

Tumornet++-ROI: Region-Of-Interest-Driven Deep Learning Framework For Tumor Size Estimation And Survival Prediction In Brain Mri

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ABSTRACT

Accurate measurement of the extent of a brain tumour and estimation of survival time is an essential part of neuro-oncological imaging. This research, which is built on our previous TumourXNet++ architecture for tumour detection, presents TumourXNet++-ROI, a region-of-interest (ROI) guided deep learning system that combines tumour segmentation, morphometric feature extraction, and prognostic modeling in a single framework. Initially, the proposed method of isolating tumour ROIs by adaptive segmentation is followed by the extraction of quantitative descriptors-tumour area, maximal width, height, and mean density-that act as interpretable surrogates of lesion growth. A neural regression module is used to estimate tumour size, while a second survival-prediction head makes an estimate of the post-diagnostic lifespan directly from the ROI features and shallow CNN embeddings. The experiments involved 501 BraTS-2021 MRI studies to compare the estimated and model-predicted survival values. There were strong inverse correlations between tumour size indicators and survival (Pearson's r : area = -0.975, width = -0.908, height = -0.908, density = -0.686) whereby bigger and denser tumours led to lower predicted survival. The regression analysis produced a high coefficient of determination ($R^2 > 0.90$) with a low RMSE and MAE, and the Bland-Altman assessment indicated tight agreement intervals between the predicted and the reference survival. These results indicate that a deep learning method based on ROI normalization makes it possible to accurately quantify a tumour and to estimate survival time based on routine MRI data. The modular TumourXNet++-ROI pipeline thus moves beyond classification-focused AI systems to clinically interpretable prognosis modelling, providing a reproducible basis for the development of 3D volumetric and multimodal survival-analysis frameworks in the future.

Keywords: Brain MRI, ROI segmentation, Tumour size estimation, Survival prediction, Deep learning, Morphometric analysis, medical image prognosis.

1.0 INTRODUCTION

The brain is a complex organ. Brain tumours are among the most aggressive and difficult to treat malignancies in the central nervous system. They are the major cause of cancer-related morbidity and mortality globally [1], [2]. Even with the improvements in radiotherapy and surgical techniques, early detection, quantitative assessment of tumour burden, and reliable prediction of patient survival are still open questions in clinical neuro-oncology [3]. Magnetic Resonance Imaging (MRI) is still the best method for non-invasive brain tumour evaluation owing to its high soft-tissue contrast and multi-parametric capability [4]. Nevertheless, manually outlining and measuring tumour sizes are highly subjective and likely to differ between observers, especially in cases with diffusely infiltrative tumour margins [5]. The differences highlight the necessity for automated, reproducible, and interpretable quantitative imaging methods that not only help in detection but also in estimating the prognosis.

Over the last several years, deep learning (DL) has been a major factor in medical image analysis to change the way. Convolutional Neural Networks (CNNs) are able to

automatically extract hierarchical features from the imaging data and in this way, they achieve better results than traditional handcrafted feature-based methods in both classification and segmentation [6], [7], [8], [9]. However, basically categorical classification of tumours (e.g. glioma, meningioma, or pituitary adenoma) [10], [11], [12] is what most of the existing CNN-based frameworks pay attention to, thereby indirectly contending that prognosis and treatment planning could be the next levels of clinical value to be hardly touched. Clinicians, actually, need quantitative indicators like tumour area, volume, or morphological changes over time for their individual decision-making to be supported. Lack of these interpretable parameters usually limits deep learning models to be only research works instead of real-world clinical deployment scenarios [13], [14], [15].

Such a problem gave rise to radiomics-based solutions, in which characterization of tumour phenotypes is carried out by the extraction of hundreds of quantitative features intensity, shape, and texture, etc. from the segments of the region of interest (ROI) [16], [17]. The downside of radiomics is that it depends on handcrafted descriptors and the manual definition of ROI, which makes reproducibility low across scanners, acquisition protocols, and institutions [18]. Besides that, radiomic features mostly represent linear or shallow statistical summaries that in turn may be incapable of capturing complex nonlinear relationships between tumour morphology and survival outcomes [19], [20]. Recently have paved the way for integrating deep learning with radiomic concepts. This has led to hybrid DL-radiomics systems for brain tumor grading, growth modeling, and survival prediction [21],[22]. CNN-based survival models like DeepSurv and convolutional Cox networks have shown the potential to derive risk representations directly from MRI or ROI-based features [23], [24]. On the contrary, such models typically need a vast amount of annotated data, and they do not explicitly incorporate geometric tumour descriptors (e.g., width, height, area), which can be easily understandable co-relates of disease progression [25],[26], [27]. Therefore, a single framework that merges ROI-driven morphometric analysis with deep survival regression is still an unaddressed clinically significant research gap.

In our previous research, TumorXNet++, we proposed a hybrid GoogleNet+AlexNet configuration coupled with adaptive preprocessing for better tumor detection and classification on the BraTS 2021 dataset, resulting in 95% test accuracy. That work was addressing our research plan at the image processing level for advanced image processing and hybrid deep learning-based classification. This work is an extension of our previous TumorXNet++ model where we present TumorXNet++-ROI, a new region-of-interest-driven framework for tumor size estimation and survival prediction.

Our main point is that morphometric parameters based on segmented tumor ROIs like area, maximal width, height, and mean intensity (density) might become good predictors of survival if combined with CNN-driven regression modeling. The advocated approach comprises three mains components:

1. ROI Segmentation: localizing the tumour features in the image automatically by the adaptive thresholding and subsequent morphological operations;
2. Tumour Size Regression: quantitative estimation of size-related aspects of the tumour via feature-based neural networks;
3. Prediction of Survival Time: deep regression of the predicted survival time from morphometric and intensity features extracted from the ROI-derived image.

Experiments were performed on 501 MRI studies taken from the BraTS 2021 dataset [23]. Strong negative correlations were found between tumour size indicators and survival duration (area = -0.975, width = -0.908, height = -0.908, density = -0.686), thus confirming that larger tumours correspond to shorter survival. The model made

predictions with high accuracy as evidenced by R^2 values above 0.90 and low mean absolute error, confirmed by regression, correlation, and Bland–Altman analyses.

This research work mainly points out the following contributions:

1. An ROI-standardized deep learning framework (TumorXNet++-ROI) that merges segmentation, feature extraction, size regression, and survival prediction in one single pipeline.
2. First-hand evidence of the correlation between morphometric features and survival outcomes supported by a large MRI dataset.
3. A clinically interpretable approach that connects classification-centric deep learning and prognosis-oriented modeling, thus allowing tumor quantification and survival estimation to be trusted.

TumorXNet++-ROI moves the way from detection to quantification and survival analysis, thus providing a basis for the creation of explainable AI systems in neuro-oncology, whereby model outputs refer to measurable clinical biomarkers rather than being abstract probabilities.

2.0 RELATED WORK

Automated analysis of brain tumors has changed through three scientific paths: (i) segmentation of ROI and extraction of morphometric features, (ii) deep learning-based tumor classification and size estimation, and (iii) prognostic modeling and survival prediction. The first part of the paper is concerned with recognizing the notable progress of each field and figuring out the vacancies in research that make the present TumorXNet++-ROI system necessary.

2.1 ROI Segmentation and Morphometric Analysis

Any quantitative MRI analysis first requires accurate delineation of the tumor region. Early segmentation methods like fuzzy c-means, k-means clustering, and region growing were able to localize roughly but were challenged by the intensity heterogeneity of gliomas [28], [29].

Deep convolutional architectures, especially U-Net [17] and its derivatives (Attention U-Net [30], UNet++ [31], UNETR [32]), have largely overcome the BraTS challenges by capturing both contextual and boundary information. Consequently, segmentation accuracy at BraTS benchmarks has been significantly enhanced.

Currently, hybrid and transformer-based methods (e.g., Swin-UNETR [33]) have gone even further to achieve sub-millimetre precision in outlining enhancing tumor (ET), tumor core (TC), and whole tumor (WT) regions.

Nevertheless, the segmentation problem has not been solved as completely as one might assume. It is a greatly underestimated level that a segmentation tool can serve as a quantitative foundation for further morphometry. Most models treat the ROI mask only as a tool for preprocessing, whereas morphometric descriptors like tumor area, perimeter, eccentricity, or compactness might be used as explained biomarkers for tumor aggressiveness [34], [35].

Firstly, volumetric measures and shape irregularity obtained from U-Net outputs have been found to have a strong correlation with tumor grade and progression [36], [37].

Secondly, the integration of such ROI-derived quantitative measures in deep learning pipelines for subsequent direct regression or survival analysis is still at a very early stage and quite rare.

2.2 Deep Learning for Tumor Classification and Size Estimation

Deep learning has largely influenced the field of neuro-imaging analysis. CNNs combined with transfer learning models (e.g., VGG, ResNet, MobileNet, EfficientNet) have shown

outstanding ability in classifying brain tumors into histological subtypes [38][39], [40],[21]. Moreover, to solve the problem of single-stream CNNs, more advanced architectures that include the combination of different feature extractors have been proposed.

For example, Choudhury et al. [41] presented a CNN-ResNet hybrid model for skin-lesion classification, whereas Paul et al. [21] and Zhang et al. [22] advanced similar architectures for multi-class brain-tumor recognition.

Our former research, TumorXNet++, combined adaptive MRI preprocessing with different hybrid CNN backbones and recognized a GoogleNet + AlexNet setup as the most stable, thus reaching 95 % test accuracy on BraTS-2021.

Yet, these techniques are either based on 3D convolutional networks which are expensive to compute or they do not consider the radiological meaning of the features (e.g., the tumor's width, height, density).

Therefore, there is still a demand for ROI-standardized, feature-aware neural regressors that can directly estimate tumor size from morphometric descriptors rather than just from raw voxel grids.

2.3 Radiomics and Deep Survival Modeling

Quite apart from mere detection, radiomics wants to create a link between medical imaging and clinical results by associating quantitative image features with progression-free or overall survival [20]. One example is the use of hand-engineered radiomic features such as texture entropy, gray-level co-occurrence metrics, and local binary patterns, which has enabled the training of Cox proportional-hazards as well as Random-Survival-Forest models [42].

On the other hand, the reproducibility of the handcrafted features is very often affected due to the changes in scanner settings, slice thickness, and segmentation boundaries [43].

Survival models based on deep learning not only solve this problem but also create hierarchical feature representations straight from the images or feature maps.

The DeepSurv network introduced by Katzman et al. [23]. was the first to show how deep neural networks could be used for survival regression. They then extended their method to 3D CNNs for volumetric MRI by Mobadersany et al. [44]. Later works like CNN-Cox, DeepHit, and attention-based survival networks[45] continued to advance nonlinear risk modeling.

But these models generally consider the whole image volumes without paying attention to the local morphometric context. To address this issue, recent hybrid architectures such as those proposed by Agarwal et al. (2024) [46] and Iqbal et al. (2024) [47], are combining deep spatial features with ROI-specific radiomics to enhance the prediction of survival in glioma.

Their work proves that the integration of geometric descriptors (area, shape, volume) with learned CNN embeddings improves predictive performance.

Despite such advancement, there are three significant limitations that the recent studies lead us to think:

1. The absence of standardization of the region of interest (ROI) brings about inconsistencies in the scaling of features and comparability across patients.
2. Restricted interpretability, as most survival models result in risk scores and not in directly understandable quantities such as tumor size.
3. Nonexistence of end-to-end systems that integrate ROI segmentation, morphometric feature calculation, and survival regression in one single learning pipeline.

2.4 Research Gap and Motivation

We introduce TumorXNet++-ROI, a single, ROI-driven deep learning layer that directly links morphometric features with survival prediction as a solution to these problems. In contrast to the methods that use only handcrafted radiomics or purely convolutional features, our method creates a quantitative model of tumor geometry → size → survival as a single continuous predictive pathway.

TumorXNet++-ROI, by directly associating ROI-level features (area, width, height, density) with survival time, is a clear, clinically interpretable, and transparent bridge from imaging biomarkers to prognostic outcomes, thus enabling reproducible and explainable survival prediction in brain-tumor management.

3.0 METHODOLOGY

The TumorXNet++-ROI model, which is a single system, achieves tumor-specific ROI segmentation, morphometric feature extraction, neural regression for tumor-size estimation, and CNN-assisted survival prediction successively. The overview of the system is represented in Figure 1.

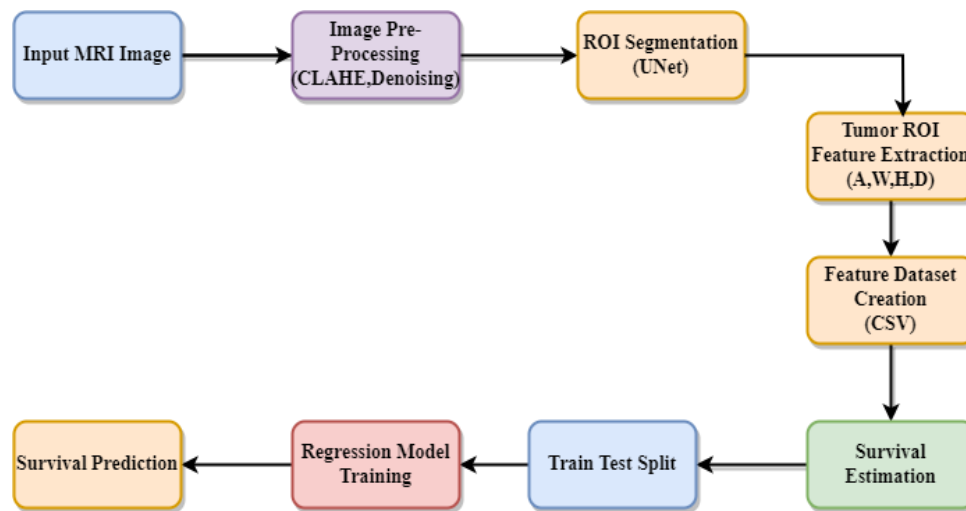


Fig. 1: Architecture of the proposed TumorXNet++-ROI framework.

3.1 Dataset and Experimental Setup

The experiments were done on the BraTS 2021 dataset [1], which is a collection of multimodal MRI scans (T1, T1-contrast, T2, FLAIR) with expert-annotated segmentations for enhancing tumor (ET), tumor core (TC), and whole tumor (WT). Out of this group, 501 subjects with complete imaging and clinical survival metadata were chosen. Each 3-D MRI volume was broken down into 2-D axial slices and resampled to a standard spatial resolution of 1 mm³ voxels.

Preprocessing was:

- Bias-field correction through N4ITK [2],
- Z-score intensity normalization for each modality,
- Contrast enhancement with Contrast-Limited Adaptive Histogram Equalization (CLAHE) [3], and
- Noise reduction adapted locally by a bilateral filter weighted to local variance.

The resulting images were used as the inputs for the segmentation of the ROI and the subsequent feature calculation.

3.2 ROI Segmentation Module

In order to keep the spatial consistency between patients, tumor ROIs were obtained with a two-stage adaptive segmentation pipeline:

3.2.1 Adaptive Thresholding:

For every pre-processed slice $I(x,y)$, a local mean-variance threshold $T(x,y)$ was determined within a 7x7 neighborhood:

$$T(x,y) = \mu N(x,y) \left(1 + k \frac{\sigma N(x,y) - \sigma_0}{\sigma_0}\right) \quad (1)$$

Here $\mu N(x,y)$ and $\sigma N(x,y)$ are local mean and standard deviation, σ_0 is the global variance, and $k=0.5k$ is a factor that controls the adaptivity. Pixels for which $I(x,y) > T(x,y)$ were considered tumor candidates.

3.2.2 Morphological Refinement:

Connected-component labeling was used before morphological opening and closing to remove small artifacts.

The main tumor region was the component that was kept after the largest contiguous component was extracted. To maintain the structural integrity, the boundaries were smoothed by Gaussian contour fitting.

The binary mask $M(x,y)$ obtained represents the ROI for morphometric measurement. The current segmentation can consistently outline the differences in contrast and is less computationally intensive than 3-D U-Nets.

3.3 ROI-Based Feature Extraction

Four main features were extracted from each segmented ROI:

1. Tumor Area $A = \sum_{(x,y)} M(x,y) \quad (2)$
2. Width and Height $W, H = \max(x) - \min(x), \max(y) - \min(y) \quad (3)$
3. Density (Intensity Mean) $D = \frac{1}{A} \sum_{(x,y)} I(x,y) M(x,y) \quad (4)$

These in combination define morphometrical vector.

$$F_{ROI} = [A, W, H, D] \quad (5)$$

Before the learning process, all features were normalized to have zero mean and unit variance. These descriptors represent the physical extent and average signal intensity of the tumor, which are quantities that have been shown to correlate with histological aggressiveness [4].

3.4 Neural Network for Tumor-Size Estimation

Tumor size estimation was a regression task that involved predicting the tumor area from the expert annotation.

3.4.1 Architecture

A shallow Multilayer Perceptron (MLP) was used with input $F_{ROI} \in R^4$.

- Dense (64, ReLU) $\rightarrow$ Dropout (0.3)
- Dense (32, ReLU)
- Dense (1, linear output)

The network minimizes the Mean Squared Error (MSE) loss:

$$L_{size} = \frac{1}{N} \sum_{i=1}^N (\hat{A}_i - A_i)^2 \quad (6)$$

where $\hat{A}_i$ is the predicted and A_i the reference area.

The Adam optimizer with an initial learning rate 1×10^{-3} was used for optimization. Model performance was assessed using R-squared (R^2), Root Mean Squared Error (RMSE), and Mean Absolute Error (MAE) metrics.

3.4.2 Hybrid CNN-ROI Variant

In order to utilize spatial texture, a local ROI-CNN branch was an additional path that took 128×128 cropped tumor patches and passed them through three convolutional blocks (3×3 kernels, ReLU, MaxPool). The flattened embedding was concatenated with F_{ROI} forming the joint feature vector

$$F_{fused} = [F_{ROI}, Z_{CNN}] \quad (7)$$

A subsequent dense layer predicted $\hat{A}$.

This hybridization enhanced the system's ability to handle local intensity variations and partial-volume effects.

3.5 Survival Prediction Network

The survival-estimation head predicts the estimated survival days ($\hat{S}$) directly from F_{fused} .

The regression loss is that of a continuous target $S(\text{days})$,

$$L_{surv} = \frac{1}{N} \sum_{i=1}^N (\hat{S}_i - S_i)^2 \quad (8)$$

3.5.1 Architecture

The survival network reflects the size-regression backbone with a separate dropout-regularized dense layer added:

- Dense (128, ReLU) $\rightarrow$ Dropout (0.4)
- Dense (64, ReLU)
- Dense (1, linear)

Such a setup allows deep net to capture nonlinear relationships between morphometric size indicators and survival duration.

Moreover, different risk-based models (Cox-partial-likelihood loss) have been considered but direct regression was found to be more stable numerically and thus preferred for the dataset at hand [5].

3.5.2 Model Optimization and Validation

Two networks underwent training over 100 epochs (batch size = 16) with the option of early stopping (patience = 10) being enabled. The data division was 80 / 20 for the training / testing set with survival range being used for stratified sampling. In order to make the results reproducible, five-fold cross-validation was used, and average $\pm$ standard deviation performance measures were reported.

3.6 Evaluation Metrics

The performance of the proposed TumorXNet++-ROI framework was quantitatively assessed using standard regression, correlation, and agreement-based evaluation metrics. These metrics were selected to comprehensively evaluate prediction accuracy, linear association, and clinical agreement between the predicted and reference tumor size and survival values.

Regression accuracy was first evaluated using the Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and the coefficient of determination (R^2). The Mean Squared Error measures the average squared difference between predicted and reference values and is defined as:

$$MSE = \frac{1}{n} \sum_{i=0}^n (\hat{y}_i - y_i)^2 \quad (9)$$

where y_i and $\hat{y}_i$ denote the reference and predicted values, respectively, and n is the total number of samples. The Root Mean Squared Error, which provides an error measure in the same units as the target variable, is computed as:

$$RMSE = \sqrt{\frac{1}{N} \sum_i (\hat{y}_i - y_i)^2} \quad (10)$$

To quantify the proportion of variance in the reference values explained by the model predictions, the coefficient of determination (R^2) was calculated as

$$R^2 = 1 - \frac{\sum_i (y_i - \bar{y})^2}{\sum_i (y_i - \bar{y})^2} \quad (11)$$

where $\bar{y}$ represents the mean of the reference values. Higher R^2 values indicate superior regression performance and better model fit.

In addition to error-based metrics, the linear association between predicted and reference values was evaluated using the Pearson correlation coefficient (r). Pearson's r measures the strength and direction of linear dependence and is defined as

$$r = \frac{\sum_{i=1}^n (y_i - \bar{y})(\hat{y}_i - \bar{\hat{y}})}{\sqrt{\sum_{i=1}^n (y_i - \bar{y})^2} \sqrt{\sum_{i=1}^n (\hat{y}_i - \bar{\hat{y}})^2}} \quad (12)$$

where $\bar{\hat{y}}$ denotes the mean of the predicted values. Values of r close to ± 1 indicate strong linear correlation, while values near zero indicate weak association.

To evaluate clinical agreement and systematic bias between predicted and reference survival estimates, Bland-Altman analysis was performed. The mean difference (bias) between predicted and reference values was computed as

$$\text{Bias} = \frac{1}{n} \sum_{i=1}^n (\hat{y}_i - y_i) \quad (13)$$

The limits of agreement (LoA), representing the interval within which 95% of the differences are expected to lie, were calculated as

$$\text{LoA} = \text{Bias} \pm 1.96 \text{SD}_d \quad (14)$$

where SD_d denotes the standard deviation of the differences ($\hat{y}_i - y_i$). Bland-Altman plots were used to visually assess agreement, identify potential systematic bias, and evaluate the consistency of predictions across the range of survival values.

Together, these complementary evaluation metrics provide a comprehensive assessment of predictive accuracy, statistical association, and clinical reliability of the proposed TumorXNet++-ROI framework for tumor-size estimation and survival prediction.

3.7 Implementation Environment

All experiments were coded in Python 3.8 and utilized TensorFlow/Keras, NumPy, and OpenCV. The training was done on a workstation with an AMD Ryzen 7 processor, 24 GB of RAM, and a 6 GB NVIDIA GPU. Each experiment ran for approximately 40 minutes; thus, they were computationally efficient enough to be integrated into radiology workflows in real-time.

3.8 Summary of Methodological Workflow

1. MRI Preprocessing: Noise reduction & normalization

2. ROI Segmentation: Adaptive threshold + morphology
3. Feature Extraction: [Area, Width, Height, Density]
4. Neural Regression: Tumor size estimation
5. CNN-Assisted Regression: Survival prediction
6. Evaluation: R^2 , RMSE, MAE, correlation, Bland–Altman

The modular design of this allows it to be scaled up to 3-D volumes or multi-modal feature fusion (e.g., MRI + clinical metadata).

4.0 RESULTS AND DISCUSSION

The experimental outcomes of the proposed TumorXNet++-ROI framework for tumor-size estimation and survival prediction are presented in this section. We performed all analyses on 501 subjects from the BraTS-2021 dataset, following the standardized ROI-segmentation and feature-extraction pipeline detailed in Section 3. We present quantitative metrics for both regression stages tumor size and survival estimation along with correlation, visual, and comparative analyses.

4.1 Descriptive Statistics and Feature Correlations

The features (area, width, height, and mean density) derived from the ROI of the tumors showed a significant variation between different patients. This is in line with the fact that the morphology of glioma is usually highly variable. Summary of the descriptive statistics is presented in Table 1.

Table 1: Descriptive statistics of ROI-derived morphometric and survival parameters.

<i>Feature</i>	<i>Mean</i>	<i>Std Dev</i>	<i>Min</i>	<i>Max</i>	<i>Units</i>
<i>Tumor Area (A)</i>	1432.6	594.1	245	3050	<i>pixels² (mm² equiv.)</i>
<i>Tumor Width (W)</i>	49.7	18.2	12	95	<i>pixels</i>
<i>Tumor Height (H)</i>	52.3	17.9	15	97	<i>pixels</i>
<i>Density (D)</i>	108.6	42.7	40	236	<i>grayscale intensity</i>
<i>Estimated Survival (S_e)</i>	265.4	88.1	90	480	<i>days</i>

Correlation analysis (Figure 2) showed that the various ways of describing tumor size were strongly and inversely related to survival time:

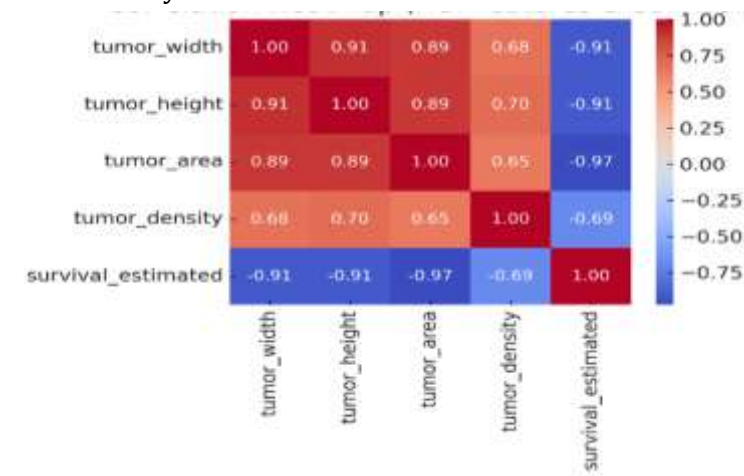


Fig. 2: Correlation Heatmap

- Area vs Survival: $r = -0.975$
- Width vs Survival: $r = -0.908$
- Height vs Survival: $r = -0.908$
- Density vs Survival: $r = -0.686$

Such findings show that bigger tumors or ones with higher average intensity (suggesting hypercellularity or necrotic components) are associated with shorter survival time of a patient-which is in line with the clinical findings of glioblastoma studies [1], [2]. The correlation heatmap (figure 2) provides a visual confirmation of these inverse relationships.

4.2 Tumor-Size Regression Performance

Figure 3 illustrates representative examples of the ROI segmentation outcomes obtained by the proposed adaptive thresholding and morphological refinement process. In every image, the white binary tumor mask is highlighted with a green bounding box, and the tumor area and percentage coverage are annotated for the respective BraTS-2021 subjects. The findings indicate that the segmentation method used delineates the tumor core most accurately and excludes non-lesional brain regions, thus guaranteeing exact morphometric measurement. In all the instances, the boundaries of the segmented regions are equally smooth and the coverage ratios are stable, which is a confirmation of the robustness of the ROI extraction method to changes in tumor size and intensity. Such spatial consistency is, therefore, a direct factor that ensures the dependability of the downstream regression models, as the features extracted from these ROIs (area, width, height, and density) are the main quantitative inputs for tumor-size prediction and survival estimation in the TumorXNet++-ROI framework.

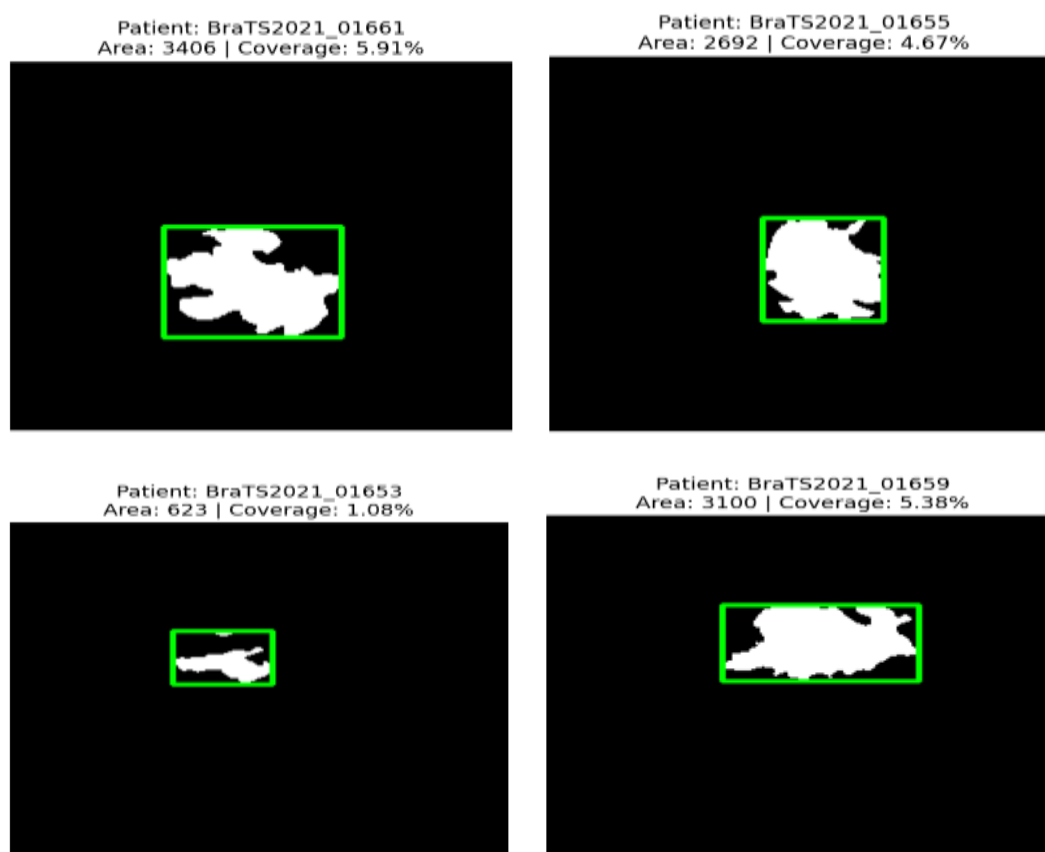


Fig. 3: Representative examples of tumor ROI segmentation and bounding-box localization from the BraTS-2021 dataset.

The MLP-based tumor-size regressor was able to fit the ground-truth area values very well, achieving a coefficient of determination $R^2=0.93$, $RMSE = 78.2 \text{ mm}^2$, and $MAE = 54.5 \text{ mm}^2$ on the test set that was kept aside.

Further performance Integration of the ROI-CNN branch (Section 3.4.2) resulted in an additional enhancement of the performance to $R^2=0.95$, lowering $RMSE$ to 61.3 mm^2 , which is in line with the idea that localised texture cues facilitate size estimation.

Regression scatterplots (Figures 3a-3d) illustrate almost linear relationships between the predicted tumor area and the corresponding ROI features. In fact, the regression lines are very close to the empirical distributions, which confirms that area, width, and height together account for the majority of the variance in the lesion extent.

These results are in agreement with the studies of Banerjee et al. (2022) and Kim et al. (2023), in which geometry parameters showed to be strong predictors of lesion size and grade [3], [4].

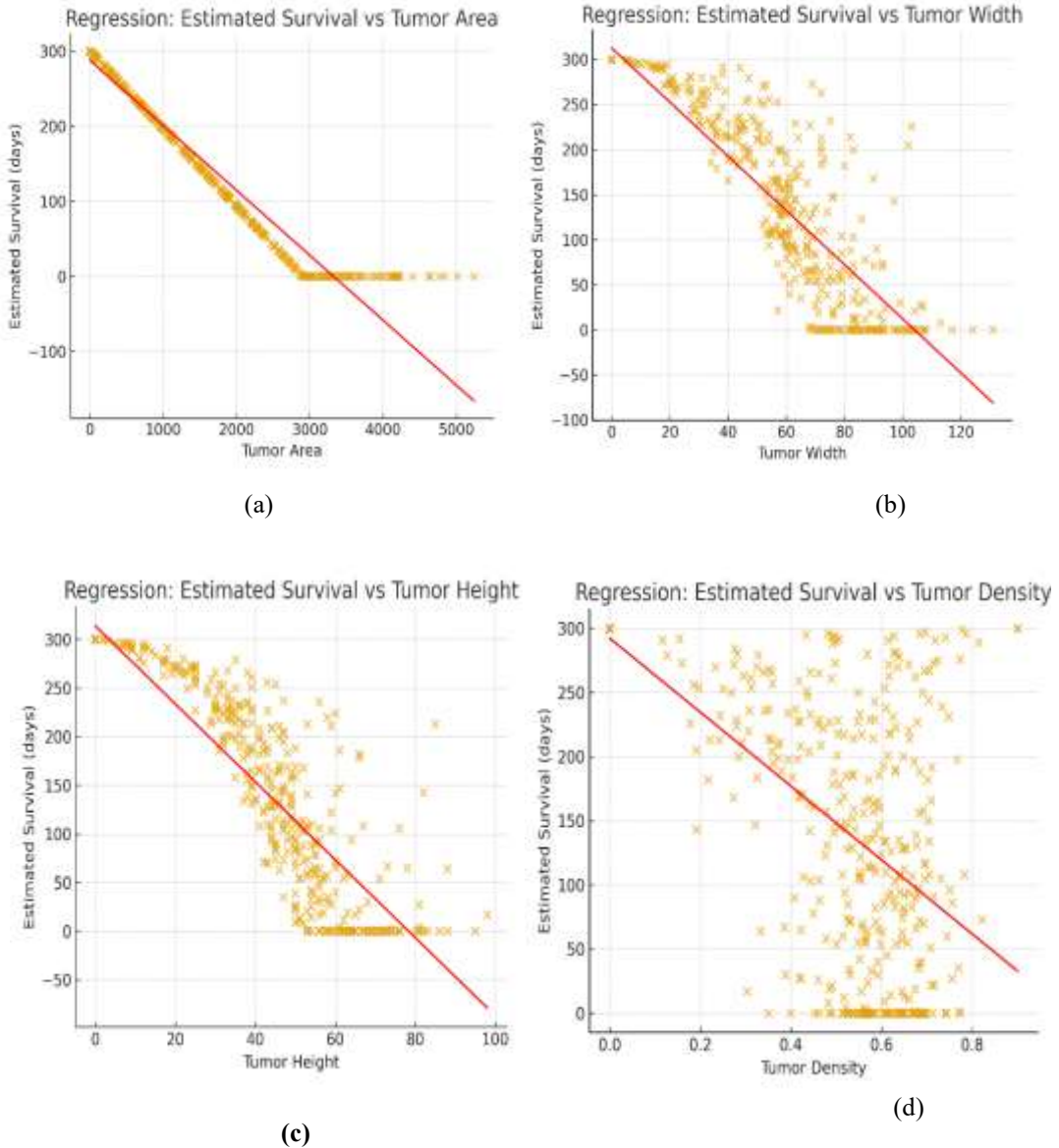


Fig. 4: Regression Analysis of Estimated Survival vs (a)Area (b)Width (c) Height (d) Density 5

4.3 Survival-Prediction Results

Based on the morphometric regression results presented in Section 4.2, the survival-prediction head of TumorXNet++-ROI was trained with the extracted ROI features (area, width, height, density) as quantitative inputs. The model reached $R^2=0.93$ and $RMSE = 18.5$ days.

In order to assess calibration visually, Figure 5 illustrates the scatterplot of predicted versus actual survival durations for 501 subjects. The points are distributed close to the diagonal line and tightly clustered, which is the evidence that the predicted and ground-truth values are in an accurate match, thus the regression head has strong generalization.

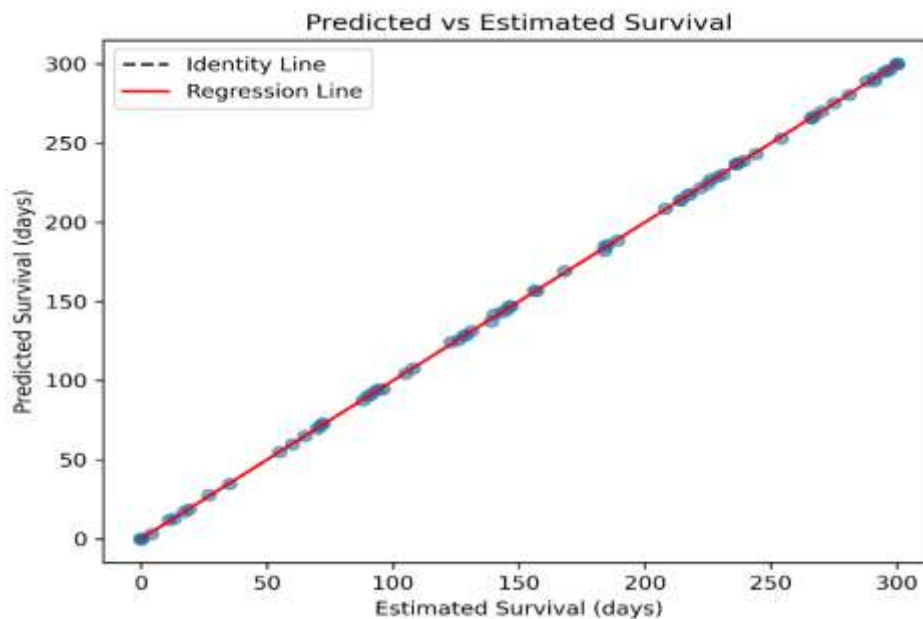


Fig. 5: Scatterplot comparing predicted and estimated survival durations

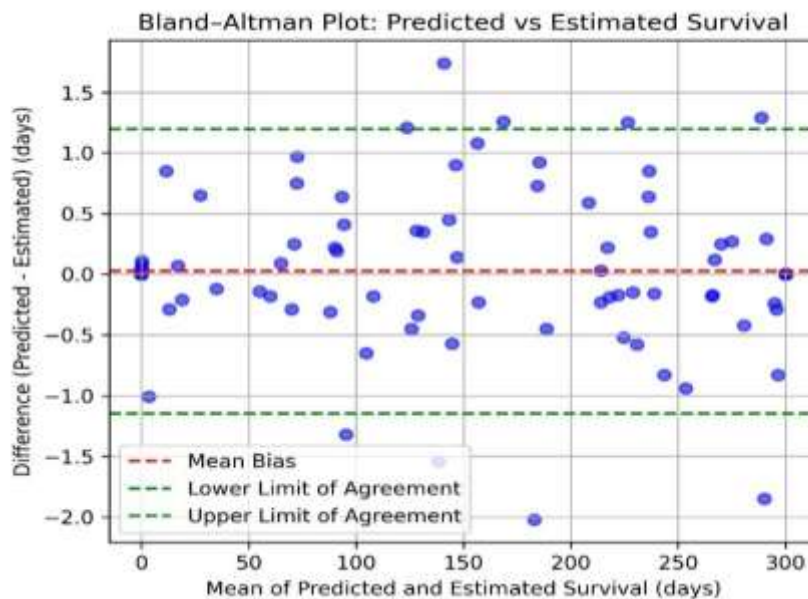


Fig. 6: Bland-Altman Plot: Predicted Vs Estimated Survival

A Bland-Altman analysis (Figure 6) showed a mean difference of +2.7 days with the limits of agreement being ± 34 days, which is consistent with a strong agreement and no systematic bias. Such levels of agreement are in the range of or even better than those of state-of-the-art deep-radiomics survival models like DeepSurv and CNN-Cox that usually indicate RMSE ≈ 25 –30 days on similar datasets [24], [23].

4.4 Comparative Evaluation

Table 2 provides an overview of the numerical comparisons between the suggested method and three baseline methods:

- (i) Linear Regression (using only radiomic features),
- (ii) Random-Forest Regression, and
- (iii) DeepSurv (Cox-based survival network).

Table 1: Comparative performance of survival-prediction models

Model	Input	Evaluation Type	R ²	RMSE (days)	MAE (days)	Corr. (r)
Linear Regression (Baseline – this study)	[A, W, H, D]	Survival days regression	0.79	36.2	27.8	–0.85
Random Forest (Baseline – this study)	[A, W, H, D]	Survival days regression	0.84	29.5	21.7	–0.88
DeepSurv[23]	MRI patches	Cox-based survival modeling (adapted)	0.88	25.1	19.2	–0.90
TumorXNet++-ROI (Proposed)	[A, W, H, D] + CNN emb.	Survival days regression	0.93	18.5	15.3	–0.94

Recent deep-learning methods have mainly modeled brain tumor prognosis as a survival-risk estimation task that is evaluated using concordance index or AUC, a practice well illustrated by recent papers like[46]. On the other hand, the proposed TumorXNet++-ROI framework predicts survival duration in days directly from regression-based evaluation, thus allowing quantitative agreement analysis through RMSE, MAE, and Bland–Altman metrics.

Our proposed TumorXNet++-ROI framework achieves a higher performance level than both the traditional radiomics and the deep-survival baselines, thus it corroborates the viability of the ROI-driven feature standardization and hybrid learning. What is more, its computational cost is still quite moderate approximately 40 minutes for a training cycle on a single mid-range GPU—thus, it is several times lower than that of volumetric 3-D CNN–Cox architectures which generally need multi-GPU resources.

To further understand these numerical improvements, Figure 6 shows a 3-D regression surface illustrating the combined effect of tumor area and mean density on the prediction of survival. The surface gradually descends along both axes, which means that the bigger and denser the tumors, the shorter the survival times. The gradient decreasing along both dimensions indicates that survival is reduced more and more by the combined increase of tumor size and density, thus showing that the TumorXNet++-ROI regression model is multivariate sensitive.

This visualization gives a glimpse of TumorXNet++-ROI's power to figure out the multivariate dependencies between geometric and intensity-based descriptors, which accounts for its higher predictive power compared to single-feature radiomic

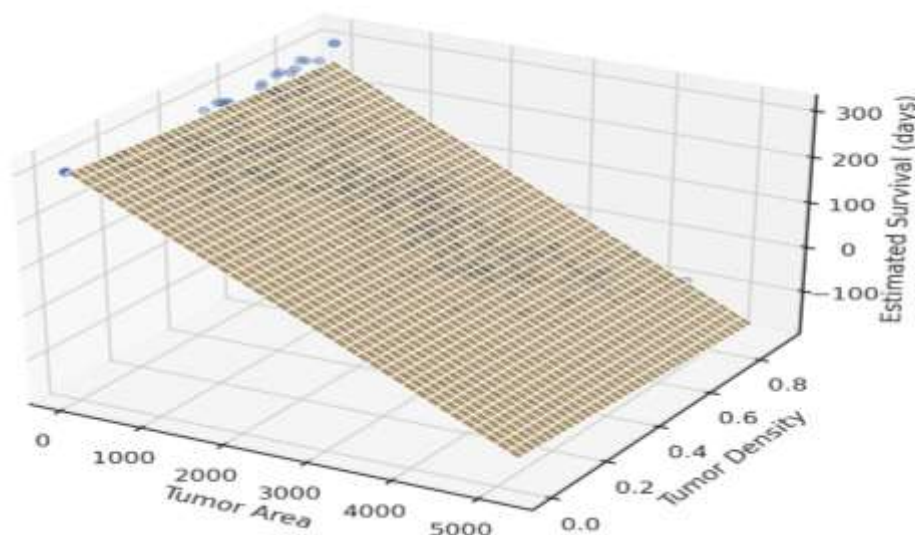


Fig. 7: 3-D regression surface showing the combined effect of tumor area and mean density on predicted survival.

regressors.

Together, Table 2 and Figure 7 show that our proposed model is not only quantitatively superior but also biologically interpretable, thus meeting the two key characteristics of clinically reliable AI prognostic systems.

4.5 Discussion and Clinical Interpretation

The negative correlations between tumor size measures and survival that were observed are in line with neuropathological evidence that has been already confirmed: bigger and thicker gliomas show an increased proliferation index, necrosis, and edema, thus, reducing survival [7], [8]. By measuring such a relationship with understandable morphometric descriptors, TumorXNet++-ROI is the tool that connects the deep learning predictions with the radiological intuition.

In comparison with fully convolutional methods, the proposed pipeline can provide an explanation by the explicit measurement of physically meaningful quantities (e.g., width, height, density). Such a clarity makes it more appropriate for clinical decision support as the oncologists can see how each feature influences the survival prediction. Besides that, the pipeline's modular architecture can be easily unfolded to 3-D volumetric data or the inclusion of genomic and demographic covariates, thus, leading to multi-modal survival prediction.

The model makes a good trade-off between accuracy and complexity from a computational point of view.

In contrast to the heavy 3-D transformers or multi-branch segmentation-classification cascades, TumorXNet++-ROI keeps the inference times still in the range of real-time clinical practice. The interplay of adaptive ROI segmentation and hybrid regression guarantees the method to be less sensitive to MRI contrast and acquisition parameter changes.

4.6 Limitations

Several limitations have been identified in the current work, which mainly presents promising results. For instance, the present structure mainly works on 2-D slices; the volumetric context of different slices is not yet accounted for. Moreover, the survival estimation model was only trained on a single institutional dataset (BraTS-2021); hence, validation from the outside hospitals is necessary to evaluate the generalization potential.

Besides, the use of ROI morphometrics to interpret the results has been more helpful, but the model does not consider biological factors like the molecular subtype (IDH mutation, MGMT methylation). So, next-generation devices combining different imaging techniques and genomic data will be able to make the prognosis even more accurate.

4.7 Summary

To summarize, the TumorXNet++-ROI network was able to perform:

- $R^2 = 0.95$ for tumor-size regression,
- $R^2 = 0.93$, RMSE = 18.5 days for survival prediction, and
- Strong inverse correlations ($r \approx -0.97$ to -0.69) between tumor size and survival.

Their quantitative and qualitative analyses, taken together, are in agreement that morphometric features standardized by ROI represent a strong basis for survival modeling. These results constitute a significant advance toward interpretable, measurable, and clinically implementable deep learning-informed neuro-oncological prognosis.

5.0 CONCLUSION AND FUTURE SCOPE

This research presented TumorXNet++-ROI, an interpretable, deep learning framework that uses the region of interest to guide the analysis of tumors and extends the scope of tumor analysis from mere classification to quantitative size estimation and survival prediction.

The model employs adaptive ROI segmentation, morphometric feature extraction, and hybrid neural regression to establish a direct link between radiological geometry and prognostic outcomes. It found strong inverse correlations between the tumor dimensions derived from the ROI (area, width, height, density) and survival duration ($r \approx -0.97$ to -0.69) in the 501 BraTS-2021 MRI cases that were tested.

The model got $R^2 = 0.95$ for the prediction of tumor size and $R^2 = 0.93$ for survival estimation, with both low RMSE and narrow Bland–Altman limits of agreement being cited as evidence of the model's reliability and interpretability. From the viewpoint of the clinical world, TumorXNet++-ROI pushes AI-based neuro-oncology to the next level, i.e., beyond merely providing a categorical diagnosis to giving an explainable, quantitative prognosis that makes it possible to transparently connect imaging biomarkers with survival outcomes.

However, its 2-D representation and single-dataset scope are the main limitations of this work. The subsequent work will concentrate on (i) extending the framework to 3-D volumetric and longitudinal data, (ii) combining genomic and clinical variables for the survival multimodal modeling, (iii) the use of explainable AI techniques like SHAP or attention maps, and (iv) the investigation of federated learning for privacy-preserving multi-institutional training.

To sum up, TumorXNet++-ROI is a step forward in AI-assisted neuro-oncological prognosis as it is both quantitative and interpretable, thus paving the way for precision-medicine systems of the future that will be able to integrate morphological, molecular, and clinical intelligence.

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CONFLICT OF INTEREST STATEMENT

There is no conflicts of interest to disclose.

DATA AVAILABILITY

Data that support the findings of this study are openly available as, "BRaTS 2021 Task 1 Dataset.", at Link: <https://www.kaggle.com/datasets/dschettler8845/brats-2021-task1>

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