

A Multitask Deep Learning Approach Toward Brain Tumor Prediction and Analysis

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Abstract

Brain tumor diagnosis and survival prediction are among the major challenges because of high variability and the lack of precise detection and estimation. Despite prominent progress in deep learning-based brain tumor analysis, most existing approaches address segmentation, classification, and survival prediction as independent tasks, limiting their ability to exploit shared representations and reducing clinical interpretability. To address these limitations, this paper proposes 3D-UMT-Net, a multi-task framework for brain tumor segmentation, tumor classification, and patient survival prediction from multi-modal magnetic resonance imaging data. The proposed framework employs a shared encoder with task-specific decoders with additional layers, enabling effective feature sharing while preserving task-level discrimination. An improved stage-based training strategy is introduced to enhance multi-task optimization, allowing revised loss computation across different clinical tasks. Experiments are performed and evaluated on the BraTS 2020 dataset. Dice scores of 0.8657 for the mean Dice, 0.8981 for the whole tumor, 0.8733 for the tumor core, and 0.8258 for the enhancing tumor regions are achieved by the proposed method. For classification, it shows a promising accuracy of 0.9324, an area under the curve of 0.9627, and an F1-score of 0.8387. Similarly, the survival prediction task achieves a concordance index of 0.6167. These results justify that 3D-UMT-Net provides an efficient and usable multi-task solution for competitive brain tumor analysis, providing improved performance and predictions. Although the proposed framework achieved promising results on publicly available datasets, further validation using clinically acquired datasets and real-world clinical environments is necessary before assessing its clinical utility. The proposed framework is projected as a computational and strategic advancement and can be used as a base study to derive solutions for clinical decision-making only after clinical validation under institutional and medical supervision.

Categories: Health Informatics, Image Processing and Analysis, Deep Learning

Keywords: deep learning, u-net architecture, dice score, tumor detection, brain tumor segmentation, medical image analysis, stage based training, brain tumor classification, cnn model, task isolation

Introduction

Brain tumor prediction from multimodal MRI (Magnetic Resonance Imaging) plays a critical role in tumor diagnosis, planning, and prognosis. Accurate prediction of tumor sub-regions, tumor classification, and survival prediction are essential and necessary for understanding tumor progression and improving patient outcomes. The availability of large-scale benchmark datasets such as BraTS made deep learning methods a robust approach for brain tumor segmentation and clinical tasks [1,2].

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Sun et al. [3] proposed a framework that performs segmentation followed by radiomic feature extraction for survival prediction. Pei et al. [1] proposed a context-aware CNN model for tumor segmentation, subtype classification, and survival prediction, showing the potential of shared representations. Similarly, Yogananda et al. [4] developed a fully automated framework combining segmentation, classification, and prognosis estimation. Nazir et al. [2] further extended this direction by introducing an end-to-end multitask architecture that jointly optimized all three objectives. Yeafi et al. [5] justify that fully joint multitask frameworks optimize all objectives simultaneously, which results in unstable training behavior due to conflicting gradients and the imbalance of task learning dynamics. Several studies employ cascaded strategies, where segmentation is first performed and contributes to clinical tasks through radiomics or feature extraction [6]. While such pipelines reduce task interference, they prevent effective end-to-end feature learning and may suffer from error propagation. Recent studies have also discovered hybrid and multitask frameworks for segmentation and survival prediction [6-8], or segmentation and classification, presenting improved performance through shared feature learning. In particular, progressive and stage-based learning strategies that train tasks sequentially within a unified architecture have not been sufficiently tested or experimented with. Rastogi et al. [9] explored segmentation and survival modeling. Kickingreder et al. [10] and Bakas et al. [11] utilize radiomic features for segmentation and further use the obtained feature data downstream for other tasks.

Integrated brain tumor analysis frameworks

The importance of unified frameworks for effective brain tumor analysis is justified by recent studies. Pei et al. [1] introduced a context-aware deep learning CNN model, as discussed above. Effective capturing of tumor sub-regions and clinical information is demonstrated by their work. Likewise, Yogananda et al. [4] developed a fully automated learning pipeline to perform segmentation, classification, and prognosis estimation using a deep CNN. Nazir et al. [2] further advanced this direction by presenting an end-to-end multitask architecture that optimizes all three objectives simultaneously, but they primarily depend on joint optimization, which can lead to performance degradation.

From these studies [1-4], we adopt the concept of using a shared backbone with multiple task-specific heads for all three tasks. This architectural design forms the basis of our unified framework.

Pipeline-based and radiomics-guided approaches

Wu et al. [6] and Kickingreder et al. [10] similarly utilized predicted tumor regions to derive specific features for downstream prognosis modeling. Agravat and Raval [7] introduced a multi-stage pipeline in which segmentation outputs are sequentially processed for survival estimation, hence reducing direct task interference by separating learning stages.

From these pipeline-based studies [3,6,7,10], we adopt the idea of sequential task integration. However, instead of employing independent models or specific features, we implement progressive optimization within a shared deep network, enabling end-to-end feature learning.

Multitask learning for segmentation and prognosis

Recent research has explored multitask learning for combinations of segmentation and clinical tasks. Huang et al. [8] proposed a multitask framework for segmentation and tumor characterization. Rastogi et al. [9] integrated deep segmentation with survival modeling in a unified system. These methods demonstrate that shared feature representations can enhance predictive performance.

From these works [8,9], we derive our multi-head network design and the use of shared convolutional features for supporting multiple clinical tasks.

Optimization strategies in multitask learning

Optimization remains a critical challenge in multitask learning. Nazir et al. [2] and Yeafi et al. [5] adopt fully joint loss optimization, assuming that simultaneous learning yields optimal performance.

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Survey studies and systematic reviews further support the necessity of upgraded training strategies in integrated medical imaging systems [12]. These studies highlight the lack of standardized methodologies for balancing multiple objectives in complex clinical tasks.

From these studies [2,5,9,10,12], we identify the limitations of joint optimization and the need for controlled training mechanisms, which motivate our stage-based learning strategy.

Additionally, Menze et al. [13] and Kundal et al. [14] focused on segmentation from multimodal MRI data, specifically from BraTS, while Hamza and Damaševičius [15] and Akter et al. [16] extended this work to integrate classification as well.

The major research gap found by reviewing the above works and studies is the lack of efficient multitasking frameworks that perform segmentation, classification, and survival prediction at the same time. Also, multitasking frameworks often have optimization imbalances and task interference during joint training; i.e., segmentation influences and degrades the learning of clinical tasks during the learning stage.

In this study, we have improvised a stage-based multi-task training strategy (sequential training) for brain tumor segmentation and clinical tasks (classification and survival prediction) using a single deep learning CNN architecture trained on the BraTS 2020 dataset. This partial end-to-end strategy aims to mitigate task interference while preserving effective feature sharing. Furthermore, we perform a direct comparison between the partial end-to-end and true end-to-end joint training under identical experimental conditions, enabling a fair comparison of convergence behavior and predictive performance. The current study is primarily validated using the publicly available BraTS 2020 dataset, which is a widely adopted benchmark for brain tumor segmentation, classification, and survival prediction research. We do not have access to clinical data due to ethical and institutional challenges, so we employed the benchmark dataset for both training and validation since it is used for various studies [2,5,8,9,15,16].

Materials And Methods

Hyperparameters and configurations

Table 1 summarizes the experimental settings and hyperparameters used for training the proposed multitask framework. The model was implemented using PyTorch and trained on a Kaggle Tesla P100 GPU with CUDA acceleration. Mixed-precision training and the AdamW optimizer with a learning rate of 1×10^{-4} were employed to improve computational efficiency and convergence. MRI volumes from four modalities were resized to $128 \times 128 \times 128$ and processed through a shared 3D U-Net encoder with Group Normalization and ReLU activation. Training was performed for 120 epochs using a stage-wise strategy, with DiceCELoss and BCEWithLogitsLoss utilized for the segmentation and classification tasks, respectively.

Parameter	Configuration
Processing Platform	CUDA-enabled Kaggle Tesla P100 GPU
Data Split	80% Training, 20% Testing
Data Sampling Sequence	Random
Learning Rate	1×10^{-4}
Training Approach	Mixed Precision Training
Optimizer	AdamW
Number of Epochs	120 (30 + 60 + 30 stage-wise training)
Batch Size	2
Number of Workers	2
Pin Memory	True
Persistent Workers	True
Input Image Size	$128 \times 128 \times 128$
File Format	NIfTI (.nii)
Input Modalities	4 (T1, T1ce, T2, FLAIR)
Encoder Channels	32, 64, 128
Bottleneck Channels	256
Segmentation Classes	3 (WT, TC, ET)
Normalization Layer	GroupNorm
Pooling Operation	MaxPool3D
Activation Function	ReLU
Dropout Rate	0.5
Classification Head	Fully Connected Classification Network
Survival Prediction Head	Fully Connected Regression Network
Segmentation Loss Function	DiceCELoss

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Classification Loss Function	BCEWithLogitsLoss
Survival Prediction Loss Function	Cox_PH_Loss

TABLE 1: Hyperparameters, model configurations, and learning rates table with all the necessary variables
CUDA, Compute Unified Device Architecture; ET, Enhancing Tumor; MRI, Magnetic Resonance Imaging; ReLU, Rectified Linear Unit; TC, Tumor Core; WT, Whole Tumor

Data acquisition

In this study, 3D-UMT-Net (the proposed multitask framework) is utilized along with a progressive training strategy to improve the existing multitask frameworks. The BraTS 2020 dataset is used, which is an available benchmark dataset actively used for brain tumor segmentation, classification, and survival analysis research. This dataset collectively contains over 369 multimodal 3D MRIs. Each subject includes four MRI modalities - T1, T1ce, T2, and FLAIR (Fluid-Attenuated Inversion Recovery) - as demonstrated in Figure 7. BraTS 2020 comes with survival data and label mapping files to support all three core functionalities of our study, i.e., segmentation, classification, and survival prediction.

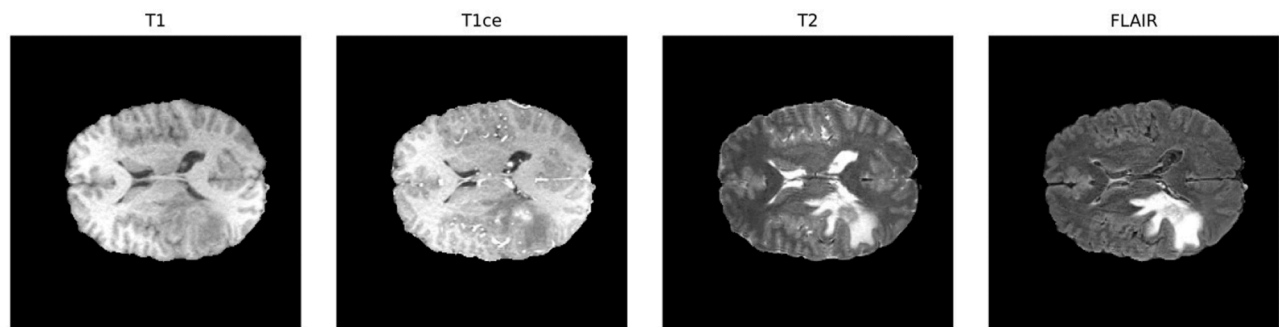


FIGURE 1: MRI modalities used for brain tumor segmentation
The figure shows MRI modalities: T1 (T1-weighted), T1CE (Contrast-Enhanced T1-weighted), T2 (T2-weighted), and FLAIR. FLAIR, Fluid-Attenuated Inversion Recovery; MRI, Magnetic Resonance Imaging

Data preprocessing

The original MRI volumes have a standardized spatial resolution of $1 \times 1 \times 1 \text{ mm}^3$ with dimensions of $240 \times 240 \times 155$ voxels. The BraTS 2020 dataset contains approximately 369 training cases, of which a subset includes clinical metadata such as patient age and survival duration, enabling survival prediction studies. From 369 cases, 270 cases were used for training, and 99 cases were used for validation. Furthermore, after filtering and validation, out of 270 training cases, 1 was found to have a missing modality, and 188 cases were found where segmentation, classification, and survival prediction were present together.

Model architecture

The proposed architecture, 3D-UMT-Net, is a unified 3D U-Net-based multitask framework for simultaneous brain tumor segmentation, classification, and survival prediction. It employs a hierarchical encoder to extract multi-scale volumetric features, followed by a decoder with skip connections to recover fine-grained spatial details missed during encoding. The

shared feature vector collectively contributes to the classification and survival branches to enable comprehensive tumor analysis. This approach stabilizes the model capacity to 256 channels and is suitable for lightweight model presentation, as demonstrated by Figure 2.

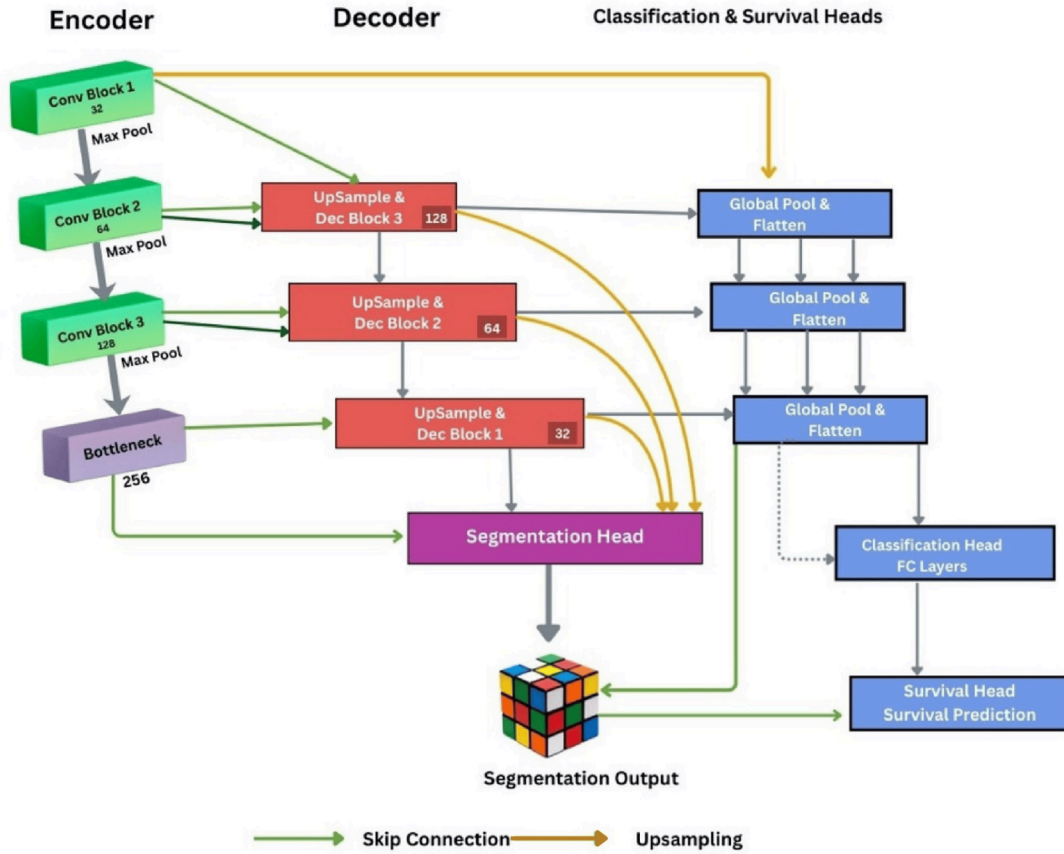


FIGURE 2: Model architecture comprises encoders, decoders, and pooling blocks

Convolutional block

$$Z_1 = \sigma(\text{GN}(W_1 * X)) \quad (1)$$

$$Z_2 = \sigma(\text{GN}(W_2 * Z_1)) \quad (2)$$

$$C(X) = Z_2 \quad (3)$$

where * denotes 3D convolution, W_1, W_2 are convolution kernels, GN is Group Normalization, and σ is ReLU.

The below equation represents that the encoder extracts low-level spatial features while reducing the spatial resolution by a factor of 2.

$$E_1 = C_1(X) \quad (4)$$

$$E_2 = C_2(P(E_1)) \quad (5)$$

$$E_3 = C_3(P(E_2)) \quad (6)$$

$$B = C_4(P(E_3)) \quad (7)$$

Decoder restores spatial resolution while integrating high-level encoder features through skip connections.

$$D_3 = C_5([U_3(B), E_3]) \quad (8)$$

$$D_2 = C_6([U_2(D_3), E_2]) \quad (9)$$

$$D_1 = C_7([U_1(D_2), E_1]) \quad (10)$$

Hence, segmentation becomes

$$Y_{\text{seg}} = W_s * D_1 + b_s \quad (11)$$

where W_s is a $1 \times 1 \times 1$ convolution kernel.

The classification branch learns discriminative representations for tumor type prediction using regularized fully connected layers.

$$H_c = \text{ReLU}(W_{c1}F + b_{c1}) \quad (12)$$

$$H'_c = \text{Dropout}(H_c) \quad (13)$$

$$y_{\text{cls}} = W_{c2}H'_c + b_{c2} \quad (14)$$

The survival branch models patient prognosis by mapping deep features to continuous survival estimates.

$$H_s = \text{ReLU}(W_{s1}F + b_{s1}) \quad (15)$$

$$H'_s = \text{Dropout}(H_s) \quad (16)$$

$$y_{\text{surv}} = W_{s2}H'_s + b_{s2} \quad (17)$$

Final Output

The proposed network simultaneously optimizes segmentation, classification, and survival prediction in a unified multitask framework.

$$F(X) = (Y_{\text{seg}}, y_{\text{cls}}, y_{\text{surv}}) \quad (18)$$

Algorithm

Require: MRI dataset $\{(X, Y_{\text{seg}}, Y_{\text{cls}}, T, E)\}$; 3D-UMT-Net M; Losses: Dice, BCE, Cox, L1; Optimizer: Adam

Ensure: Independently trained segmentation, classification, and survival module within the same model.

1: Stage-I: Survival Training

2: Train encoder and survival head using Cox loss, L1

3: Stage-II: Segmentation Training

4: Train encoder and segmentation decoder using Dice loss

5: Stage-III: Classification Training

6: Train classification head using GAP features and BCE loss

7: Inference

8: Given test volume X

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9: Predict $(Y_{\text{seg}}, y_{\text{cls}}, y_{\text{surv}}) = M(X)$

10: Return output

Training strategy

3D-UMT-Net utilizes a sequential stage-wise training strategy, which allows the architecture to train specific tasks in a completely isolated environment. To ensure stable optimization across tasks, training is performed in three sequential stages. The survival prediction task is trained in the first stage because of the design choice. It is often categorized as a challenging problem, with C-index values ranging from 0.45 to 0.60. In the second stage, the network is trained on the segmentation task to reinforce the learning of detailed spatial representations, allowing it to focus on segmentation performance. This strategy prioritizes Dice scores while preserving previously learned model parameters and task-specific heads. The third stage involves training the network for classification. Throughout this stage, parameter updates are driven only by the classification loss. This isolates class-relevant features while retaining the representations learned from prior stages, thereby maintaining stability.

Results And Discussion

The proposed framework is a partial end-to-end multitask deep learning architecture designed to perform brain tumor segmentation, tumor grade classification, and patient survival prediction from multi-modal MRI scans during a single inference step. The model aims to use shared representations across related tasks while maintaining task isolation to enhance overall performance and clinical relevance, which can be further explored after clinical trials under controlled clinically validated environment.

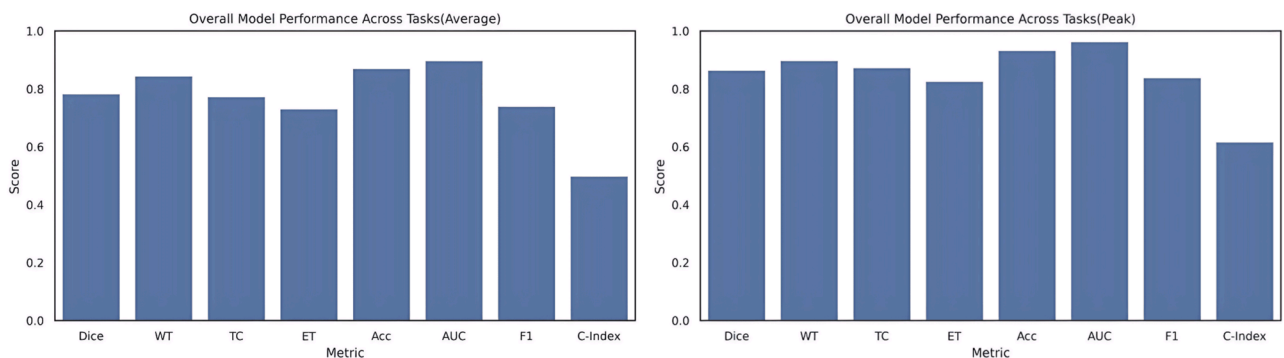


FIGURE 3: Model average performance and model peak performance

The figure demonstrates the average and peak performance statistics of the 3D-UMT-Net model. These scores were achieved under the same setup and computed from the same results CSV file.

Acc, Accuracy; AUC, Area Under the Curve; ET, Enhancing Tumor; TC, Tumor Core; WT, Whole Tumor

On average, the model's accuracy and AUC (Area Under the Receiver Operating Characteristic Curve) stats indicate strong classification, along with efficient segmentation performance justified by Dice scores. The peak results show further improvement across all metrics, further justifying the model's ability to perform properly under favorable training conditions, as demonstrated in Figure 3. However, the comparatively lower C-index suggests that survival prediction remains the most challenging task and requires additional refinement.

Segmentation

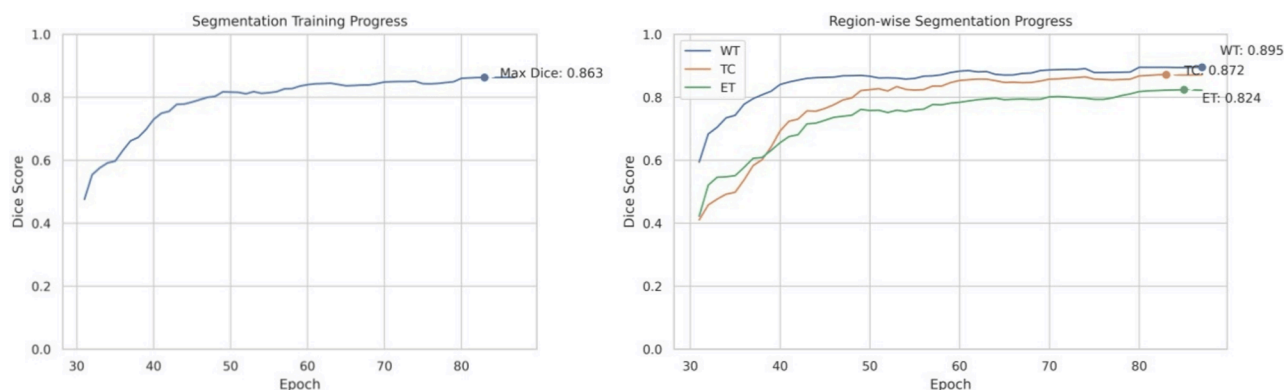


FIGURE 4: Segmentation - mean Dice and region-wise Dice

The figure demonstrates the overall Dice performance, i.e., the mean Dice score, which starts at around 0.4 at epoch 30 and converges to a maximum value of 0.863 at epoch 84. It also provides the WT, TC, and ET values.

ET, Enhancing Tumor; TC, Tumor Core; WT, Whole Tumor

The proposed solution obtains a mean Dice score of 0.8657, with individual values of 0.8981, 0.8733, and 0.8258 for WT, TC, and ET, respectively, as shown in Figure 4. These results demonstrate the ability of the network to accurately capture both global and fine-grained tumor structures. The high WT score indicates reliable identification of the complete tumor extent, while the strong TC and ET scores justify effective learning of complex intra-tumoral patterns. The segmentation of the ET region remains a computational challenge, and it is hard to capture due to its small size and irregular distribution. The proposed method achieves a Dice score of 0.8257, which highlights its efficiency in capturing important enhancing regions.

Survival prediction and classification

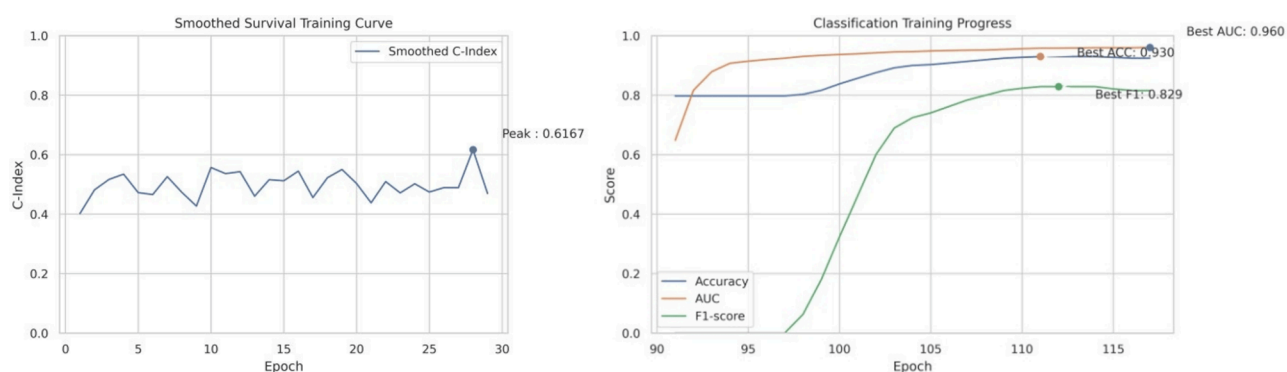


FIGURE 5: Survival prediction and classification

The figure represents the survival prediction performance, which oscillates around 0.50 and periodically reaches 0.60. On the other hand, it also represents the classification performance, where the model takes time to learn distinctive features, after which the accuracy starts to improve.

Acc, Accuracy; AUC, Area Under the Curve

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The proposed solution achieves a classification accuracy of 0.9324, an AUC of 0.9627, a C-index of 0.6167, an MAE of 214 days, and an RMSE of 345 days, indicating strong discrimination performance between tumor categories on the benchmark dataset, as presented in Figure 5. The high accuracy suggests consistent prediction capability across samples, while the strong AUC value demonstrates strong class separability. The comparatively low MAE and RMSE values make the proposed approach a possible fit for survival estimates, with low sensitivity to extreme prediction errors. The shared encoder may have facilitated the learning of representations that are useful across multiple tasks. However, the specific contribution of shared feature learning to classification performance was not explicitly evaluated in this study and warrants further investigation through dedicated ablation experiments.

Comparison study

Table 2 presents a comprehensive comparison between the proposed 3D-UMT-Net framework and recent multitask learning approaches for brain tumor segmentation and clinical tasks. Early multitask studies, such as Pei et al. [1], adopted a partial end-to-end learning strategy on the BraTS2018 dataset and achieved scores of 0.850, 0.902, and 0.589 for segmentation, classification, and survival prediction, respectively. Huang et al. [8] further explored shared encoder architectures under a partial end-to-end setting and reported a mean Dice of 0.793, with a classification accuracy of 0.901. Nazir et al. [2] introduced fully joint training on the BraTS2020 dataset, achieving a mean Dice of 0.859 and classification accuracy of 0.914. Even after the benefits of true end-to-end optimization, their survival prediction performance remained limited (CI = 0.578, MAE = 456), suggesting that joint optimization of all tasks may lead to task interference. Yeafi et al. [5] reported the highest segmentation accuracy (mean Dice = 0.940) using a non-end-to-end pipeline combined with a random forest-based survival model. The proposed 3D-UMT-Net employs a stage-based partial end-to-end training strategy that balances task-specific learning and shared representation refinement. This design achieves segmentation performance (mean Dice = 0.8657), with classification accuracy (0.9324) and AUC (0.9627). Our framework demonstrates superior survival prediction capability, with a concordance index of 0.6167 and a reduced MAE of 214 days.

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Method	Training Type	Dataset	Segmentation (Dice)	Classification	Survival	Remarks
Pei et al. [1]	Partial E2E	BraTS 2018	ET = 0.821, WT = 0.895, TC = 0.835, Mean = 0.850	Acc = 0.902	CI = 0.589	Early multitask work
Nazir et al. [2]	True E2E	BraTS 2020	Mean = 0.859	Acc = 0.914	CI = 0.578, MAE = 456	Fully joint training
Yeafi et al. [5]	Non-E2E	BraTS 2020/21	Mean = 0.94	Acc = NA	CI = 0.528, MAE = 327	Non-E2E (RF-based survival)
Huang et al. [8]	Partial E2E	BraTS 2018	ET = 0.75, WT = 0.86, TC = 0.77, Mean = 0.793	Acc = 0.901	CI = 0.569	Shared encoder
3D-UMT-Net	Stage-based Partial E2E	BraTS 2020	WT = 0.8981, TC = 0.8733, ET = 0.8258, Mean = 0.8657	Acc = 0.9324, AUC = 0.9627, F1 = 0.8387	CI = 0.6167, MAE = 214, RMSE = 345	Balanced optimization, Partial E2E

TABLE 2: Model comparison

The table represents a comparison of the model with studies involving multitasking models from the same segment.

Acc, Accuracy; ET, Enhancing Tumor; MAE, Mean Absolute Error; RMSE, Root Mean Square Error; TC, Tumor Core; WT, Whole Tumor; E2E, End-to-End

True End-to-End Multitask Learning vs Partial End-to-End Multitask Learning

The performance of true end-to-end joint training and partial end-to-end sequential training was evaluated across segmentation, classification, and survival prediction tasks. Both training strategies were tested and evaluated on BraTS 2020 benchmark using same configuration with two batches. True end-to-end multitask learning was used initially for model evaluation but switched to partial end-to-end multitask learning after testing task isolation, dataset filtering, and valid case processing.

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Task	Metric	True End-to-End	Partial End-to-End	Improvement
Segmentation	Dice	0.8236	0.8657	5.11%
	WT	0.8667	0.8981	3.62%
	TC	0.8137	0.8733	7.32%
	ET	0.7904	0.8258	4.47%
Classification	Acc	0.7984	0.9324	16.78%
	AUC	0.8433	0.9627	14.15%
Survival	MAE	338	214	-36.68%
	RMSE	466	345	-25.96%
	C-Index	0.5449	0.6167	13.17%

TABLE 3: Comparison of two training strategies

The table compares the True End-to-End training strategy with the Partial End-to-End training strategy. Additionally, the percentage improvements are calculated using the following formula: $\text{change\%} = [(\text{final-initial})/\text{initial}] * 100$

Acc, Accuracy; ET, Enhancing Tumor; MAE, Mean Absolute Error; RMSE, Root Mean Square Error; TC, Tumor Core; WT, Whole Tumor.

Sequential training consistently outperformed joint training in segmentation, with the overall Dice score increasing from 0.8236 to 0.8657 and notable gains across all tumor sub-regions, as demonstrated in Table 3. The percentage improvements were calculated using the following:

$$\frac{\text{Final Value} - \text{Initial Value}}{\text{Initial Value}} \times 100\%.$$

Similarly, accuracy improved from 0.7984 to 0.9324, and AUC improved from 0.8433 to 0.9627, demonstrating improved feature discrimination. Survival prediction results also favored the sequential approach over the joint approach, with reduced MAE and RMSE and an increased C-index, reflecting more reliable prognostic modeling.

There is reduced task interference and more stable optimization in the sequential framework. Partial end-to-end training enables effective knowledge transfer and balanced multitask performance. Due to combined learning, segmentation dominated classification and was therefore unable to capture distinctive features; meanwhile, sequential learning increased feature discrimination, which led to better accuracy. Partial end-to-end training provides the privilege of achieving the best results in individual tasks without overfitting the other tasks. In true end-to-end multitask training, we were left with 94 training cases per batch that had both grade variables and survival data because of mismatches and missing values. On the other hand, in partial end-to-end, there are 268 cases available for segmentation, of which 147 have grade variables and 188 have survival data; hence, 94 cases per batch were processed, and it provides a better training protocol.

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Discussion

While the proposed framework showed promising computational performance for brain tumor segmentation, classification, and survival prediction on the BraTS benchmark dataset, several key points limit its efficient translation into clinical practice. The study was conducted using publicly available benchmark datasets that provide standard imaging protocols. Although such datasets are valuable for developing and evaluating machine learning algorithms, they may not fully represent the variable challenges in real-world healthcare environments. Clinical MRI data have differences in hardware, imaging protocols, image quality, orientation, patient demographics, tumor heterogeneity, and institutional practices, which can alter model performance because the model is not trained on these variabilities. The raw performing model cannot be deployed under a medical setup with necessary micro-threshold arrangements. One such important variable is the Youden J Statistic in binary classification, as this technique can be exercised as future work for this study. This approach reduces false-negative predictions compared to the default threshold. The method works by providing multiple decision threshold values and a range of thresholds where false-negative predictions are found to be minimum, which might help in improving the practical reliability and decision-making of the model in a medical setup. In medical diagnosis and detection, false-negative predictions are considered much more dangerous than false positives. A false positive might cost unnecessary expenses, but a false negative might delay a lifesaving treatment. Therefore, the current work should be regarded as a computational research framework and a proof-of-concept study instead of a clinically validated diagnostic or prognostic tool. Noticeably, the results obtained are achieved from a publicly available benchmark dataset, and there is a need for multi-center clinical validation and clinically guided evaluation before actually deploying the proposed framework in real-world settings or clinical decision-making.

Limitations and future work

A noticeable limitation of the present study is the absence of external validation using independent clinical datasets. External validation is essential for assessing model robustness, reproducibility, and generalizability across different medical centers. Accordingly, the reported results are presented as evidence of computational effectiveness under a benchmark dataset instead of proof of clinical utility. Additional evaluation using multi-center datasets and prospective clinical studies would be necessary before the proposed framework could be considered for medical and clinical use. The proposed framework is positioned as a computational and strategic improvement at benchmark data settings.

Although the proposed framework achieved encouraging quantitative results, clinical adoption requires much more aspects than just high accuracy metrics. Practical deployment would require micro-adjustments using analytical variables suitable for medical analysis, diagnosis, or prognosis; extensive validation across diverse patient populations; integration into existing clinical workflows; regulatory approval; compliance with data privacy regulations; continuous performance monitoring; and assessment by multidisciplinary clinical experts.

Future scope of this work will be focusing on dataset processing improvements, integrating larger and more diverse datasets, detailed clinical comparisons, and explainable models to enhance clinical applicability and trust, as well as validating the proposed framework using clinically acquired patient datasets and real-world clinical settings. Such validation will help us assess the model's robustness, generalizability, and potential to be used in clinical decision-making under healthcare institutions.

Conclusions

The proposed multitask framework demonstrates strong performance in brain tumor segmentation and clinical tasks (classification and survival prediction), favoring the effectiveness of partial end-to-end learning. The achieved results suggest that integrating spatial and semantic information improves prognostic modeling. By jointly addressing tumor segmentation, classification, and survival prediction within a unified architecture, the proposed approach demonstrated the effectiveness of shared feature learning while reducing task interference through sequential optimization. The partial end-to-end training strategy enables effective information sharing among tasks while maintaining task isolation, leading to improved learning efficiency compared to joint learning approaches. We need to reconsider the possibilities of improvements even after achieving promising results. The study was conducted using publicly available datasets without

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access to institution-specific patient data, extensive ethical approvals, and data governance procedures. Overall, the proposed framework provides an efficient solution for integrated brain tumor analysis and prediction from multimodal MRIs.

Additional Information

Author Contributions

All authors have reviewed the final version to be published and agreed to be accountable for all aspects of the work.

Concept and design: Archana Uniyal, Pooja Sharma

Acquisition, analysis, or interpretation of data: Archana Uniyal, Pooja Sharma

Drafting of the manuscript: Archana Uniyal, Pooja Sharma

Critical review of the manuscript for important intellectual content: Archana Uniyal, Pooja Sharma

Supervision: Pooja Sharma

Disclosures

Human subjects: All authors have confirmed that this study did not involve human participants or tissue. **Animal subjects:** All authors have confirmed that this study did not involve animal subjects or tissue. **Conflicts of interest:** In compliance with the ICMJE uniform disclosure form, all authors declare the following: **Payment/services info:** All authors have declared that no financial support was received from any organization for the submitted work. **Financial relationships:** All authors have declared that they have no financial relationships at present or within the previous three years with any organizations that might have an interest in the submitted work. **Other relationships:** All authors have declared that there are no other relationships or activities that could appear to have influenced the submitted work.

Data Availability Statements

The data (and/or code) supporting this study are openly available in Kaggle at <https://www.kaggle.com/datasets/awsaf49/brats20-dataset-training-validation> and https://drive.google.com/drive/folders/1Vk_GNxt5Qpkx7nr9BI-D_I97xIJWl6pG?usp=sharing.

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