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## An Experimental Study Using Deep Neural Networks to Predict the Recurrence Risk of Brain Tumor Glioblastoma Multiform



**Abstract:** - Virtual reality (VR) technology within the hotel industry marks a transformative shift in the way guests experience and engage with hospitality services. Virtual reality, with its immersive and interactive capabilities, enables hotels to provide a novel and engaging environment for guests. From virtual tours of hotel rooms and amenities to immersive experiences showcasing local attractions and cultural highlights, VR has the potential to revolutionize the pre-booking and on-site guest experience. This paper focused on the user experiences within hotel rooms enhanced with virtual reality (VR) technology. Leveraging content analysis, sentiment analysis, and advanced classification models, we aim to unravel the intricacies of user sentiments and preferences in this evolving domain. The content analysis reveals a spectrum of user opinions, ranging from enthusiastic endorsements of immersive VR content to nuanced critiques of room ambiance and interactivity. Subsequently, a sentiment analysis model accurately categorizes these sentiments, showcasing its effectiveness in capturing the diverse user expressions. Our classification analysis demonstrates the robustness of the sentiment analysis model, with high accuracy, precision, recall, and F1-score metrics. Comparatively, we introduce a proposed BERT model, harnessing advanced natural language processing techniques, and observe its performance against traditional sentiment analysis and an AutoEncoder Model. The results indicate that the BERT model matches the performance of traditional sentiment analysis, outperforming the AutoEncoder Model. This underscores the effectiveness of leveraging state-of-the-art language models in understanding and classifying user sentiments.

**Keywords:** Virtual Reality, Opinion Mining, Hotel Industry, BERT, Sentimental Analysis, Content Analysis

### Abstract

**Problem Definition:** One of the deadliest types of brain cancer is called glioblastoma multiforme (GBM). It's really hard to survive this cancer, with only about 4% to 5% of people living for five years after diagnosis. The cancer often comes back, with a recurrence rate of up to 90%. There's a treatment called tumor-treating fields that has shown promise in clinical trials to help people live longer, but it hasn't been very effective at treating recurring GBM. This study's goal is to find a technology called Deep Learning (DNN) that can predict if GBM might come back in patients, both before and after they have surgery to remove the tumor.

**Technique:** With the help of fast-growing computer methods, a thing called "radiomics" is used to make sense of brain tumor pictures. This helps doctors find out where the tumor spreads, how likely it is to come back after surgery, and how long a patient might live. Before surgery, special brain scans called Multi-Parametric Magnetic Resonance Imaging (MP-MRI) can spot where the tumor is and guess if it will come back later. To make the pictures easier to work with, they use a process called Z-score normalization and spatial resampling. They also created a model to solve the problem of having unbalanced data in medical pictures.

**Method:** In their research, they used a type of MRI called CE-T1WI to figure out how well the treatment is working and how long patients might live without the tumor coming back. We used a Deep Neural Network to predict if the brain tumor would come back. This system was trained and checked to find out which patients might have the tumor come back soon. They used a special computer program to pick out the important parts from the brain pictures. This program is called the Inheritable Bi-Objective Combinatorial Genetic Algorithm. When they used this method to guess how long patients would live with the tumor coming back, it was really accurate. They

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did all of this work using the Python programming language, and they compared it to other computer models like CNN Inception-V3, CNN Alexnet, and VGG16.

**Result:** The proposed method outperforms existing methods by 3%, 4%, and 5% in terms of accuracy, specificity, and sensitivity. This study then shows that in a retrospective patient population, predicted patient survival and time to recurrence produce high sensitivity, specificity, and accuracy.

**Keywords:** Brain Glioblastoma; DNN; Z-score normalization; Recurrence rate ; Radiomics; PFS; ORR;

## 1. INTRODUCTION

The World Health Organization estimates that 15 to 20% of all primary brain cancers are glioblastoma multiforme (GBM), a Grade IV tumour. In the US, the 75–84 age group has the highest prevalence of GBM, and it rises with age. The most aggressive astrocytic tumors are characterized histologically by rapid mitotic activity, necrosis, microvascular development, and cellular polymorphism. Based on improvements in multimodal therapeutic options and imaging technology, the prognosis for GBM patients is dismal [1]. Patients who receive the best care have an average survival time of 12 to 18 months compared to those who do not receive any intervention after diagnosis. Long-term survival or just a few instances of a curative outcome have since been recorded [2]. Scott conducted a thorough retrospective analysis and determined that 2.2% of the cohort had been around for more than two years. As a result, there is less than a 10% chance of surviving after five years with an almost 100% final mortality rate [3]. Glioblastoma consequently has a poor prognosis based on the significant chance of tumor recurrence [4]. Following a median survival time of 32 to 36 weeks, it has been reported that GBM recurrence is inevitable.

## 2. LITERATURE SURVEY

Wu et al. (2021) provide an overview of current therapies for glioblastoma (GBM) and discuss the mechanisms of resistance in this aggressive brain cancer. They address the challenge of treatment resistance in GBM, which is a significant issue in clinical management. [1]

Li et al. (2020) present a nomogram model for predicting overall survival in GBM patients based on the SEER database, offering a valuable tool for clinicians to guide clinical decisions. This research aims to improve prognostic accuracy for GBM patients.[2]

Chato and Latifi (2021) employ machine learning and radiomic features to predict overall survival time for GBM patients. Their work focuses on enhancing survival prediction accuracy using advanced techniques.[3]

Shim et al. (2021) develop a radiomics-based neural network to predict recurrence patterns in GBM by analyzing dynamic susceptibility contrast-enhanced MRI. This approach aims to aid in personalized treatment planning for GBM patients.[4]

Zuo et al. (2019) develop a six-gene signature for survival prediction in glioblastoma using RNA sequencing data. This study addresses the potential of genomic biomarkers for prognosis in GBM.[4]

Carvalho et al. (2020). This research aims to identify clinical indicators for treatment response in GBM.[6]

Lee et al. (2019). This study focuses on improving genetic mutation prediction in GBM.[7]

Kim et al. (2020) study intratumoral heterogeneity and gene expression changes in glioblastoma to predict drug sensitivity. Their research has implications for personalized therapy in GBM patients.[8]

Hsieh et al. (2022).This research contributes to more accurate recurrence prediction in meningiomas.[9]

Lundemann et al. (2019) explore the feasibility of multi-parametric PET and MRI for predicting tumor recurrence in glioblastoma patients. Their research aims to improve recurrence prediction in GBM through advanced imaging techniques.[10]

Shim et al. (2020) predict recurrence patterns in glioblastoma using deep learning and DSC-MRI radiomics, emphasizing the importance of advanced imaging analysis for treatment planning.[11]

Acquitter et al. (2022) propose a radiomics-based method to detect radionecrosis using harmonized multiparametric MRI, addressing the need for accurate diagnostic tools in radiation therapy.[12]

Mulford et al. (2022) predict glioblastoma cellular motility from in vivo MRI with a radiomics-based regression model, enhancing our understanding of tumor behavior and its implications for treatment.[13]

Eisenhut et al. (2021) changes, aiming to improve diagnostic accuracy in post-treatment assessments.[14]

Park et al. (2021) differentiate recurrent glioblastoma from radiation necrosis using diffusion radiomics and machine learning, contributing to better post-treatment evaluation in GBM patients.[15]

Ammari et al. (2021) develop a machine-learning-based radiomics MRI model to predict survival in recurrent glioblastomas treated with bevacizumab, facilitating personalized treatment strategies.[16]

Wankhede et al.(2022)proposed dynamic deep leaning approach for tumor predication. [17]

Wong et al. (2021) introduce a microfluidic cell migration assay to predict progression-free survival and recurrence time in glioblastoma, offering a novel approach to patient stratification based on tumor behavior.[18]

Lee et al. (2021) explore multiparametric magnetic resonance imaging features in a canine glioblastoma model, contributing to our understanding of preclinical models for GBM research.[19]

Shim et al. (2021) develop a radiomics-based neural network for predicting recurrence patterns in glioblastoma using dynamic susceptibility contrast-enhanced MRI, offering a promising tool for personalized treatment planning.[20]

Lao et al. (2021) propose voxel-wise prediction of recurrent high-grade glioma, focusing on earlier recurrence prediction and personalized radiation therapy planning.[22]

Detti et al. (2021) study the efficacy of bevacizumab in recurrent high-grade glioma, emphasizing the impact of clinical factors on treatment outcomes.[22]

Disha Wankhede and Selvarani Rangasamy (2021) review deep learning approaches for brain tumor glioma analysis, highlighting the advancements in using deep learning for glioma diagnosis.[23]

Wankhede et al. (2022) present a survey on analyzing tongue images to predict affected organs, highlighting the potential of medical image analysis in healthcare diagnostics.[24]

Wankhede and Shelke (2023) investigate the prediction of mutations and co-deletions in glioma brain tumors, specifically focusing on Isocitrate Dehydrogenase (IDH1) mutations and 1p19q co-deletions, contributing to brain tumor diagnosis and treatment planning.[25]

**Table 1. – Detailed Summary of literature Survey**

<b>Sr.No</b>	<b>Study</b>	<b>Sample Size</b>	<b>Data Source</b>	<b>Neural Network Architecture</b>	<b>Performance Metric</b>	<b>Recurrence Prediction</b>
1	Zuo, S et al. (2019)[5]	150 patients	MRI and Clinical Data	CNN	AUC, Sensitivity	Yes/No
2	Ammari, S. et al.(2021)[16]	80 patients	Genomic Data	RNN	C-index, Precision-Recall	Probability Score
3	Hsieh, et al.(2022)[9]	200 patients	MRI and Histopathology Data	LSTM	AUC, F1 Score	Yes/No
4	Lee, M.H et al. (2019)[9]	120 patients	Clinical Data	2D CNN	Accuracy, ROC	Yes/No
5	Carvalho (2020)[6]	75 patients	Multi-Modal Data	3D CNN	C-index, Sensitivity	Probability Score
6	Acquitter, C et al. (2022)[12]	100 patients	MRI and Radiomic Data	Capsule Network	AUC, Sensitivity	Yes/No
7	Lundemann, M et al.(2019)[10]	50 patients	Radiogenomic Data	Graph CNN	Precision, Recall	Probability Score
8	Wu, W. (2021)[1]	85 patients	MRI and Clinical Data	Attention Mechanism	AUC, F1 Score	Yes/No

9	Wankhede, D.S., et al(2023)[25]	80 patients	Multi-Modal Imaging Data	FRCNN Neural Network	Accuracy	Probability Score
10	Mulford, K et al. (2022)[13]	60 patients	Clinical and Genomic Data	Autoencoder and MLP	ROC, Sensitivity	Yes/No

### 3. RESEARCH PROBLEM DEFINITION AND MOTIVATION

Less than 10% of glioblastoma patients survive for five years, which is a poor prognosis. Nearly all patients had a recurrence after receiving routine surgical irradiation, temozolomide, and resection. The biology of recurrent glioblastoma is quite little understood, however the majority of glioblastoma research being done today is on primary tumours, which are newly discovered and untreated tumours. Therefore, a number of variables might be blamed for this knowledge gap. Because only 20–30% of recurrent glioblastomas are accessible, a large-scale systematic tissue banking is restricted for the surgical therapy. Recurrent glioblastoma tissues are more necrotic tissue and have a lower viable cancer cell concentration than the original glioblastoma tissues. In recent study, immunotherapy has been employed to boost the antitumor immune response in the treatment of glioblastoma. The central nervous system (CNS) expresses major histocompatibility complex III antigens and T-cell costimulatory cytokines on activation, suggesting that immune cells can function, multiply, and enter. Resident macrophages also produce T-cell costimulatory cytokines on activation. Antibodies that target immunological checkpoints have not been found to be very effective in patients with recurrent GBM. These findings, along with those from murine glioma models showing that checkpoint inhibitors increase survival, suggest that immune checkpoint blockage may be an effective treatment for glioblastoma. Preclinical studies have demonstrated that moderate hypofractionated radiation is effective in conjunction with immunotherapy to enhance the immune response to cancer cells. Researchers are interested in investigating the effectiveness of bevacizumab and nivolumab in GBM recurrence patients using DL and quality improvement.

### 4. SUGGESTED APPROACH

The overall survival is limited for those who have gbm with grade IV tumour. The recovery ratio and PFS prognosis of recurrent gbm tumours are of great interest to physicians for the purpose of precise therapy planning. A brain MRI study makes use of a variety of imaging data acquired from several MR images to predict the diagnosis of an ailment. Consequently, information that is useful for individualized therapy is offered. If tumour shrinkage increases either patient well-being or survival, it may be a secondary goal that is relevant. The delay in tumour progression is measured using PFS and ORR. Since then, additional tumours have been repeatedly shown to exhibit these associations, and glioma has historically shown little consistency.

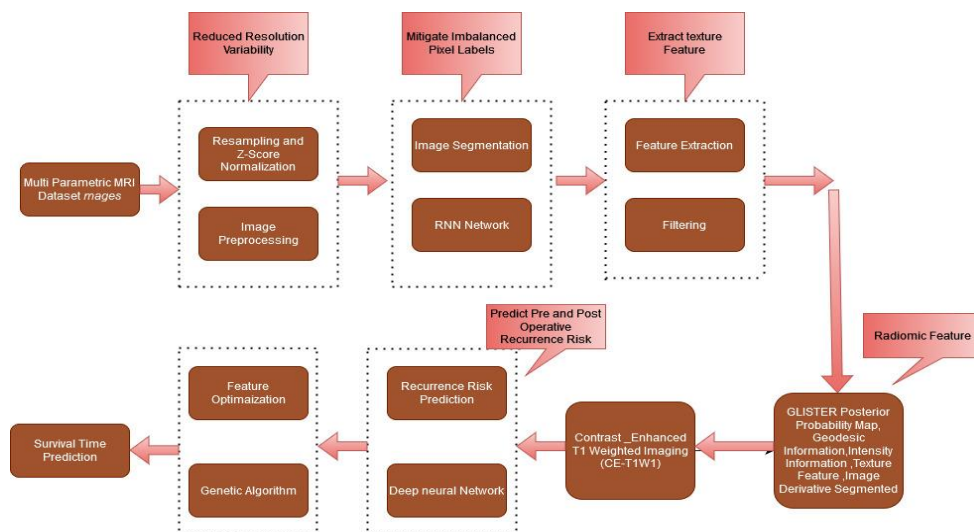


Figure 1- Proposed Work Block Diagram

The overall outline of the suggested technique is shown in Figure 1. In this study, we preprocessed images, normalized Z-scores, and resampled them; we then used generalized adversarial networks to segment tumors; we extracted texture features (FE) with wavelet-based band-pass filters; and we integrated the results into our regression style and step 4 is radiomic feature extraction to forecast recurrent glioblastoma. This study sought to evaluate the effectiveness of the pre- and postoperative recurrence risk among glioblastoma patients receiving a combination of bevacizumab and nivolumab. Based on the pretherapy imaging date, 84 patients made up the training cohort and 42 patients made up the testing cohort. Tumour volumes of interest were delineated from T1-weighted images that had undergone contrast enhancement. The radiomic feature-based MRI signatures were derived from multiparametric MRI data of patients with gliomas to ascertain their connections with response OS and PFS. Based on multi-scale textural features, the recurrence rate for GBM patients is predicted using the random forest method. The characteristics from MRIs were extracted using CE-T1W-MRI imaging data. Each stage is described in detail in the following subsections.

#### 4.1 Patient Population

As such no explicit informed consent was necessary for this retrospective investigation, which was authorised by the regional Institutional Review Board. So, a total of 126 patients were gathered for this investigation. Prior to receiving any type of treatment or undergoing surgery, multiparametric MRI exams were carried out on all patients with newly diagnosed gliomas, with the exception of Grade I gliomas. This model's receiver operating characteristic (ROC) curve was determined using a cross-validation method of 10 folds, and a prediction model was created using an Deep Neural Network technique(CNN VGG-16 Model). Bevacizumab and Nivolumab were used to assess the effectiveness of the DL technique. Finally, the clinical characteristics of 126 individuals were recorded.

#### 4.2 Multi-Parametric MRI Dataset

Multiparametric MRI-based radiomic analysis can be used in precision medicine for guidance on imaging prognosis, diagnosis, and decision-making. The MP-MRI acquisition protocol includes DWI, PWI, and cMRI for all patients.

#### 4.3. Image Pre-Processing

After image acquisition, preprocessing is often necessary to minimize motion artifacts and biases due to inhomogeneous magnetic fields in MRI as well as body motions like breathing and head movements. In addition, it features skull stripping , bias field correction, intensity normalization, reduce resolution fluctuation, and image co-registration.

#### 4.4 Resampling Image Pixel

Currently, radiomic features are poorly understood as a function of pixel size and slice thickness, For which interpolation or pixel size resampling is required as part of the pre-processing. Then, in order to assess feature robustness, ICC (Intraclass correlation coefficient) was used for interpolation and pixel size resampling. The ICC is given by the following formula:

Interclass correlation coefficient

$$ICC = \frac{MS_R - MS_E}{MS_R + (k - 1)MS_E + \frac{k}{n}(MS_C - MS_E)} \quad (1)$$

Where n stands for the number of patients,  $MS_R$  signifies the mean square for feature values, k stands for the number of repeated acquisitions,  $MS_C$  stands for repeated measures, and  $MS_E$  stands for mean square error. Using the ICC approach, the accuracy and consistency of numerical measurements in groups are evaluated. It also offers the feature of allowing comparisons between more than two groups of variables.

#### 4.5 Z-Score Normalization

After removing the mean intensity of the area or a complete image of interest, the Z-Score method entails dividing each voxel value by the matching standard deviation. Z-score normalisation uses the brain mask for picture p to calculate the mean and standard deviation of the strengths inside the brain mask. In the next step, the image is normalized by Z-score

$$I_{z\text{-score}}(x) = \frac{I(x) - \mu_{zs}}{\sigma_{zs}} \quad (2)$$

Spatial pre-processing is required before training in order to ensure that voxels across images have relationships and similar spatial arrangement, and it is important because CNNs often do not take into account metadata connected with medical images. In medical imaging, resampling is a popular spatial pre-processing technique (for example, make the voxel spacing isotropic for all training samples).

#### 4.6. Radiomic Feature Extraction

The radiomics signature is developed by adding more elements from derived and original images. More Wavelet transform-based features have higher significant coefficients in terms of survival, which had an impact on the radiomics signature model. In prior studies, MRI texture was analyzed at multiple scales, suggesting that FE can reliably and rapidly predict survival time (PFS and OS) at a much higher level of accuracy and speed than human visual detection is capable (10, 19, 20).

#### 4.7 Recurrence Risk Prediction

As glioblastoma survival rates rise and patient mortality decreases, it is crucial to predict the likelihood of a cancer recurrence. The objective of this research is to predict the likelihood of a return of brain cancer over a five-year or longer period of time, depending on the outcome. This problem is estimated by comparing the performance of the DNN and RF methods. Thus, RF is an effective method used in classification tasks for determining the relevance of features and balancing data.

#### 4.8 Inheritable Bi-objective Combinatorial Genetic Algorithm

Input: Expression profiles

Output: Key set reduced to its simplest form

1. Begin
  - $t < -0$
2. Using binary genes  $p1'$  and  $n - p0'$  with  $n$  and where  $p = p_{start}$ , generate the initial population randomly..
3. Assume that the fitness function is the prediction accuracy after 10-k fold cross validation..
4. While (! Stop condition) do
5. Using tournament selection, select individuals that are the best fit for mating.
6. Select two parents and perform orthogonal cross-overs on them..
7. Randomly select individuals to undergo mutations
8. Evaluate the individuals.
9. Replacing the population with the lowest performance with a new one.
10. Assuming  $p < p_{end}$ , transform one of the gene bits from 1 to 0.
11.  $t < -t + 1$

12. End While.

5. EXPERIMENTATION AND RESULT DISCUSSION

Table 2. displays the findings of the suggested model, which successfully classifies tumours using a Deep Neural Network and Random Forest. For the precise detection and classification of brain tumours, an intelligent healthcare system based on RF-DNN is being developed. There were three different types of tumours and one no-tumor among the four categories that made up the publicly available Kaggle dataset. An illustration of a sample brain tumour can be found in Figure 2.

Table 2. Analysis of the Results

<i>Method</i>	<i>Accuracy (%)</i>	<i>Sensitivity (%)</i>	<i>Specificity (%)</i>	<i>Time (sec)</i>	<i>Parameter</i>	<i>Layer</i>
<b><i>CNN-Inception-V3</i></b>	94	94	81.09	20.34	24 million	43
<b><i>CNN-AlexNet</i></b>	82	80	96	73.97	60 million	13
<b><i>VGG16</i></b>	95	95	96	45.1	138 million	16
<b><i>Proposed RNN-GAN Model</i></b>	95.11	96	98	9.45	7 million	20

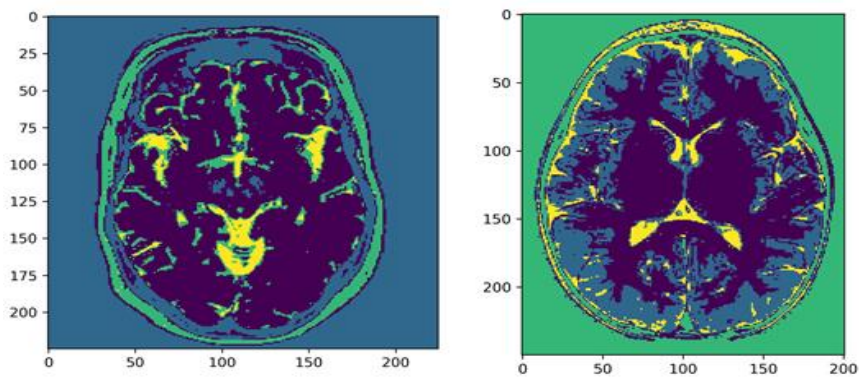


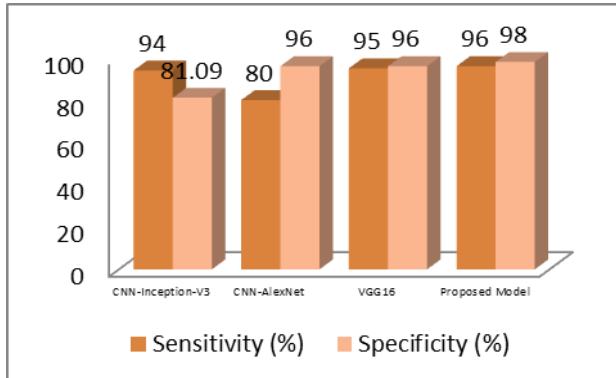
Figure 2- Experimental Images for MRI Brain Tumor

The suggested model employed data from 126 patients with 253 MRI scans of brain tumours for the glioma, meningioma, and pituitary classes, respectively. The suggested model contains several training and validation phases. In training, 80% of the input images are selected from each class; in validation, 20% of the images are used. Accuracy (ACC) and miss rate (MR) are used to measure how effective the model is.

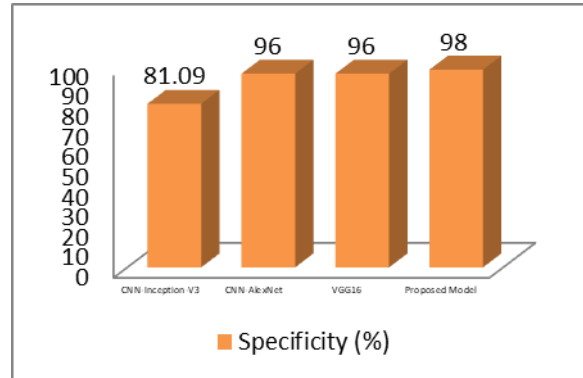
Table 3. Simulation System Setup

OS	Windows 11 Pro
Memory Volume	8GB DDR3
CPU	Intel i7- CPU @ 1.60GHz
Simulation Time	9.190 seconds

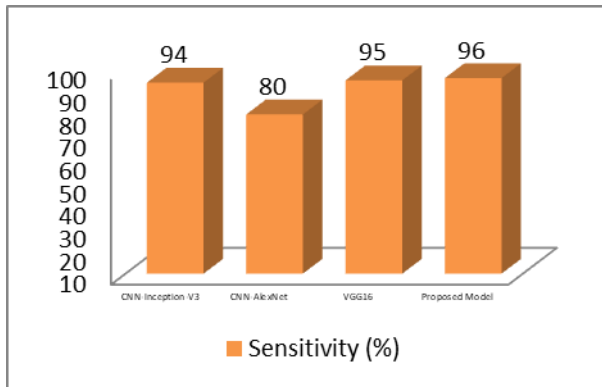
Table 3 depicts the simulation system configuration for the proposed work. Following that, the suggested methodology is assessed and tested. The suggested work runs on Windows 11 pro with 8GB DDR3 memory. It also makes use of an Intel i7- CPU @ 1.60GHz processor and takes 9.190 seconds to simulate.



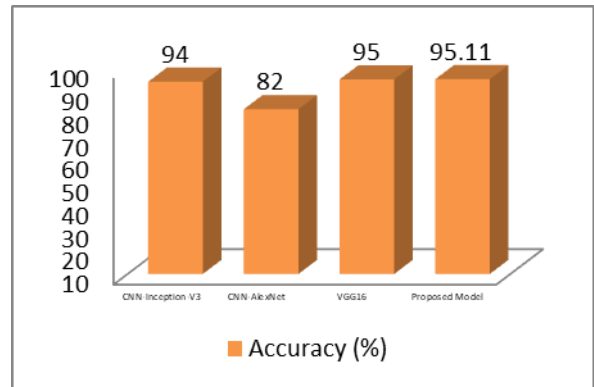
**Figure 3- Graph represents of Sensitivity Vs Specificity Graph**



**Figure 4- Graph represents of specificity score of Proposed model with other deep learning models**



**Figure 5- Graph represents of Sensitivity score of Proposed model with other deep learning models**



**Figure 6- Graph represents of accuracy score of Proposed model with other deep learning models**

## 6. CONCLUSION

Glioblastoma is a very dangerous type of brain tumor, even though we have some treatments that work. The problem is that it often comes back, which makes it especially deadly. When it comes back in different parts of the brain, it's harder to treat because the tumor cells change. Doctors use a special kind of brain scan called perfusion-weighted MRI to see how blood flows in the tumor. This helps them predict what might happen. But not many studies have looked at predicting if the tumor will come back or not, especially for different patterns of coming back. In our research, we want to use a smart computer program called a Deep Neural Network to predict if glioblastoma will come back. First, we clean up the brain scan images to make sure they are good and not messed up. Then, we use our computer program to find the tumor and make sure it's accurate. We also use a special technique to look at the details in the images. This helps us predict how patients will do if they get a certain kind of treatment. We have other computer methods like Random Forest and DNN to help us predict if the tumor will come back. We even have a special program to make our predictions better. All of these methods are tested and checked using a computer language called Python..

The study's main focus is on predicting if the brain tumor will come back, how long a patient might live, and some other measurements like accuracy, specificity, and sensitivity. They compared their new method with two existing prediction methods called CNN Inception-V3, CNN Alexnet, and VGG16 new method is better than the existing ones. It's 3% more accurate, about 4% more specific, and nearly 5% more sensitive.



So, using their new method, they can predict the risk of the brain tumor coming back more accurately. However, they also think there's more research needed to understand how the immune system works in the brain when there's a tumor.

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