**RESEARCH PAPER**

# A Hierarchical CNN Model for Brain Tumor Classification and Survival Rate

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**ABSTRACT**
Automatic brain tumor segmentation and classification of MRIs are very important for diagnosing and treating brain tumors. Early and accurate detection greatly increases the chances of getting medical help on time, which in turn raises the chances of survival for patients. The dependability of these detection systems has a direct effect on how well doctors can make diagnoses and come up with effective treatment plans. Glioblastoma is among the most aggressive and lethal brain tumors; therefore, perfect accuracy in diagnosis and prognosis is essential to improving patient outcomes. This paper presents a Hierarchical Convolutional Neural Network (HCNN) model that utilizes relevant clinical data and tumor severity analysis to predict the overall survival of glioblastoma patients. The HCNN is a complex deep learning structure that combines structured rate of patient data with medical imaging to make tumor classification and survival prediction better. The model enhances MRI image feature extraction through transfer learning, thereby augmenting diagnostic accuracy and efficiency. The HCNN uses the image analysis capabilities of convolutional neural networks along with clinical records to quickly assess how a tumor is growing and how it will affect a patient's prognosis. The model works well, with a prediction accuracy of 99.67%. This shows that it could be a useful tool for making clinical decisions and planning personalized treatment. Fuzzy neural networks (FNNs) are often used to deal with unclear medical data, but they aren't very accurate, which makes them less useful in real-time clinical settings. So, the proposed HCNN architecture is a better and more reliable way to diagnose medical problems.

**Keywords**: MRI, Image Processing, CNN, Transfer Learning, Brain Tumor, Classification, Detection.
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## 1. INTRODUCTION

Brain tumors are characterized by abnormal cell proliferation and are primarily distributed into two categories: benign (non-cancerous) and malignant (cancerous). Brain tumors can lead to various symptoms, including headaches, visual disturbances, speech difficulties, disorientation, impaired decision-making, personality alterations, and hearing loss [1]. New techniques like machine learning (ML) and deep learning (DL) have made it possible to automatically analyze MRI brain images. This helps radiologists, doctors, and researchers find and classify brain tumors more accurately. Because delayed diagnosis and treatment can lead to death, it is very important to find the problem early and correctly [2]. The National Brain Tumor Foundation (NBTF) says that approx 29,000 new brain tumor cases are found in the US each year. The disease kills more than 13,000 people each year. MRI is still an important way to find brain tumors, and it has shown promising results when used with computer programs to measure tumor severity [3].

Medulloblastomas are tumors that grow quickly and are usually found in children. They are most often found in the cerebellum. Ependymomas, which come from the ependymal cells that line the ventricular system of the brain, can have different effects depending on the properties of the cells [4].

Gliomas, meningiomas, and pituitary tumors are the most frequent types of brain cancers. Predicting patient outcomes, evaluating surgical choices, and choosing suitable treatment approaches all depend on the accurate and timely detection of these malignancies [5]. With commonly utilized modalities like Computer Tomography (CT), Magnetic Resonance Imaging (MRI), and Ultrasound (US), medical imaging is essential in the detection of brain malignancies. Because of its remarkable capacity to distinguish between soft tissues, its multi-planar imaging capabilities, and its effectiveness in identifying both structural and functional problems in the brain, MRI is typically preferred among these. Manually interpreting MRI scans, however, can be time-consuming and could result in variations across radiologists. Tumors in their early stages may have modest symptoms that are

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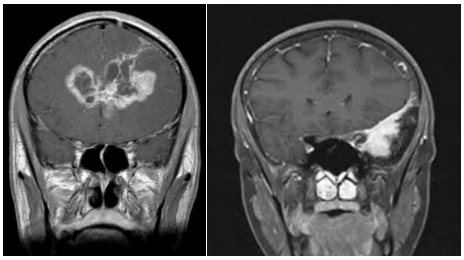
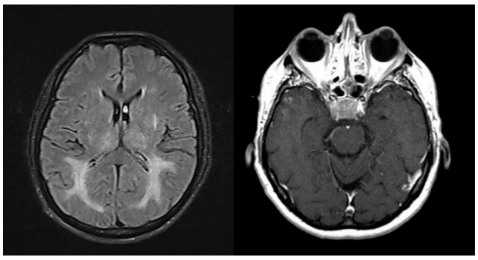
**Author for Correspondence: agarwal.shivam88@gmail.com* easy to miss. The images must go through segmentation [6], a basic image processing step, to increase diagnostic precision. By properly separating the tumor from normal brain tissue, proper segmentation improves the analysis. Semi-automatic or automated techniques can be used to accomplish this. Even though automatic segmentation facilitates large-scale applications, it occasionally lacks accuracy or requires additional computing work to produce reliable results [7].

By fixing the problems with fully automated methods, semi-automatic segmentation strikes a balance between accuracy and user control. In earlier studies [8], machine learning techniques like Random Forests (RF) and Support Vector Machines (SVM) were often used to find patterns in tumors on MRI scans. As machine learning has improved, for finding, classifying, and judging brain cancers, deep learning algorithms are more popular. Utilizing diverse MRI modalities has significantly enhanced the accuracy of these deep learning models in automatic segmentation. Convolutional Neural Networks (CNNs) are especially good at getting detailed information from medical images because they have a multi-layered structure [9, 10]. In addition to CNNs, two more deep architectures that have been used for tumor segmentation are Convolutional Restricted Boltzmann Machines (CRBM) and Stacked Denoising Autoencoders.

Various segmentation strategies—like thresholding, region-based, edge-based, contour-based, and atlas-based techniques—are already used in previous studies to extract crucial biological features like the region of tumor, which is termed as area of interest (ROI). Following feature extraction, classification algorithms such as SVM, k-nearest neighbor (k-NN), Random Forest (RF), Naive Bayes (NB), and Decision Trees (DT) are utilized to distinguish between cancerous and non-cancerous tissue regions [11,12]. Figure 1 shows a MRI scans, where Figure 1(a) displays a scan with a visible tumor, whereas Figure 1(b) represents a normal brain image without any signs of a tumor.





(a) (b)

**Figure-1**. Sample MRI Images; (a). MRI with tumor, (b). MRI without Tumor

Various earlier research works have proposed conventional methods, mathematical models, AI methods, and machine learning algorithms. But the efficiency in classification accuracy is less, time and computational complexity are high, and not provided survival rate. Estimating the patient survival rate is used to decide the appropriate treatment to extend the lifespan, the precautionary treatment to avoid other diseases, and to plan their life with their family. Only a few of the earlier research works have discussed MRI brain tumors and glioblastoma based on patient survival rates. This study addresses a significant and ongoing research challenge in the biomedical field. The main aim is to develop and implement a hierarchical deep learning framework to analyze MRI brain scans, along with patient medical records and associated metadata, to estimate patient survival rates. The proposed hierarchical model leverages deep learning techniques to automatically detect, analyze, and categorize brain MRI images, while incorporating survival data for comprehensive assessment. The main focus of this research is to forecast the overall survival duration of patients, particularly focusing on the severity of glioblastoma, by utilizing clinical information through a Hierarchical Convolutional Neural Network (HCNN) approach. The HCNN represents an innovative deep learning architecture designed specifically to assess the severity of brain tumors and estimate patient survival outcomes based on their classification. To achieve this, transfer learning is employed to increase the automated diagnosis and classification process of brain tumors. Additionally, CNN are utilized to integrate image-based results with clinical datasets, enabling a more accurate prediction of patient survival based on tumor severity. Existing literature elucidates a range of both traditional and contemporary methodologies employed for the classification and detection. The methodology section goes into more detail about the algorithms and methods used in this study. The study suggests a hierarchical predictive model that uses CNN to figure out survival rates. The results section shows the experimental results, then there is a conclusion and a discussion of possible future directions for this research.

**The contributions of this work are:**

- This method has used BRATS dataset (57195 images) segregated and used for training and validation purposes which consists of 50 patients with HGG

(Glioblastoma - Grade IV) and LGG (Lower-Grade - Grade II & III)

- The HCNN has multiple CNN architectures for identifying, detecting, segmenting, and classifying the Gliomas from the input image. The CNN architectures are integrated into a single model using a U-Net structure. The proposed HCNN model was implemented, experimented and the output found that the proposed HCNN obtained 99.67% of accuracy in prediction.
- It is done with the help of 3D Slice. It applies transfer learning with the help of a dataset. Here, the dataset is segregated and used for validation and testing purposes. The dataset is collected from different repositories.

The remaining sections are categorized as discussed in section 2, which has discussed the Literature work, which is used in this work. Section 3 has given the methodology, and 4 has given the results and discussion. Finally, section 5 has the conclusion of this work.

## 2. LITERATURE REVIEW

Compared to normal machine learning techniques, deep learning methods have gained significant traction in medical data analysis and medical image processing due to their superior performance and automated capabilities. To increase the model accuracy, Aamir M. et al. [13] introduced a hierarchical deep learning framework that merges VGG16 and VGG19. This integrated approach outperformed the standalone models, reaching a classification accuracy of 92% when combined with average pooling and SVM classifiers. Similarly, Gómez-Guzmán M. A. et al. [14] assessed the effectiveness of seven different CNN architectures for classifying brain tumors. An automated two-phase system for brain tumor identification that integrates segmentation and classification procedures was created by Asiri A. A. et al. [15] in a different methodology. With the use of independent component analysis, adaptive Wiener filtering, and neural network-based picture augmentation, their method used Support Vector Machines (SVM) for categorization. Furthermore, Bhagyalaxmi K. et al. [16] carried out an extensive evaluation of deep learning approaches for MRI image analysis in the diagnosis and categorization of brain tumors. An efficient and accurate MRI-based tumor detection model that combines fuzzy C-means segmentation, CLAHE preprocessing, and SVM classification was also shown by Alqhtani S. M. et al. [17]. It achieved a high accuracy rate of 0.982 while requiring little computing power.

CNN-based models detect, classify, and locate brain tumors in deep learning. CNN models are often used to analyze image data because of their high level of accuracy. Many different designs are put together to make up what is known in the industry as CNN. It is necessary to display a CNN model image that it can understand at a basic level to train it [18]. One model is not sufficient for all categorization tasks. It is possible to categorize the tumor in various ways using the same brain MRI picture. It is possible to think of this classification as a multi-layer classification problem because of the structure of the difficulty. The number of layers depends on the task at hand. A CNN based multi-task classifier is included in this module [19]. The neural nets in this model are trained using multi-labels and preprocessed picture data from the data preprocessing module. The test data is used to verify the model's accuracy. This module also describes whether a tumor is a present and its grade and kind. Multi tasking may be categorized according to the findings of this study. Residual Network is used for the CNN-based multi-task categorization, whereas these CNN are known as ResNets. ResNet34 is one of the first layers, broken down into sub-layers for specific classification tasks. Three different layers are required for each of the three classes [20].

Javeria A. et al. [21] introduced an automated method designed to differentiate malignant brain MRI scans from non-malignant counterparts. Sarmad M. et al. [22] make a hybrid diagnostic system that integrates multi-class SVM with deep neural networks to enhance the accurate position of brain tumor detection. Vatika J. et al. [23] conducted a comprehensive examination of diverse deep learning techniques utilized in the automated diagnosis of brain tumors through medical imaging. To make a more robust method, Kambham P. J. et al. [24] presented the VSA-GCNN-BiGRU model, which combines attention-driven graph convolutional networks with a Bidirectional Gated Recurrent Unit (BiGRU) classifier. Classification using MRI scans, Kerem G. et al. [25] gives a hybrid deep learning framework that contains the EfficientNetB0 architecture with a quantum genetic algorithm. An early detection of tumors from MRI data was presented by Parameshachari B. D. et al. [26]. Their methodology utilizes the Watershed technique with Particle Swarm Optimization (PSO) for segmentation, and employs Discrete Wavelet Transform (DWT) and Principal Component Analysis (PCA) for feature extraction. To ensure accurate classification and localization despite limited data, Chalapathiraju K. et al. [27] employed dual subnetworks with transfer learning methodologies to develop a deep learning approach for the detection and segmentation of brain tumors.

The problem with MRI segmentation and classification using neural networks is it performs better only on large-scale datasets. The images are acquired in various planes, and it broadens the database. It disturbs the classification results based on preprocessing overfitting before feeding into a neural network. Though there are many advantages to transferring learning-based CNN, it does not require preprocessing and feature engineering. It learns the data within the closest region, fetches more accurate information, and transfers it to the next layer for comparison. From the above discussion, it is noticed that a particular method is applied for each stage of image processing. It is semi-automatic, has more coding, and has more complex computational time and cost. Hence it requires a fast, efficient, and automatic image processing solution for the medical industry since it demands the same. Thus, this paper aimed to utilize deep learning algorithms for diagnosing MRI images to provide good accuracy. The motto of this paper is to examine the tumor and tumor types using deep learning algorithms on an imbalanced dataset. Since each database considered in this paper comprises a smaller number of images, a larger quantity of images is obtained from different databases to evaluate the performance. The above survey identified that the existing methods are semi-automatic and require an automatic, advanced model with deep learning for better MRI brain tumor detection and classification accuracy.

## 3. MATERIAL AND METHODOLOGY

### 3.1 Dataset

The BRATS dataset helps to train the HCNN. It applies transfer learning with the help of a dataset. Here, the dataset is split into training and validation sets. The dataset is collected from different repository [30,31]. The training phase utilizes imaging data from 107 patients, while validation is conducted using data from 50 patients. Additionally, the trained model is evaluated on a separate test set consisting of another 50 patients. To check the performance of the CNN approach, experiments are carried out on multiple datasets. These datasets are used to train the CNN model and annotate the data, enhancing its testing efficiency. The annotation process is carried out using 3D Slicer. As illustrated in Figure-2, Label-1 corresponds to the contrast-enhancing region, Label-2 identifies the necrotic core, and Label-3 represents the peritumoral edema.

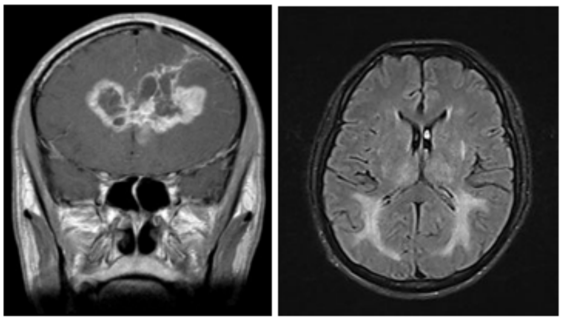


**Figure 2:** Illustration of segmentation of tumor subregions and imaging sequences: (a) T1 post-contrast, (b) T2 fluid-attenuated inversion recovery (FLAIR), (c) whole-tumor mask.

**The BraTS 2017 - HGG vs. LGG Distribution**

| Grade | Number of Patients | Percentage |
|---|---|---|
| HGG (Glioblastoma - Grade IV) | 210 | ~73.7% |
| LGG (Lower-Grade - Grade II & III) | 75 | ~26.3% |
| Total | 285 | 100% |

**Training Set (210 patients with ground truth labels)**

- **HGG: 146 patients** (~69.5%)
- **LGG: 64 patients** (~30.5%)

**Validation + Test Set (75 patients, no public labels)**

- Exact HGG/LGG split is **not publicly disclosed** (used for challenge evaluation).

**BraTS 2018 - HGG vs. LGG Distribution**

| Grade | Number of Patients | Percentage |
|---|---|---|
| **HGG (Glioblastoma - Grade IV)** | 259 | ~74% |
| **LGG (Grade II & III)** | 94 | ~26% |
| **Total** | 353 (with known grades) | 100% |

**Notes:**

1. **Training Set (285 patients):**
   - o **HGG:** 210 patients (~74%)
   - o **LGG:** 75 patients (~26%)
2. **Validation + Test Set (132 patients):**
   - o Grades **not publicly disclosed** (used for challenge evaluation).
3. **Total Confirmed Grades:** 353/485 (~73% HGG, 27% LGG).

### 3.2 Methodology

Gliomas are among the most aggressive and prevalent malignant brain tumors, playing a critical role in determining a patient's survival rate. They are typically detected through MRI scans [32]. Manually specifying the brain tumor with various stages is very difficult from MRI images. It can be obtained only by automatic learning data analytical methods. Many earlier researchers proposed multiple conventional methods, AI methods, and Machine learning algorithms. Still, the medical industry needs an efficient method to provide higher accuracy in identification and classification [33]. This research paper has proposed a Hierarchical Convolution Neural Network (HCNN) model for fulfilling the requirement mentioned above. The HCNN has multiple CNN architectures for identifying, detecting, segmenting, and classifying the Gliomas from the input image. The CNN architectures are integrated into a single model using a U-Net structure. The proposed HCNN is implemented and experimented with in Python software, and the results are verified.

The performance evaluation concludes that the proposed HCNN is a better model for Glioma's detection. Many developed techniques, like conventional MRI, CT scan, and ultrasonic scanning, can quickly scan the brain tumor areas present in the brain [34]. After detecting the brain, the scanned images are sent to the neurosurgeons who extract the tumor tissue to analyze Glioblastoma's severity. Based on the above-said information, this research suggests a hierarchical deep learning method for analyzing the medical images, providing cell information. To enhance the accuracy of the whole proposed method, it splits the entire work into stages, such as identifying the abnormality in the input image using CNN-1, segmenting the tumor using CNN-2, and classifying the tumor stage using CNN-3. Proceeding to CNN-2 and CNN-3, the output of CNN-1 should say the input image is abnormal [35]. This novelty helps to avoid the waste of time and computational complexity. The literature survey motivated this research to design and implement an efficient hierarchical CNN model for diagnosing MRI brain images with improved accuracy. The proposed HCNN model focused on overcoming the challenges and issues faced by the previous research works. It provides a solution based on classification accuracy.

The proposed HCNN model shown in figure 3, comprises three stages of the CNN model named CNN-1, CNN-2, and CNN-3 to increase overall performance time, computation, and cost complexity. The output of all three CNN is integrated to get the single result using U-Net architecture, where the production of CNN-1 is fed as input to CNN-2, CNN-2 to CNN-3, and vice versa. CNN-1 is used to learn the whole image, identify the highly differed portion (tumor), and label it as abnormal. To identify the abnormality, 3000 abnormal images are used to train the CNN-1 model, increasing the testing accuracy. Then the abnormal portion is applied to CNN-2 for segmenting the gliomas. CNN-3 learns, extracts the features, and classifies the severity of the gliomas, and finally, the CNN-4 analyzes, extracts survival data features, and classifies the tumor class based on the CNN-3 and CNN-4 output.

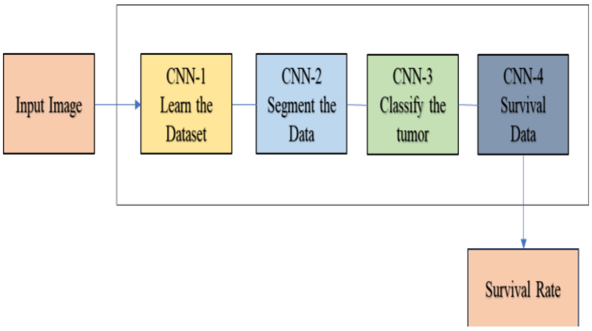


**Figure 3:** Proposed framework of HCNN model.

In the proposed HCNN architecture, a learning rate of 0.001 is used, with a 0.004 rate of decay. The model undergoes training for 300 iterations with a batch size of 5. The CNN-4 architecture has two convolutional layers, two max-pooling layers, and culminates in three fully linked layers, as depicted in Figure 4.

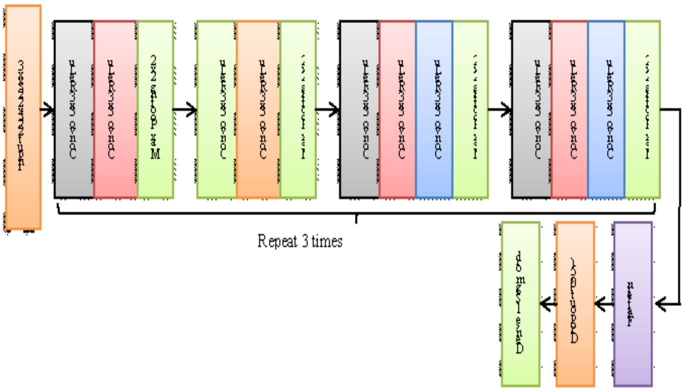


**Figure 4:** Architecture framework of Proposed HCNN model.

There are 4-convolution layers, 4-Pooling layers are involved in the CNN-1. Thirteen convolution layers with activation functions are used in CNN-2. In CNN-3, 5-convolution layers, 5-maximum pooling layers are involved with 1-flatten, 1-dropout, and 1-dense layers.

### 3.3 Survival Data for CNN-4

In HCNN Workflow as shown in Figure 3, the CNN-4 analyzes the patient survival data and sends the output to U-Net, where it combines all the results and predicts the survival rate [36]. The survival data are given in the form of *.csv format. It comprises both patient behavioral data and imaging data. From the data, the summary of the values is used for evaluation. Finally, the expected data is compared with the predicted data in figure 5.

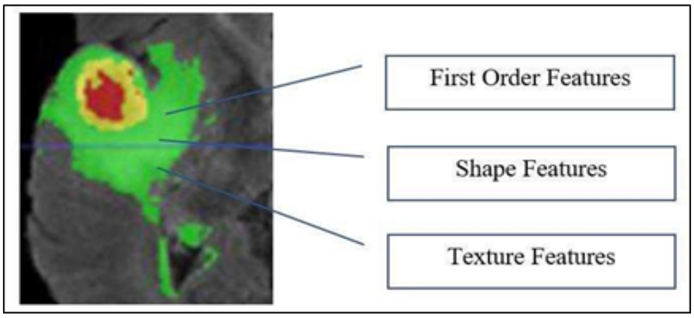


**Figure 5:** Feature Extraction from Abnormal Image (CNN-3)

Survival prediction has relevant or irrelevant features. Here, feature selection is introduced to choose some features relevant to the survival information given in Figure 5. Selecting the relevant features can improve the performance and minimize over-fitting. The ranking and cross-validation are the parameters used for Feature selection. The features are graded by merging the convolution classifiers and the gradient boosting during the training phase. Max-pooling layers reduce the feature dimensionality. Next, the selection of optimal numbers for the finest features is made through cross-validation. The finalized features are given in Table-1.

**Table-1.** Survival Features Selected for Classification

| Extracted from | Name | Subregion | Score |
|---|---|---|---|
| clinical | age | N/A | 0.037375134 |
| wavelet-LHL | glcm_ClusterShade | WT | 0.036912293 |
| log-sigma-4.0mm-3D | glcm_Correlation | TC | 0.035659833 |
| log-sigma-2.0mm-3D | gldm_LargeDependenceHighGrayLevelEmphasis | TC | 0.026891052 |
| wavelet-LHL | glcm_Informational Measure of Correlation | ET | 0.022191975 |
| wavelet-HLL | firstorder_Maximum | ET | 0.021211927 |
| wavelet-LHL | firstorder_Skewness | ET | 0.019402119 |
| original image | glcm_Autocorrelation | ET | 0.014046403 |
| wavelet-HHH | gldm_LargeDependenceLowGrayLevelEmphasis | FULL | 0.014085406 |
| log-sigma-4.0mm-3D | firstorder_Median | WT | 0.013031154 |
| wavelet-LHH | glcm_JointEntropy | WT | 0.013025344 |
| wavelet-LHL | glcm_ClusterShade | TC | 0.012335471 |
| wavelet-HLL | glszm_LargeAreaHighGrayLevelEmphasis | FULL | 0.011890386 |
| original image | firstorder_10Percentile | WT | 0.011803132 |

The Figure 6 represents the significance of various features obtained from clinical information and medical imaging in terms of their impact on a predictive model. Among all, the clinical feature age stands out with the highest score, indicating its strong influence on the model's outcome. Several texture-related features extracted from wavelet-transformed images, like glcm_ClusterShade and glcm_Correlation, also rank highly, particularly those related to specific tumor areas such as the whole tumor (WT) and tumor core (TC). Additionally, features derived from gray-level patterns and spatial relationships—such as gldm and glszm—play a substantial role, capturing structural and intensity-based variations within tumor regions. First-order statistical measures, including Maximum, Skewness, and Median, offer moderate importance but still contribute meaningful insights into pixel intensity distribution. Overall, the graph helps pinpoint which features are most valuable, aiding in the refinement of model inputs and improving the interpretability of medical image-based predictions.

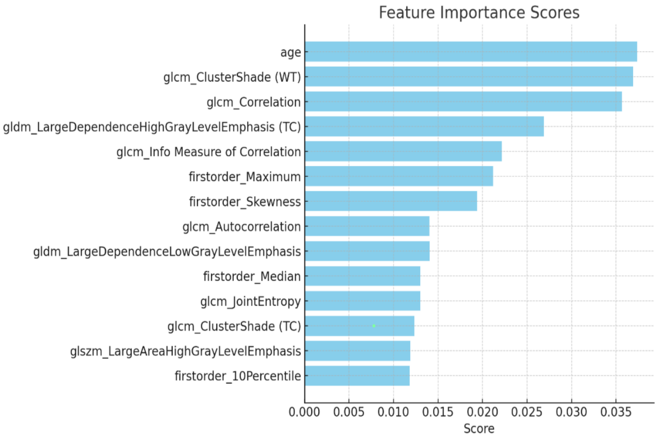


**Figure 6:** Graph of Survival Features Selected for Classification

The HCNN model is introduced for overall survival prediction based on the above 14 features. It works based on 4 different CNN models. For presenting randomness and diversity, every base convolutional layer is used to accomplish on sub-dataset that are bootstrapped. The average prediction values are calculated from base classifiers that help to enhance the prediction accuracy and reduce over-fitting. Finally, a loss function acts as a mean squared error obtained from every convolution model.

The patients above 18 years identified primary Glioblastoma from July 2016 to January 2018. This study must not include the previous patients of glioma and cranial surgery. The records of the patients are collected electronically based on the characteristics of the clinical tests. Power reduction is the motor deficit in brain tumor detection, and sensation reduction is the sensory deficit in modality cases. Speech problems are termed expressive dysphasia [37,38, 39, 40, 41]. It is used to indicate speech difficulties. The records help to derive the factors electronically, such as the American Association of Anesthesiologists (ASA) grade and utilization of 5-aminolevulinic acid (5-ALA). It may also include the surgery of neurostimulation. After the surgery, it is necessary to record the Postoperative neurological deficit and Isocitrate dehydrogenase (IDH) mutation. It also includes the MGMT promoter methylation. The differentially methylated regions are thus pyro sequenced to determine the MGMT promoter methylation. It is done with a value of 10% cutoff. Chemoradiation and radiotherapy will help to treat brain tumors disease in patients. It increases stabilization with supportive care. The national records help to produce the patient's date of death accurately. The NHS Spine database is queried about the date that indicates the last follow-up. The data that relates to the research are recorded based on the patient demographics and imaging. The local research ethics committee is used to approve this research.

### 3.4 Evaluation Metrics

In brain tumor classification using deep learning, it is crucial to assess the model's performance using appropriate statistical measures. Commonly used metrics include Sensitivity, Specificity, and Accuracy. Each of these offers distinct insights into the model's effectiveness in distinguishing between tumor and non-tumor MRI scans.

**1. Sensitivity (Recall or True Positive Rate)**

$$Sensitivity = \frac{True\ Positive}{True\ Positive + False\ Negative}$$

Eq. 1

Sensitivity in equation 1 indicates the model's ability to correctly identify patients who actually have a brain tumor. A high sensitivity means the model successfully detects most of the true tumor cases, minimizing the chances of missing a tumor (false negatives) [36]. This metric is especially important in medical diagnosis because missing a tumor can have severe consequences.

**2. Specificity (True Negative Rate)**

$$Sensitivity = \frac{True\ Negative}{True\ Negative + False\ Positive}$$

Eq. 2

Specificity reflects how well the model identifies patients who do not have a tumor as given in equation 2. A higher specificity means fewer healthy individuals are wrongly diagnosed with a tumor (false positives). This helps reduce unnecessary treatments, tests, and anxiety for patients who are actually healthy.

**3. Accuracy**

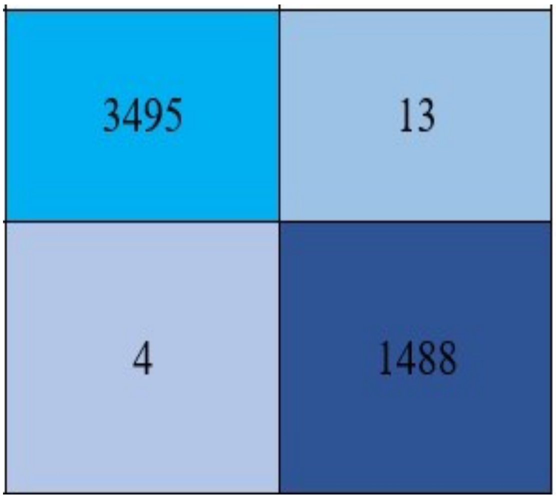
$$Accuracy = \frac{True\ Positive + True\ Negative}{True\ Positive + True\ Negative + False\ Positive + False\ Negative}$$

Eq. 3

Accuracy represents in equation 3 shows the overall correctness of the model by considering both correctly predicted tumor and non-tumor cases. While it provides a general measure, it may not fully reflect performance in situations with class imbalance (e.g., when tumor cases are much fewer than non-tumor cases).

## 4. RESULT AND DISCUSSION

From the results, it is easy to understand the performance of the proposed method used in this research work. For doing that, some of the performance measures, like accuracy is calculated and compared with one another. The HCNN architecture contains two parallel pathways, where they extract four features associated with 53 kernels. Finally, it has three layers, in which two are fully connected, and the other layer is used for final classification. The input channels process the multi-scale data and the final classification. This methodology minimizes the computational cost. The original image is operated on the first pathway. A down- sampled version helps manage the second pathway. The coefficient of the Dice and the segmentation volumes are compared to determine the segmentation quality. The overlapping of two segmentation is the Dice coefficient. It lies between zero and one. The current dataset is tested to compare the segmentation of the sub-regions and the automated labels. Finally, each tumor's sub-regions are compared with differences in both the volumes of both manually and corrected segmentation. Consider the n value to be 500 for the test data of BRATS. Hence, this model effectively generates the Dice coefficient for the automated labels. These ground truths, which are manual, are noted by the experts. The performance of HCNN model is estimated using the true positive, true negative, false positive, and false negative values. The estimated values are TP - 3495, TN - 1488, FP - 13, FN - 4. Based on these values the confusion matrix is calculated for analyzing the efficiency of the proposed method and it is shown in Figure 7.



| | |
|---|---|
| 3495 | 13 |
| 4 | 1488 |

**Figure 7:** HCNN Confusion Matrix

The deep learning network integrates with the processing pipeline to measure the volumetric features of the semi-automated Glioblastoma. It is derived from the preoperative MRI. The BRATS dataset helps to train the CNN. The training is done before testing the common clinical dataset. The manual corrections of the automated segmentations can generate the labels of the final segmentation. For evaluating the performance, both the clinical and BRATS datasets are compared with the help of the Dice coefficient. The volumetric features' performance is evaluated by assessing the validity based on the segmentation approach. The overall death risk is high. Here, the CER/TC and NC/TC are highly independent. The death risk of biopsy patients is low associated with NET/WT. RTV is used to associate with CER/TC to evaluate overall survival (OS). The angiogenesis and hypoxia are correlated with the genes and CER in the radiogenic research. The NC and the CER are not linear. Though the CER/TC and the volume of the core tumor are independent, necrosis has high proportions of the corresponding tumor volume. The glioblastomas are associated as a false negative with the volume of CER for survival. Hard-copy imaging provides limited accuracy of the volumetric measurements. If the VASARI variables are adjusted, survival is worsened for the CER volume. However, it cannot be controlled in the adjuvant treatment. CER/TC is associated with overall survival (OS). For achieving more accuracy, CER/TC is used. CER is related to the volume of the core tumor. The usage of steroids will affect the components of the edema. From the overall discussion and experimental analysis, it is found that the proposed HCNN model obtained high accuracy in analysis and prediction accuracy.

**Table 2:** Performance Comparison in terms of different metrics.

| Methods | Sensitivity | Specificity | Accuracy |
|---|---|---|---|
| AFNSS | 88.59 | 98.19 | 98.80 |
| VGG-16 | 92.51 | 93.15 | 92.84 |
| VGG-19 | 99.31 | 98.54 | 99.11 |
| HCNN | 99.90 | 98.94 | 99.67 |

From the above results, the overall prediction accuracy obtained using ANFSS, VGG-16, VGG-19, and HCNN-OS are compared and given in Table-2. From the comparison, it is identified that the proposed HCNN outperforms in accuracy than others. Thus, it is decided that HCNN algorithm is highly suitable for brain tumor diagnosis and survival prediction.

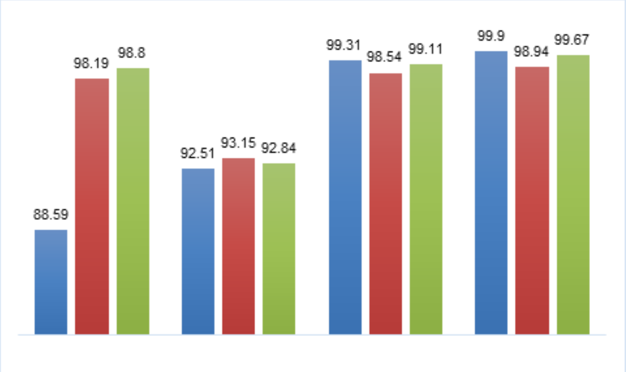


**Figure 8:** Graphical representation of evaluation metrics.

Figure 8 illustrates a comparison of four deep learning models—AFNSS, VGG-16, VGG-19, and HCNN—based on three essential evaluation metrics: sensitivity, specificity, and accuracy. Sensitivity indicates the model's effectiveness in detecting true positive cases, whereas specificity measures its capability to accurately identify true negative cases. Accuracy denotes the overall rate of correct predictions made by the model. Among the models**,** HCNN shows the highest performance with nearly perfect scores in all three metrics: 99.90% sensitivity, 98.94% specificity, and 99.67% accuracy, indicating it is highly reliable for classification tasks. VGG-19 also performs exceptionally well, with 99.31% sensitivity and 99.11% accuracy, slightly outperforming VGG-16 in all areas. AFNSS, although slightly behind the others in sensitivity (88.59%), maintains a strong accuracy score of 98.80%, making it a competitive model. Overall, HCNN leads the group, followed closely by VGG-19, based on these evaluation metrics.

## 5. CONCLUSION

The final stage of this research work motivated the design and implementation of a novel Hierarchical CNN model for MRI brain image analysis, gliomas detection, and patient survival classifications. Since gliomas are dangerous eye diseases, it needs to be identified and treated immediately to avoid vision loss. Compared to the earlier approaches, this research highly focused on improving the accuracy of tumor detection classification, identifying it as a glioma, analyzing the patient and other survival characteristics or features, and predicting the overall survival rate. It can be obtained only by automatic learning data analytical methods. Many earlier researchers proposed multiple conventional methods, AI methods, and Machine learning algorithms. Still, the medical industry needs an efficient method to provide higher accuracy in identification and classification. The proposed a Hierarchical Convolution Neural Network (HCNN) model for fulfilling the requirement mentioned above. The HCNN has multiple CNN architectures for identifying, detecting, segmenting, and classifying the Gliomas from the input image. The CNN architectures are integrated into a single model using a U-Net structure. The proposed HCNN model was implemented, experimented and the output found that the proposed HCNN obtained 99.67% of accuracy in prediction. In future, The Fuzzy neural network is applied most on uncertainty data, and the prediction accuracy is less, which cannot be used in the real-time medical industry. In future work, it can compare the proposed model with the other transfer learning models, such as ResNet, Inception-V3. Classifying the Tumor helps to provide appropriate treatment for extending people's lifetime. The survival data given in this research work is too complex that an ordinary reader cannot understand. Hence, the survival data should be collected in person from the patients, analyzed, and predicted the overall survival rate in future work.

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