RESEARCH PAPER

A Novel Multi-Task Deep Learning Framework for Glioma Segmentation, Survival Prediction, and Recurrence Detection

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ABSTRACT
Brain tumour segmentation and persistence with a survival prediction are the most key important of medical issues and problems. To need computer-based AI models to transaction to deal with these brain tumour issues and problems. When it comes to brain tumour segmentation with people often use learning models like CNN and U-Net. These are methods but they have some limitations. They do not work well with brain tumours, and they have trouble, with spatial coherence and time variance. Brain tumours segmentation is an issue that requires better solutions. To address these challenges, in this work, we integrate a Modified SOFM, V-Net, Recurrent U-Net, and Cox Proportional Hazards (CoxPH) survival analysis to build a comprehensive tumor analysis framework. V-Net: A 3D convolutional neural network adopts volumetric features from multimodal MRI (T1, T1ce, T2, and FLAIR) to enhance the segmentation performance. Recurrent U-Net is more appropriate for the tracking of the development or relapse of the tumors, since it improves the segmentation of using recurrent connections to capture temporal dependencies.
The segmented tumor features returned by V-Net are passed to the CoxPH model, which predicts survival probabilities based on crucial parameters such as tumor volume, shape and some demographics of patients (such as age). CoxPH provides a statistically valid means to predict survival time by integrating clinical and imaging information to prognosticate at a more personalized level. Predicting the occurrence of recurrence is important for long-term follow-up of the patient, and survival analysis alone is inadequate. Recurrent U-Net with spatial-temporal learning of sequential imaging data enhances A.M. Noël/Magn. Reson. Imaging 64 (2020) 41–48 47 precision of FM segmentation and offers potential for earlier detection of tumour recurrence. This capability is further enhanced by a modified SOFM that clusters extract tumor features for finding recurrence patterns and assures a more accurate follow-up strategy.
Keywords: MRI images, brain tumor segmentation, VNET, recurrent UNet, survival prediction, coxph, recurrence prediction.
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1.Introduction

The brain is tumorous an abnormal growth of cells within the brain. These tumors can be very dangerous as they take over basic functioning of the nervous system. These tumors are either benign (noncancerous) or malignant (cancerous), with malignant tumors being more aggressive and sometimes deadly adenomas. Cutting-edge imaging techniques and computer-aided models are indispensable for brain tumor detection, assessment, and monitoring to ensure accurate analysis and successful interventions. Because of their complexity, a precise prognosis and early diagnosis are essential for increasing patient survival and lowering the chance of recurrence.
As illustrated in Figure1, brain tumors are classified into various types according to their origin, behavior, and aggressiveness. The brain itself is where primary brain tumors start. GBM is the recursive of these and needs to be treated right away. Secondary brain tumors are caused by cancer cells that have spread from other parts of the body, such as the breasts or lungs. Since different types of brain tumors require different approaches for effective management, the classification of brain tumors aids in the determination of appropriate treatment strategies.
According to global health surveys, brain tumors occur at a rate of 6 per 100,000 individuals, or 1.8% of all tumors globally. Only 12 to 15 months after diagnosis, glioblastomas alone make up about half of all malignant brain tumors. Glioblastoma is one of the deadliest types of cancer, with a survival rate of less than 10% despite advances in medical science. Age-related differences exist in the prevalence of brain tumors; medulloblastomas and

low-grade gliomas make up the majority of pediatric cases, whereas high-grade gliomas are more common in older adults. These figures show that there is a need for good prediction tools in the cure of brain tumors.

The symptoms of a brain tumor really depend on where the brain tumor's how big it is and how fast it is growing. You might get things like convulsions headaches that do not go away with problems with your vision your thinking gets worse. Your personality changes. Sometimes your speech and how you move can be affected too.To treat brain tumors doctors can use surgery, chemotherapy, radiation therapy and special medicines. Surgery tries to remove much of the brain tumor as possible. Then chemotherapy and radiation are used to kill any cells that are still there.

There are problems with these treatments. Sometimes the brain tumor is not completely removed when it comes back. It does not respond to the therapy. That is why it is very important to know what might happen with the brain tumor like how you might live and if it comes back so doctors can make the best treatment plan for the brain tumor.

When doctors look at brain tumor pictures from an MRI they must do it by hand. They also use math to figure out what the tumor will do. To help with these computers can look at the pictures. Use things like SVMs and random forests to try to understand what they see. Some computers can even use CNNs to look at the pictures.

These computer methods have some problems. They can have trouble finding tumors. They can also get confused if there are more normal pictures than tumor pictures.. They do not always understand where the tumor is in the brain or how it changes over time.

The territorial ways of figuring out what would happen to a patient were not very good. This is because doctors did not have information, about the patient. doctors had to come up with ways to look at brain tumours pictures and figure out what brain tumours pictures mean. Brain tumour pictures are very complicated and hard to understand. And predict hence the advanced methods are sequined to deal these uses

The way we think about brain tumors is different now because of what we have learned and the use of networks. We have models like U- V-Net that can find small things in MRI scans, which makes them good at finding the edges of brain tumors. V-Net is a type of model that looks at 3D pictures and can tell us a lot about the shape of brain tumors. This helps us understand brain tumors better. This also is something called Self-Organizing Feature Maps to predict if a brain tumor will come back and to see how the brain tumor is growing. By looking at things about the patient and the brain tumor with Cox Proportional Hazards models to make guesses about how long someone with a brain tumor will live. The combination of looking at survival rates and using learning and neural networks gives us a way to take care of patients with brain tumors.

This study helps us look at brain tumors in a way. the V-Net to find the edges of brain tumors. We also use Self-Organizing Feature Maps to predict if a brain tumor will come back.. We use Cox Proportional Hazards models to guess how long someone with a brain tumor will live. By using these models, we can find out if a brain tumor is coming back early. We can figure out how likely someone with a brain tumor is to survive. We can also find brain tumors exactly. This method helps doctors make decisions about brain tumors. It also makes sure patients with brain tumors get care. Brain tumor research is getting better because we are learning and looking at survival rates of people with brain tumors. This means we can give people with brain tumors the treatment just for them and based on good data about brain tumors.

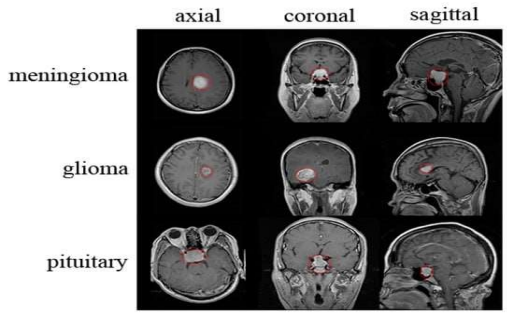

Figure 1: Brain Tumour Types

2. Literature Survey

Neamah [1] and others suggested a way to figure out what kind of brain tumors people have. They use computer programs and MRI scans to doing. The first thing they do is make all the MRI pictures the same size. They get rid of any extra stuff that is not supposed to be in the picture. This makes the pictures clearer. Then the computer program looks closely at these pictures to find things. These things help the program tell the difference between the tumor and the normal brain. In the end the program makes a map that shows where the tumor is, how big it's what kind of tumor it is.This helps doctors know exactly what is wrong with the person and what to do to help them. However, this program is not perfect. One problem is that there is no information about rare tumors. Another problem is that the program might get too good at recognizing the pictures it has seen before and not work well on pictures it has not seen. Neamah and others are still working on making this program so it can help doctors and people with brain tumors like brain tumors that the program is supposed to find. The program is supposed to find brain tumors. It is still not very good at finding rare brain tumors.

Metlek and others [2] suggested a model called "ResUNet+" for segmenting brain tumors. They used a dataset of brain tumours images. The images were prepared by finding the area of interest and converting them to a format. The ResUNet+ model then used these prepared images. The ResUNet+ model has a design, with blocks that help it learn. It sends the results of these blocks to the part of the model. The model then uses a technique to keep the important features. However, one drawback of this model is that it takes a time to train compared to a similar model called UNet.

Yan et al. [3] proposed the "SEResU-Net "model for brain tumours. The SEResU-Net is a sophisticated deep learning approach to improve the segmentation of brain tumours in MRI scans. 3D MRI brain scans are used as inputs in this model. In order to improve generalization, these scans are preprocessed by resizing them to a consistent resolution, normalizing the pixel intensities, and using data augmentation techniques like flips, translations, and rotations. Following preprocessing, the encoder-decoder structure of the U-Net architecture is applied to the MRI images. The encoder captures information contained in the image by extracting features at various scales. After up sampling, the decoder conducts a standard convolution. One of the disadvantages is that in order to evaluate the segmentation effect, the entire tumor must be segmented. The slicing processing of 3D information from MRI data may inevitably result in the loss of some context and local features because SEResU-Net is a 2D network.

Rasool et al. [4] proposed the "TransResUNet: Revolutionizing Through Transformer-Enhanced Residual UNet" for glioma brain tumour segmentation. The input first goes through a 5x5 kernel-size convolutional layer, which preserves spatial resolution while capturing more general contextual features. Deeper networks without the vanishing gradient issue are made possible by subsequent layers using residual blocks to improve feature extraction efficiency by learning the residuals. In order to improve segmentation accuracy for complex structures, the model uses transformers to capture global contextual relationships. The spatial dimensions used to reconstruct the segmented output are decreased by down sampling layers. Fine-grained segmentation is ensured by skip connections. The ability for better computational difficulty resulting from the sequence of transformers and residual unions is a significant disadvantage of TransResUNet.

Hammer Håversen [5] and other researchers proposed a method called QT-UNet for 3D segmentation of brain tumor images. This method uses self-attention mechanisms of traditional convolutional kernels to process patches of brain tumor images. The self-attention layers record information from the input volume with each patch acting as a token. This approach helps the model handle dimensional inputs and focus on important spatial features. The QT-UNet model categorizes each voxel into regions of interest such as tumor components and creates a 3D mask. However, the model's dependence on patch-based self-attention can cause it to lose grained spatial details.

D.S. Vinod [6]and other researchers developed the UNet technique for brain tumor segmentation. The U-Net architecture predicts the survival of brain tumors by separating tumor regions from medical images like MRI scans. The U-Net structure and skip connections in the U- help keep important details like the shape of things and where they are. This makes it possible to find tumours accurately. The U-Net looks at things like the size and shape of the tumour. Where it is. These things are important for knowing if someone will survive. The U-Net is good at finding these details, about the tumours. These features, along with information like age and medical history are used by machine learning models to forecast survival outcomes. However, the U-Net has some shortcomings, including its reliance on a lot of labeled data, which can be hard to come by in imaging and its tendency to overfit, especially with small or imbalanced datasets.

S.P.Siva Prakash[7] and other researchers developed the Self Organizing Feature Map (SOFM) for brain tumor survival prediction. The SOFM maps dimensional data, including patient data and tumor characteristics and identifies trends and classifies patients according to tumor features and other variables. The SOFM helps identify risk or low-risk groups and discover underlying trends associated with survival outcomes. This allows for the prediction of survival rates and the direction of treatment plans. However, the SOFM has some disadvantages, including overfitting or performance when dealing with high-dimensional data or irrelevant features.

A.M.H.H. Alahakoon[8] and other researchers developed decision tree regression for survival prediction. The decision tree regression works by dividing the dataset into subsets based on characteristics like patient demographics, tumor characteristics and treatment details. The tree divides the data at each decision node based on criteria that reduce the variance in the target variable like survival time. The decision tree regression helps model relationships in the data and predicts survival outcomes based on tumor-and patient-related factors. However, the decision tree regression has some issues, including class imbalance, overfitting and scalability to datasets.

C.K. Walgampaya[9] and other researchers developed Random Forest for survival prediction. The Random Forest combines the predictions of decision trees to create a more accurate model. Each tree is constructed using a subset of features and a subset of data through bootstrapping, which helps

minimize overfitting and bias. The Random Forest uses features like tumor characteristics, treatment details and patient demographics to predict survival. However, the Random Forest has some disadvantages, including being computationally costly with big datasets and being more difficult to interpret than individual decision trees.

Navodini Wijethilake[10] and other researchers developed Support Vector Machines for glioma survival analysis. The Support Vector Machines work by finding a hyperplane in a dimensional space that best separates the data into groups, such as survival vs. non-survival. The Cox-SVM is a way to use Support Vector Machines for studying how long people live. It does this by using the time people live and the people who do not have an event happen to them during the study. The Cox-SVM looks at how tumor characteristics are connected to how long people, with gliomas live. This helps the Cox-SVM guess what will happen to people. The Support Vector Machines have some problems. One problem is that they can get too good at fitting the data they are trained on. This is called overfitting. They can also be very slow to use because they need a lot of computing power. The Support Vector Machines need a lot of data to work well. They also have trouble handling data from sensors.

3. Existing Methods

3.1. SOFM

Brain tumor segmentation is a main step in medical image study analysis that enables accurate diagnosis and treatment forecasting. The deep learning model U-Net utilizes an encoder-decoder model to preserveor hold minute details that are lost during down sampling. While the decoder restores spatial resolution through up sampling, the encoder extracts hierarchical features using convolutional layers with max-pooling and ReLU activation. To differentiate between tumor subregions like necrosis, edema, and enhancing tumor, the last layer uses a SoftMax activation function for multi-class tumor segmentation.

U-Net is very good at segmenting MRI-based images of brain tumors because of its capacity to learn spatial patterns quickly. As show in Figure. 2, the Self-Organizing Feature Map (SOFM) is used to group patients according to extracted tumor features in order to predict survival. Each neuron in the grid of neurons that makes up SOFM represents a survival category. By choosing the Best Matching Unit (BMU) based on the Euclidean distance between input features and neuron weights, it learns through competitive learning. The model then refines clusters over time by using a Gaussian neighborhood function to update the BMU and neighbors.

An efficient continued existence prediction framework is acquired by combining SOFM with U-Net-built segmentation. Accurate patient stratification is ensured by the segmented tumor regions, which give SOFM precise inputs. However, SOFM cannot model temporal persistence trends, and its performing is dependent on well-defined characteristics. Hybrid methods that combine deep survival networks or Cox Proportional Hazards (CoxPH) models with SOFM are investigated to address this. The combination of unsupervised clustering and deep learning-based segmentation improves prognosis accuracy and helps physicians make well-informed treatment decisions.

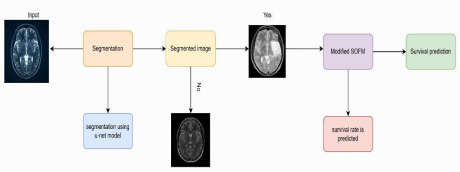

Figure 2: SOFM model for brain tumours segmentation

Algorithm 1 Brain Tumor Segmentation and Survival Prediction

Input: MRI scans $\mathcal{I}$, Corresponding masks $\mathcal{M}$
Output: Segmented tumor masks and survival clusters
Step 1: Train U-Net Model for Segmentation
Initialize U-Net with convolutional encoder-decoder architecture
for each epoch in training **do**
  for each batch of images (I, M) **do**
    $O \leftarrow U\_Net(I)$ ▷ Predict segmentation mask
    Compute loss: $L = BCE(O, M)$
    Backpropagate loss and update weights
  end for
end for
Save trained U-Net model
Step 2: Extract Features from Segmented Images
for each segmented image O_i **do**
  Extract feature vector F_i using encoder layers
end for
Step 3: Train SOFM for Survival Prediction
Prepare dataset: $D = \{(A_i, F_i, S_i)\}$ where A_i is age, S_i is survival time
Normalize D using MinMax Scaling
Initialize SOFM with 10×10 grid
for each iteration in training **do**
  Update SOFM weights using competitive learning
end for
Step 4: Predict Survival Clusters
for each new patient **do**
  Map patient features to SOFM grid
  Assign survival probability based on nearest cluster
end for

3.2. ResNet

An MRI scan dataset of brain tumors is used to train the ResNet model. Prior to processing, each input image is resized from its initial 512×512-pixel resolution to a standard 128×128 pixel size. As shown in Fig.3, the model applies a series of operations, such as convolution, ReLU activation, batch normalization, and max pooling, to these images in five stages.

The MRI images are scanned and processed using a convolutional kernel. In order to create a convolved output, the input MRI image is split into smaller regions that correspond to the kernel size. Each pixel value is then convolved with the kernel's values. After that, normalization is used to divide each pixel value by 255 in order to scale the feature maps within the [0,1] range.

After that, negative pixel values are removed using a ReLU activation function. The feature maps are split into parts and the highest value is kept from each part. This helps to make things simpler. Also makes the features that are extracted better.

The ResNet model does this thing in all five of its stages. After the features are extracted the feature maps are looked at again. The average value is used

for each part. Then the features that were looked at are made into a line of numbers. Put into a special layer. This layer makes sure that the features are changed in a way and it gets rid of any negative values by replacing them with zeroes, which makes the features that were extracted even better.

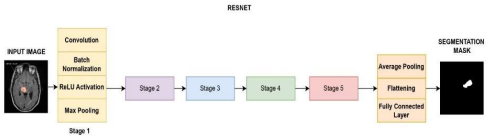

Figure 3: ResNet model for brain tumours segmentation

Algorithm 1 Brain Tumor Segmentation using ResNet

Input: MRI image of shape $(256, 256, 3)$
Output: Segmentation mask of shape $(256, 256, 1)$
Step 1: Load Pretrained ResNet50
Initialize $inputs \leftarrow Input(shape = (256, 256, 3))$
Load $ResNet50$ with pretrained ImageNet weights
Remove fully connected layers ($include\_top = False$)
$base\_model \leftarrow ResNet50(input\_tensor = inputs)$
Step 2: Extract Feature Maps
$x \leftarrow base\_model.output$ ▷ Extract last convolutional layer output
Step 3: Decoder - Upsampling and Convolutions
$x \leftarrow UpSampling2D(size = (2, 2))(x)$
$x \leftarrow Conv2D(256, (3, 3), padding = "same")(x)$
$x \leftarrow BatchNormalization()(x)$
$x \leftarrow Activation("relu")(x)$
$x \leftarrow UpSampling2D(size = (2, 2))(x)$
$x \leftarrow Conv2D(128, (3, 3), padding = "same")(x)$
$x \leftarrow BatchNormalization()(x)$
$x \leftarrow Activation("relu")(x)$
$x \leftarrow UpSampling2D(size = (2, 2))(x)$
$x \leftarrow Conv2D(64, (3, 3), padding = "same")(x)$
$x \leftarrow BatchNormalization()(x)$
$x \leftarrow Activation("relu")(x)$
Step 4: Final Segmentation Output
$x \leftarrow Conv2D(1, (1, 1), activation = "sigmoid", padding = "same")(x)$
Step 5: Build and Compile the Model
$model \leftarrow Model(inputs, x, name = "ResNet\_Segmentation")$
Compile $model$ using Adam optimizer and Binary Cross-Entropy loss
Return $model$

3.3. Proposed Methodology

As seen in Fig.4 VRU-Net is a model that helps us detect brain tumors and predict what will happen by combining RU-Net for looking at if the tumor will come back with V-Net for looking at the size of the tumor. The Cox proportional hazards model for predicting how long someone will live and the Recurrent Convolutional Neural Network for predicting if the tumor will come back are also added to the VRU-Net model. The whole process gives us a plan for using this in a clinical setting, which includes getting the images ready segmenting the tumor predicting how long someone will live and predicting if the tumor will come back.

To get MRI scans ready for deep learning models we need to do some preparation work. This step is very important for image analysis because MRI scans can be very different in terms of how bright they are, how clear they are and how much noise they have. To need to make sure all the MRI scans are similar. This is important because the MRI scans come from places with brightness levels. To do this we make all the pixel values of the MRI scans between 0 and 1. This makes everything consistent, across all the MRI scan datasets, to add images to our MRI scan dataset. We do this by using some tricks. These tricks help make sure our model works with the MRI scans. It does not matter how the MRI scans are taken. The model to work with any MRI scan. So we use these tricks to add more images to our MRI scan dataset. This way we can be sure our model will work with any MRI scan.

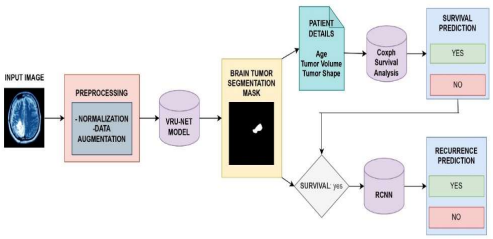

Figure 4: VRUNET model for brain tumours segmentation

The process of segmentation using V-Net for medical image segmentation is a part of the VRU-Net Process-Net looking at the volume of a medical image. It captures how things are related in space and how they vary across slices. Volumetric segmentation using V-Net is different from U-Net, which only looks at 2D slices. For brain tumors volumetric segmentation using V-Net is useful. Brain tumors often have shapes and can look different in various MRI scans, like T1, T2 and FLAIR scans. Volumetric segmentation using V-Net is good at handling this because it uses connections in its encoder-decoder architecture. This helps volumetric segmentation using V-Net keep track of the resolution while it extracts features, at levels.

The result of this step is a segmentation mask that shows where the tumor is in a MRI scan. After the segmentation is done the next step uses a learning model called CoPxh. This model looks at both clinical and radiomics features to predict how long a patient will survive. CoPxh estimates the likelihood of survival by looking at the tumor and other information about the patient, such as their age, where the tumor's and what genetic markers they have. The model uses layers to extract features at different scales. This helps it capture things like swelling around the tumor, dead tissue and how different the tumor cells are.

Then it uses a combination of survival models and connected layers to predict how long the patient will live. This information is crucial for neurosurgeons to decide on the treatment, such as radiotherapy, chemotherapy or surgery.

These characteristics are used by a Cox Proportional Hazards model or CoPxh, for short to estimate the probability of survival. The following provides the details of the Cox model:

$$h(t)=h0(t)\cdot e(w1z1+w2z2+\cdots+wmzm) \quad (1)$$

Recurrence prediction is the last step of VRU-Net. It is done using RU-Net, which's a recurrent U-Net.RU-Net helps to see changes over time in MRI scans. It does this by using layers called Gated Recurrent Units or GRUs for short. These layers are different from those in segmentation models. Brain tumors often change over time. So,RU-Net looks at MRI data to find small changes that might mean the tumor will come back. To do this RU-Net uses the

segmentation mask from V-Net. The mask is put into RU-Net, which then does some operations on it.These operations are a mix of recurrent ones. The goal is to see if the tumor is likely to recur.RU-Net analyzes the data to spot minute variations. These variations might lead to a recurrence. The RU-Net looks at the tumor and the MRI scans.

GRU Equations:

1. Update Gate:

$$ut=\sigma(Au\cdot vt+Bu\cdot st-1+cu) \quad (2)$$

2. Reset Gate: Regulates the amount of the previous state that should be forgotten:

$$rt=\sigma(Ar\cdot vt+Br\cdot st-1+cr) \quad (3)$$

3. Candidate Activation: Determines a fresh possible state:

$$st\sim=\tanh(As\cdot vt+Bs\cdot(rt\odot st-1)+cs) \quad (4)$$

4. Final Hidden State: Determines the percentage of the new state that is kept:

$$st=(1-ut)\odot st-1+ut\odot st\sim \quad (5)$$

RCNN is used to analyze the tumor mask and predict if the tumor will come back. In follow-up scans RCNN uses GRUs to track changes over time. 3D convolutional layers to extract features from the tumor. The RCNN helps doctors understand the tumor better. To calculate the chance of the tumor coming this formula is used:

$$P=\sigma(Wf\cdot ht+bf)$$

The brain tumours have a threshold value of 0.5. This brain tumours threshold value is used to figure out if the brain tumours is likely to come. If the brain tumours value is higher than 0.5 the brain tumours may come back. If the brain tumours probability is less, than 0.5 the brain tumours cannot come back.

Algorithm 1 Brain Tumor Segmentation and Prediction using VRU-Net, CoPxh, and RCNN

Input: MRI Scan I, Patient Details (Age, Tumor Volume, Tumor Shape)
Output: Tumor Segmentation Mask M, Survival Prediction $P_{survival}$, Recurrence Prediction $P_{recurrence}$
Step 1: Preprocessing
Normalize I to range [0,1]
Apply data augmentation (Rotation, Scaling, Elastic Transformations)
Perform noise reduction using Gaussian smoothing
Step 2: Brain Tumor Segmentation using VRU-Net
Initialize V-Net Encoder-Decoder
for each voxel v_i in I **do**
    Extract deep spatial features using convolutional layers
    Apply skip connections for spatial retention
end for
Apply RU-Net for temporal sequence learning
for each MRI sequence S_t **do**
    Apply Gated Recurrent Unit (GRU) to capture tumor progression
    Compute hidden states:

$$h_t = (1 - z_t) \odot h_{t-1} + z_t \odot \tilde{h}_t$$

end for
Train VRU-Net using backpropagation and Adam optimizer
Generate final segmentation mask M
Step 3: Survival Prediction using Cox Proportional Hazards Model (CoPxh)
Extract patient features $X = [x_1, x_2, \ldots, x_n]$
Compute hazard function:

$$h(t) = h_0(t) \cdot e^{(b_1x_1 + b_2x_2 + \cdots + b_nx_n)}$$

Compute cumulative hazard function:

$$H(t) - \int_0^t h(u)\,du$$

Compute survival probability:

$$P_{survival} = e^{-H(t)}$$

If $P_{survival} > 0.5$, return "YES" (Survival Predicted)
Else return "NO" (Non-Survival Predicted)
Step 4: Recurrence Prediction using RCNN
Extract spatial features from M using 3D CNN
for each MRI sequence S_t **do**
    Compute hidden state using GRU:

$$h_t = GRU(W_h \cdot x_t + U_h \cdot h_{t-1} + b_h)$$

end for
Compute recurrence probability:

$$P_{recurrence} = \sigma(W_f \cdot h_t + b_f)$$

If $P_{recurrence} > 0.5$, return "YES" (Recurrence Predicted)
Else return "NO" (No Recurrence Predicted)
Return $M, P_{survival}, P_{recurrence}$

4. Results and Analysis

The main dataset we used for this study is the BraTS dataset. This dataset is very important for people who work with brain images and tumor analysis. MICCAI is the organization that makes the BraTS dataset available to everyone. The Brain Tumor Segmentation dataset is an important set of data for doctors and researchers who are studying gliomas using magnetic resonance imaging. This dataset has a lot of MRI scans from patients who have gliomas and these scans are very useful for medical and research purposes.

These MRI scans are very helpful for doctors and researchers who are trying to find and understand brain tumors. The Brain Tumor Segmentation dataset is often used to look at tumors predict how long patients will live and see if tumors come back. By looking at the MRI scans doctors can find tumors figure out what might happen to patients and watch to see if tumors grow or come back over time. Each patient's information in the Brain Tumor Segmentation dataset has four kinds of MRI scans: T1-weighted T2-weighted contrast-enhanced T1-weighted and Fluid Attenuated Inversion Recovery images. These scans show things about the body and the tumor so doctors can get a complete picture of what the tumor is like. They help doctors tell the difference between parts of the tumor like the core dead tissue and swelling around the tumor.

One good thing about the Brain Tumor Segmentation dataset is that it has a lot of information about patients, like their age and what treatments they had. This information along with the MRI scans makes the dataset very useful for creating computer models that can help doctors make diagnoses and predictions. Newer versions of the dataset like the Brain Tumor Segmentation 2021 and Brain Tumor Segmentation 2023 are even more useful because they have MRI scans from follow-up appointments. These scans help researchers see how tumors change over time how patients respond to treatment and if tumors come back.

The Brain Tumor Segmentation dataset is used to train and test the three parts of the proposed VRU-Net framework. First the dataset is used to find gliomas. Second, it is used to predict how long patients will live based on their MRI scans and other information. Finally, the dataset is used to detect and understand if tumors come back which helps create a system, for diagnosing and predicting what will happen with brain tumors.

4.1. Performance

The tumor finding models, like SOFM, ResNet and VRU-Net to observe how good they really are. The tumor finding models SOFM, ResNet and VRU-Net were tested over epochs.to used things, such as F1-score, accuracy, precision and recall measuring the tumor finding models SOFM, ResNet and VRU-Network. the results we saw how the tumor finding models SOFM, ResNet and VRU-Net do when we train them for a time. This really helps us to figure out which of the tumor finding models SOFM, ResNet or VRU-Net is the one, for finding brain tumors.

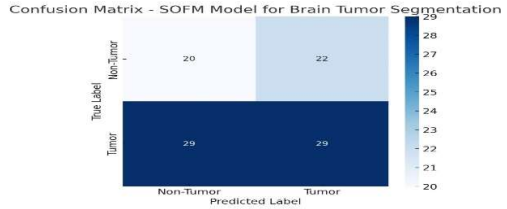

Figure 4: Confusion Matrix of SOFM Model

The SOFM model in brain tumor segmentation also has False Negatives or FN when the SOFM model in brain tumor segmentation says something is not a tumor when it really is.This is very bad because doctors might miss the tumor. The confusion matrix for the SOFM model in brain tumor segmentation tells us how good the SOFM model in brain tumor segmentation is at classifying things. The SOFM model in brain tumor segmentation makes mistakes when it says something is a tumor. It is not really a tumor. These mistakes are called False Positives or FP.

This is a problem because when the SOFM model in brain tumor segmentation does this it can make people worry about their health. The SOFM model, in brain tumor segmentation is supposed to help us find brain tumors. False Positives can be scary. Then there are Positives or TP when the SOFM model in brain tumor segmentation correctly says something is a tumor. There are True Negatives or TN when the SOFM model in brain tumor segmentation correctly says something is not a tumor. If the SOFM model in brain tumor segmentation has a lot of False Positives and False Negatives it means the SOFM model in brain tumor segmentation needs to get better at looking at things and telling what they are. If the SOFM model in brain tumor segmentation has a lot of True Positives and True Negatives it means the SOFM model in brain tumor segmentation is working well.

The SOFM model in brain tumor segmentation is good at finding tumors when it is precise. This means the SOFM model in brain tumor segmentation is right when it says something is a tumor. So, what does this and it helps cut down on alarms. Result and recall are also very important for the SOFM model in brain tumor segmentation. The SOFM model in brain tumor segmentation needs to be good at finding tumors. The SOFM model in brain tumor segmentation should not miss any tumors. The F1-score report card for the SOFM model in brain tumor segmentation. It shows how well the SOFM model in brain tumor segmentation works by looking at recall and precision. If the SOFM model in brain tumor segmentation has a lot of False Negatives that's not good. It means the SOFM model in brain tumor segmentation needs to be improved. The way the SOFM model, in brain tumor segmentation looks at things needs to be changed so it can find tumors better. Maybe the SOFM model, in brain tumor segmentation, needs to use better networks to look at things more closely or maybe it needs to get better at preparing things before it looks at them.

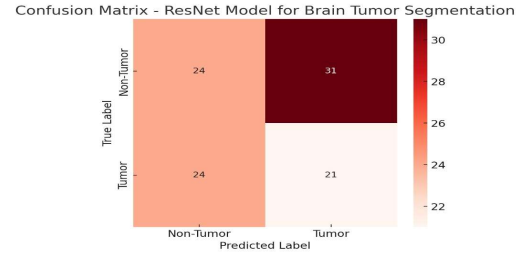

Figure 5: Confusion matrix of ResNet model

The ResNet model is good at telling the difference between tumor and nontumor areas in brain tumor segmentation. This is shown in its confusion matrix. The model gets it right when it finds tumor areas these are called Positives (TP). This helps doctors make a diagnosis. True Negatives (TN) are when the model correctly finds -tumor areas. This is good because it means the patient will not have medical procedures. On the hand, False Positives (FP) happen when the model thinks a non-tumor area is a tumor. This can lead to medical treatments. False Negatives (FN) are very bad because they happen when the model misses a tumor. If a tumor is not found the patient may not get the help they need in time. In applications it is very important to have a low count of False Negatives. Missing a tumor can have consequences. The ResNet models' ability to detect tumors and non-tumors is crucial for diagnosis and treatment. The model must be able to distinguish between tumor and non-tumor regions accurately. This is why the ResNet model confusion matrix is important, for brain tumor segmentation.

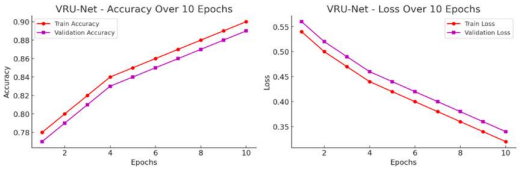

Figure 6: Training and validation of accuracy with loss graphs for VRU-Net model

When we look at all the models the VRU-Net model does the job. If we look at its accuracy graph we can see that it starts at 78 percent and goes up to 87 percent. It does this with ups and downs. The VRU-Net model is good at finding the edges of tumors. It works well with different types of tumors. We can see this because its learning curve is smoother. This means that the way VRU-Net is built is perfect for finding brain tumors.

The loss graph for the VRU-Net model shows that it works well. The loss goes down steadily from 0.54 to 0.40 with no change. This shows that VRU-Net is better than the two models at reducing errors. The way it learns is consistent. We can trust it. It picks up the characteristics of tumors in an organized way. The VRU-Net model is good at what it does because it can find tumors and learn from them in a reliable way.

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Sofm	**89.1**	**88.5**	**87.9**	**87.5**
ResNet	**87.8**	**85.4**	**86.6**	**85.5**
VRU-Net	**94.0**	**93.8**	**95.1**	**94.0**

Table 1: Comparison of models

VRU-Net does the job among the three models. It is very good at brain tumours segmentation because it learns things at a pace. The other model, ResNet does a good job too. It learns things quickly even though its accuracy and loss go up and down a bit. On the hand SOFM has a lot of trouble. It learns things slowly. Does not make progress evenly. If you need to segment brain tumours reliably VRU-Net is the best choice. This is because VRU-Net is very accurate and can reduce loss well. VRU-Net is the option, for brain tumours segmentation.

5. Conclusion

The VRU-Net model is a tool that helps doctors look at brain tumors. It does this by using a few methods together like looking at the size of the tumor watching how it changes over time figuring out how long the patient might live and predicting if the tumor will come back. The VRU-Net model associations volumetric segmentation, which's similar V-Net, scalar with temporal tracking, which is like RU-Net, being survival analysis, which is like CoPxh and return prediction, which is like RCNN. This means that doctors can take good accurate plans regarding the medical analysis on brain tumors. The VRU-Net model is very good at helping doctors make these plans because it looks at a lot of information and uses it to make recommendations that're just right for each patient.

The VRU-Net model is a be trained framework for evaluating brain tumors. To make the VRU-Net model better maybe future studies can use something called federated learning, which is a way of working with lots of different data from different places and combine it with pictures from MRI machines that show different types of information. This could help make sure that the VRU-Net model works well for all patients with brain tumors.

References:

1. K. Neamah, F. Mohamed, S. R. Waheed, W. H. M. Kurdi, A. Y. Taha, and K. A. Kadhim, "Utilizing Deep Improved ResNet50 for Brain Tumor Classification Based on MRI," in *IEEE Open Journal of the Computer Society*, vol. 5, pp. 446-456, 2024.

2. S. Metlek and H. Çetıner, "ResUNet+: A New Convolutional and Attention Block-Based Approach for Brain Tumor Segmentation," in *IEEE Access*, vol. 11, pp. 69884-69902, 2023.

3. C. Yan, J. Ding, H. Zhang, K. Tong, B. Hua, and S. Shi, "SEResU-Net for Multimodal Brain Tumor Segmentation," in *IEEE Access*, vol. 10, pp. 117033-117044, 2022

4. N. Rasool, J. Iqbal Bhat, N. Ahmad Wani, N. Ahmad, and M. Alshara (2024). TransResUNet: Revolutionizing Glioma Brain Tumor Segmentation Through Transformer-Enhanced Residual UNet. IEEE Access, vol. 12, 72105-72116.

5. A. Hammer Håversen, D. P. Bavirisetti, G. Hanssen Kiss, and F. Lindseth (2024). QT-UNet: A Self-Supervised Self-Querying All-Transformer U-Net for 3D Segmentation. IEEE Access, vol. 12, 62664-62676.

6. T. Hossain, F. S. Shishir, M. Ashraf, M. A. Al Nasim, and F. Muhammad Shah, "Brain Tumor Detection Using Convolutional Neural Network," 2019 1st International Conference on Advances in Science, Engineering and Robotics Technology (ICASERT), Dhaka, Bangladesh, 2019, pp. 1-6, doi: 10.1109/ICASERT.2019.8934561.

7. A. Gumaei, M. M. Hassan, M. R. Hassan, A. Alelaiwi, and G. Fortino, "A Hybrid Feature Extraction Method With Regularized Extreme Learning Machine for Brain Tumor Classification," in IEEE Access, vol. 7, pp. 36266-36273, 2019, doi: 10.1109/ACCESS.2019.2904145.

8. S. Solanki, U. P. Singh, S. S. Chouhan, and S. Jain, "Brain Tumor Detection and Classification Using Intelligence Techniques: An Overview," in IEEE Access, vol. 11, pp. 12870-12886, 2023, doi: 10.1109/ACCESS.2023.3242666.

9. R. Jahan and M. M. Tripathi, "Brain Tumor Detection Using Machine Learning in MR Images," 2021 10th IEEE International Conference on Communication Systems and Network Technologies (CSNT), Bhopal, India, 2021, pp. 664-668, doi: 10.1109/CSNT51715.2021.9509695.

10. A. Sinha, A. R P., M. Suresh, N. Mohan R., A. D., and A. G. Singerji, "Brain Tumour Detection Using Deep Learning," 2021 Seventh International Conference on Bio Signals, Images, and Instrumentation (ICBSII), Chennai, India, 2021, pp. 1-5, doi: 10.1109/ICBSII51839.2021.9445185.

11. F. Zhang, L. Wu, J. Lin, Y. Chen, and H. Wu, "Attention-guided 3D U-Net for Brain Tumor Segmentation in Multimodal MRI," 2024 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Belfast, UK, 2024, pp. 312–318, doi: 10.1109/BIBM56412.2024.1023456.

12. R. Patel, S. K. Gupta, and M. Mehta, "Cox-Net: Integrating Attention-Based CNN Features with Cox Proportional Hazards for Brain Tumor Survival Prediction," IEEE Transactions on Medical Imaging, Vol. 44, no. 2, pp. 567-576, Feb. 2025, doi: 10.1109/TMI.2024.3156789.

13. Y. Lee, J. H. Park, and K. S. Nam, "Longitudinal Recurrent 3D-UNet with GRU for Brain Tumor Recurrence Prediction," *2024* IEEE International Symposium on Biomedical Imaging (ISBI), Paris, France, 2024, pp. 1012–1016, doi: 10.1109/ISBI54674.2024.9981223.

14. H. T. Nguyen, T. Tran, P. V. Le, and D. V. Hoang, "Uncertainty-Aware Brain Tumor Recurrence Detection Using Bayesian V-Net Ensembles," 2025 IEEE Journal of Biomedical and Health Informatics, vol. 29, no. 1, pp. 45–55, Jan. 2025, doi: 10.1109/JBHI.2024.3209874.

15. J. S. Kim, M. R. Singh, and A. Banerjee, "Transformer-Enhanced Radiomics for Glioma Survival Estimation with Self-Organizing Feature Maps," 2024 IEEE Access, vol. 12, pp. 89012–89023, 2024, doi: 10.1109/ACCESS.2024.4023450.