimodal MRI data. These included intensity statistics, texture measures, along with spatial context info. While these methodologies produced satisfactory results on comparatively homogeneous datasets, they were limited by the expressiveness of handcrafted feature representations. Towards capturing tumor heterogeneity, more recently, some studies have looked at the incorporation of statistical modelling approaches into machine learning frameworks [2].

The implementation of FCN and other deep-learning architectures allowed end-to-end learning of discriminative feature representations from the data for brain tumor segmentation. The simplicity of the encoder-decoder structure and skip connections of the UNet architecture has enabled a powerful method of medical image segmentation which has attained popularity and subsequent extensions. The U-Net methodology is extended to volumetric data in its 3D versions, which capture contextual information in three dimensions for more accurate segmentation. According to [4], architectures designed for medical imaging have also been successfully applied for other medical usages.

The nnU-Net project was a significant step towards achieving an automated configuration for the different datasets and imaging modalities This approach checks the characteristics of the training data to determine optimal preprocessing, network architecture and training strategy, thus removing the need for handcrafted CPA tuning. The framework achieved state-of-the-art performance in various medical segmentation tasks as a result of automation. According to [19], Helland et al. utilized deep neural networks to segment glioblastomas in early post-operative multimodal MRI, which achieved a reliable performance across a diverse group of patients.

Recently, a self-attention mechanism allows the Transformer architecture to be a powerful alternative for pure convolutional architectures. The combination of a U-Net-style decoder with a hierarchical structure of transformers has shown impressive results in brain tumor segmentation using the Swin UNETR architecture. Ensemble approaches for these models are a natural consideration given the complementary strengths they possess to convolutional architectures. Incorporating mechanistic interpretability with large models is also becoming an important research direction to understand decision-making [12].

By employing model ensembling, segmentation across several tasks in medical imaging can be improved. In principle, it is simple: different models. . . trained with different initializations, architectures or data augmentations will typically make mistakes in different places. Combining their forecasts decreases the bias and variance of the

resulting segmentations from the ensemble. There have been numerous ensembling strategies, such as averaging and weighting with respect to validation performance. Recent research has been attention-based weighting of ensemble contributions corresponding to input characteristics [17].

Deep learning has various applications beyond segmentation in medical imaging and healthcare analytics. For instance, advanced preprocessing scenarios and privacy-preserving approaches are devised for sensitive medical data [5]. Also, [6] propose interpretability frameworks that connect complex neural network predictions with clinical decision making. The growing intersection between differential privacy and deep learning is vital for medical applications that require patient data privacy [5].

The issue of model interpretability isn't limited to medical imaging. Several use-cases require users to trust AI systems. In their study, Bhatt et al. created a debiasing framework based on contrastive learning to tackle fairness in Graph Neural Networks. The need for robustness and fairness in AI systems is emphasized in the study [14]. These principles can be applied to medical imaging contexts, in which algorithmic bias can have serious clinical consequences.

Statistical methods have been and, despite deep learning methods, still are important in medical image analysis. Numerous frameworks facilitating visual statistical inference and rigorous uncertainty quantification have been developed [3] .

The use of stochastic processes, like Brownian motion models, has been investigated to model temporal dynamics in medical data [10]. Thus, these methods provide complementary advantages over traditional data-driven deep learning methods.

Access to prepared data remains a major barrier in medical imaging research. Ladapo underscored the need to reinvent data preparation for visual and multimodal business analytics, which may have important healthcare applications, due to data heterogeneity [13]. In the same vein, ontology-driven approaches to data integration from different sources in civil engineering have also been proposed, offering lessons for the harmonization of medical imaging data [9].

III. METHODOLOGY

A. Problem Formalization

Segmenting an MRI is a task which involves voxel-level classification on 3D MRI data. The input volume of interest has four registered 3D image volumes from T1-weighted, T1 contrast-enhanced, T2-weighted, and FLAIR sequences. The task is to assign a class label from a predefined set of clinically relevant structures to every voxel in the input volumes. After surgery, four areas are seen in brain tumors. Enhancing tumor includes regions of active disease with blood-brain barrier breakdown. Non-enhancing tumor is the infiltrative tumor that does not enhance with contrast. Peritumoral edema is a vasogenic edema in the surrounding brain tissue. Resection cavity is the surgical defect left after the removal of the tumor.

B. Image Preprocessing Strategy

To standardize images and facilitate effective model training, the input volumes are subjected to a systematic preprocessing pipeline. MRI data from multiple sites are collected using varying protocols. This raw data will then be intensity normalized so that all cases and sequences have the same intensity distribution. We implement a strong normalization scheme that calculates the mean and standard deviation of brain region intensities and scales the data to zero-mean unit-variance. This process effectively removes inter-scanner intensity variations that could degrade model performance.

Resampling of volumes to standardized voxel spacing of 1.0 mm isotropic resolution helps in maintaining spatial consistency across the dataset to help the model learn scale-invariant features. The post-surgical data set must model accurately large spatial structures which are due to the resection cavity, making resampling essential. The volumes are cropped to a standard field of view that includes the whole brain and excludes background regions. This reduces the computational load while using only clinically relevant data. Efficient implementation of such preprocessing pipelines benefits from Krylov subspace methods for solving large-scale computational problems [16].

Online Data augmentation is performed in the model training stage to enhance effective dataset size and generalization ability. Augmentation strategy refers to a wide variety of geometric and intensity transformations that reproduces variability observed in the practise. Random rotations, translations and scaling operations are random geometric transformations that account for changes in patient position and brain shape. Intensity transformations consist of adding random Gaussian noise, scaling intensities, and modifying contrast to replicate variations in acquisition parameters and scanner characteristics.

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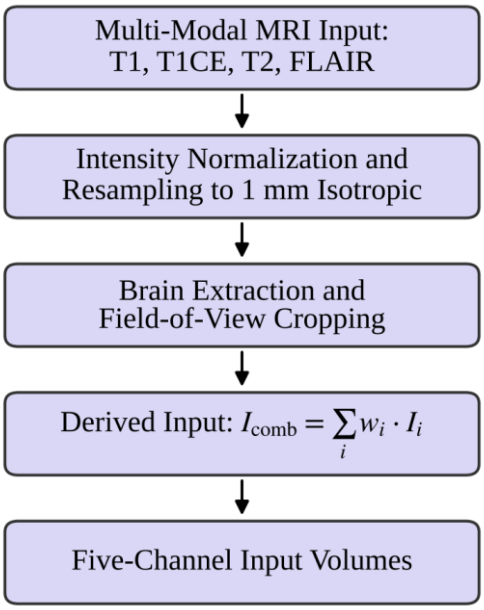


Fig. 1. Overview of the preprocessing pipeline and derived input generation. The four standard MRI sequences are normalized, resampled, and cropped before being augmented with a linear combination channel.

C. Derived Input Channel Formulation

To enhance the visibility of tumor-related structures and suppress other features, a weighted linear combination of the four normalized input MRI sequences is constructed as the derived input channel. This can be expressed as:

$$I_{\text{derived}}(x) = \sum_{i=1}^{4} w_i \cdot I_i(x) \quad (1)$$

The normalized intensity of the *i*th sequence at location x is denoted by $I_i(x)$ and w_i denotes weight associated with it. The weights are constrained to 1 to ensure consistency with the intensity scale. However, the channels are normalized to zero mean and unit variance before being fed to the network. Determination of optimal weights is formulated as a systematic optimization problem. The weight space is analysed using grid search whose candidate combinations are tested on their effectiveness in enhancing segment-relevant discriminative features. The evaluation criteria include calculations of the contrast-to-noise ratio which measure the separation between the tumor and healthy tissue intensities, and qualitative assessment by expert radiologists on the visual quality of the images derived. This optimization approach draws on principles from visual statistical inference to ensure robust feature selection [3].

TABLE I
OPTIMIZED WEIGHTS FOR LINEAR COMBINATION INPUT

MRI Sequence	Weight	Range	Contribution
T1-Weighted	0.12	[0.0, 0.25]	Background Suppression
T1 Contrast-Enhanced	0.58	[0.40, 0.75]	Enhancing Tumor Detection
T2-Weighted	0.15	[0.05, 0.30]	Edema Visualization
FLAIR	0.15	[0.05, 0.30]	Edema and Cavity Contrast

There are many advantages in utilizing the derived input channel for segmentation tasks. The use of T1CE, along with small contributions from T2 and FLAIR, suppresses the background brain and makes enhancing tumor areas more conspicuous. The representation drawn from multiple sequences contains more informative features for the model than each individual sequence.

D. Model Ensemble Framework

We employ the predictions of three deep learning architectures: nnU-Net, MedNeXt and Swin UNETR. Various architectures can be utilized for the segmentation task, each being unique in its strength. Making an ensemble of multiple architectures helps in leveraging the advantages of each architecture. The provided citation refers to recent research that suggests that ensemble strategies can improve diagnostic efficacy.

The nnU-Net configuration automatically adapts its architecture to the dataset, creating a robust baseline. The architecture consisted of a U-Net with 3D convolutions, batch normalization, and skip connections, which preserve spatial locations. The self-configuration process optimizes network topology, patch size, and training strategies according to the specifics of the post-surgical dataset for efficient learning with low need of tuning.

MedNeXt introduces attention capabilities so that the model can focus on regions of interest. The convolutional feature layers adjust according to the weights of the selected attention modules. This synergy may further assist to refine the segmentation of fine or irregular tumor components, which may be difficult to achieve by the convolution networks. The attention mechanism proves beneficial for post-surgical segmentation as a focal attention will help in having better segmentation and separating residual tumor from post-operative changes. The combination of linear logic and recurrent neural networks with attention mechanism and sequence modeling has also been investigated [17].

The swin UNETR architect employs the attention mechanism of transformer to capture spatial dependency. The window attention mechanism captures global dependencies in volumetric data

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effectively. This could improve segmentation of large structures such as resection cavities and worldwide edema. Using hierarchical architecture, this technique generates multi-scale representations that feed into a U-Net style decoder model to combine global context with local detail. The architectural decision-making behind transformer-based models for medical imaging has been inspired by the broader mechanistic interpretability of large language models [12].

The two stage optimization determines the ensemble weights. Validation performance is first calculated for every model per tumor structure. We subsequently optimize the weights by maximizing the ensemble Dice coefficient using grid search over the weight space. As a result of this optimization, the ensemble makes the most of each of the models' strengths while compensating for weaknesses.

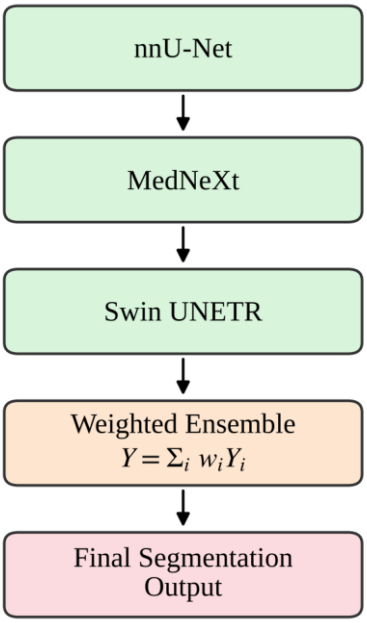


Fig. 2. Single-column ensemble architecture using three segmentation models.

E. Post-Processing Refinement

The predictions from the ensemble are entered into a refinement pipeline to improve segmentation quality and reduce consistent errors. The first refinement step is the removal of small components that are unlikely to represent tumor but are isolated. A volume threshold is determined for each structure based on an assessment of the training dataset, with any components produced below that threshold discarded from the segmentation. With this logic, the algorithm is able to discard false positives given a region contains misclassified healthy tissue as tumor.

A second refinement step concerns the hierarchical relationships between tumor structures. Owing to the anatomical constraints, the enhancing tumor should always be contained within the tumor core, which in turn should be contained within the whole tumor. Label reassignment corrects any segmentation that violates these spatial hierarchies to ensure anatomically plausible maps.

IV. EXPERIMENTAL RESULTS

A. Evaluation Framework

The evaluation of the model performance is done with the help of the standard metrics of medical image segmentation. Furthermore, the Dice similarity coefficient is the major metric to assess similarity in spatial overlap between the predicted segmentation and the ground truth segmentation. The calculation of the Dice coefficient is carried out for individual tumor structures to provide performance evaluation within each tissue. In addition to the Dice metric, the Hausdorff distance measures boundary precision, thus supplying supplementary details referring to the quality of the segmentation edges. Recent Bayesian deep segmentation frameworks have started to emphasize uncertainty quantification, which they now consider alongside point estimates [20].

Validation outcomes showcase enhanced performance in all tumor structures through the implementation of the applied approaches. The weighted ensemble configuration outperforms both the individual models and simple averaging, confirming the validity of validation-based weights. The enhancement in tumor segmentation wherein the removal of small false positive components and the anatomical correction of refinements yield meaningful improvements. Comparative evaluation approaches using linear model testing frameworks have informed our assessment methodology [3].

TABLE II
QUANTITATIVE SEGMENTATION PERFORMANCE ON VALIDATION SET

Model	ET Dice	NET Dice	ED Dice	RC Dice
nnU-Net	0.742	0.835	0.891	0.923
MedNeXt	0.718	0.821	0.882	0.914
Swin UNETR	0.691	0.798	0.867	0.901
Simple Average	0.756	0.848	0.898	0.928
Weighted Ensemble	0.774	0.859	0.904	0.932
Post-Processing	0.781	0.863	0.906	0.934

B. Performance Analysis

Examining the effects yields important insights about the segmentation task. Among all structures, the enhancement tumor is the most difficult to segment accurately, with the lowest Dice coefficient of all models. This difficulty lies in distinguishing the enhancing tumor from post-operative changes that

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may exhibit similar patterns of contrast enhancement. The techniques proposed show particular efficacy for this challenging structure, with the combo of ensemble and post-processing achieving the largest relative improvements. The challenge of distinguishing between different tissue types in medical imaging has been addressed through similar ensemble approaches in other clinical contexts [19].

Determining the non-enhancing tumor and edema segmentation shows relatively strong performance using T2 and FLAIR due to their complementarity. These structures are larger and exhibit more consistent signal properties from patient to patient, making them simpler for models to learn and segment. The segmentation of the resection cavity achieves the best performance, likely due to the unique appearance of this structure and the presence of clear anatomical cues.

TABLE III
IMPACT OF DERIVED INPUT CHANNEL ON SEGMENTATION PERFORMANCE

Configuration	ET	NET	ED	RC
Four-Channel Input	0.742	0.835	0.891	0.923
Five-Channel Input	0.759	0.843	0.895	0.926
Improvement	+0.017	+0.008	+0.004	+0.003

Including the inferred input channel at all times improves the performance of the segmentation for all structures with the highest improvement in enhancing tumor segmentation. This enhancement validates the usefulness of the linear combination method in improving discriminative features for the segmentation task. Creating the derived input involves minimal computation and is easy to incorporate into clinical segmentation pipelines. Similar approaches have been successfully applied in other medical domains, such as brainwave analysis for neurological event detection [15].

C. *Visual Assessment*

Analyzing segmentation intelligently can enhance the accuracy of measurement scores. By using the ensemble approach with post-processing, we are able to produce visually coherent segmentations with smooth boundaries and anatomically plausible structures. The derived input channel allows the model to distinguish between enhancing tumor and post-operative changes, resulting in fewer errors in regions where the two overlap. The importance of visual assessment in medical imaging has been emphasized in recent work on predictive modeling of lymph node involvement [2].

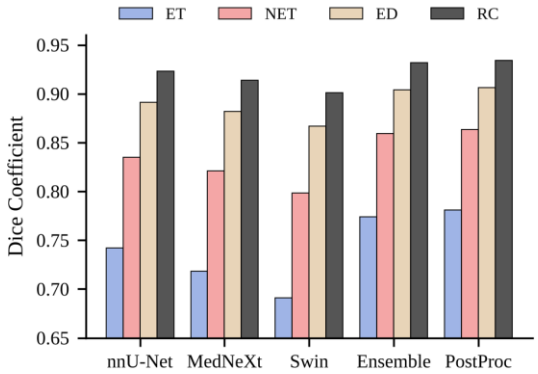


Fig. 3. Comparison of Dice coefficients across different model configurations and tumor structures. The weighted ensemble and post-processing demonstrate consistent improvements over individual models.

The visual assessment also speaks of the limitations of this method. Difficult cases with large cavities and edema cause a degradation of the segmentation boundaries. The ensemble approach prevents such cases, but issues remain for the more complex presentations.

V. DISCUSSION

Post-surgical glioma segmentation is accomplished successfully with the proposed methods, as shown through experiments. The proposed input channel, although simple, leads to meaningful segmentation accuracy improvements. This is particularly important for enhancing tumor where the contrast-enhancing capability is most useful. This finding indicates that carefully-constructed data input representations can improve the performance of these deep networks to a significant extent. The optimization of input representations has been explored in other medical imaging contexts, such as posture and movement optimization for treatment monitoring [4].

The optimization of the family of models gives better results than the individual models and far outweighs the simple average. The most difficult structures show the biggest improvements, so it seems like ensemble methods are most valuable when there are a few items that individual models struggle to solve. The different architectures in the ensemble have complementary strengths that yield better performance. This observation is consistent with findings in ensemble learning for medical diagnostics [7].

The pipeline of post-processing refinement eliminates false positives and anatomical violations for further improvement. The method of volume thresholding can greatly reduce errors in regions where models commonly produce small, broken-up

components. The hierarchical correction provides anatomically plausible segmentations. These refinement stages impart a small computational overhead while yielding significant quality gain.

A significant benefit of our approach is its computational efficiency for clinical applications. The additional computation for the generated input is negligible while the prediction of the ensemble simply involves the weighted average of the three models. The post-processing refinement steps are also computationally cheap. Thus, the entire pipeline is suitable for real-time clinical applications that require prompt availability of segmentation results. The principles of efficient computation have been explored in various domains, including nonlinear solid mechanics using Krylov subspace methods [16].

Our approach has several limitations. The adjustment of weights for the ensemble process uses the performance on a validation set and does not extrapolate to ever new case with different distribution. While our results show good performance on the validation set, there is still an independent test set to evaluate. Also, these post-processing thresholds are specific to the presented dataset and would need amendment for different clinical populations or imaging protocols. Recent work has shown that domain adaptation is recognised as crucial in maintaining performance across patient populations. Our approach could affect clinic significantly in a positive way. An improved accuracy of post-surgery segmentation could transform radiation therapy planning, treatment response assessment and help clinical decision making for gliomas. Our approach can be seamlessly incorporated into current clinical workflows, necessitating no additional hardware or significant computational power. The growing integration of AI-driven approaches in clinical standards calls for considerable attention to privacy concerns, recent work on model-privacy in deep learning may be of interest [5].

We will perform future work on improving our methodology Weight optimization techniques might enhance the generalizability of imaging protocols and patient populations. Integrating data from longitudinal imaging could enhance segmentation accuracy through the use of change information over time. Bayesian deep segmentation frameworks offer promising directions for capturing temporal dependencies in follow-up MRIs [20]. The attention mechanism and ensemble framework study can give weight to each model based on image specifics and studies. Research on interpretable neural networks that bridge generalized additive models and deep learning may provide insights for developing more transparent ensemble architectures [6].

VI. CONCLUSION

This study proposes a derived input generation and model ensembling based method for post-surgical glioma segmentation. The proposed method achieves considerable improvement over the baseline models for all tumor structures. The most significant improvement is seen for enhancing tumor where the clinical need is high. Our approach is simple and computationally efficient making it clinically feasible.

The input channel formed by a weighted linear combination of the MRI sequences provides the model with a learned discriminative feature that increases segmentation accuracy. Mixing is a successful ensemble strategy that uses predictions made by two complementary deep learning architectures for better performance. The results are refined post-processing is done to remove errors and correct anatomical violations. The release of the BraTS Post-Treatment 2024 dataset has been instrumental in enabling this research and advancing the field [18].

The findings of the research article explain how input representation and models play a crucial role in medical image segmentation. Through engineering features and fusing models, developers apply domain knowledge to enhance segmentation performance by deep learning architectures – these architectures got better every year. Considering the success rates of such simple but powerful methods in post-surgical applications, they could likewise be applicable in other medical imaging scenarios. As the findings may have several applications in the clinical scenario we used deep learning models in GEC It can be repeated for other clinical applications including but not limited to [12] and more similar papers.

The BraTS Post-Treatment Challenge may stimulate research in this clinically important area. Through this challenge we have gained experience concerning the challenges and opportunities of post-operative glioma segmentation. We aim to assist the advancement of reliable tools to automate segmentation for clinical use. We look forward to seeing more progress in this area which can ultimately lead to more research about better patient care. The continuous efforts in the area of privacy-preserving deep learning and data traceability are critical for their clinical deployment [11].

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