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RESEARCH ARTICLE

Ensemble Technique for Brain Tumor Patient Survival Prediction

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ABSTRACT Brain Tumours pose a significant health challenge, demanding the immediate development of reliable and automated detection methods within the medical sphere. Swift and accurate identification of these Tumours are crucial for effective treatment and the well-being of patients. These growths stem from uncontrolled cell multiplication, depleting vital nutrients from healthy brain tissue and leading to organ dysfunction. Presently, the conventional method involves a manual examination of brain MRI scans by medical professionals, but this is hindered by the varied shapes and sizes of Tumours, resulting in time-consuming and occasionally imprecise evaluations. The emergence of automation holds immense potential, promising to bolster efficiency and allow medical practitioners more time for direct patient care. Traditional machine learning approaches have historically depended on labor-intensive feature engineering. In our research, we introduce an innovative approach: a combination of the U-Net model, a Convolutional Neural Network (CNN), and Self Organizing Feature Map (SOFM) in an ensemble technique for precise brain Tumour segmentation using the BRATS 2020 dataset. Our evaluation not only focuses on segmentation accuracy but also utilizes valuable survival data from the dataset to predict patient survival rates. The proposed model resulted in average training accuracy, mean Intersection over Union (mIoU), and dice coefficient scores of 0.967, 0.521, and 0.990 respectively for different epochs. Also, average validation accuracy, mIoU, and dice coefficient scores of 0.965, 0.546, and 0.992 respectively. The proposed model showcases a 98.28% accuracy in the segmentation of brain Tumours. The proposed methodology has the potential to revolutionize the landscape of brain Tumour diagnosis and treatment.

INDEX TERMS Automated brain tumor detection, BRATS 2020 dataset, U-Net, convolutional neural network (CNN), modified self-organizing feature map (MSOFM), survival information, survival prediction, tumor identification.

I. INTRODUCTION

Brain Tumour signifies an aggregation of abnormal cells within the brain, a vital organ protected by the rigid confines of the skull. The growth of such Tumours within the limited cranial space can give rise to significant complications. Brain Tumours are typically classified into two main categories: primary and secondary. Primary brain Tumours originate within the brain itself, with a majority being non-cancerous or benign [1]. In contrast, secondary brain Tumours, also referred to as metastatic brain Tumours, emerge when cancer cells from other parts of the body, such as the lungs or chest, spread to the brain [2]. The severity of brain Tumours varies according to their location and size, with some directly damaging brain tissue and others exerting pressure on adjacent neural structures. The detection of brain Tumours commonly entails the use of MRI (Magnetic Resonance Imaging) scans, offering detailed images of the brain's structure without the use of radiation, in contrast to CT scans. Consequently, MRI images serve as the primary data source in our dataset.

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Our model is trained using the Brats-2020 dataset [3], [4], [5], which comprises NIfTI files containing T1, T1ce, T2, and FLAIR images, alongside corresponding ground truth images, enabling us to advance our understanding and management of these complex conditions. The presence of a brain Tumour presents a formidable challenge in the realm of healthcare, characterized by the intricate structure of the brain. Therefore, the development of precise and robust algorithms for the automated prediction of overall survival and segmented regions in patients diagnosed with gliomas holds paramount importance. Such algorithms can provide invaluable guidance for diagnosis, treatment planning, and outcome prognostication [6]. In the context of successful surgical interventions, segmentation plays a pivotal role in efficiently identifying and delineating brain Tumours. While manual segmentation, the first approach, is inherently subjective and often fails to yield desired outcomes due to the difficulty in fully extracting Tumours without impacting surrounding healthy tissue, an automated segmentation approach becomes imperative. The latter method, relying on automatic segmentation, ensures swift and accurate detection of brain Tumours, proving essential for meticulous treatment planning and quantitative assessment. The following are the highlighting contributions of this work:

- U-Net for Brain Tumour Image Segmentation: The U-Net model is used to segment brain Tumour images from the BRATS 2020 dataset. U-Net is known for its effectiveness in image segmentation tasks and provides a foundation for precise Tumour identification.
- Modified Self-Organizing Feature Map (Modified SOFM): Proposed a novel Modified Self-Organizing Feature Map (Modified SOFM) approach to predict patient survivability based on the segmented images. The Modified SOFM [7] is designed to capture complex patterns in the data, enabling accurate patient survival predictions.
- Ensemble Approach: The U-Net-based image segmentation and Modified SOFM are combined for survival prediction, creating an ensemble technique that enhances both Tumour identification accuracy and survival rate forecasting.

The rest of the paper is organized as follows: Section II presents the related works carried out by various researchers. The problem that is addressed in this work is stated in Section III. The system model having objectives and solutions is defined in Section IV. The proposed methodology and the working principle are presented in Section V. The proposed algorithm is described in Section VI. The results are discussed in Section VII and the conclusion and the future work is summarised in Section VIII.

II. LITERATURE REVIEW

The study conducts performance comparisons using TensorFlow on the Google Colab platform. Havaei et al. [8] proposed a novel approach to address the limitation of resolution in the BraTS dataset. They performed segmentation on MRI images slice by slice, using CNN techniques. The architecture involves convolutional layers hierarchically stacked to extract incremental features.

Soltaninejad et al. [9] introduced a machine learned approach based on FCN to detect coarse Tumour regions. The model employs Random Forest for classification, albeit with higher computational time. A Cascade Deep Learning model reduces overfitting challenges by focusing on smaller image regions.

Zhou et al. [10] introduced the 'One-pass Multi-task Network' (OMNet) to address class imbalance in brain Tumour segmentation. OMNet significantly reduces model size and system complexity, though its implementation introduces increased complexity. Raut et al. [11] introduced a Convolutional Neural Network (CNN) model designed for the detection of brain Tumours. The approach involves augmenting brain MRI images to create a dataset suitable for deep learning. Following this augmentation, a preprocessing phase eliminates noise and prepares the images for analysis. The system is trained using preprocessed MRI brain images to classify new images as Tumourous or normal, based on learned features during training. Backpropagation is utilized to enhance result accuracy and minimize errors. Autoencoders are used to generate images devoid of irrelevant features. Tumour region segmentation is achieved using the K-Means algorithm, with potential for further classification accuracy improvements using different algorithms. Tamilselvi et al. [12] introduced the concept that integrating new technologies alongside existing imaging modalities could enhance brain Tumour screening. Many brain Tumour databases are inaccessible to the public. To address this, the authors presented BRAMSIT, a valuable resource for the MRI image analysis research community. BRAMSIT, 'Brain MRI Dataset for Screening and Imaging Technologies,' aims to provide a diverse collection of both normal and malignant brain Tumour images. The database includes patient-specific details such as age and MRI axial position. Diverse datasets hold the potential to further enhance the accuracy of brain Tumour analysis.

Three distinct CNN models achieve an impressive 99.33% accuracy rate for brain Tumour detection. Someswararao et al. [13] highlighted the significance of early detection in reducing the fatality rate associated with brain Tumours. They propose a novel approach using machine learning algorithms, especially the CNN model, for effective Tumour detection. Increasing the training dataset and fine-tuning model hyperparameters can bolster accuracy. Divyamary et al. [14] focused on the early detection of brain Tumours through a systematic sequence of steps, including noise removal, segmentation, feature extraction, and Naive Bayes classification. Ganasala et al. [15] emphasized the invaluable attributes of magnetic resonance imaging (MRI) for visualizing brain lesions. However, the volume of data generated by MRI scanners poses a challenge for manually delineating Tumour regions. The study focuses on identifying precise brain

Tumour segmentation approaches and evaluating various methods through image segmentation metrics. While higher accuracy is achievable, certain methods may trade accuracy for processing time. Baranwal et al. [2] introduced a system to classify brain Tumour images into three sub-types using CNN and SVM. Downsizing images and introducing controlled noise enhance model robustness.

Ranjbarzadeh et al. [16] addressed the challenges of brain Tumour segmentation through a deep learning framework featuring an attention mechanism. Irmak et al. [17] presented their work on the multiclassification of brain Tumours using CNN technology. Rani et al. [18] focused on precise computation of 3D Tumour volumes from 2D MRI images. They introduced an effective volume rendering technique for well-defined Tumour edges and 3D segmented Tumour models.

Asthana et al. [19] proposed brain Tumour segmentation using a U-Net-based model, achieving good results on various MRI datasets. Additionally, they introduced a novel regression model for predicting brain Tumour patients' survival rates, showing moderate accuracy on the tested datasets. Al Nasim et al. [20] focused on segmenting necrotic, edematous, growing, and healthy tissue regions within the brain Tumours. The use of U-Net's encoder-decoder architecture and image segmentation to exclude background details enhances efficiency. The obtained dice scores on the different BraTS datasets suggest that the model performs consistently well across multiple years, demonstrating its effectiveness in brain Tumour segmentation. Tran et al. [21] presented a comprehensive framework that leverages deep feature information from FLAIR MRI data to predict survival in brain Tumour patients, showing promising results with high accuracy and correlation scores. The suggested future research directions, including the integration of additional imaging modalities, exploration of different deep learning models, and conducting large-scale multi-center studies, indicate a commitment to improving clinical applicability and advancing the field.

The literature review showcases advancements in brain Tumour detection and segmentation using CNNs and machine learning techniques. Integrating new technologies and diverse datasets, exemplified by BRAMSIT, offers valuable resources for researchers. However, challenges such as class imbalance, increased computational complexity, and the need for optimization in processing time highlight the ongoing need for research and algorithm enhancements.

The field of radiology faces challenges in the manual analysis of MRI brain Tumour results, leading to extended diagnostic times. The reviewed papers address computational demands, existing model complexity, and accuracy limitations, stressing the necessity for more efficient and accurate automated diagnostic methods for brain Tumours.

III. PROBLEM STATEMENT

The diagnosis and prediction of survival for patients suffering from brain Tumours is a formidable challenge in the field of medical science. Traditional machine learning methods rely on manual and time-consuming feature engineering, which often limits the accuracy of patient survival predictions. The problem at hand can be defined as Feature Engineering Complexity, Segmentation, Survival Prediction Accuracy, and Effective Utilization of BRATS 2020 Dataset.

IV. SYSTEM MODEL

Let D represent the data source (BRATS 2020 dataset), P denote the preprocessing module and Tumour segmentation module be represented as S. For the Survival Prediction Module, M is used to denote the survival prediction module (Modified SOFM). The ensemble module is represented as E. The objectives are symbolized as O and the system's output as Y, representing patient survival predictions. The D provides data to the system and P processes and prepares the data. S segments Tumour images, M predicts patient survivability, and E combines the results from the Segmentation and Survival Prediction Modules. The system optimizes its components and processes according to defined objective functions. The system generates patient survival predictions (Y). The Tumour Segmentation Module receives preprocessed images and produces segmented Tumour regions: $S : P \rightarrow S$. The Survival Prediction Module uses the segmented Tumour regions and survival data: $M : S \rightarrow Y$. The Ensemble Module combines the results from the Tumour Segmentation and Survival Prediction Modules: $E : (S, M) \rightarrow Y$. The Objective Functions guide the optimization process: O : minimize $O(D, P, S, M, E)$. The system incorporates the feedback as part of the optimization process representing F for feedback.

A. OBJECTIVE FUNCTIONS

1. Feature Engineering Complexity The objective is to minimize the complexity of feature engineering:

$$Minimize : O_{feature} = f(t, e) \tag{1}$$

where t represents time and e represents effort.

2. Segmentation and Survival Prediction Accuracy The objective is to maximize accuracy for both Tumour segmentation and patient survival prediction:

$$Maximize : O_{segmentation} = A_{segmentation} = f(data) \tag{2}$$

where $A_{\text{segmentation}}$ is the accuracy of Tumour segmentation as a function of data. A_{survival} is the accuracy of patient survival prediction as a function of data.

3. Effective Utilization of BRATS 2020 Dataset The objective is to maximize the effective utilization of the BRATS 2020 dataset:

$$Maximize : O_{BRATS} = C_{BRATS} \tag{3}$$

where C_{BRATS} represents the challenge of effectively utilizing the dataset.

B. PROPOSED SOLUTION

The proposed solution involves the integration of the U-Net model for image segmentation and the Modified Self-Organizing Feature Map (Modified SOFM) for patient survivability prediction within the system.

1. U-Net-Based Image Segmentation

The objective is to maximize the accuracy of Tumour segmentation using the U-Net model:

$$Maximize : O_{U-Net} = S_{U-Net} \tag{4}$$

where $S_{\text{U-Net}}$ represents the accuracy of Tumour segmentation.

2. Modified SOFM for Survival Prediction

The objective is to maximize the accuracy of patient survival prediction using the Modified Self-Organizing Feature Map (Modified SOFM):

$$Maximize : O_{SOFM} = P_{SOFM} \tag{5}$$

where P_{SOFM} represents the accuracy of patient survival prediction. This is achieved during training by maximizing the validation accuracy and minimizing the validation loss.

3. Ensemble Approach The ensemble approach combines the accuracy of U-Net-based segmentation and Modified SOFM for an overall objective:

$$Maximize : O_{ensemble} = E = S_{U-Net} + P_{SOFM} \tag{6}$$

where E represents the overall ensemble approach accuracy, which combines segmentation and prediction accuracy.

V. PROPOSED METHODOLOGY AND WORKING PRINCIPLE

A. METHODOLOGY

In this sub-section, we describe the methodology adopted to achieve the research objectives of brain Tumour patient survival prediction using the U-Net model for image segmentation and the Modified Self-Organizing Feature Map (Modified SOFM) for survivability prediction. Figure 1 shows the proposed methodology in survival prediction. The ensemble technique is used to improve the accuracy of patient survival prediction, an ensemble technique is introduced. This involves combining the outputs from U-Net-based Tumour segmentation and the Modified SOFM-based survival prediction. The ensemble approach leverages the strengths of both segmentation and prediction models.

- **Data Collection and Preprocessing:** The research begins with the collection of data from the BRATS 2020 dataset. This dataset contains brain Tumour images and corresponding patient data. Data preprocessing is carried out to ensure data quality and consistency. This includes tasks such as:
  - Normalization: The data is scaled and normalized to facilitate further processing.
  - Feature Extraction: Relevant features are extracted from the images to represent Tumour characteristics.

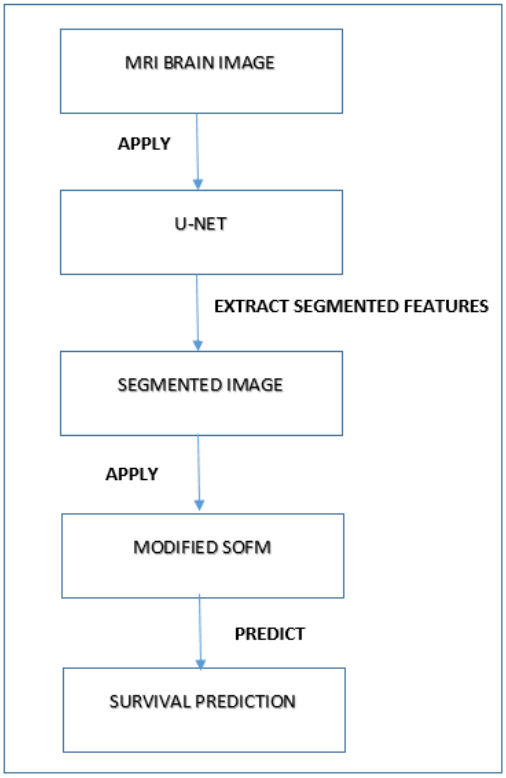


FIGURE 1. Proposed methodology.

- **Tumour Segmentation with U-Net:** The U-Net model, a Convolutional Neural Network (CNN), is employed for precise Tumour segmentation. The segmentation process is as follows:
  1) Training: The U-Net model is trained using a portion of the dataset. The model learns to delineate Tumour regions from the images.
  2) Validation: The trained U-Net model is applied to the remaining dataset to perform Tumour segmentation. The output is a binary mask indicating Tumour regions.
- **Survival Prediction with Modified SOFM:** Survival prediction is carried out using the Modified Self-Organizing Feature Map (Modified SOFM). This step involves:
  1) Training Modified SOFM: The survival data is used for training the Modified SOFM. The model learns to map Tumour features to patient survivability.
  2) Prediction: The trained Modified SOFM is applied to the segmented Tumour regions to predict patient survivability. The output is a prediction of survival rates

B. WORKING PRINCIPLE

1) U-NET ARCHITECTURE

The U-Net is a convolutional neural network (CNN) widely used for semantic segmentation tasks, including medical

image segmentation such as brain Tumour segmentation using the BRATS dataset. Ronneberger et al. proposed U-Net [1] convolution neural network for biomedical image segmentation. It is characterized by its U-shaped architecture, which resembles the letter ''U.'' The U-Net architecture consists of several sections, each with a specific function. The U-Net has three sections Encoder, Bottleneck, and Decoder sections. Here's an explanation of the different sections of a U-Net model:

- Encoder Section: The top part of the ''U'' shape is called the encoder. Its primary purpose is to capture contextual information from the input image. It consists of several convolutional layers followed by pooling layers (typically max-pooling). These layers help extract hierarchical features from the input image. Each convolutional layer increases the number of feature channels, allowing the network to capture more complex patterns.
- Bottleneck: The bottleneck, located at the bottom of the ''U,'' is a narrow portion of the network. It acts as a bridge between the encoder and decoder sections. The bottleneck has multiple convolutional layers to maintain spatial information and capture high-level features.
- Decoder Section: The lower part of the ''U'' shape is the decoder. Its primary function is to recover the spatial information lost during the encoding phase and generate the segmentation mask. The decoder consists of up-sampling layers (often transposed convolution or bilinear up-sampling) to increase the spatial resolution. Each decoder layer is paired with skip connections that bring feature maps from the encoder section at the same scale. These skip connections allow the decoder to use contextual information from earlier layers, aiding in precise segmentation.

  Skip Connections: Skip connections are crucial to U-Net's success. They facilitate the flow of detailed information from the encoder to the decoder. These connections merge feature maps from the encoder with feature maps at the same scale in the decoder. Skip connections help the model recover fine-grained details, making it suitable for tasks like Tumour segmentation.

  Final Layer: The final layer of the U-Net architecture typically consists of a single convolutional layer with a sigmoid activation function. It generates the segmentation mask, where each pixel is assigned a value between 0 and 1, indicating the probability of belonging to the Tumour region.

The U-Net architecture's distinctive ''U'' shape, skip connections, and encoder-decoder structure make it highly effective for tasks that require pixel-wise segmentation, such as identifying Tumours in medical images. It can capture both low-level and high-level features, ensuring precise and accurate segmentation.

The segmentation of the images categorizes tissue. It assigns numerical labels to these classes: 0 for ''not Tumour,'' 1 for ''necrotic or core'' Tumour regions, and 2 for ''edema'' regions. Additionally, class 3 represents ''enhancing'' Tumour regions. In the next stage, the segmented image is considered for survivability prediction.

2) MODIFIED TRAINING SCHEME FOR SOFM FOR SURVIVABILITY PREDICTION

Self Organizing Feature Map (SOFM) is an unsupervised neural network architecture that has found wide applications in data clustering. The network architecture was originally proposed by T. Kohonen in 1982 [22], [23] and many of its variants have appeared in the literature [24], [25], and [26]. The SOFM partitions the input space into several regions where each region has similar data. Thus SOFM exploits the statistical dependencies among the data in the input space for partitioning and hence a modified training scheme has been proposed for survivability prediction.

The ''Modified Training Scheme for Self-Organizing Maps (SOM)'' creates a cluster of data with a specified number of clusters. It begins by applying a two-stage Condensed Nearest Neighbours rule to extract features from the segmented image. The concept of the standard set was proposed by N.V. Subba Reddy [27]. The Condensed Nearest Neighbours rule retains the basic approach of the nearest neighbour [28], [29], [30] rule but uses only a subset of the training set of samples [31].

The ratio of the volume of the segment representing Tumour to the total volume of the Brain in each channel and the age of the patient represents the features for survivability prediction. Through iterative training, the algorithm updates weight vectors based on the Best Matching Unit (BMU) for each sample in the feature-extracted data. Once training is complete, it generates a cluster that is used to predict survivability.

VI. ALGORITHM

In the initial phase, data acquisition is initiated, which involves the retrieval of the MRI image dataset, specifically BRATS 2020. After this, image pre-processing is carried out, which encompasses the normalization of the images to a standardized scale within the range of 0 to 1, achieved through the application of the Min-Max Scalar. Additionally, modalities displaying a significant quantity of regions of interest are integrated. Continuing the procedure, the subsequent step is the cropping of unlabeled volumes. This cropping process is paramount in minimizing the presence of extraneous dark areas that may exist outside the volume of interest. Following this crucial step, the MRI images are loaded utilizing a Custom Data Generator, which plays an instrumental role in the meticulous preparation of the data for both training and testing purposes. The U-net model is then effectively and accurately employed to execute these tasks.

Algorithm 1 outlines the process of creating and training a survival prediction model using deep learning techniques.

Initialization: An empty neural network model is created, consisting of two layers. The first layer comprises 8 neurons and utilizes a Rectified Linear Unit (ReLU) activation

Algorithm 1 Brain Tumour Patient Survival Prediction Algorithm

Data: BRATS 2020 dataset
Result: EnsembleResult, Dice, C-index
Data Collection and Preprocessing
Collect data from the BRATS 2020 dataset;
Perform data cleaning, normalization, and feature extraction;
Tumour Segmentation with U-Net
Split the dataset into training and testing sets;
for *each image in the training set* **do**
    Train the U-Net model with the image;
for *each image in the testing set* **do**
    Apply the trained U-Net model to the image for Tumour segmentation;
Survival Prediction with Modified SOFM
for *each patient in the dataset* **do**
    Train the Modified SOFM with the patient's survival data;
    for *each segmented Tumour region* **do**
        Predict patient survivability using the Modified SOFM;
Ensemble Technique
Combine U-Net segmentation and Modified SOFM prediction results;
for *each patient's prediction* **do**
    if *U-NetResult* > *SOFMResult* **then**
        Use U-NetResult;
    else
        Use SOFMResult;
Evaluation and Validation
Calculate accuracy metrics for Tumour segmentation, Dice coefficient;
if *Dice* > *Threshold* **then**
    Segmentation is accurate;
else
    Segmentation is not accurate;
Evaluate patient survival prediction accuracy using C-index;
if *C-index* > *Threshold* **then**
    Prediction is accurate;
else
    Prediction is not accurate;

function. The second layer consists of 2 neurons and employs a Softmax activation function. This model is tailored to handle input data with four features.

Compilation: The model is compiled with specific settings. It utilizes the categorical cross-entropy loss function and the Adam optimizer for updating model parameters. Accuracy is tracked as a metric during training.

Algorithm 2 U-NET

Data: BRATS 2020 dataset
Result: EnsembleResult, Dice, C-index
Contracting Path (Encoder):
Input: X (Input Image);
$C_1 \leftarrow \text{ConvBlock}(X)$;
$P_1 \leftarrow \text{MaxPooling}(C_1)$;
$C_2 \leftarrow \text{ConvBlock}(P_1)$;
$P_2 \leftarrow \text{MaxPooling}(C_2)$;
...;
$C_n \leftarrow \text{ConvBlock}(P_{n-1})$;
$P_n \leftarrow \text{MaxPooling}(C_n)$;
Bottleneck:
$B \leftarrow \text{ConvLayer}(P_n)$;
Expansive Path (Decoder):
Input: B (Bottleneck Features);
$U_1 \leftarrow \text{Upconvolution}(B)$;
$M_1 \leftarrow \text{Concatenate}(U_1, C_{n-1})$;
$C_1' \leftarrow \text{ConvBlock}(M_1)$;
$U_2 \leftarrow \text{Upconvolution}(C_1')$;
$M_2 \leftarrow \text{Concatenate}(U_2, C_{n-2})$;
...;
$U_n \leftarrow \text{Upconvolution}(C_{n-1}')$;
$M_n \leftarrow \text{Concatenate}(U_n, C_1)$;
$C_n' \leftarrow \text{ConvBlock}(M_n)$;
Output Layer:
$Y \leftarrow 1 \times 1$ ConvLayer with Sigmoid Activation(C_n');
Output: Y (Segmentation Mask);

Training: The model is trained using the provided training data. This involves adjusting its internal parameters (weights and biases) across 300 training epochs. The training data is segmented into batches comprising five samples for every training iteration. Algorithm 1 incorporates two subroutines, described in algorithms 2 and 3.

The algorithm 2 description represents the U-Net architecture for semantic image segmentation, tailoured for the analysis of the BRATS 2020 dataset in a report format. The U-Net architecture comprises three key components: the Contracting Path (Encoder), Bottleneck, and Expansive Path (Decoder). In the Contracting Path, the input image X undergoes a series of convolutional operations followed by max-pooling layers, progressively reducing spatial dimensions while increasing feature maps. The Bottleneck section acts as a bridge between the encoder and decoder, preserving essential features. The Decoder path upscales the features and progressively concatenates them with corresponding features from the Contracting Path, allowing the network to capture both high-level information and fine-grained spatial details. The final output is a segmentation mask Y, generated by a 1×1 convolutional layer with a sigmoid activation, facilitating detailed medical image segmentation for tasks like Tumour detection, with evaluation metrics such as the Dice coefficient.

The proposed modified self-organizing feature map (MSOFM) for survivability prediction algorithm 3

incorporates two stages condensed nearest neighbourhood and SOFM.

The MSOFM predicts two categories of survivability:

- **SHORT**: 0 - Denotes the short survival category, including intervals from 0 to 300 days.
- **LONG**: 365 - Represents the long survival category, including intervals of 365 days or more.

This algorithm is designed to predict survivability based on segmented medical images and patient data. It begins by calculating the ratio of segmented volume to brain volume for different image slices, normalizing the features, and combining them with the patient's age. The algorithm employs a two-stage condensed nearest neighbor rule to obtain a standard subset from these features. It initializes parameters such as learning rate and neighborhood size and iteratively updates weight vectors associated with the features using the farthest neighbor method. After training, the algorithm predicts survivability into two categories, 'SHORT' and 'LONG'. In summary, it combines patient age, and segmented image information, and employs a self-organizing map to make survival predictions based on the provided data.

VII. RESULT AND DISCUSSION

A. DATASET AND PREPROCESSING

The BRATS (Brain Tumour Segmentation) dataset serves as the foundation of this study.The BRATS 2020 dataset is a substantial multi-institutional collection of routine clinically-acquired pre-operative multimodal MRI scans, including glioblastoma (GBM/HGG) and lower grade glioma (LGG), with updated datasets featuring 3T multimodal MRI scans. This dataset contains a comprehensive collection of brain MRI scans, including multiple sequences like T1-weighted, T2-weighted, T1-weighted with contrast (T1c), and Fluid-Attenuated Inversion Recovery (FLAIR) images. The BRATS dataset comprises a substantial number of MRI scans, each with varying characteristics. These images are acquired with different imaging sequences, resulting in diverse features:

- T1-weighted: Provides structural information about the brain.
- T2-weighted: Offers insights into brain tissue abnormalities.
- T1-weighted with contrast (T1c): Highlights regions with contrast-enhancing lesions.
- FLAIR: Enhances contrast between lesions and normal tissue by suppressing cerebrospinal fluid.

The dataset includes images from both Tumour and non-Tumour cases, with variations in Tumour size, location, and shape. The resolution of the images may vary as well. To prepare the dataset for training the U-Net model, a series of preprocessing steps are applied. MRI images are often subjected to pixel intensity normalization to bring all images within a consistent intensity range. This step ensures that the model isn't biased by variations in pixel values across images.

Algorithm 3 Modified Training Scheme for SOM

Data: Segmented image obtained by the application of U-Net

Result: Survivability prediction into two categories **SHORT** and **LONG**

1 Calculate the ratio of volume segment to the volume of Brain for Flair, T1ce and T2 slices respectively for $masks[1]$, $masks[2]$ and $masks[3]$: $masks[1] \leftarrow masks[1]/brain\_vol$ $masks[2] \leftarrow masks[2]/brain\_vol$ $masks[3] \leftarrow masks[3]/brain\_vol$ Extract the patient's age $age\_dict[i]$. Merge all the features one vector to $merged$: $merged \leftarrow [age\_dict[i], masks[1], masks[2], masks[3]]$

2 Apply the 2 stage condensed nearest neighbourhood rule to the features extracted to obtain the standard subset;

3 Set the values for initial learning rate $\eta(0)$ and initial neighborhood size $\sigma(0)$;

4 Set the number of iterations and the number of clusters $n_{clu} = 2$ required;

5 Normalize the samples in the extracted features and the standard data set by the maximum of the feature values;

6 Assign weight vectors from the extracted features using the farthest neighbor method at random.

7 **for** *each iteration* **do**

8 **for** *each sample in the extracted features* **do**

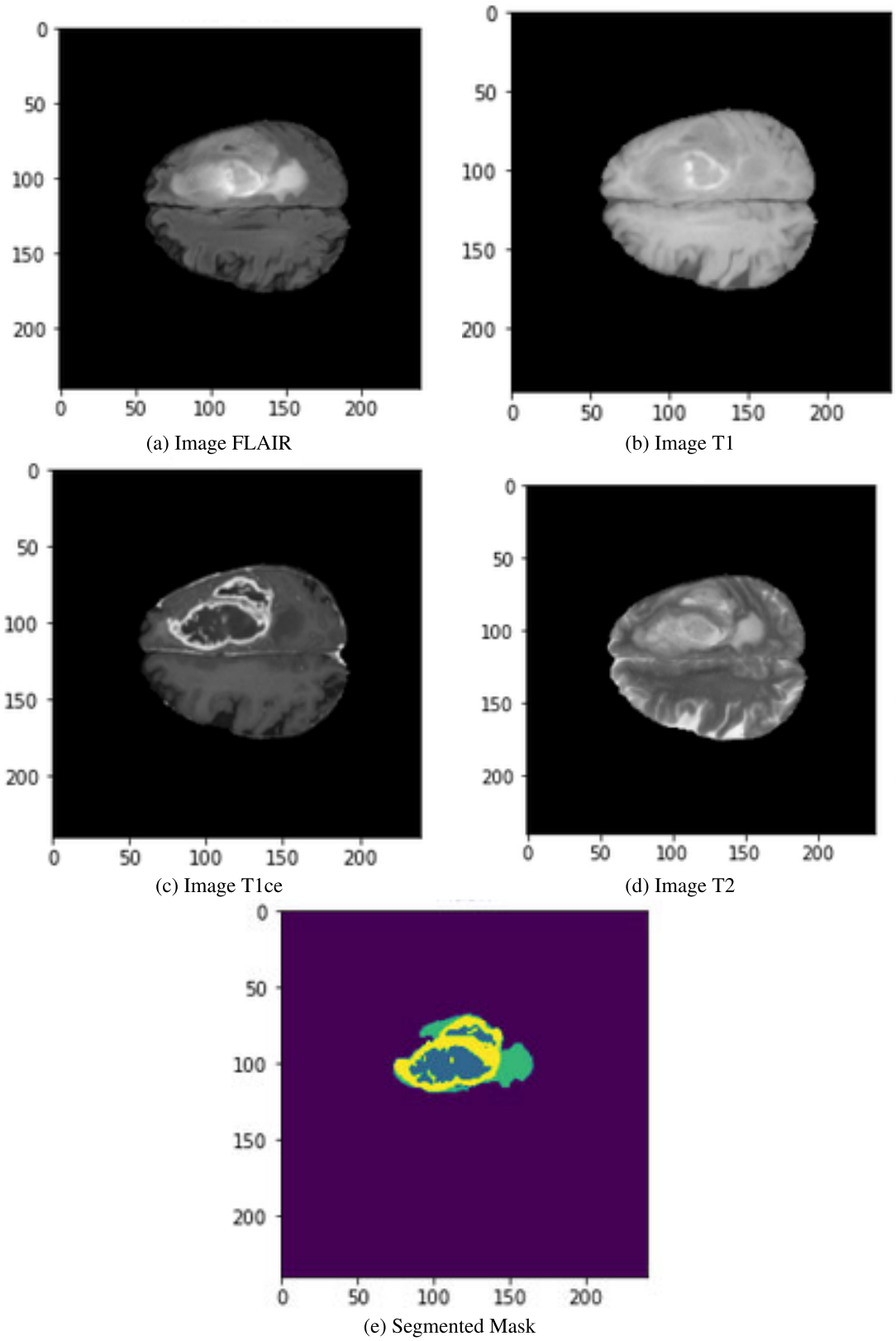
9 Find the winner or BMU for each sample present in the standard subset;

10 Update the weight vectors of the winner neuron and the neighborhood by the respective samples present in the extracted features;

11 Predict the survivability;

Output: Survibality Prediction

Images may be resized to a common resolution to standardize input dimensions. This ensures that the U-Net model can handle inputs of consistent size and facilitates training. Data augmentation techniques are employed to artificially increase the dataset's diversity. The augmentation method includes Rotation, Horizontal and vertical flipping, Adding noise, Contrast and brightness adjustments, and Elastic deformations. Data augmentation helps the model generalize better and cope with variations in Tumour appearance. For supervised training of the U-Net model, corresponding ground truth masks are generated from the segmented regions in the BRATS dataset. These masks serve as the target for the model, helping it learn to accurately segment Tumours. The dataset is split into training, validation, and test sets. The typical split ratio is 70 : 15 : 15, respectively. The training set is used to teach the model, the validation set to fine-tune hyperparameters and monitor training progress,



(a) Image FLAIR (b) Image T1

(c) Image T1ce (d) Image T2

(e) Segmented Mask

FIGURE 2. A randomly selected slice from the BraTS 2020 dataSet.

and the test set to evaluate the model's performance on unseen data.

Figure 2 displays the visualization of a sample image from BraTS dataset. The image encompasses T1-weighted

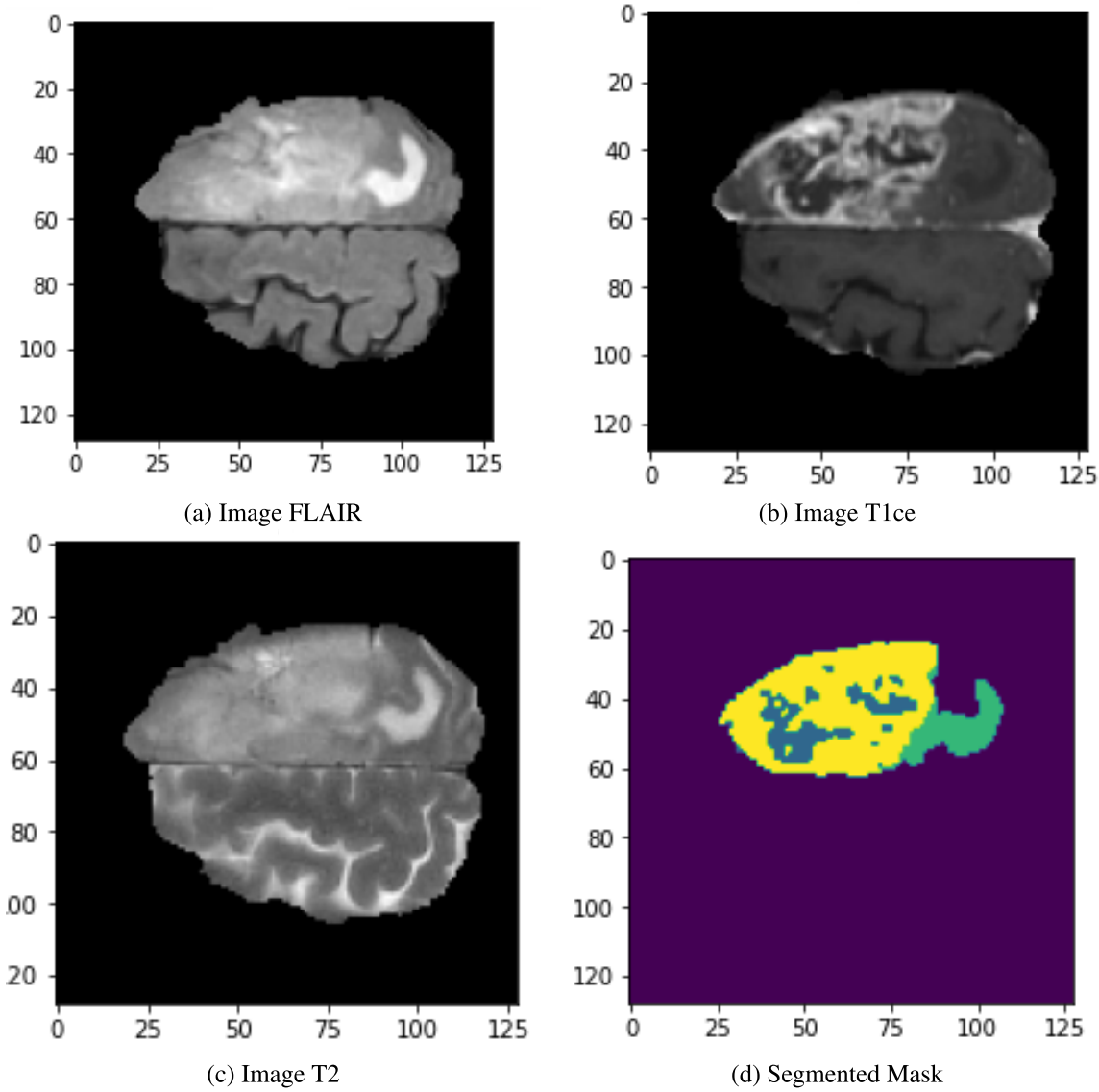


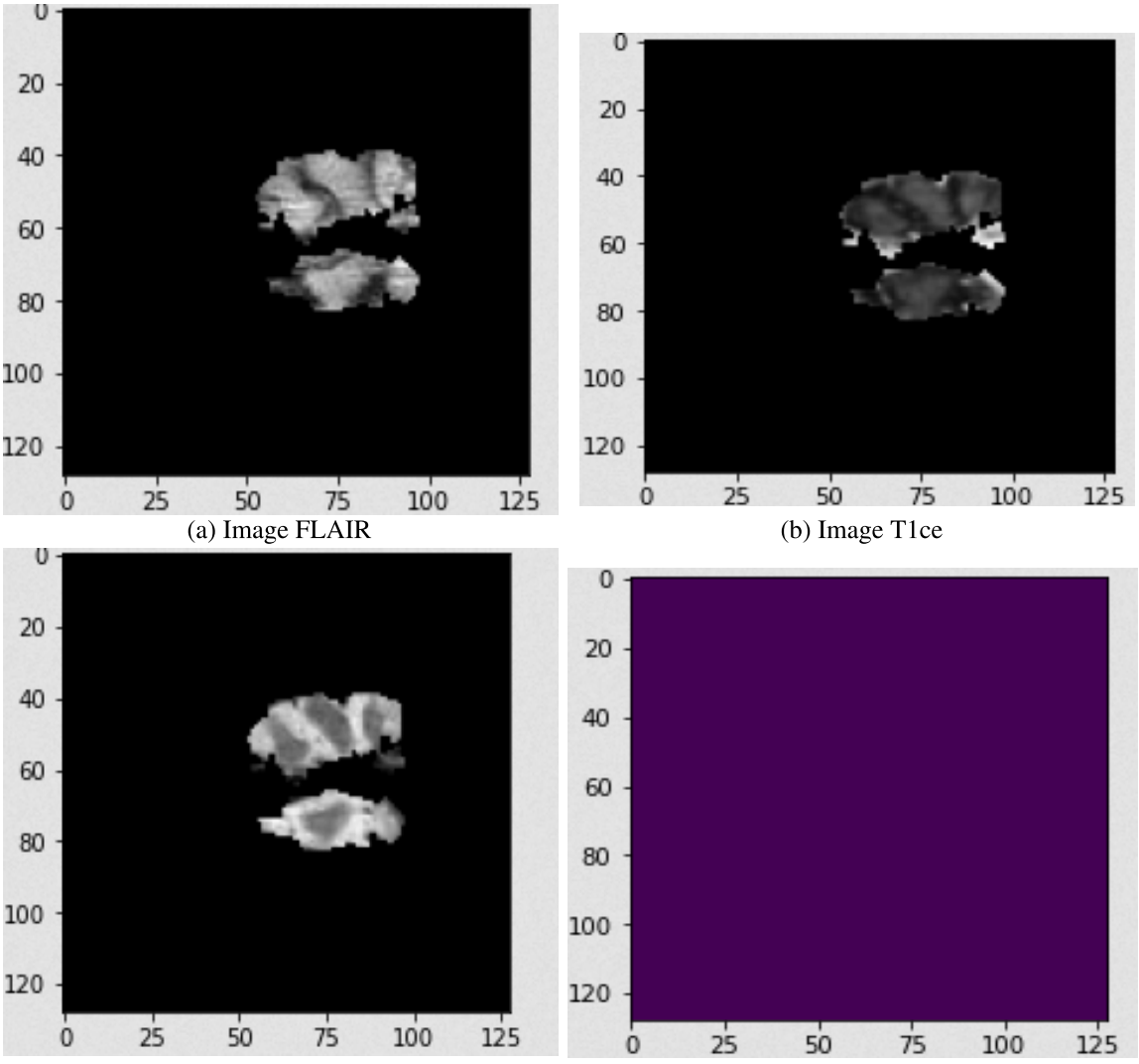
FIGURE 3. Multichannel input data and image and mask.

(T1) and T1-weighted contrast-enhanced(T1ce) images, the former with native 2D acquisitions and the latter using 3D acquisitions. Additionally, T2-weighted (T2) and T2-weighted Fluid-Attenuated Inversion Recovery (FLAIR) images are acquired with axial, coronal, or sagittal 2D methods, with slice thickness ranging from 2 to 6 mm, providing enhanced visibility of cerebral fluid. Figures 2 (a), (b), (c), and (d) illustrate the FLAIR, T!, T1ec, and T2 images. Figure 2 (e) displays the segmented mask.

The FLAIR, T1ce, and T2 images and the corresponding segmented mask are cropped to size $128 \times 128 \times 128$. A sample cropped image is displayed in Figure 3. The data is split into training and validation datasets. The image loader is implemented as a generator that provides a continuous stream of image and mask data in batches, making it suitable for training deep learning models on large datasets. The generator is designed to apply various data augmentation techniques to the loaded images and masks, which could include operations like rotation, scaling, and flipping. This generator setup is crucial for efficiently training deep learning models on large datasets. Figure 4 depicts a sample augmented dataset. Figures 4 (a), Figure 4 (b), Figure 4 (c) and Figure 4 (d) represents FLAIR, T1ce T2 and mask generated after augmentation.

B. TRAINING USING U-NET

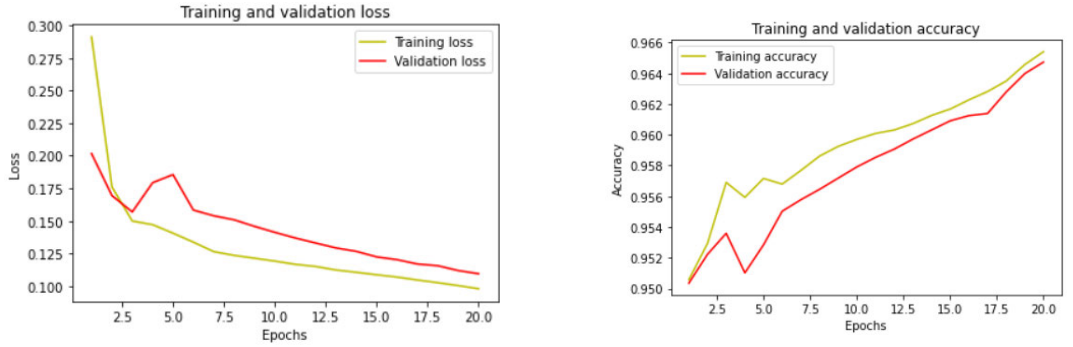
During training, the batch size is set to 2, Batch size represents the number of data samples processed simultaneously during each training or validation step. It's a key parameter that can affect training efficiency and model performance. Batch generators are mechanisms used to load and handle data in smaller, manageable portions during training. A 3D



(a) Image FLAIR (b) Image T1ce

(c) Image T2 (d) Segmented Mask

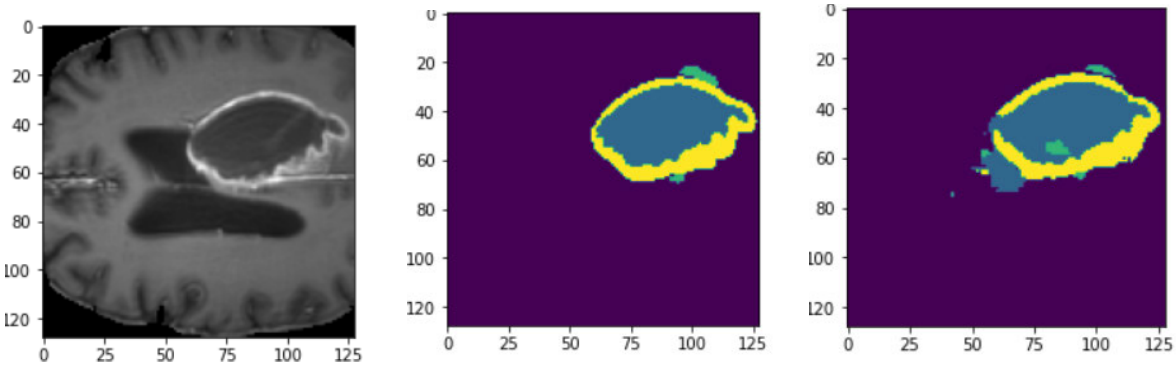
FIGURE 4. Image and mask after augumentation.



(a) Training and Validation Loss (b) Training and Validation Accuracy

FIGURE 5. Plot of loss and accuracy.

U-Net model for image segmentation with input images of dimensions 128 × 128 × 128 and 3 color channels is constructed. The model is compiled with the Adam optimizer using a learning rate of 0.001 and a suite of evaluation



(a) Testing Image (b) Testing label (c) Prediction of Test Image

FIGURE 6. Sample image after validation.

TABLE 1. Training accuracy, mIoU and Dice coefficient score for different epochs.

Number of epochs	Accuracy	Mean IoU	Dice coefficient
10	0.944	0.382	0.9665
15	0.951	0.426	0.9752
20	0.956	0.475	0.9879
40	0.963	0.511	0.9992
60	0.971	0.558	0.9996
80	0.982	0.589	0.9997
100	0.984	0.608	0.9998
120	0.987	0.623	0.9999
AVG	**0.967**	**0.521**	**0.990**

TABLE 2. Validation accuracy, mIoU, and Dice coefficient score for different epochs.

Number of epochs	Accuracy	Mean IoU	Dice coefficient
10	0.947	0.389	0.977
15	0.955	0.435	0.979
20	0.956	0.487	0.987
40	0.964	0.535	0.999
60	0.967	0.558	0.999
80	0.974	0.631	0.999
100	0.977	0.716	1.000
120	0.987	0.623	0.999
AVG	**0.965**	**0.546**	**0.992**

metrics, including accuracy, mean Intersection over Union (mIoU), dice coefficients, and more. The model is trained.

Figure 5 (a) illustrates the changes in training and validation losses across epochs using line plots. The training loss is denoted by the yellow line, while the validation loss is represented by the red line. These visualizations are instrumental in evaluating the model's performance and detecting signs of overfitting, where the model excessively optimizes for the training data at the expense of validation performance.

In Figure 5 (b), line plots showcase the training and validation accuracy over epochs. Similar to the previous plot, the yellow line corresponds to training accuracy, and the red line corresponds to validation accuracy. These visual representations offer insights into how effectively the model learns from the training data and how well it generalizes to unseen validation data. It is crucial to analyze these plots throughout the training process to ensure the model's performance aligns with the intended objectives and to identify potential issues like overfitting or underfitting.

C. VALIDATION AND SURVIVAL PREDICTION

Figure 6 depict the sample image after validating on the trained U-Net. Figures 6 (a), 6 (b) and Figure 6 (c) are the test image, ground truth image, and predicted result.

The data presented in Table 1 demonstrates a direct correlation between the increase in the number of epochs and the enhancement in various performance metrics such as accuracy, Mean IoU, and Dice coefficient. The accuracy exhibits a gradual ascent from 0.944 at 10 epochs to 0.987 at 120 epochs. Both Mean IoU and Dice coefficient display significant improvements, signifying the model's increased proficiency in accurately segmenting objects within images with extended training duration.

The table in 2 compiles essential validation metrics across various epochs in a segmentation task. It records the number of epochs, validation accuracy, mean Intersection over Union (mIoU), and Dice coefficient. The equations for Intersection over Union (IoU) and Mean Intersection over Union (mIoU) are provided below: To calculate IoU:

$$\text{IoU} = \frac{\text{Area of Overlap}}{\text{Area of Union}} \tag{7}$$

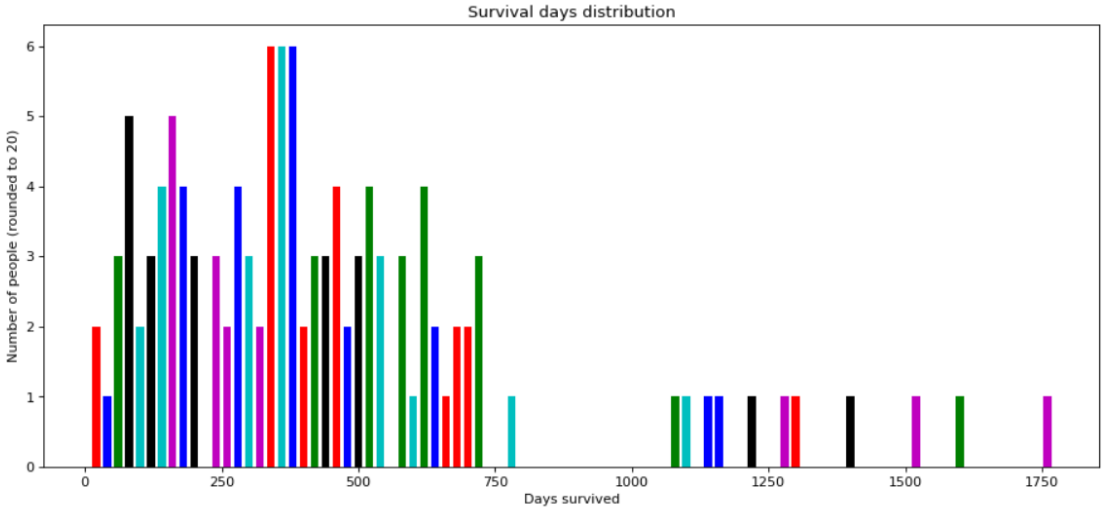
To calculate mIoU:

$$\text{mIoU} = \frac{1}{N}\sum_{i=1}^{N} \text{IoU}_i \tag{8}$$

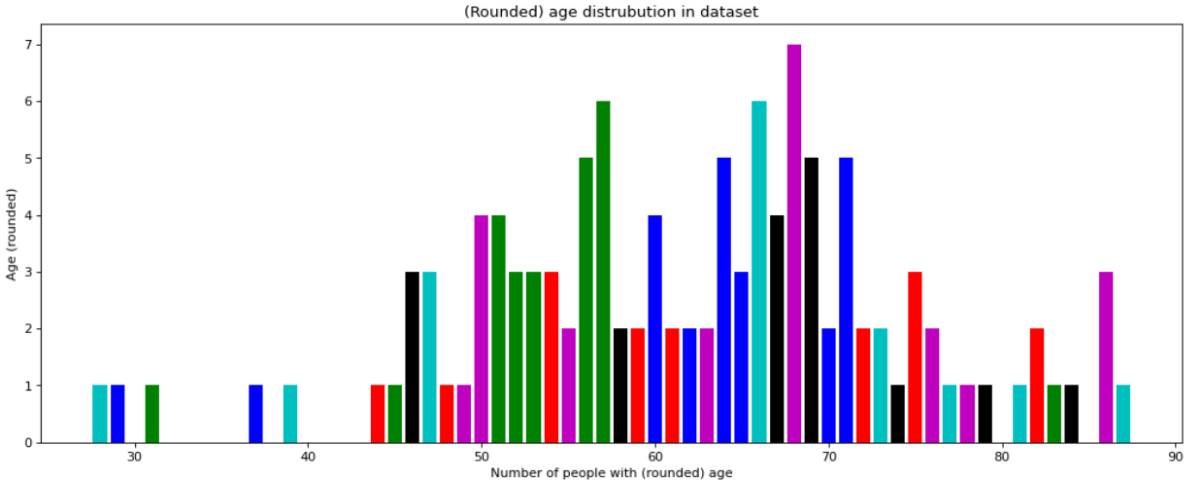
The test accuracy is calculated using

$$\text{Test Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}} \times 100\% \tag{9}$$

The results show an improvement in validation accuracy with increasing epochs, signifying the model's ability to



(a) Age distribution in the dataset



(b) Survival days predicted

FIGURE 7. Age distribution and survival prediction.

TABLE 3. Mean IoU and test accuracy.

Metric	Value
Mean IoU	0.62
Test Accuracy	0.98

accurately classify pixel segments. Both the Mean IoU and Dice coefficient increase over time, indicating enhanced overall segmentation performance and greater alignment between predicted and ground-truth masks.

The data within table 3 showcases performance metrics evaluating a machine learning model. The Mean Intersection over Union (IoU), at a value of 0.62, serves as a metric for segmentation accuracy, illustrating the model's effectiveness in delineating objects within images. Additionally, the Test Accuracy, marked at 0.98, represents the proportion of correctly classified instances within the test dataset, reflecting the model's overall classification accuracy.

D. SURVIVAL PREDICTION

The age distribution of patients in tin the BraTs 2020 dataset is illustrated in Figure 7 (a). Figure 7 (b) illustrates the predicted survival after the application of MSOM.

VIII. CONCLUSION AND FUTURE WORK

The primary focus of this work lies in the efficient segmentation of Tumour regions, aiming to expedite the diagnosis process for doctors and pathologists. Taking into consideration the performance and intricacy of the U-Net Model, the proposed model achieved mean scores of 0.967, 0.521, and 0.990 for training accuracy, mean Intersection over Union (mIoU), and Dice coefficient across various epochs. Additionally, for the validation phase, the model attained mean scores of 0.965, 0.546, and 0.992 for accuracy, mIoU, and Dice coefficient respectively. Furthermore, the model demonstrates a high accuracy of 98.28% in segmenting brain Tumours. This innovative methodology holds promising

potential to transform the field of brain Tumour diagnosis and treatment. Instead of relying on manual segmentation methods, a web-based interface has been developed for doctors, showcasing segmented regions and assisting medical professionals in their analysis. This interface facilitates doctors in assessing Tumour impact and estimating survival rates based on historical data, ultimately streamlining the diagnostic process and saving considerable time. To further improve this approach, future enhancements could involve enlarging the training dataset and meticulously selecting appropriate test samples to reduce misclassification. Additionally, the creation of three-dimensional (3D) anatomical models from individual patient data holds promise in enhancing surgical planning and guidance. Moreover, for improved testing accuracy and reduced computation time, exploring classifier-boosting techniques such as dataset augmentation, fine-tuning hyperparameters, extending training duration, and incorporating more layers could prove beneficial.

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