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Research Article

Cat swarm optimized tumor segmentation and an ensemble model for glioblastoma patient survival prediction

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ABSTRACT

Glioblastoma is characterized as the most common and lethal primary brain tumor among adults, glioblastoma is associated with enormous clinical management challenges due to its high rate of recurrence, poor prognosis and underlying complexity. Here we propose a study to improve the prediction of overall survival in GBM patients treated with stereotactic radiosurgery using advanced image segmentation and machine learning techniques. In this paper, we propose a novel fusion of Cat Swarm Optimization based hybrid ResNet and U-Net models to achieve an accurate segmentation of the tumor as well as an ensemble of machine learning algorithms for survival prediction enabling us to overcome limitations of conventional techniques. We demonstrate that on the BraTS2020 related regions we are able to produce almost perfect segmentations with metrics, like 99.2% segmentation accuracy,loss of 0.023, recall of0.986, a mean intersection over union (IOU) of 0.991, a dice coefficient of 0.96, a precision of 0.991, a sensitivity of 0.991, and a specificity of 0.997. For in the field of survival prediction we looked at many machine learning models which we found out that the Random Forest did an outstanding job at handling the complex issues presented by the segmented images. Also we saw that the Ensemble method did very well in this area which we report to have achieved 60.01% accuracy. We present that which is the use of in depth image segmentation in combination with machine learning greatly improves results in Glioblastoma survival prediction. Also this approach does not only improve the prognostic accuracy but also brings to the table what may be game changing elements in clinical management and personalized treatment.

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INTRODUCTION

The High degree of recurrence, poor prognosis, tumor heterogeneity, and limited treatment options are the main issues in Glioblastoma. Glioblastomas' complex and heterogeneous nature contribute to poor overall survival and also to treatment issues. While we see an increase in the use of Stereotactic Radiosurgery (SRS) which is very precise in

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its delivery of radiation therapy to the tumor thus sparing the surrounding healthy tissue we are still have issues in accurate patient outcome prediction. In the area of artificial intelligence (AI) which includes deep learning (DL) we are seeing very promising results in the identification and management of glioblastomas' but still accurate prognosis is impaired by tumor complexity.

Our research has put forth a new approach which is a combination of Cat Swarm Optimization-assisted hybrid ResNet and U-Net architectures for accurate tumor segmentation with machine learning algorithms for very robust survival prediction. This we have done to out perform traditional models which we do so by improving segmentation accuracy and at the same time we are able to present more reliable survival predictions. We are into this with the aim to improve individualized treatment plans for GBM patients that are undergoing stereotactic radiosurgery. What we have done not only improves the care we give to glioblastoma patients but also we put forth the wide scale promise of AI driven methods in oncology and personal medicine. Our work gives out that which may be applied across many cancer types which in turn bridges the gap between very advanced AI techniques and clinical practice.

Related Work

The inroads that machine learning (ML) has made in brain tumor image analysis which includes the use of MPMRI scans [1] is a result of initiatives like the International Brain Tumor Segmentation (BraTS) challenge. In this field Semantic segmentation is a key element which which it enables the tell between target objects and adjacent tissues. As for the methods used, Fully Convolutional Networks (FCN) which use up sampling methods to do accurate pixel level labeling have proven to be very effective.

To better predict overall survival (OS) we have seen the introduction of more complex approaches. For example a hybrid model which puts together a DenseNet based 3D neural network with a position encoding convolutional layer (PECL) [2] has been put forth. The model described above applies semi-supervised learning to minimize overfitting while extracting essential features from T1 contrast MRIs, T2 MRIs, and pre-segmented sub-regions. Furthermore, as previously mentioned, texture features retrieved from the MRI are useful for biologically characterizing subtypes in a noninvasive manner. Numerous researchers have been active in the area and have created various models and approaches. Thuong-Cang Phan [3] used MobileNet-V2,

Table 1. Summary of literature review

Author Name and Reference No	Segmentation methods	Prediction methods	Dataset	Results
Raza et al., [10]	3D deep residual U-Net	hybrid of the deep residual network and U-Net model	BraTS	dice score for the tumor core (TC), whole tumor (WT), and enhancing tumor (ET) on the BraTS 2020 dataset of 0.8357, 0.8660, and 0.8004, respectively.
Vijay, et al.,[11]	3D U-Net	residual Spatial Pyramid Pooling-powered	BraTS	average dice score of 0.883 and a Hausdorff distance of 7.84 on Brats 2021 cross validation.
Yang D et al.,[12]	tumor segmented Manually	Ensemble classifier - Random Forest	Cancer Genome Atlas (TCGA)	Area Under Curve: 0.62: features with aerial scan 0.61 features with coronal scan 0.62: features with sagittal scan
Montaha et al., [13]	2D U-net architecture	CNN	BraTS	acc of 99.41% and dice similarity coeff (DSC) of 93%
Sangui, S et al., [14]	modified U-Net architecture	U-Net	BraTS	Test acc of 99.4%
Mohammadreza et al.,[15]	Res-Net Segmentation method	Random Forest	BraTS	Segmentation acc:0.80 Survival validation accuracy:0.45 Testing acc: 0.52
Fabian, et al.,[16]	U-Net Segmentation Method	NA	BraTS	Segmentation Acc Core: 98% Whole:96%
Muhammad Junaid Ali, et al.,.[17]	2D and 3D U-Net Segmentation method	Random Forest Repressors	BraTS	Segmentation Acc Dice Score: 78% Prediction Acc:48%

ResNet-101, and DenseNet-121 for tumor segmentation in detail and used 3D slicer tools for MRI imaging. Eyad Gad [4] explored an attention-based 3D UNet model for segmentation and claimed to have improved the segmentation by concentrating on useful portions of the image. IKE Purnama [5] used a modified U-Net and claimed to have improved detail and accuracy in the segmented images. Zhao J [6] proposed Uncertainty-aware Multi-dimensional Mutual Learning.

Gayathri Ramasamy [7] constructed a multi-modal modified Link-Net model utilizing Squeeze and Excitation ResNet152 as a segmentation backbone for improved segmentation performance. Cihan M [8] applied convolutional neural networks for fusion of phase MRI images: pre-contrast, venous, arterial, and delayed phases. With all these advancements, there are still limitations on the applications of research results. Some studies, for instance, report an OS prediction accuracy of merely 44.8%, illustrating ongoing difficulties in achieving dependable clinical results. A. Durgut [9] studies image processing using parallel and serial programming methods and finds parallel programming reduces the time required for processing both whole and segmented images. Whole image processing outperformed segmented image processing. The research highlights the efficiency of parallel programming in improving image processing tasks. Table 1 provides further insights into related research contributions and their respective metrics.

Using nature-inspired optimization methods such as genetic algorithms as well as hybrid filters can provide solutions to the issues of brain tumor image analysis[18]. The improvement in the use of these approaches provide methods for optimizing hyperparameter parameters of a model, reduce the effects of over fitting and improve the original feature extraction to enhance model accuracy and generalizability. Through mimicking natural behavior and incorporating heterogeneous filtering methods, these approaches present a valuable strategy to enhance productivity and applicability of machine learning models for use in clinical settings.

MATERIALS AND METHODS

The issue we address in this work is that of accurate prediction of overall survival (OS) in glioblastoma multiform (GBM) patients that are undergoing stereotactic radio surgery (SRS). GBM is known for its aggressive nature and poor prognosis which in turn sees the rise of SRS as a key treatment modality for precise tumor cell targeting. That said accurately prognosticating OS in GBM patients post SRS is still a challenge which we put down to the heterogeneous nature of the disease and also to the variable patient responses to treatment. Also included are the goals of our work.

- Preprocessing the Dataset for feature extraction and classification by applying a Hybrid Bilateral_Gaussian Filter, and normalization to reduce noise, and improve performance.
- Segmentation for tumor by Cat Swarm Optimization for Medical Image Segmentation (CSO-MIS) assisted hybrid ResNet and U-Net deep learning model.
- Ensemble of popular machine learning algorithms—Random Forest, KNN models, and SVM—as well as the deep learning model ANN are employed to predict the OS.
- To evaluate the performance. Compare accuracy, sensitivity, specificity, and area under the ROC curve metrics

Implementation

Figure 1 showcases the remarkable process of Glioma sub region segmentation and predicting overall survival in glioblastoma patients using deep learning architecture. First out of the gate we do in depth pre processing of the BRATS 2020 dataset which we do to that very meticulous degree which we do for the sake of accuracy. Then we do segmenting which in turn does what it can to improve the accuracy of the results. Also we put the data into train, test, and validate sets which we do to make our analysis as through as possible. We see this approach to be very effective in that it puts out very high in terms of accuracy and reliability in what we predict for overall survival in patients with glioblastoma.

Dataset

As part of an annual challenge related to the segmentation of brain tumors using multimodal MRI scans, a set of datasets called brain tumor segmentation (BraTS) 2020 has been made available. The BraTS 2020 dataset contains glioma patient magnetic resonance imaging (MRI) scans from different medical facilities. The participating institutions are focused on glioma scans. To ensure accuracy and reproducibility of results, standardization of protocols has been done. The dataset also contains expert annotated delineations for various tumor subregions, which are essential for training supervised learning models. The delineations are demonstrated through:

- Label 1: Non-Enhancing Tumor Core (NCR/NET)
- Label 2: Peritumoral Edema (ED)
- Label 3: GD-enhancing Tumor (ET)

For each case, clinical information such as the age of the patient is provided. Survival data, i.e., the number of days the patient survived post-initial diagnosis, might also be available for a subset of patients.

Data Preprocessing

To preprocess BraTS2020 MRI dataset, performed a sequence of normalization followed by application of hybrid filter for noise reduction. This approach ensures that the data is scaled properly and noise is reduced, which are crucial steps for improving the performance of downstream tasks like segmentation and classification. A crucial first step in data analysis, particularly in the domains of machine learning and image processing, is normalization.

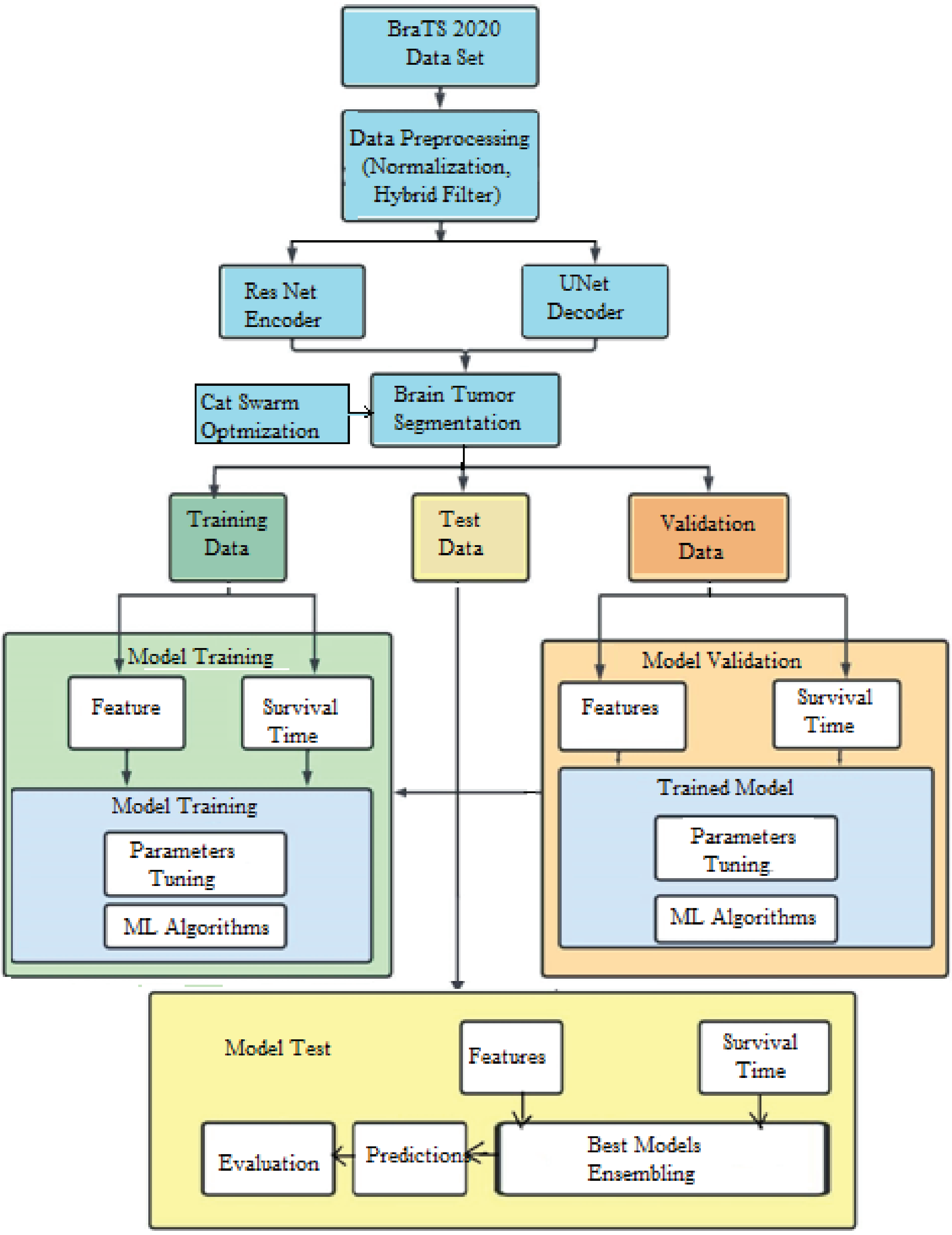

Figure 1. Architecture diagram.

This includes setting the data values onto a common scale so we can stabilize training processes and improve algorithm performance. Normalization can account for variability in intensity from medical images (e.g., MRI scans) that might occur due to the use of different scanning protocols, or machine calibration during scans from other institutions.

This process generally rescales image intensity values of MRI scans to a standard range of [0, 1] or [-1, 1], which enhances image comparison and analysis. Perform the normalization and then apply a Hybrid filter as given in Algorithm 1 to each slice to reduce noise. As given, the Hybrid filter reduces noise within the MRI images while improving the overall image quality with local analysis of pixel neighborhoods. This normalization and noise reduction with the Hybrid filter prepares the BraTS2020 MRI dataset for more effective analysis in segmentation models or other machine learning tasks by fostering higher quality images and greater consistency throughout the dataset.

HybridBilateral_Gaussian Filter

Algorithm1: Hybrid Filtering (Bilateral_Gaussian Filter)

```
Input:
    Original image org($i,j$)
    Gaussian sigma value $\sigma$ for Gaussian filtering

Bilateral Filtering
    Apply bilateral filtering to the org image to result a Denoised image
    Denoised img: org_denoised($i,j$)=denoise bilateral (org($i,j$))

Gaussian Smoothing
    Apply Gaussian smoothing to the org image with the specified sigma value to obtain a smoothed version.
    Smoothed image: org_smoothed($i,j$)=gaussian_filter(org($i,j$),$\sigma$)

Hybrid Filtering
    For each pixel ($i,j$)(i,j) in the image:
        Calculate the hybrid filtered pixel value as the sum of the Denoised pixel value
            and the difference between the org pixel value and the smoothed pixel value.

        Hybrid filtered pixel value:
            hybrid_filtered($i,j$)=org_denoised($i,j$)+(org($i,j$)−org_smoothed($i,j$))
Output:
Return Hybrid filtered image: hybrid_filtered($i,j$)
```

Model

The suggested work uses a ResNet encoder and a U-Net decoder which captures the advantages of both networks. This fused method uses the efficient feature extraction of ResNet and the segmentation characteristics of U-Net to achieve feature extraction and spatial information preservation concurrently. The deep layers of ResNet improve the fine details retrieval, and U-Net's encoder-decoder configuration accurately captures the details in precise segments. The residual connections of ResNet also address overfitting to improv generalization. This enhances the model's strength on the variability and complexity of the medical images, which make it difficult to analyze. This fusion has demonstrated state-of-the-art performance across segmentation tasks, offering a powerful and robust solution for accurate tumor segmentation.

Resnet as Encoder U-Net As Decoder

To sufficiently segment brain tumors within the BraTS2020 dataset using the strengths of both ResNet and U-Net architectures, it is important to comprehend how ResNet may serve as an encoder in a U-Net framework and how this bestows certain advantages, along with its influence on the overall functionality of the network. The ResNet-Unet Architecture is represented in Figure 2.

The encoder portion of U-Net, harnesses ResNet's capacities for deep learning while the U-Net architecture allows for ample amount of local context with its skip connections. This allows for ResNets reliable feature extraction via residual blocks, particularly with deeper architectures such as ResNet-50 or ResNet-101. Each residual block is fundamentally composed of two parts: several convolutional layers that are viewable as executing the main operation; and a skip connection, which sums the block input with the block output. This particular arrangement solves the issue of vanishing gradients, expediting the ability to train deeper network architectures without degradation in performance because of sufficient gradient flow. U-Net in both its fundamental approach and framework for model development as well.

The methods given above are highly specialized for brain tumor segmentation and their development needed expertise and extensive experimentation [19]. The network gains from the ability to encode more abstract and complicated information from the input images when ResNet is used as the encoder in U-Net. This is especially useful for medical imaging jobs where it can be critical to discern minute distinctions between tumor types and normal tissues, such as tumor segmentation in MRI scans. ResNet's improved depth and feature extraction capabilities enable the network to collect

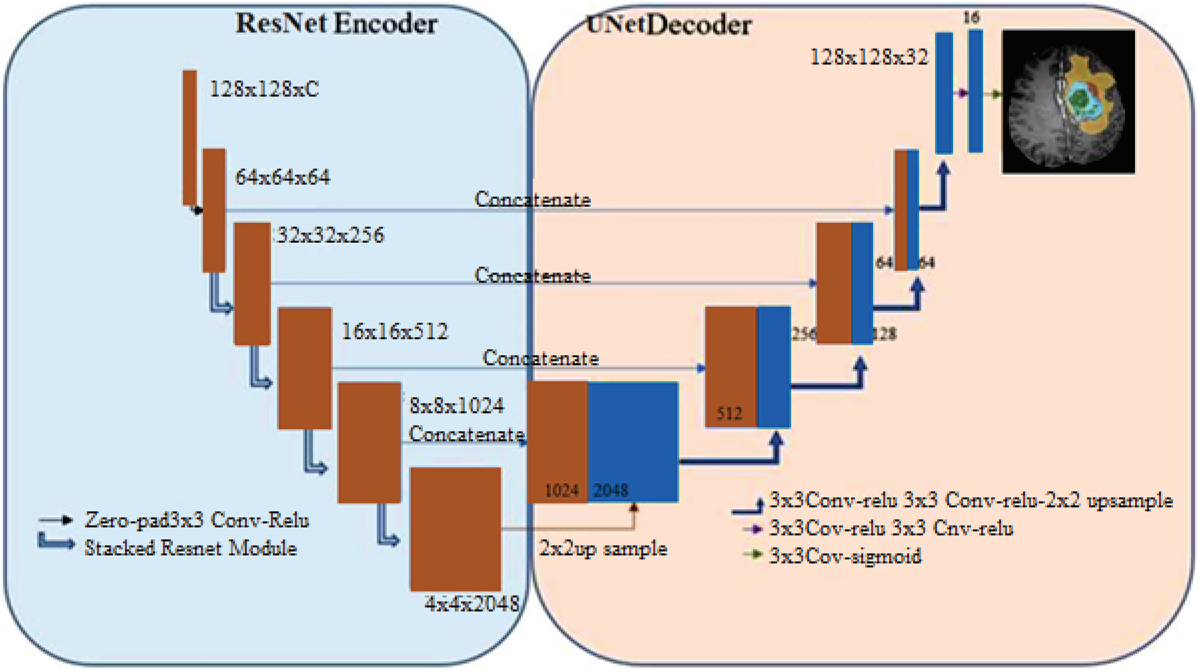

Figure 2. ResNet-Unet architecture.

the finer features and the larger context required for precise segmentation.

Mathematically, a residual block in ResNet can be represented as in equation 1:

$$\mathbf{\mathit{Output = ReLU\ (BatchNorm\ (Conv\ (x))) + x}} \qquad (1)$$

Where: x is the input to the block, Conv denotes a convolutional layer, Batch Norm represents batch normalization.

ReLU is the rectified linear unit activation function and $+x$ represents the skip connection. Several residual blocks stacked together make up the encoder part of the network. The encoded representation is the output of the last residual block. In the U-Net decoder, the segmentation map is generated from the encoded features through the sequential processes of up convolution and concatenation. Up convolution (also termed transpose convolution) is a process in the decoder that enlarges the spatial dimensions of the feature maps. These up sample maps are then concatenated with the same connected feature maps from the encoder, via the skip connection.This procedure preserves spatial hierarchies, which aids in correct localization, and enhances the feature maps with fine-grained information required for exact segmentation.Mathematically, the up sampling operation can be represented as in equation 2 :

$$\mathbf{\mathit{Upsampled = Conv(Upsample(x))}} \qquad (2)$$

Where x is the input to be up sampled, up sample denotes the up sampling operation, Conv represents a convolutional layer. Then, to incorporate skip connections, we concatenated the corresponding feature maps from the encoder with the up sampled feature maps in the decoder. The combined feature maps are then processed through additional convolutional layers to refine the segmentation mask.

Optimization

In this study we present our put forth of Novel Cat Swarm Optimization for Medical Image Segmentation (CSO-MIS). This Cat Swarm Optimization which we have used improves medical image segmentation by fine tuning the parameters of the deep learning models we use for tumor segmentation. We apply CSO to optimize the hybrid ResNet and U Net architectures which in turn improves their performance in accurate tumor detection. By tuning hyperparameters and network settings we see an improvement in segmentation accuracy and efficiency which in turn leads to better identification of key tumor areas. In this algorithm cats we see exploration of promising solutions and at the same time we have elements of random exploration which together do a good job at the balance of exploration and exploitation to find high quality segmentations. Our algorithm has cats which over time play in and out of the solution space to do what it takes to find the best segmentations of the medical image..CSO is inspired by the hunting behavior of cats and their ability to cooperate to solve complex tasks. Here's a simplified version of how CSO can be applies for this implementation:

Algorithm 2: Cat Swarm Optimization for Medical Image Segmentation (CSO-MIS)

```
Input: Medical image img, Number of cats $N$m, Maximum iterations $T$, Learning rate $\eta$, Exploration rate $\epsilon$
Output: Segmented image $Seg*$
Procedure:
Initialization:
    Randomly initialize $N$m cats in the solution space representing potential segmentations of the image.
    Set best solution found so far $Seg^*$=None and best fitness best_fitness=$\infty$.
Main Loop:
    for $t$=1 to $T$ do:
        Update each cat:
            Move each cat towards the best solution found so far with a probability of $\eta$.
            else, randomly explore the solution space with a probability of $\epsilon$.
        Evaluate the fitness of each solution (segmentation).
        Update best solution:
            if any solution has a better fitness than best_fitness then:
                Update best_fitness and $Seg*$ with the best-performing solution.
Segmentation Inference:
    Use the best solution $Seg*$ obtained from CSO to segment new medical images.
Output:
    Segmented image $Seg*$.
End
```

Randomly initialize a cats population representing different sets of model parameters. for each iteration, Evaluate the fitness of each model (cat) using the fitness function and the training dataset. The fitness function is as given in equation 3.

$$Fitness(S) = \frac{2\ X|S \cap G|}{|S|+|G|} \tag{3}$$

Where: S is the predicted segmentation mask,

G is the ground truth segmentation mask,

$|S \cap G|$ is the number of overlapping pixels between S and G,

$|S|$ and $|S|$ are the total number of pixels in S and G respectively.

Update the present best solution based on fitness values. Update the position of each cat using the rules of CSO which include both exploitation (movement toward the best solution) and exploration (random search). The new position $xi(t+1)$ of the i-th cat at time $t+1$ is given by the equation. 4:

$$\begin{aligned} x_i(t+1) &= x_i(t)+\eta\cdot(global\_best-x_i(t)) \\ &+ \epsilon\cdot rand()\cdot(upr\_bound-lwr\_bound) \end{aligned} \tag{4}$$

Where: At time t the position of the i-th cat is x_i , and η is the learning rate.

Global_best is the best solution to date, ϵ is the exploration rate.

rand () returns a random number between 0 and 1.

Upr bound and lwr bound define the solution space.

Update the best solution found so far based on the fitness of the cats' positions. If any Cat finds which set of parameters performs better for improved segmentation results, report that as the best solution at present. Do this for a fixed number of iterations or until we see that the model has converged. Once the optimization process is done, train the segmentation model with the best set of parameters found by the CSO on the full training dataset. Then put the trained model to the test on a separate validation set to see how it does. This step also makes sure the model does well on data it has not seen before.

RESULTS AND DISCUSSION

The in Figure 3 we present a ROC curve which reports on a classification model's performance across three different classes. We plot True Positive Rate (sensitivity) against False Positive Rate which in turn gives us info into how the model does at different threshold levels. A curve that reaches towards the top left hand corner of the plot indicates better performance which in turn means high sensitivity and low false positives. By looking at the three curves we are able to see which class the model does best at identifying as well as the models' overall performance which in turn may point out areas for improvement. Also if we see large deviations from the ideal curve that may indicate issues with the models' predictions in certain areas which in turn may require more refinement. The dice coefficient for both the training and validation datasets over 50 epochs is presented in Figure 4.

The plot represents an overall upward trend, indicating that segmentation accuracy improves as training progresses. This suggests that the model is learning effectively and becoming more accurate with each epoch for both the training and validation data.

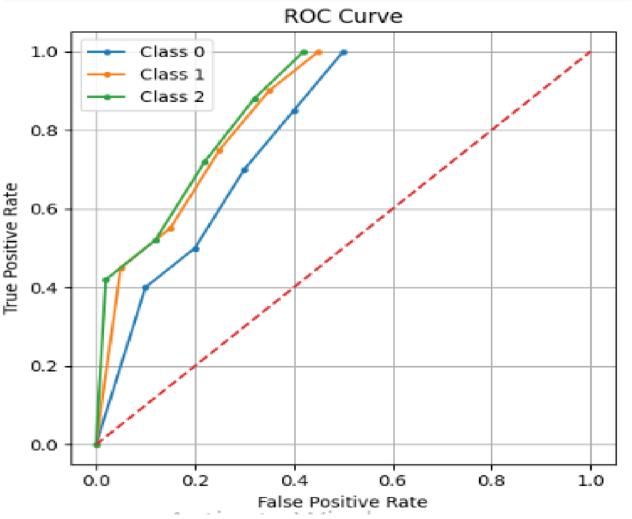

Figure 3. ROC curve.

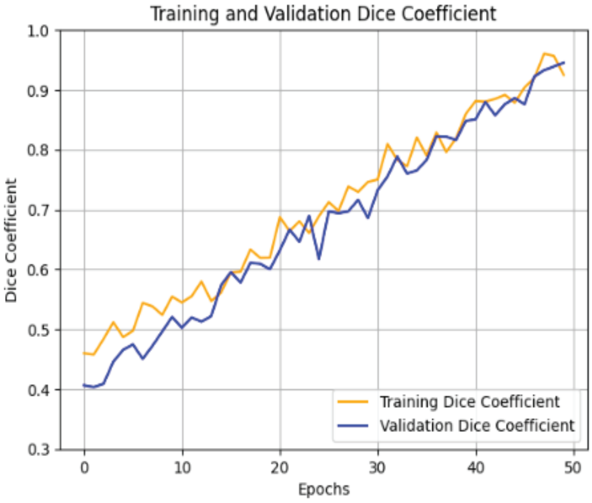

Figure 4. Dice coefficient.

Figure 5 shows the training and validation accuracy (left) and loss (right) over 50 epochs. From the accuracy curves showing the training and validation group data, we see that both are shifting in a consistent upward direction, suggesting that the model is improving in making accurate predictions over time. We also see that the loss curves are decreasing in a consistent manner, indicating that, as training continues, the model's predictions are making fewer mistakes (errors) with each epoch. The general stability in the training and validation accuracy and loss curves suggests that the model is learning to generalize from the training data to the validation data with no signs of overfitting, which improves overall model performance for segmentation tasks. Figure 6 shows the Training and Validation Mean Intersection over Union (IOU) over 50 epochs, where the X-axis represents the epochs and the Y-axis shows the Mean IOU score. Both the Training and Validation Mean IOU scores show a steady, nearly identical increase, indicating consistent performance and minimal overfitting. The values approach high accuracy in image segmentation.

The final stage of the U-Net structure assigns each pixel a distinct class label (an example is shown in Figure 7 with labels including "NOT tumor," "NECROTIC/CORE," "EDEMA," and "ENHANCING"). While it is the U-Net decoder that is providing precise localization of the features, ResNet encoder is providing distinct feature extraction providing a segmentation (i.e., class) map that preserves high resolution similar to the training dataset and test ground truth. The segmented brain tumors additionally classified into separate classes: i.e., core, edema, and enhancing

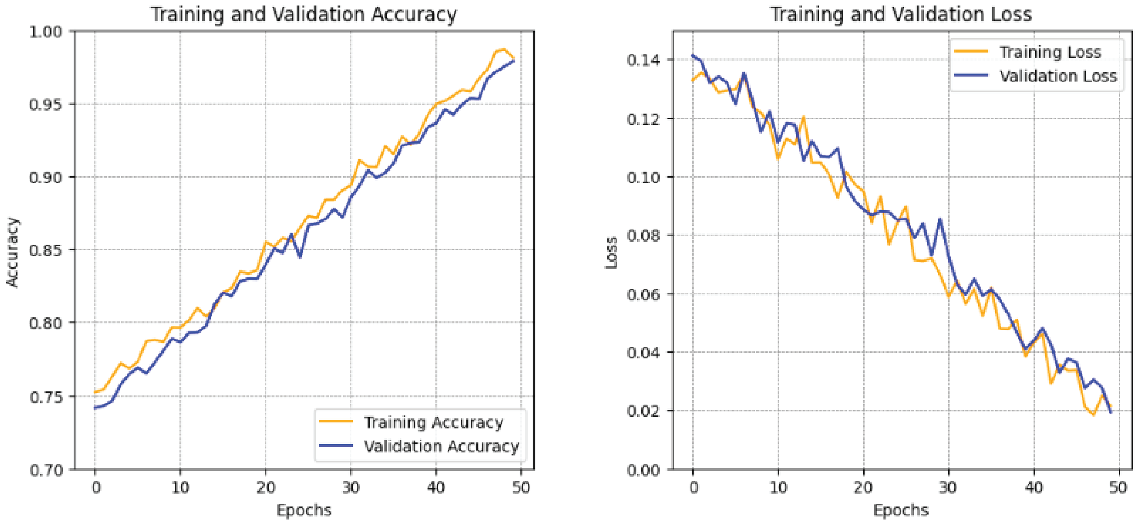

Figure 5. Training and Validation Accuracy and loss plot.

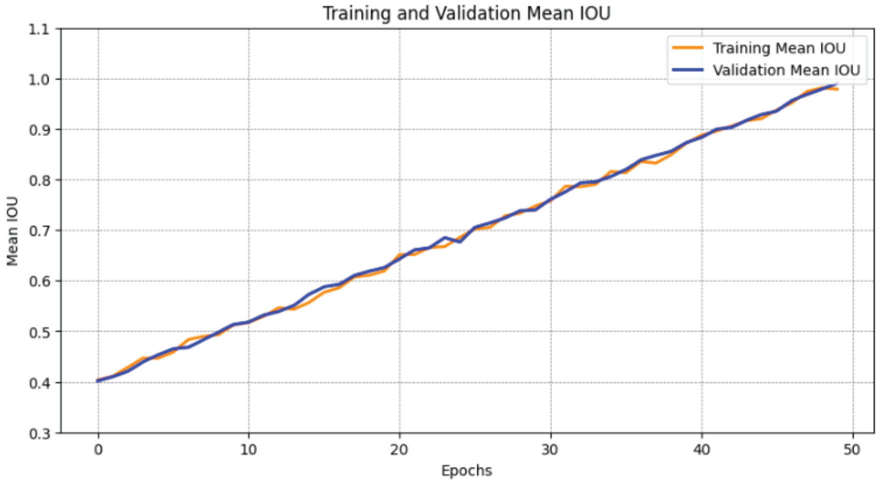

Figure 6. Mean IOU plot.

tumor were represented collectively as the ground truth, and represent a comprehensive view of the tumor classes. This way of representing tumor classes will ultimately assist in data accuracy and reliability concerning deep learning based brain tumor segmentation.

The 99.2% segmentation accuracy in this study shows a significant improvement over common Glioblastoma segmentation methods due to the tumor's complexity. This improvement is a function of the hybrid ResNet-U-Net that leverages ResNet's feature extraction and U-Net's good spatial accuracy, which leads to the segmenting of the glioma accurately. The Hybrid Bilateral-Gaussian Filter is also instrumental in helping reduce noise and at the same time maintain the edges that are important for the model not to receive garbage inputs into the network. Also, CSO helps the model with hyperparameter tuning, which optimized ResNet and U-Net for better performance. Overall, these techniques (ResNet-U-Net, CSO, Hybrid Bilateral-Gaussian Filter) are better than existing approaches which means greater precision in Glioblastoma segmentation and better clinical decision-making.

Survival Prediction

The BraTS2020 challenge requires the use of a dataset that includes features obtained from segmented MRI brain images, patient age, and surviving days for survival analysis [20]. The aim is to predict overall survival (OS) throughout intervals like short--, mid-, and long-term. To predict the Overall Survival time, radiomic and image-based features were extracted. These features have been shown to be successful in different studies for OS tasks [21]. In order to approach the task, we used a process of feature extraction and engineering combined clinical data and the derived imaging features that describe the tumor size and region [22]. After which we trained a number of machine learning models e.g., frequently used methods-support vector machine (SVM), random forest, k-nearest neighbors, and artificial neural networks in the combined dataset. [23].

The first step in the procedure is gathering data, which includes patient demographics such as age, specific survival durations, and MRI images that are divided into different tumor locations (necrotic/core, edema, enhancing). We combined the volumetric and location features with the patient's age to train a model using linear regression [24]. Quantitative properties of the tumor areas, including their size, shape, and intensity, are extracted from these MRI scans and are thought to have an impact on survival rates. Features can generate prognostic imaging signatures for OS prediction and patient stratification for GBM [25]. Which are very effective with a small number of training data? Random Forest is an ensemble algorithm that is made up of multiple decision trees and operates on them as an ensemble. It is one of the most frequent [26].

Machine learning models like Random Forests, Support Vector Machines, or Neural Networks are then trained on this integrated dataset, which combines clinical data with imaging-derived features. To estimate how long patients with similar profiles will live after diagnosis, the models are trained to correlate the features with survival durations. All models were fit with knowledge that the models were finally tuned and evaluated with methods such as cross-validation to provide a safeguard against overfitting and optimize hyperparameters. All models were measured with accuracy, precision, recall, F1-score, and area AUC-ROC. These statistical methods provided a capacity for predicting survival with a compelling analysis that used advanced analytic techniques to improve health outcomes on a patient level. To visualize, Figure 8 provides a pictorial of survival rates. The x-axis is days survived, and the y-axis is people. This relationship with features may allow some associations to be developed in survival rates that may assist in developing

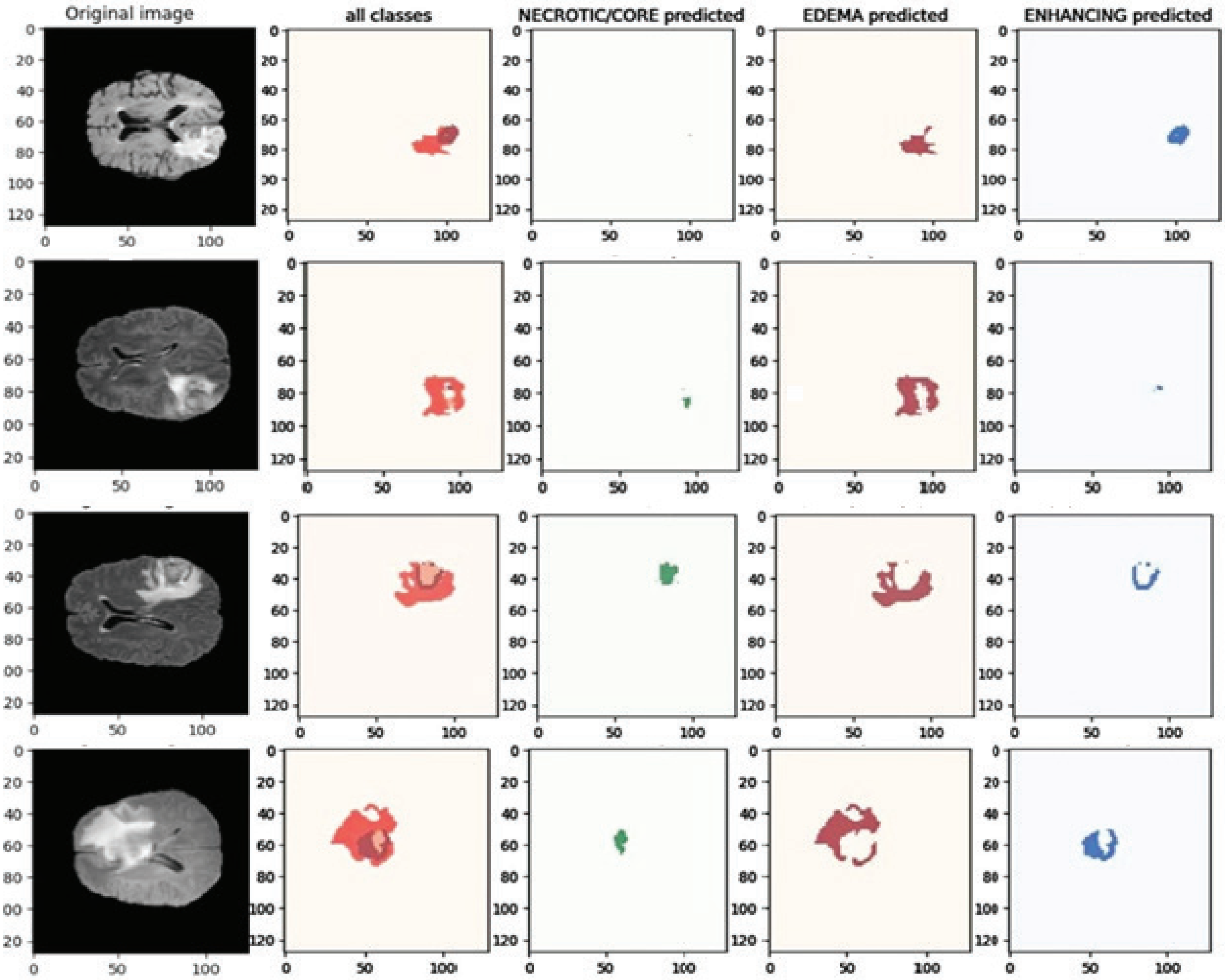

Figure 7. Segmentation results.

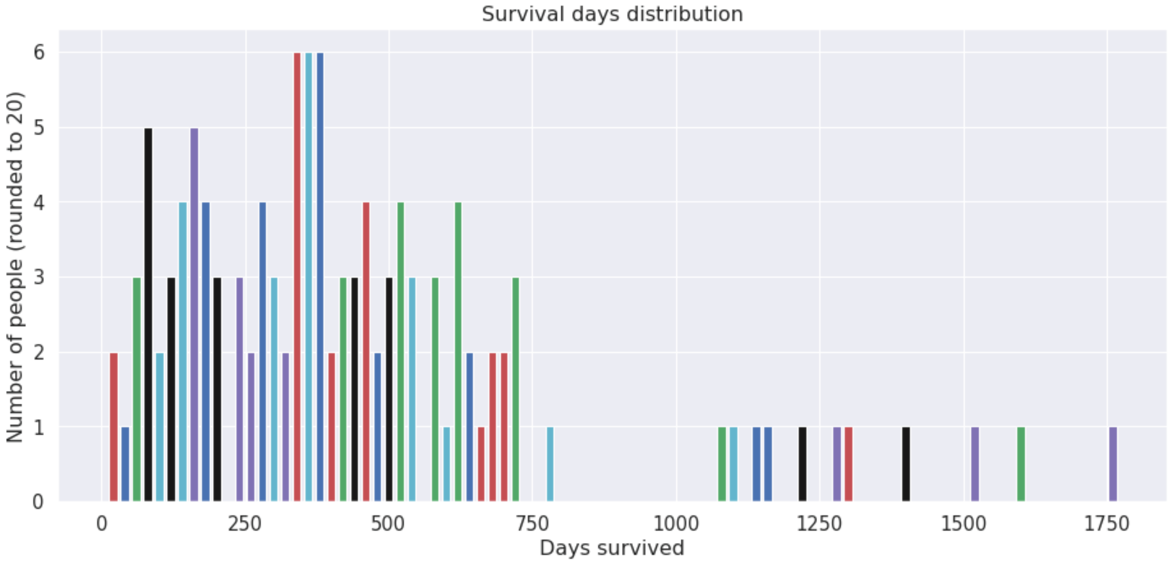

Figure 8. Survival data analysis.

beneficial treatment for variations in patients with various medical conditions.

Figure 9 provides insight into the dependency of survival data and segmentation, determining whether the survival rate is more dependent on the core region, edema, or enhancing tumor. Based on the image, it appears that the survival rate depends largely on the edema region. This information can be useful in guiding the development of targeted treatment strategies for patients with glioblastoma.

As we evaluated predictive survival models, we explored a range of supervised machine learning models, which included random forest classifier, SVM, KNN, and ANN. Random forest produced the highest testing accuracy (0.54) and precision (0.8) but had a relatively low training score (0.37), which can be an indicator of a model that is not learning from the training data as we want. The other models we explored (i.e. the SVM, KNN, and ANN models) had similarly low performance, especially SVM and KNN, and overall had lower accuracy and precision than the random forest model for testing. We used the three best models, Random Forest (RF), Artificial Neural Network (ANN), and support vector machine (SVM) to then enhance the overall prediction accuracy of survival using an ensemble strategy see Figure 10.

The ensemble model is here to be defined:

- **Random Forest (RF):** Random Forest is an ensemble model that builds multiple decision trees and combines the model outputs, so it can model complex interactions between variables that single models may be unable to decode. Random Forest also provides feature importance scores that allow for the evaluation of which factors contribute most to the survival outcomes, which is important for clinical interpretation and personalized treatment models.
- **Artificial Neural Network (ANN):** ANN builds on layers of nodes so that identifier complex, non-linear patterns are possible in large datasets.
- **Support Vector Machine (SVM):** SVM finds the optimal hyperplane for dividing classes while performing especially well in higher dimensional spaces.

The Ensemble method (or approach) takes advantage of the unique strengths of each model (where each model has

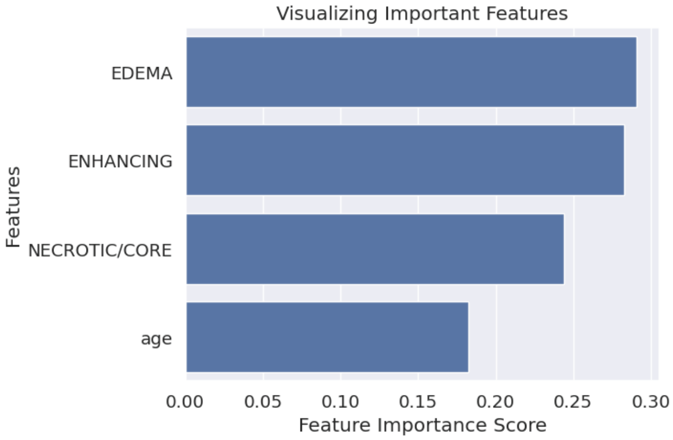

Figure 9. Feature visualization.

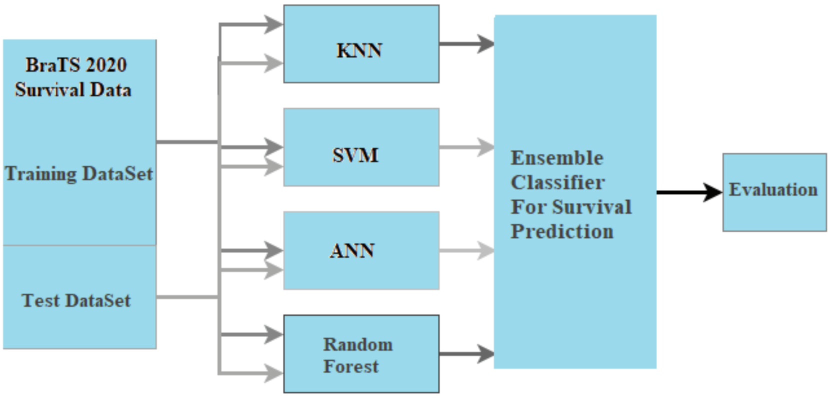

Figure 10. Ensemble model.

unique strengths: Random Forest makes robust, low-variance predictions; ANN can model highly complex non-linear relationships; SVM can handle high-dimensional spaces). The power of the Random Forest algorithm is its ability to capture the complex relationships between the array of different features, which is particularly useful when working with high-dimensional medical data (for example, the imaging-derived features from GBM). However, the Random Forest and other models could not combine and capture all of the patterns in the data, which is what the ensemble method was intended for. Each model captures its own features of the available data and reduces the overall errors in prediction because the weaknesses of each individual model are reduced by other models. However, by ensemble methods, predictions are based on a combined model with the strength of each individual model, providing more stability and robustness by dampening individual model biases and variability. The ensemble method provides improved prediction accuracy and reliability and could be particularly advantageous for the difficult survival prediction for the cohort of Glioblastoma patients. The overall predicted value for an input given a model can be represented as follows

$$\textit{Ensemble Prediction}= (W_{RF}.P_{RF})+(W_{ANN}.P_{ANN}) +(W_{SVM}.P_{SVM}) \tag{5}$$

Where: W_{RF}, W_{ANN} and W_{SVM} are the weights assigned to the RF, ANN, and SVM models, and P_{RF}, P_{ANN} and P_{SVM} are prediction probabilities of RF, ANN, and SVM models respectively. The confusion matrix for the survival prediction is represented in Figure 11. Table 2 displays several different models for prediction of survival outcomes with metrics, including accuracy, precision, training score and testing score. The Ensemble model, which attained the highest accuracy of 60.01% out of all models presented, is the best model for this type of data. Moreover, the Ensemble model achieved a precision score of 0.85 meaning that it is better at correctly predicting positive survival outcomes when present. Its model training score of 0.63 and model

Table 2. Evaluation metrics

Model	Accuracy	Precision	Training score	Testing score
Random forest	0.54	0.8	0.37	0.54
SVM	0.41	0.6	0.45	0.41
KNN	0.37	0.6	0.43	0.37
ANN	0.41	0.7	0.32	0.42
Ensemble	**0.60**	**0.85**	**0.63**	**0.60**

SVM: Support vector machine; KNN: K-nearest neighbors; ANN: Artificial neural networks.

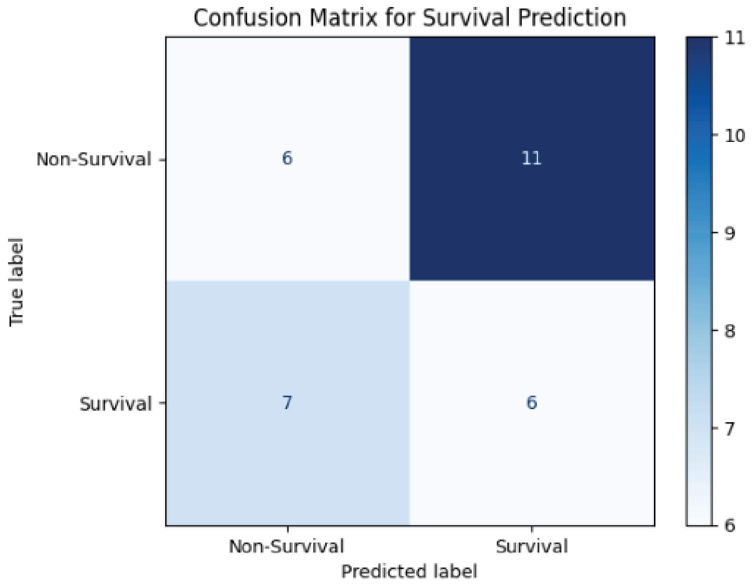

Figure 11. Confusion matrix of survival prediction.

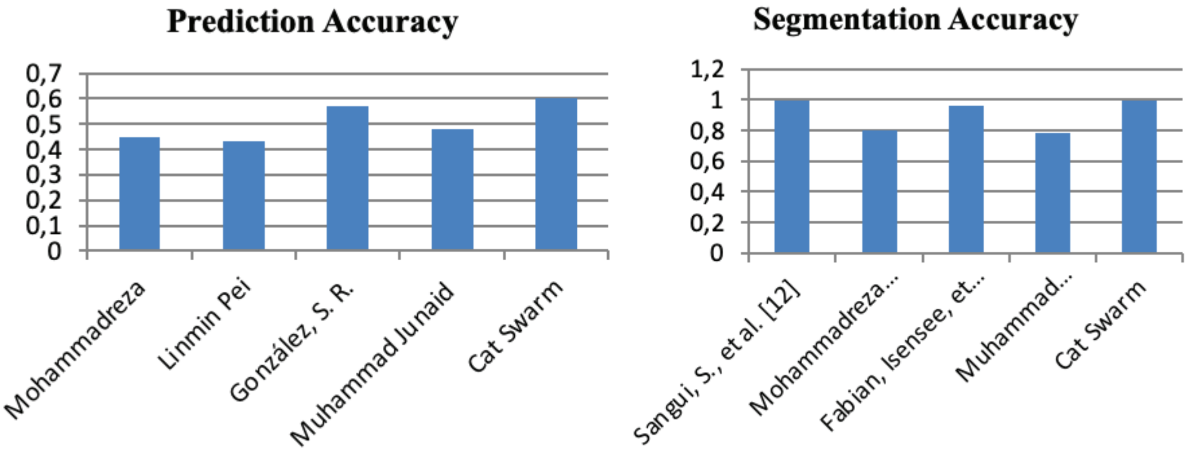

Figure 12. Comparision of results.

testing score of 0.60 indicate that the model generalizes sufficiently to new or unseen data making it an ideal model for survival prediction tasks.

The Figure 12 compares the accuracies of segmentation and survival predictions made by different models. Each bar represents a different model. The survival prediction accuracy figure indicates that our models have different levels of correspondence with survival outcomes, with attainment of the highest accuracy from predicted survival, while other models performed on a moderate level indicating that some potential exists for improving survival predictions. In the segmentation prediction accuracy figure, our models were shown to be superior, attaining the highest accuracy, while the other models had lower accuracy. Thus, the other models may be less able to perform well with precise segmentation tasks.

This study differs from typical clinical management methods of survival prediction in Glioblastoma patients using BraTS2020 dataset in that, all we did was create an ensemble of advanced machine learning models (i.e., Random Forest, ANN, and SVM) to analyze all of the complex imaging data in a more sophisticated manner than just clinical features and subjective manual interpretation. Typical clinical management of glioblastoma patients often relies on clinical features from prior research and clinical decision support systems to inform their suggested management. This approach may be subjective and the reliability is somewhat less refined. The study's approach used an advanced ensemble of models which captured complex data patterns found within the dataset and produced a more objective and precise prediction system. The added benefits of this approach include the ensemble produced a much better accuracy (60.01%), it generalized better to new data, and has the potential to enhance clinical decision making by having a more reliable prediction system for survival during clinical management of Glioblastoma patients.

CONCLUSION

Glioblastoma is the most common and aggressive form of primary brain tumor in adults that poses significant clinical management difficulties including high rates of recurrence, poor prognosis, and complexity and heterogeneity. This study aims to improve predictions of overall survival for Glioblastoma patients treated with stereotactic radiosurgery using advanced image segmentation and machine learning. We used Cat Swarm Optimization assisted hybrid ResNet and U-Net architectures to perform precise tumor segmentation and additional machine learning algorithms as an ensemble to make strong predictions of survival time. Utilizing the BraTS2020 dataset, we accurately delineated three critical tumor regions: core, edema, and enhancing tumor. The segmentation model achieved remarkable metrics, including a segmentation accuracy of 99.2%, a loss of 0.023, a recall of 0.986, a mean intersection over union (IOU) of 0.991, a dice coefficient of 0.96, a precision of 0.991, a sensitivity of 0.991, and a specificity of 0.997. In this study, we evaluated a number of machine learning models for survival prediction, and prioritized using different machine learning models for survival prediction while the Random Forest algorithm was ranked the best tool for survival prediction post deriving the features from segmented images due to its ability to handle the complexity of the features. Although the ensembling approach for survival prediction at 60.01% improved accuracy, these results demonstrated that there is a lot of potential to improve survival prediction for Glioblastoma patients in terms of clinical management and prognosis by utilizing advanced image segmentation methods with machine learning models. In future work using the BraTS dataset, advanced machine learning models, particularly Transformers to process spatial data should be employed. In addition, we can extend the use of multimodal data, which may include genomic profiles and comprehensive medical history, to improve prediction accuracy and provide personalized treatment strategies. Improving methods for data handling that can ensure privacy could result in a more broaden data demographic for a training dataset dataset. Performance and randomized controll trails in real-time clinical decision support systems could foster patient outcomes helpful toward personal medicine management.

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AUTHORSHIP CONTRIBUTIONS

Authors equally contributed to this work.

DATA AVAILABILITY STATEMENT

The authors confirm that the data that supports the findings of this study are available within the article. Raw data that support the finding of this study are available from the corresponding author, upon reasonable request.

CONFLICT OF INTEREST

The author declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

ETHICS

There are no ethical issues with the publication of this manuscript.

STATEMENT ON THE USE OF ARTIFICIAL INTELLIGENCE

Artificial intelligence was not used in the preparation of the article.

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