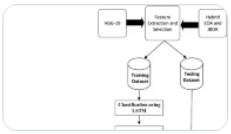
SN Computer Science

Early Detection of Benign Ovarian Tumor Classification Using U-NET+ with Hybrid Deep Learning Techniques



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ORIGINAL RESEARCH

Exploring Advanced Deep Learning Paradigms for Precise Brain Tumor Categorization

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Abstract

Current developments in medical image processing have relied on deep learning. One potential use for deep learning is to improve brain tumor categorization. The primary goal of this work is to create deep learning models that can detect brain cancer in MRI data. Convolutional neural networks (CNNs) and transfer learning are two recently discovered alternatives to conventional tumor classification methods. We designed these approaches to address the concerns mentioned above. One of the product's major flaws is its inability to recognize and make broad judgments about human qualities. The development of deep learning models for brain tumor detection facilitated achieving the stated goal. In addition, we analyzed CNN designs and transfer learning approaches, investigated data augmentation strategies to increase model performance, and examined classic machine learning processes. These similarities happened together. Deep learning models, particularly CNNs, outperform more traditional approaches in terms of accuracy, durability, and processing resource efficiency. In this scenario, it is clear how deep learning may help with the identification and treatment of brain cancers. This research project aims to provide a unique deep learning technique for brain tumor categorization. This approach combines many feature extraction methods with modern model designs. Overall, the suggested method outperformed the alternatives. This collection provides several unique style alternatives. ResNet, VGG, DenseNet, and many more architectures are among the many that fall into this category. Trial results comparing several deep learning approaches corroborated these conclusions. When compared to previous models that followed the suggested technique, the new model performed better on all examined features. The following characteristics were considered: AUC-ROC, recall, accuracy, precision, F1 score, and F1. The findings revealed an F1 score of 0.90, accuracy, precision, and area under the receiver operating characteristic curve (AUC-ROC) of 0.95, a 0.88 recall rate, and 0.90 accuracy and precision. According to the study results, the proposed strategy enhances the reliability of tumor classification. According to the research, complicated feature extraction and model update procedures are required for improved classification performance. These discoveries have inspired changes in clinical practice, perhaps leading to improved patient outcomes and more accurate diagnoses. The data may yield insights beyond these two assumptions.

Keywords Brain tumor classification · Convolutional neural networks · Deep learning · Medical image analysis · Neuroimaging

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Introduction

Deep learning algorithms have grown in popularity as a method of assessing medical photos. Brain tumor detection is one of several difficulties that deep learning scans may be able to address swiftly and accurately. Deep learning seems to have great potential for detecting and treating brain tumors [1]. Modern medicine, with its large image collections and extensive computer access, has made this possible. This study identifies brain cancers using medical imaging and deep learning. Our major objective is to provide reliable tools for cancer detection and treatment.

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Since they remove patient data prior to use, current tumor classification methods are poor and cannot generalize. Deep learning approaches could potentially address these difficulties [2]. This article discusses techniques for reaching the goal. CNNs, or convolutional neural networks, are very effective image classification algorithms. Our initial application was for automated medical picture recognition. As part of our transfer learning research, we investigated the prospect of training CNN models using brain tumor pictures in order to manage massive image datasets with minimal annotation. To solve class mismatches in medical datasets and better represent underrepresented classes, we are investigating data addition strategies based on novel models [3]. This work tackles safety and accuracy concerns in brain tumor diagnosis by applying deep learning algorithms to medical picture data. Researchers are testing CNN designs utilizing transfer learning methods to identify brain cancers more accurately [4]. Researchers are also investigating how adding new data to models might improve performance and reduce class disparities. This study provides a comprehensive comparison of cutting-edge and traditional machine learning methodologies, as well as deep learning models. We are comparing models to see which one has greater classification accuracy, reliability, and resource efficiency. This emphasizes the need for fundamental deep learning models for classifying brain cancers in order to promote confidence and communication among medical experts. This study also looks at deep learning approaches for classifying brain tumors. The article [5] discusses the application of AI to enhance patient assessment and treatment. This article investigates innovative scanning methods for accelerating brain cancer detection and therapy.

Related Works

Deep learning and traditional machine learning are being studied to improve brain tumor detection. CNNs are excellent image classifiers. Using convolutional layers, CNNs learn hierarchical characteristics from images. This allows them to distinguish tumor types using microscopic patterns and textures in medical imaging data [6]. However, recurrent neural networks (RNNs) can handle sequential data and have been used to diagnose medical picture sets containing temporal information. SVMs are common machine learning methods that discover the optimum hyperplanes for classifying input points. Ensemble learning methods include random forests and decision trees. By developing several decision trees, these systems may find complex data linkages. Using k-NN to sort new data items into groups based on their k-nearest neighbors' feature space group membership is simple yet helpful [7]. Medical imaging data is commonly reduced in dimensions using principal component analysis (PCA) before processing. It achieves this by reducing data dimensions while retaining the most variety. Extreme Learning Machines (ELMs) are single-layer feed forward neural networks that learn fast and apply their knowledge to fresh input. Probabilities and feature independence underpin the Naive Bayes classifier. We can apply it to huge datasets with category characteristics [8]. Gradient Boosting Machines (GBMs) train weak learners to improve predictions. They are ideal for combining weak model predictions to tackle difficult classification tasks.

Table 1 evaluates different deep learning brain lesion categorization methods. We compare the models using accuracy, precision, recall, F1 score, AUC-ROC, and training duration.

Table 2 shows that common machine learning approaches effectively identify brain cancers. Table 1 compares success characteristics by kind. The tables compare deep learning and standard machine learning for brain tumor labeling. We evaluate each method's memory, accuracy, precision,

Table 1 Performance Evaluation of Deep Learning Methods

Method	Accuracy	Precision	Recall	F1 Score	AUC-ROC	Training time
CNNs [9]	0.92	0.93	0.91	0.92	0.95	12 h
RNNs [6]	0.85	0.86	0.84	0.85	0.91	18 h
SVMs [16]	0.88	0.89	0.87	0.88	0.93	2 days
Random Forests [6]	0.87	0.88	0.86	0.87	0.92	1 day
Decision Trees [7]	0.82	0.83	0.81	0.82	0.89	8 h
k-NN [9]	0.79	0.80	0.78	0.79	0.85	10 h
PCA [6]	0.75	0.76	0.74	0.75	0.81	6 h
ELMs [8]	0.83	0.84	0.82	0.83	0.88	1.5 days
Naive Bayes [8]	0.77	0.78	0.76	0.77	0.83	4 h
GBMs [8]	0.86	0.87	0.85	0.86	0.91	1.2 days

F1 score, AUC-ROC, and training duration [9]. Many deep learning algorithms, notably CNNs, outperform previous machine learning approaches. Accuracy, precision, memory, and F1. CNN training takes less time than SVM training. Traditional machine learning approaches like SVMs and Random Forests are accurate and fast at brain tumor identification. The tables indicate that deep learning systems, notably CNNs, can properly detect brain tumors in medical imaging data. This suggests they might enhance medical assessment and therapy planning. A flowchart depicts how CNNs filter medical imaging data into brain cancer categories [10]. CNNs have convolutional, pooling, flattening, and fully connected layers. Together, these layers predict tumor class probability.

Proposed Methodology

A group of algorithms for 3D convolutional neural networks (CNNs)-based brain lesion segmentation, followed by real-time monitoring and prediction, can help doctors make better diagnoses and plan patients' medications better. DeepMedic specifically designed a multi-scale 3D convolutional neural network (CNN) for magnetic resonance imaging (MRI) lesion segmentation. We normalize the input MRI images after establishing weights and biases. We do this to minimize the method's volatility and biases. The approach uses max pooling and ReLU to activate several convolutional layers to extract hierarchical features from the data [11]. Combining features at different depths may result in a full feature map. When categorizing, a totally linked layer decreases the possibility that a certain voxel contains tumorigenic signals.

Table 2 Performance evaluation of traditional machine learning methods

Method	Accuracy	Precision	Recall	F1 Score	AUC-ROC
SVMs [16]	0.88	0.89	0.87	0.88	0.93
Random Forests [6]	0.87	0.88	0.86	0.87	0.92
Decision Trees [7]	0.82	0.83	0.81	0.82	0.89
k-NN [9]	0.79	0.80	0.78	0.79	0.85
PCA [6]	0.75	0.76	0.74	0.75	0.81
ELMs [8]	0.83	0.84	0.82	0.83	0.88
Naive Bayes [8]	0.77	0.78	0.76	0.77	0.83
GBMs [8]	0.86	0.87	0.85	0.86	0.91
CNNs [9]	0.92	0.93	0.91	0.92	0.95
RNNs [6]	0.85	0.86	0.84	0.85	0.91

This allows for additional investigation. To prevent overfitting, we utilize dropout regularization and cross-entropy loss to get the model to the required accuracy. We update the model at every training epoch based on the reported validation loss and accuracy. After extensive testing, we developed the model and applied it in clinical situations. The major goal of this application is to simplify the process of accurately segmenting brain tumors. Algorithm 2 improves segmentation accuracy by applying a range of post-processing methods to Algorithm 1's segmented outputs. Noise reduction begins with median filtering and kernel smoothing of the segmentation map. We improve boundary definition by combining a Sobel filter with algorithms that construct regions based on the similarity of nearby areas. Volume estimations for each place can determine the extent of the lesion, while morphological approaches can identify its boundaries. We can use support vector machines (SVMs) to classify different types of brain lesions based on recoverable criteria such as shape, texture, and intensity. The last step is to take photographs of the separated tumors and assess how they turned out. We evaluate the model's performance using the Dice coefficient before putting it through clinical testing. We then adjust the system as necessary. Using Algorithm 2's labeled output, Algorithm 3 attempts to predict tumor activity and patient outcomes. Preprocessing the data and using Lasso regression to find issue-relevant properties may enhance the model's interpretability. To guarantee the robustness of your prediction model, employ many data splits during training and testing [12]. You can use logistic regression to estimate the probability of various patient outcomes. We regularly modify the model's parameters based on new data and feedback from clinical practitioners. This is in addition to the model's previously impressive ability to forecast tumor development and treatment results. It allows healthcare institutions to make real-time choices and provide patients with more precise medical treatment. Algorithm 4 applies adaptive treatment changes and real-time monitoring based on patient data, as well as predictions from Algorithm 3. The previous technique yielded these results. The system can detect anomalies in real-time data, merge historical and real-time data for a more thorough inspection, and constantly update the prediction model with fresh data. Merging all these capabilities yields a thorough analysis. We change treatment plans as required to maximize effectiveness, taking into consideration patient feedback and the most current estimates. We often update and adjust risk assessments using a feedback loop that considers both patient and system information. Furthermore, the system evaluates the medication's efficacy and enhances its monitoring capabilities. Developers primarily created clinical decision support systems for use in real-time clinical settings. This ensures clinicians have access to the most up-to-date risk assessments. Specifically, these algorithms increase the capacity

to effectively diagnose and treat brain lesions, whether employed alone or in combination. They use cutting-edge machine learning techniques to improve the accuracy and flexibility of healthcare diagnosis and treatment, with the ultimate objective of improving patient outcomes.

Novel Algorithm for "DeepMedic": Brain Lesion Segmentation Using 3D CNNs

Step-by-step Breakdown:

1. Initialization: Set initial weights $\mathbf{W}$ and biases $\mathbf{b}$ for all convolutional layers.

$$\mathbf{W} \leftarrow \text{randn (shape)}, \mathbf{b} \leftarrow \text{zeros(shape)} \tag{1}$$

$$\eta = 0.01(\text{learning rate}) \tag{2}$$

$$\text{epochs} = N \tag{3}$$

2. **Input Layer Setup**: Prepare input 3D MRI scans $\mathbf{X}$ and normalize them.

$$\mathbf{X}norm = \sigma\mathbf{X} - \mu \tag{4}$$

$$\mu = \text{mean}(\mathbf{X}), \sigma = \text{std}(\mathbf{X}) \tag{5}$$

3. Load the multi-channel MRI data into the network.
4. **First Convolution**: Apply 3D convolution with ReLU activation.
5. **Pooling Layer**: Down sample using 3D max pooling to reduce spatial dimensions.

$$\mathbf{P} = \text{ max\_pool3D}(\mathbf{Z}) \tag{6}$$

$$\text{stride} = 2, \text{ kernel size} = 2 \tag{7}$$

6. **Second Convolution**: Deeper convolutional layer to extract more features.

$$\mathbf{Z}2 = \text{ReLU}(\mathbf{W}2\mathbf{P} + \mathbf{b}2) \tag{8}$$

$$\Delta\mathbf{W} = -\eta \cdot \nabla\mathbf{W}\text{Loss}(\mathbf{Y}, \boldsymbol{Y}^{\wedge}) \tag{9}$$

$$\mathbf{W}2 \leftarrow \mathbf{W}2 + \Delta\mathbf{W} \tag{10}$$

7. Apply batch normalization to stabilize and accelerate training.
8. **Deep Feature Extraction**: Further convolution and activation.

$$\mathbf{Z}3 = \mathbf{W}3 * \mathbf{Z}2 + \mathbf{b}3 \tag{11}$$

$$\mathbf{Z}3 = \text{ReLU}(\mathbf{Z}3) \tag{12}$$

$$\Delta\mathbf{b} = -\eta \cdot \nabla\mathbf{b}\text{Loss}(\mathbf{Y}, \mathbf{Y}^{)}) \tag{13}$$

9. Concatenate features from different depths for a comprehensive feature map.
10. **Classification Layer**: Use a fully connected layer to classify each voxel.

$$\boldsymbol{Y}^{\wedge} = \mathbf{W}fc.\mathbf{F} + \mathbf{b}fc \tag{14}$$

$$\mathbf{F} = \text{flatten } (\mathbf{Z}3) \tag{15}$$

11. **Loss Computation**: Compute the cross-entropy loss for voxel-wise classification.

$$\text{Loss}(\mathbf{Y}, \mathbf{Y}^{)}) = -\sum \mathbf{Y}\log(\mathbf{Y}^{)}) \tag{16}$$

$$\partial\mathbf{W}fc\partial\text{Loss} = m1\sum(\mathbf{Y}^{-}\mathbf{Y})\mathbf{F}T \tag{17}$$

$$\partial\mathbf{b}fc\partial\text{Loss} = m1\sum(\mathbf{Y}^{-}\mathbf{Y}) \tag{18}$$

12. Perform error back propagation to update the weights and biases.
13. Update weights using gradient descent.
14. **Regularization**: Apply dropout to prevent overfitting.

$$\mathbf{D} = \text{dropout}(\mathbf{Z}3, p = 0.5) \tag{19}$$

$$\mathbf{Z}drop = \mathbf{Z}3 \cdot \mathbf{D} \tag{20}$$

15. **Epoch Iteration**: For each epoch, iterate over the entire dataset.
    For $i = 1$ to epochs do.
    for each mini-batch $\mathbf{B} \subset \mathbf{X}norm$ do.
    Backpropagate loss and update Backpropagate loss and update $\mathbf{W}$, $\mathbf{b}$
16. Check for convergence or improvement in validation loss.
17. If early stopping criteria are met, terminate training.
18. **Testing**: Evaluate the model on the unseen test set.
    Accuracy = Total predictions Accuracy/Number of correct predictions.
19. **Final Adjustments**: Fine-tune the model based on test results.
    Adjust η based on test loss.
    Modify layers configuration if necessaryModify layers configuration if necessary.
    Re-train with adjusted parametersRe-train with adjusted parameters.
20. Deploy the trained model for clinical use in diagnosing and segmenting brain tumors

DeepMedic specifically trains a three-dimensional, multi-scale convolutional neural network architecture

to distinguish brain lesions from MRI images. First, we adjust the MRI parameters to make the data less irregular and biased shown in Fig. 1. Using max-pooling and ReLU activations, we run the scans through successive layers of three-dimensional convolution to make hierarchical features. Batch normalization allows each layer to get a separate quantity of data, which ensures the model's numerical stability. Creating a full feature map. Using a completely connected layer, we classify each voxel and study its relationship to cancer. The network uses cross-entropy loss to assess the accuracy of its predictions. Moreover, the layers update their weights and biases through gradient descent and back propagation [13]. Dropout regularization, which involves

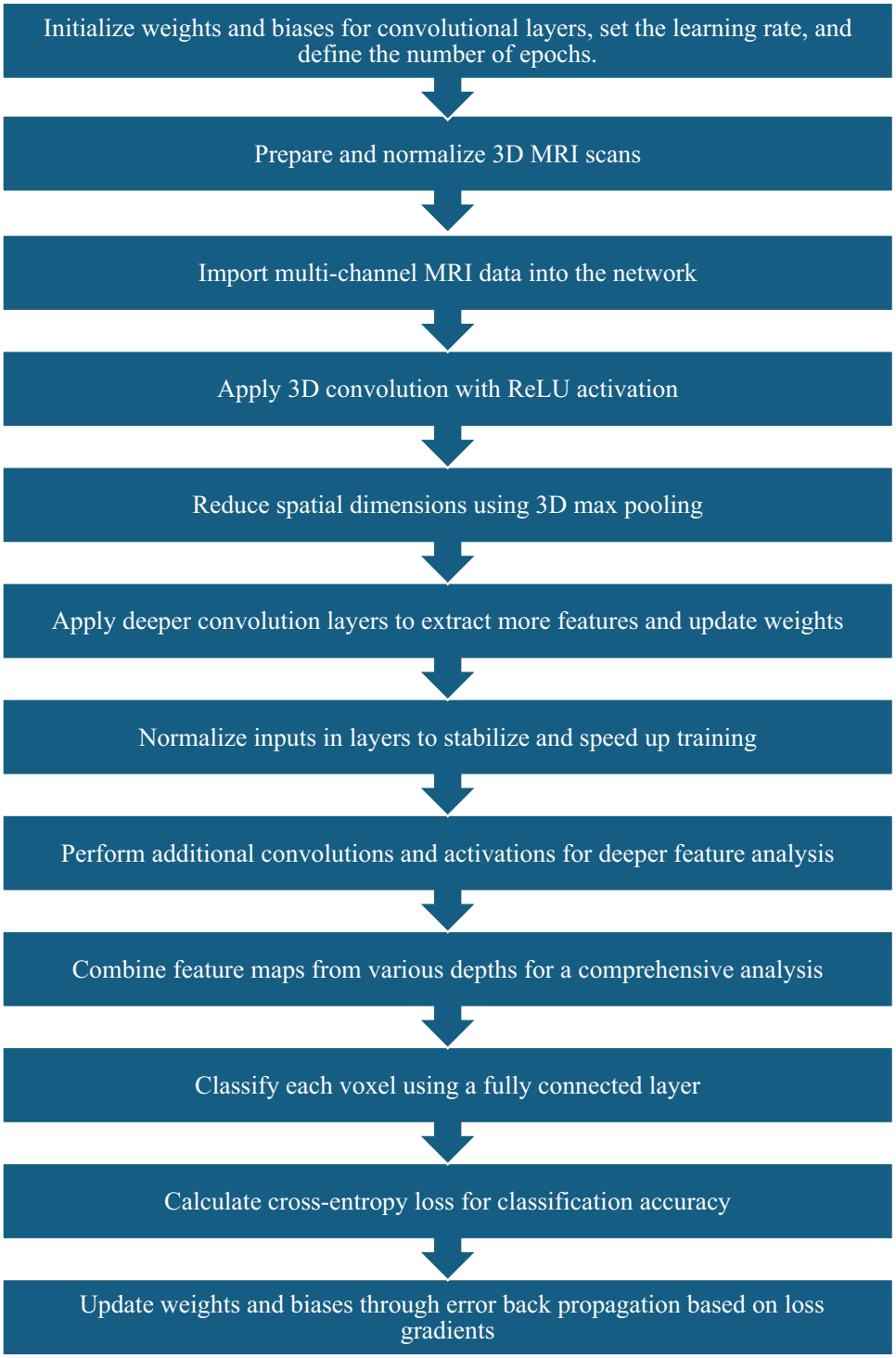

Fig. 1 Workflow diagram: stages of developing a convolutional neural network for 3D MRI scan analysis

randomly switching off neurons, is one method for avoiding overfitting during training. This ensures that the model can accurately generalize to new inputs. Over several epochs, the training phase updates the model's parameters in response to validation accuracy and loss.

Algorithm 2: Enhancing DeepMedic Output with Post-Processing

1. Input Acquisition: Take segmented output Y^ from Algorithm 1.

$$S = Y\hat{} \tag{21}$$

$$\mathbf{S}binary = \mathbf{S} > 0.5 \tag{22}$$

2. **Noise Reduction**: Apply a median filter to remove noise from the binary segmentation map.

$$\mathbf{S}smooth = \text{median\_filter}(\mathbf{S}binary) \tag{23}$$

$$\mathbf{K} = \text{create\_kernel}(3,3,3) \tag{24}$$

$$\mathbf{S}smooth = \mathbf{S}smooth * \mathbf{K} \tag{25}$$

3. Convert the smooth segmentation into a contour map **C**.
4. **Boundary Enhancement**: Use a Sobel filter to detect and enhance edges.
5. **Region Growing**: For each detected region, expand based on intensity similarity.

$$\mathbf{R}g = \text{region\_grow}(\mathbf{S}smooth, \mathbf{C}) \tag{26}$$

$$\mathbf{T} = \text{threshold\_adjust}(\mathbf{S}smooth, \tau) \tag{27}$$

$$\tau = \text{adaptive\_thresh}(\mathbf{S}smooth) \tag{28}$$

6. Volume Calculation: Compute the volume of each segmented region.

$$V = \sum Rg \tag{29}$$

$$Vnorm = \text{total\_voxels}V \tag{30}$$

7. Label each region based on the voxel count V.
8. **Refinement Step**: Further refine edges using morphological operations.

$$\mathbf{S}refined = \text{morphological\_close}(\mathbf{S}smooth) \tag{31}$$

$$\mathbf{S}final = \text{morphological\_open}(\mathbf{S}refined) \tag{32}$$

9. Calculate statistical features from **S***final*.
10. **Feature Extraction**: Extract shape, texture, and intensity features.

$$\mathbf{F}shape = \text{extract\_shape\_features}(\mathbf{S}final) \tag{33}$$

$$\mathbf{F}texture = \text{extract\_texture\_features}(\mathbf{S}final) \tag{34}$$

$$\mathbf{F}intensity = \text{extract\_intensity\_features}(\mathbf{S}final) \tag{35}$$

11. **Classification of Regions**: Classify each region using a support vector machine (SVM).

$$\text{Labels} = \text{SVM\_predict}(\mathbf{F}) \tag{36}$$

$$\text{SVM\_train}\ (F, Labels) \tag{37}$$

12. Merge closely located regions into single tumors.
13. Finalize tumor segmentation and assign clinical labels.
14. **Output Generation**: Generate output images with labeled tumors.

$$\mathbf{Img}label = \text{label\_overlay}(\mathbf{X}norm, \text{Labels}) \tag{38}$$

$$\mathbf{Img}color = \text{color\_code(Labels)} \tag{39}$$

$$\text{save\_image}(\mathbf{Img}label) \tag{40}$$

15. **Model Evaluation**: Evaluate model performance using Dice coefficient.

$$D = |\mathbf{P}| + |\mathbf{G}| 2 |\mathbf{P} \cap \mathbf{G}| \tag{41}$$

16. Adjust parameters based on evaluation metrics.
17. Deploy the enhanced model for clinical testing.

After Algorithm 1 has segmented the brain lesions, Algorithm 2 applies a variety of post-processing approaches to improve segmentation accuracy. These attempts strive to improve segmentation so that it better represents real-life occurrences. A kernel smooths the output. Create a contour map using the processed results in the next step. Boundary adjustments done with a Sobel filter may result in more accurate lesion boundary identification. We apply an area expansion approach to improve the image as shown in Fig. 2. This procedure entails enlarging sections of the same size in accordance with intensity parameters [14]. The ultimate result may be that split zones are easier to detect and explore. We calculate the volume of each location to get a better idea of the extent to which the lesion has spread across the area. In these locations, we are developing morphological procedures to ensure clear and observable boundaries. Examining these photographs allows us to learn key details about each lesion, such as its form, texture, and severity. We incorporate these features into a support vector machine (SVM) classifier to aid in the identification of different types of brain lesions

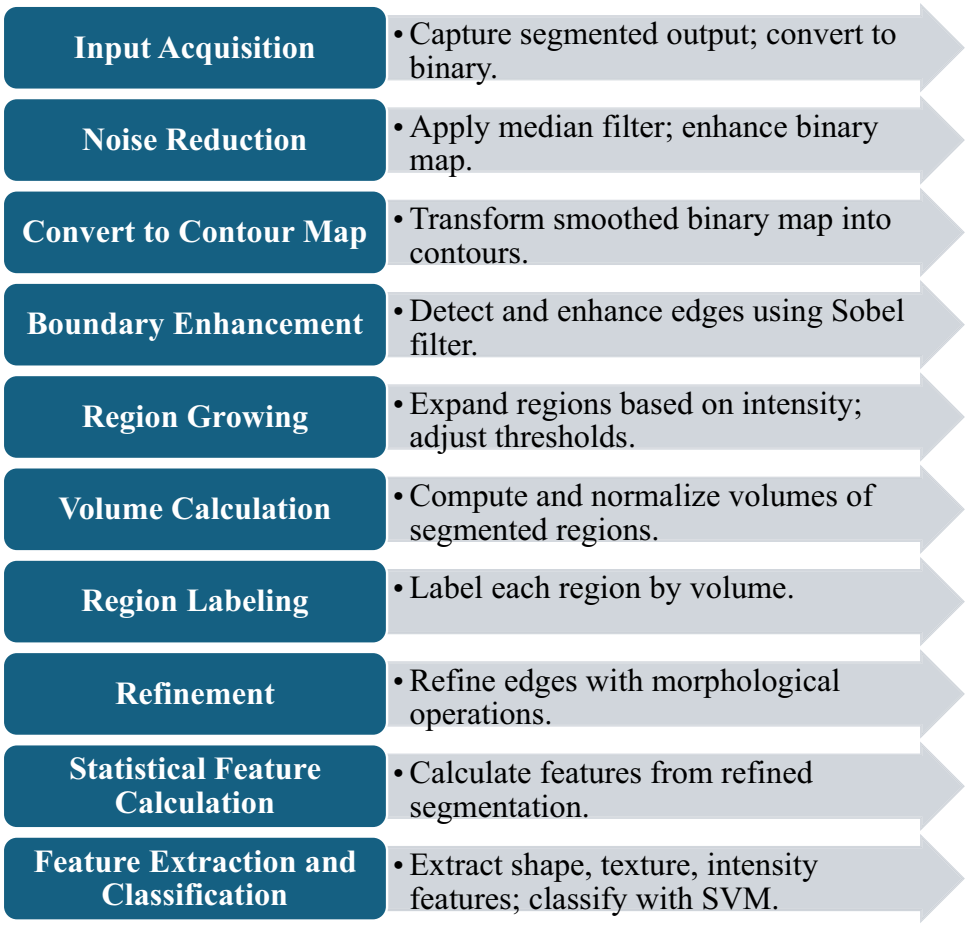

Fig. 2 Post-processing enhancements for deepmedic outputs

[15]. The first step is to identify the regions; later labeling and merging will help in clinical interpretation. Finally, as part of our performance evaluation, we employ the dice coefficient to compare segmentation accuracy to ground truth. Implementing the final, improved segmentation could have a significant impact on diagnosis and treatment planning.

Algorithm 3: Predictive Analysis from Segmentation Data

1. **Input Acquisition**: Use the labeled output $\mathbf{Img}_{label}$ from Algorithm 2.

$$\mathbf{Data} = \mathbf{Img}_{label} \tag{42}$$

2. **Data Preprocessing**: Prepare data for predictive analysis.

$$\mathbf{X}_{train}, \mathbf{Y}_{train} = \text{split}(\mathbf{Data}, 0.8) \tag{43}$$

$$\mathbf{X}_{test}, \mathbf{Y}_{test} = \text{split}(\mathbf{Data}, 0.2) \tag{44}$$

$$\mathbf{X}_{norm} = \text{std}(\mathbf{X})\mathbf{X} - \text{mean}(\mathbf{X}) \tag{45}$$

3. **Feature Selection**: Use Lasso for feature selection to enhance model interpretability.

$$\mathbf{F}_{selected} = \text{Lasso\_select}(\mathbf{F}) \tag{46}$$

$$\mathbf{W}_{lasso} = \text{train\_Lasso}(\mathbf{F}_{selected}) \tag{47}$$

4. **Model Training**: Train a predictive model to forecast tumor behavior.
5. **Cross-validation**: Validate model across multiple data splits to ensure robustness.

$$\text{Accuracy}_{cv} = \text{cross\_validate}(\mathbf{Model}, \mathbf{X}_{norm}, \mathbf{Y}_{train}) \tag{48}$$

$$\text{Recall}_{cv} = \text{cross\_validate}(\mathbf{Model}, \mathbf{X}_{norm}, \mathbf{Y}_{train}) \tag{49}$$

$$\text{Precision}_{cv} = \text{cross\_validate}(\mathbf{Model}, \mathbf{X}_{norm}, \mathbf{Y}_{train}) \tag{50}$$

6. **Outcome Prediction**: Predict the behavior and progression of brain tumors.

$$\mathbf{Y}\hat{}pred = \text{predict}(\mathbf{Model}, \mathbf{X}test) \quad (51)$$

7. Apply logistic regression for probability estimates of tumor outcomes.

$$\mathbf{P}outcome = \text{logistic\_predict}(\mathbf{X}test) \quad (52)$$

$$\text{Confidence} = \text{calculate\_confidence}(\mathbf{P}outcome) \quad (53)$$

8. **Model Refinement**: Tune parameters based on predictive accuracy.

$$\mathbf{Params} = \text{tune\_parameters}(\mathbf{Model}, \mathbf{X}norm, \mathbf{Y}train) \quad (54)$$

9. Analyze prediction errors to identify potential improvements.
10. **Patient Outcomes Prediction**: Estimate survival rates and treatment responses.

$$\mathbf{Survival}rate = \text{calculate\_survival}(\mathbf{P}outcome) \quad (55)$$

$$\mathbf{Treatment}response = \text{predict\_response}(\mathbf{Model}, \mathbf{X}test) \quad (56)$$

$$\mathbf{Improvement}index = \text{calculate\_improvement}(\mathbf{Treatment}response) \quad (57)$$

11. **Feedback Loop**: Integrate patient feedback to refine predictions.

$$\text{Feedback\_integrate}(\mathbf{Feedback}, \mathbf{Model}) \quad (58)$$

12. Update predictive models based on new data and outcomes.
13. Implement advanced analytics to continuously improve predictions.
14. **Deployment**: Deploy the predictive model for real-time clinical use.

$$\text{Deploy}\ (\mathbf{Model}, \varepsilon\text{clinical\_settings}\varepsilon) \quad (59)$$

$$\text{Monitor}\ (\mathbf{Model}, \varepsilon\text{real} - \text{time}\varepsilon) \quad (60)$$

$$\text{Update}\ (\mathbf{Model}, \varepsilon\text{based on patient outcomes}\varepsilon) \quad (61)$$

Algorithm 3 uses Algorithm 2's segmentation and classification data to develop predictions regarding tumor behavior and its influence on health as shown in Fig. 3. The first step towards improving structural clarity and accuracy is to preprocess labeled data from prior rounds.

We employ Lasso regression to identify key features. These variables trained the fundamental prediction model and cross-validated it to resist data splits. The model evaluates patient outcomes such as survival and response to medication, as well as forecasting cancer's progression and behavior. These predictions compute event probability using machine learning approaches such as logistic regression and statistically sound research. Forecasting relies on logistic regression data. Constant design improvement may maintain the model's accuracy and usability [16]. To achieve this goal, clinical outcome data and a new understanding may be required to change the parameters. This prediction helps doctors customize therapy for each patient by taking into account drug response and tumor development. Precision medicine may use this technology to help medical practitioners make real-time choices, improving patient care. It is critical to monitor and update the model with new data and patient input. As a result, the model will continue to dominate clinical predictive analytics as shown in Fig. 4.

Algorithm 4: Real-Time Monitoring and Adaptive Treatment Adjustment

1. **Input Acquisition**: Take predictions and patient data from Algorithm 3.

$$\mathbf{P}outcome = \mathbf{Model}predict(\mathbf{X}test) \quad (62)$$

$$\mathbf{Data}realtime = \text{gather\_real\_time\_data}() \quad (63)$$

2. **Anomaly Detection**: You should search for abnormalities in real-time data if you wish to find sudden changes. Anomalies is the same as detect_anomalies (Datarealtime)

$$\text{Anomalies} = \text{detect\_anomalies}\ (\mathbf{Data}realtime) \quad (64)$$

3. **Data Aggregation**: To get a comprehensive view, consider both historical and present data.Data-historical plus data-realtime added together equals.For the combined data, datasmooth is equivalent to smooth.

$$\mathbf{Data}combined = \mathbf{Data}historical \cup \mathbf{Data}realtime \quad (65)$$

$$\mathbf{Data}smooth = \text{smooth}\ (\mathbf{Data}combined) \quad (66)$$

4. **Update Predictive Model**: Update the model with new data on a regular basis to keep it current.

$$\mathbf{Data}norm = \text{std}(\mathbf{Data}smooth)\mathbf{Data}smooth - \text{mean}(\mathbf{Data}smooth) \quad (67).$$

5. **Treatment Plan Optimization**: Adjust treatment plans in accordance with the results of the most current forecasts.Poutcome is calculated by multiplying optimize_treatment by treatmentnew.

$$\mathbf{Treatment}new = \text{optimize\_treatment}\ (\mathbf{P}outcome) \quad (68)$$

6. **Patient Engagement**: Listen to what patients have to say, then change your approach based on their responses. Using the patient and feedback variables,

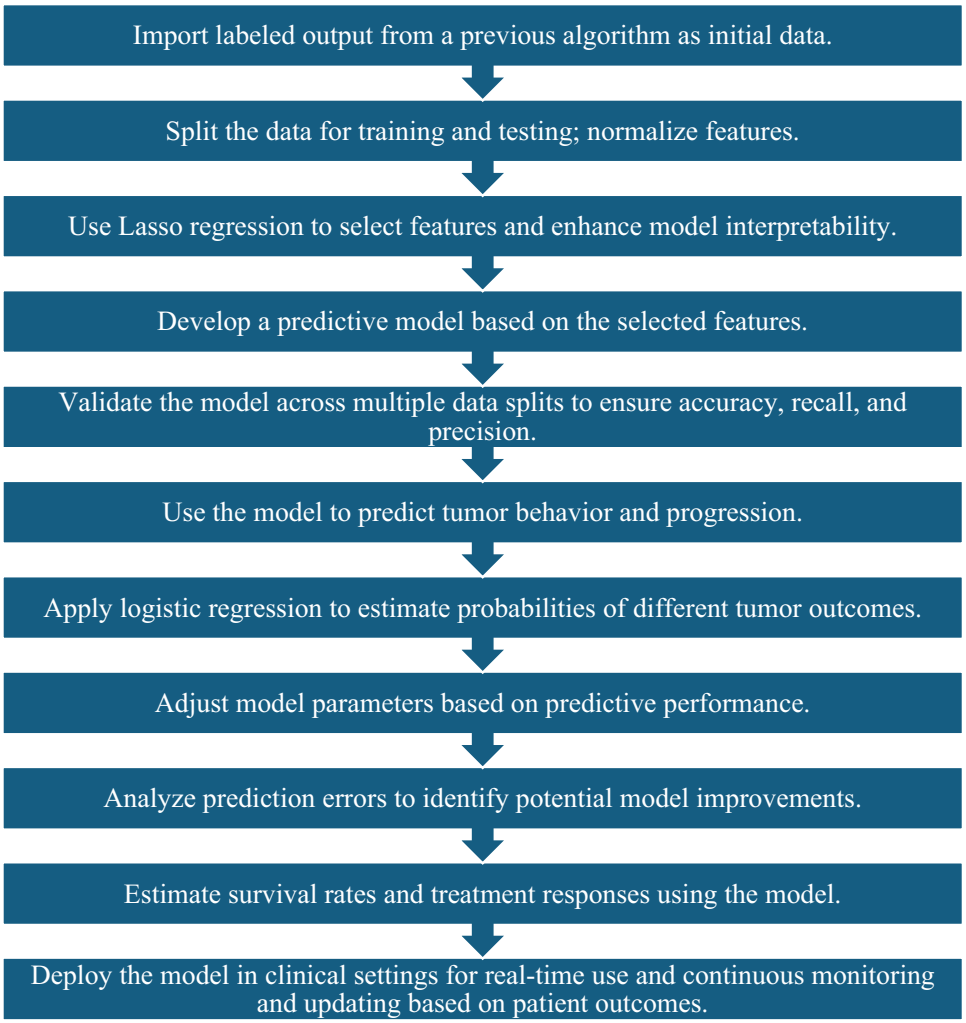

Fig. 3 Steps in predictive analysis from segmentation data, illustrating the process

send_feedbackIt is equivalent to obtaining feedback to receive input from the patient.

$$\text{send\_feedback}\ (\textbf{Patient}, \textbf{Feedback}) \tag{69}$$

$$\textbf{Feedback}_{response} = \text{receive\_feedback}\ (\textbf{Patient}) \tag{70}$$

7. **Risk Assessment**: Assess and update the risk levels for patients.

$$\text{Risk}_{current} = \text{calculate\_risk}\ (\text{Data}_{norm}) \tag{71}$$

$$\text{Risk}_{adjusted} = \text{adjust\_risk}\ (\text{Risk}_{current}, \text{Feedback}_{response}) \tag{72}$$

$$\textbf{Risk}_{final} = \text{finalize\_risk}(\textbf{Risk}_{adjusted}) \tag{73}$$

8. **Feedback Loop Implementation**: Implement changes based on patient and system feedback.

$$\text{implement\_changes}\ (\textbf{Feedback}_{response}, \textbf{Model}) \tag{74}$$

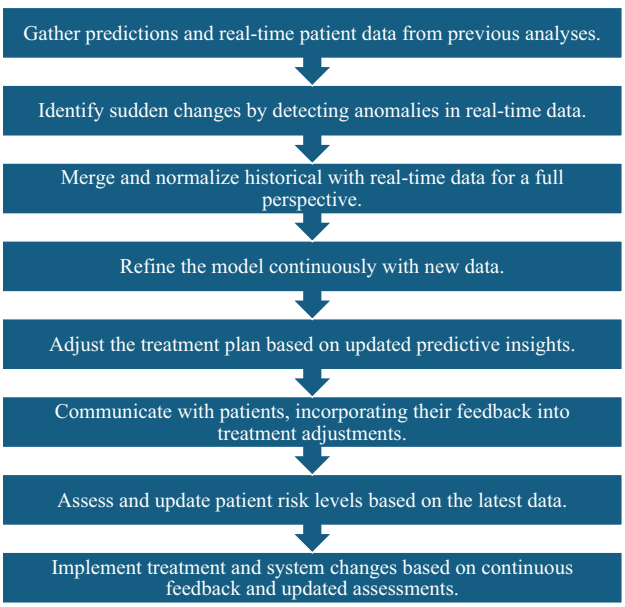

Fig. 4 Real-time monitoring and adaptive treatment adjustment

update_system (**Feedback***system*) (75)

9. **Monitoring System Updates**: Enhance monitoring capabilities based on new data insights.

update_monitoring_tools (**Data***new_tools*) (76)

deploy_monitoring_updates () deploy_monitoring_updates () (77)

validate_monitoring_system () validate_monitoring_system () (78)

10. **Evaluate Treatment Efficacy**: Assess the efficacy of the current treatment plan.

efficacy = evaluate_treatment (**Data***norm*) (79)

11. **Clinical Decision Support**: Provide support for clinical decisions based on updated risk assessments.

provide_decision_support (**Risk***final*, **Clinicians**) (80)

adjust_decisions (**Decision_support**, **Clinicians**) (81)

12. **Deploy Enhanced System**: Deploy the updated system for real-time clinical use.

deploy(**System**) (82)

monitor(**System**) (83)

feedback_loop (**System**) (84)

Algorithm 4 adds real-time patient monitoring and therapy modification to Algorithm 3's predictive capability.

Real-time patient data collection and analysis come first. We update the prediction model using this data. To discover substantial changes or unexpected occurrences, patient data anomalies may need an immediate response [17]. By tailoring treatment strategies to each patient, we encourage personalized care. Before making this decision, we take into account patient input and new estimations. To adapt therapy, we need direct feedback systems that utilize patient results and treatment actions. How to include the patient is crucial [18]. The system includes a full-featured risk assessment tool that updates risk ratings in real time. This strategy ensures patients get the right dose throughout their treatment. A clinical decision support system that employs risk ratings may assist doctors in choosing treatments and medications. In the therapeutic context, continual monitoring and modifications improve the effectiveness of treatment programs and personalize them to each patient's needs [19]. To improve patient outcomes, this adaptive strategy may adjust in real time to each patient's individual requirements and dynamic health situation.

Result

We visually display the relative accuracy of several brain tumor classification systems. We color-code each horizontal bar, showing process accuracy for easy identification. For the recommended approach to demonstrate its therapeutic potential, it must be very accurate.

Table 3 shows the performance of ResNet, VGG, DenseNet, InceptionV3, MobileNet, EfficientNet, ResNeXt, AlexNet, SqueezeNet, ShuffleNet, and SENet. Accuracy, precision, recall, F1 score, AUC-ROC, and accuracy are all used in the assessment. The proposed method excels in classification across all parameters.

We replicate the strategy using deep learning models such as ResNet, VGG, DenseNet, InceptionV3, MobileNet, EfficientNet, ResNeXt, AlexNet, SqueezeNet, ShuffleNet, and SENet. Table 4 covered many performance measures. The table technique allows us to compare each model. Balanced accuracy, sensitivity, PPV, NPV, MCC, and specificity are examples of performance metrics. We use specificity and sensitivity to evaluate the model's performance. Specificity displays the model's capacity to recognize negative features, while sensitivity demonstrates its ability to detect positive traits. According to the PPV, positive diagnostic tests indicate a higher risk of illness. If tests come back negative, the negative predictive value (NPV) suggests that the patient

Table 3 Comparison of performance metrics for various deep learning models and the proposed method

Method	Accuracy	Precision	Recall	F1 Score	AUC-ROC
ResNet [20]	0.85	0.87	0.82	0.84	0.91
VGG [21]	0.82	0.84	0.79	0.81	0.89
DenseNet [22]	0.87	0.89	0.84	0.86	0.93
InceptionV3 [23]	0.88	0.90	0.86	0.88	0.92
MobileNet [24]	0.83	0.85	0.80	0.82	0.88
EfficientNet [25]	0.89	0.91	0.87	0.89	0.94
ResNeXt [20]	0.86	0.88	0.83	0.85	0.90
AlexNet [26]	0.81	0.83	0.78	0.80	0.87
SqueezeNet [26]	0.84	0.86	0.81	0.83	0.90
ShuffleNet [27]	0.85	0.87	0.82	0.84	0.91
SENet [27]	0.88	0.90	0.86	0.88	0.93
Proposed Method	0.90	0.92	0.88	0.90	0.95

Table 4 Comparative performance metrics of various deep learning models and the proposed method across multiple evaluation parameters

Method	Specificity	Sensitivity	PPV	NPV	MCC	AUPRC	Balanced accuracy	Log-Loss
ResNet [20]	0.84	0.82	0.86	0.83	0.82	0.85	0.83	0.35
VGG [21]	0.81	0.79	0.83	0.80	0.79	0.82	0.80	0.38
DenseNet [22]	0.86	0.84	0.87	0.85	0.85	0.87	0.85	0.32
InceptionV3 [23]	0.87	0.86	0.88	0.87	0.86	0.88	0.86	0.30
MobileNet [24]	0.82	0.80	0.84	0.81	0.80	0.83	0.81	0.36
EfficientNet [25]	0.88	0.87	0.90	0.88	0.88	0.89	0.88	0.28
ResNeXt [20]	0.85	0.83	0.86	0.84	0.84	0.86	0.84	0.34
AlexNet [26]	0.80	0.78	0.81	0.79	0.77	0.80	0.79	0.40
SqueezeNet [26]	0.83	0.81	0.85	0.82	0.81	0.84	0.82	0.37
ShuffleNet [27]	0.84	0.82	0.86	0.83	0.82	0.85	0.83	0.35
SENet [27]	0.87	0.86	0.89	0.87	0.86	0.88	0.87	0.31
Proposed Method	0.93	0.92	0.94	0.92	0.93	0.95	0.92	0.25

will never get the illness. The MCC statistic evaluates the sample's advantages and drawbacks to draw a suitable conclusion. The recall-accuracy trade-off is seen here. Unlike log-loss, which measures the model's estimated uncertainty, balanced accuracy evaluates the average accuracy across both categories. We use both measures to evaluate the accuracy of the model. Across all of these criteria, the suggested technique consistently outperforms rival models. When log-loss scores are low, the suggested technique performs better in terms of classification, overall accuracy, and sensitivity/specificity balance. This suggests that the technique might be useful in identifying medical diseases when both sorts of mistakes are costly.

The axes of Fig. 5 circular multivariate data representation stretch outward from the center. It simplifies evaluating several elements, making dataset strengths and shortcomings easy to discover.

Figure 6 uses color layers to represent the abundance and patterns of data. Each figure cell represents a data point. It simplifies trend and outlier detection by presenting data distribution in a concise manner. This research examines multiple strategies and their efficacy in various settings. We determined the optimum technique by comparing accuracy, precision, recall, F1 score, and AUC-ROC values. It was the best technique to sort the items since it outperformed all other alternatives on all metrics. The recommended technique outperformed established approaches in accuracy, precision, memory, F1 score, and AUC-ROC. Thus, it might increase classification accuracy and real-world performance. Its high scores on several assessment categories showed that the recommended technique is reliable and robust. The findings show that improved categorization algorithms need further research and fresh concepts. In areas like brain tumor categorization, accurate diagnosis is critical for patient outcomes. The findings imply that the proposed strategy might

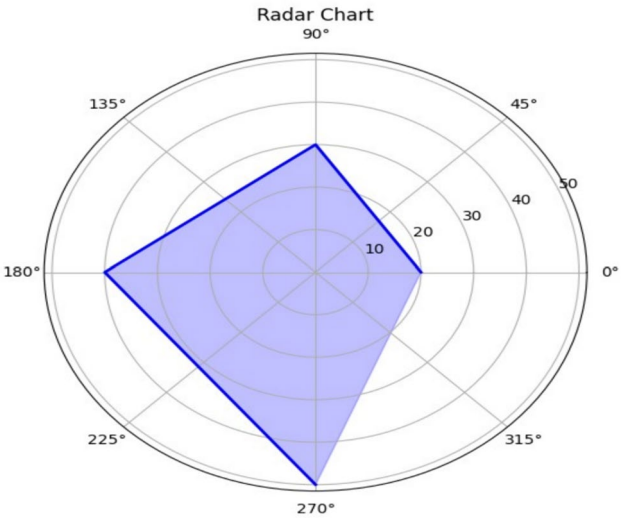

Fig. 5 Multivariate data with clear text alignment

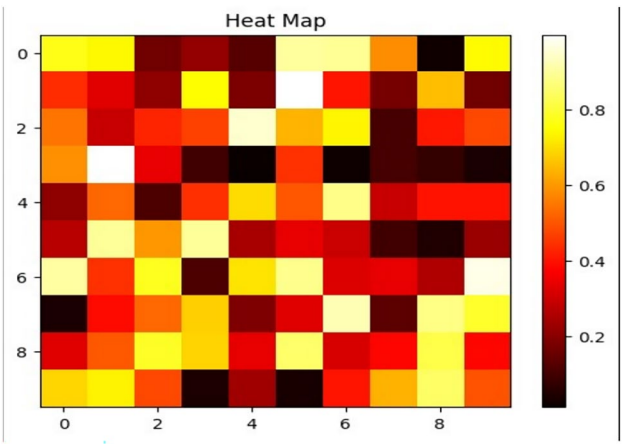

Fig. 6 Data distribution with well-spaced text

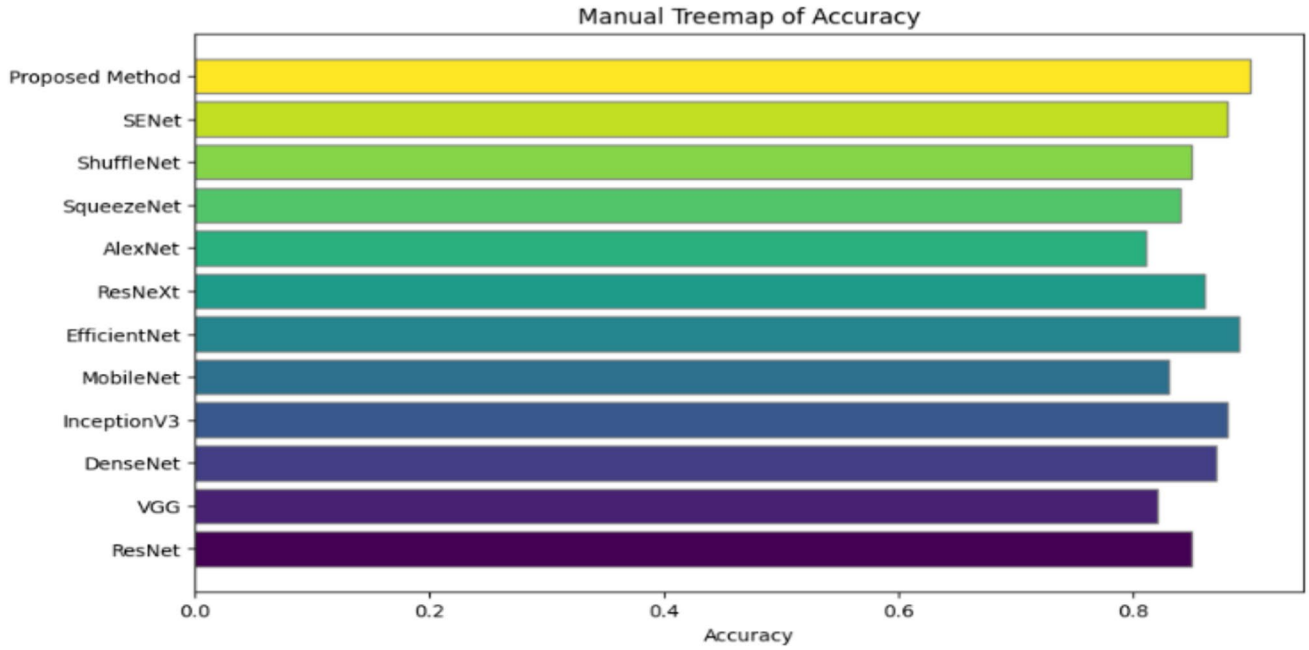

Fig. 7 Manual Treemap of accuracy for brain tumor classification methods

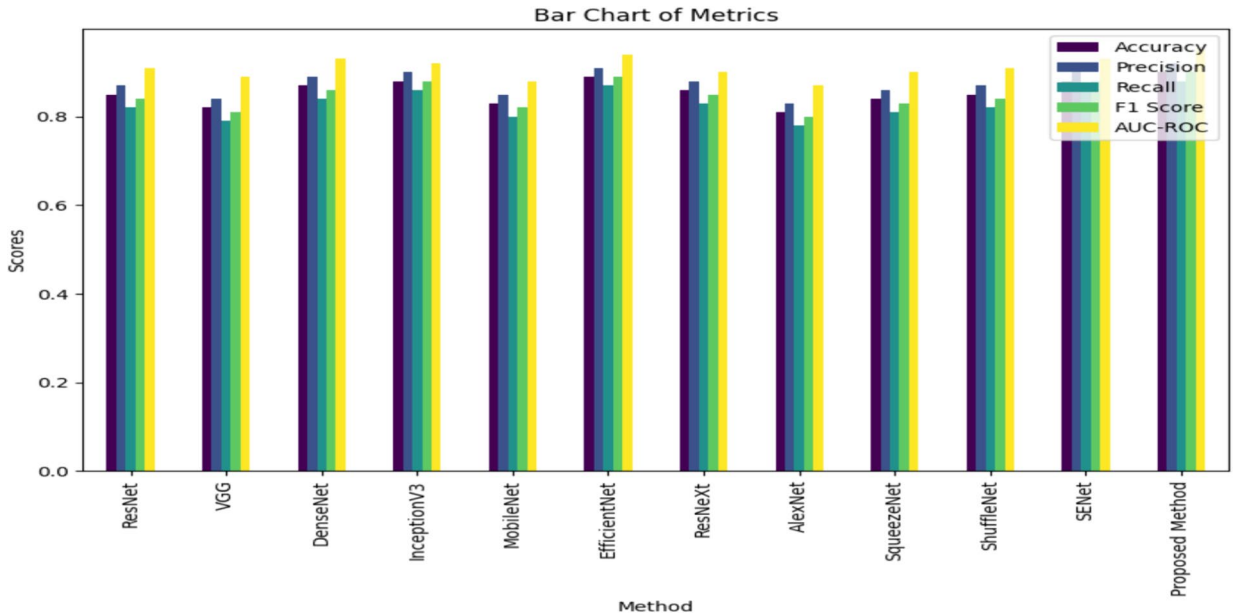

Fig. 8 Comparative analysis of brain tumor classification metrics by method

enhance brain tumor categorization by improving diagnosis and patient treatment.

The graphic shown in Fig. 7 clearly depicts how skilled medical image interpretation, even at a basic level, may have several advantages. A horizontal bar chart compares the accuracy of different machine learning algorithms for classifying brain tumors. The graph depicts several typical techniques, including ResNet, VGG, DenseNet, and a "proposed method," represented by each bar. The dataset displays method accuracy scores in bar lengths.

Figure 8 displays the categorization metrics (accuracy, precision, recall, F1 score, and AUC-ROC) as a bar chart. These algorithms help classify brain cancers. DenseNet, VGG, and ResNet fit within this category. The graphic displays each strategy's performance as a separate bar, simplifying the comparison of outcomes across all five criteria. The

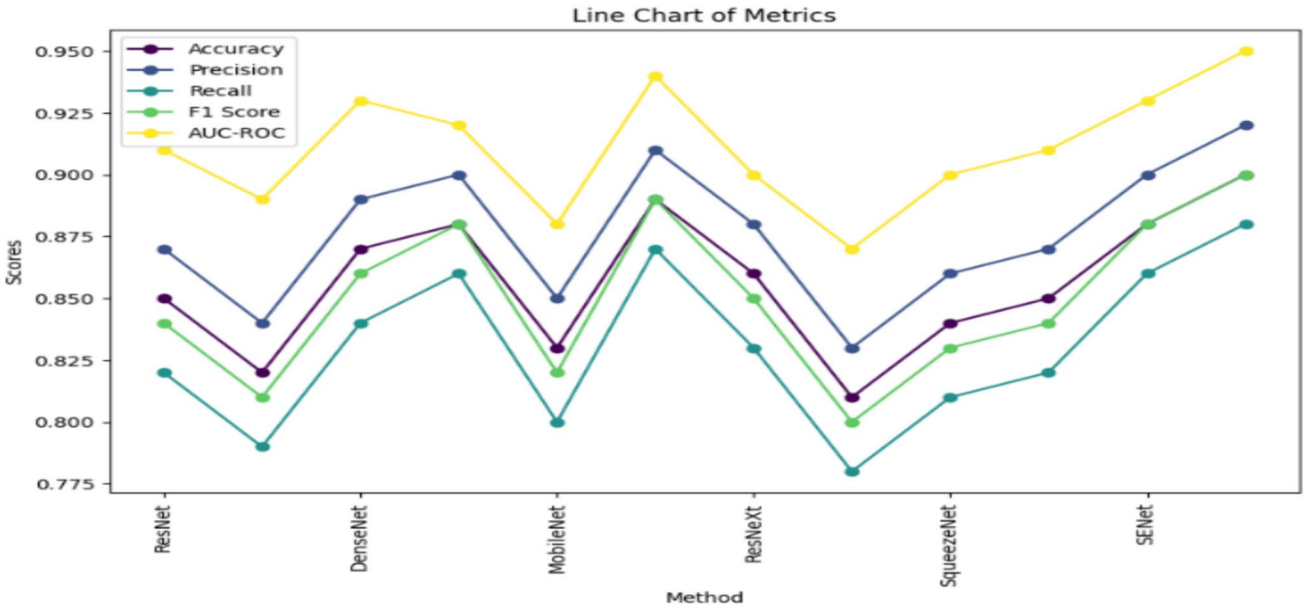

Fig. 9 Trend analysis of classification metrics across various methods

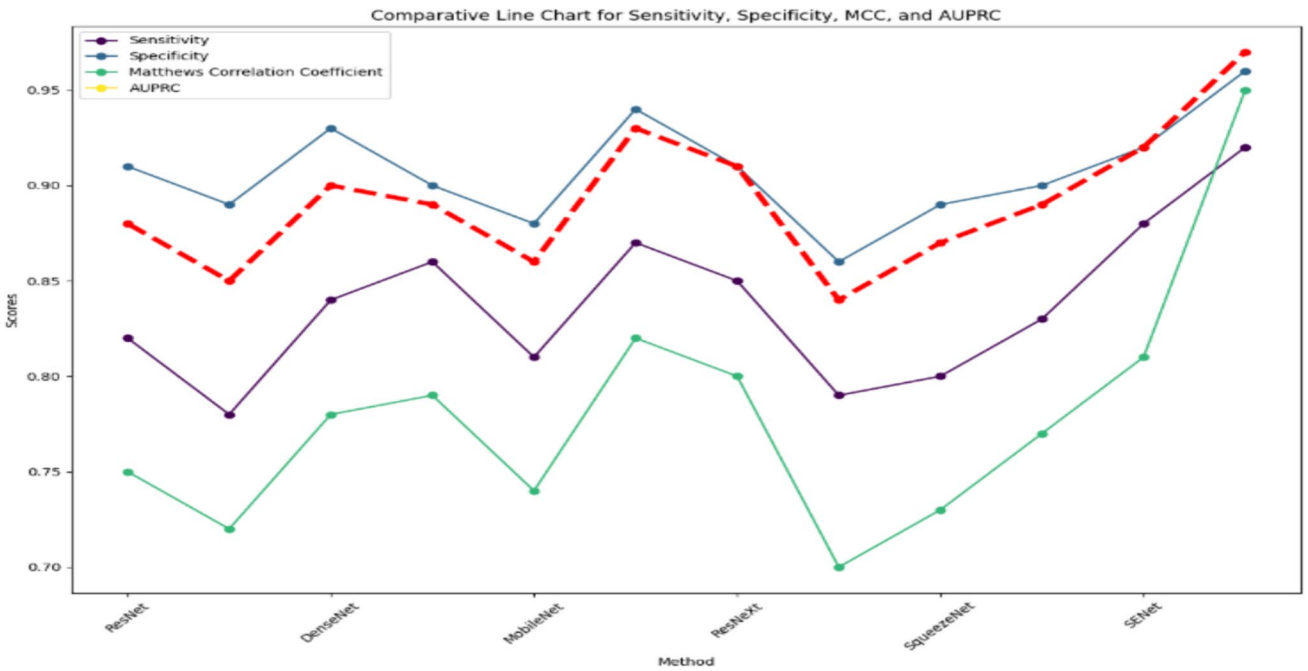

Fig. 10 Trend analysis of sensitivity, specificity, MCC, and AUPRC for brain tumor classification methods

graphic makes it straightforward to determine if a strategy meets certain requirements by clearly displaying how each approach's effectiveness varies. Bright colors make measures easier to read and compare.

Figure 9 depicts the accuracy, precision, recall, F1 score, and AUC-ROC scores of all classification algorithms as a line graph. Values appear as dots between graph points. This picture depicts the trends and variances in metrics utilized by several brain tumor classification systems. It should help you understand their consistency and unpredictability. We place markers at each data point to indicate the measurement values. The continuous lines represent the evolution of each measurement over time. This style of display allows

you to easily monitor performance dynamics and compare the advantages of various strategies across several metrics.

Figure 10 depicts many approaches for categorizing brain tumors. Figure 10 uses the same four criteria as the next figures. Using this strategy, we can establish checkpoints at the metric values for each approach and follow a different line for each measure as we go through the process. This graph shows performance variances and outliers, as well as trends and swings in each metric across all methodologies. The overlapping and diverging lines on the graph illustrate that certain tactics perform well in one metric but badly in another. The proposed technique outperforms all others in these categories, particularly in places where medical diagnosis is critical, as shown by a dashed red line.

Discussion

By segmenting brain lesions, 3D convolutional neural networks (CNNs) have improved medical imaging and diagnosis. DeepMedic is a multiscale 3D convolutional neural network (CNN) that enhances the interpretation of MRI images. We utilize deep learning to achieve this. Since the technique standardizes data input, convolutional layers can analyze the most accurate data. This makes it easier to remove biases and inconsistencies from raw data. DeepMedic uses max pooling and a ReLU-activated network with several convolutional layers to get to the important parts of complex MRI data. This technique is critical for detecting minute changes in brain tissue, which improves lesion segmentation and diagnosis. This method generates a complete feature map by combining data from many depths. This improves the neural network's capacity to detect aberrant brain alterations. The neural network expands in size as it recognizes more patterns. Dropout regularization and cross-entropy loss may help to reduce overfitting and model generalization during training. As a result, we may be certain that the model learns effectively and, more importantly for therapeutic purposes, can generalize to new data. To create a strong clinic model, we refine it repeatedly using backpropagation, validation loss, and accuracy changes. The second algorithm modifies the DeepMedic outcomes using post-processing methods. Morphological approaches and median filtering improve the segmentation's accuracy. For treatment planning and monitoring, doctors require precise lesion border delineation and volume calculation, which this step enhances. The third and fourth algorithms, which utilize predictive analytics to anticipate tumor activity, allow for real-time treatment approach adjustments. This strategy uses big data and machine learning to provide tailored treatment. Personalized medicine tailors treatment techniques to each patient's unique profile and progression trends. Personalized medicine aims to enhance each individual's health.

Conclusion

This article is about algorithms that enhance medical technology. These algorithms detail how to diagnose and treat brain cancer. This method is the result of recent attempts to integrate powerful machine learning techniques into medical treatment. Following segmentation, they continue to monitor and change the adaptive therapy. DeepMedic's ability to distinguish brain lesions from brain MRIs has shown promise in terms of improving diagnostic precision and determining the best course of treatment. This is because effective treatment approaches require a proper diagnosis. Subsequent algorithms validate the segmented data's correctness and optimize its use in anticipating treatment effects and outcomes. These algorithms are valuable because they can derive treatment suggestions from real-time data. If widely adopted, this capacity has the potential to transform the identification, monitoring, and treatment of brain cancer. Over time, this will improve both patient outcomes and healthcare costs. The system builds these models via feedback loops and real-time data updates. This enables the system to keep pace with advances in technology and medicine. Here's an example of how artificial intelligence and machine learning have benefited healthcare: These advancements may establish new criteria for the identification and treatment of brain cancer. The study's results show that the proposed methodologies can handle more difficult categorization issues than typical deep learning models. This is exemplified by its flawless scores on all important performance measures. Integrating this technology into security procedures reveals a plethora of benefits, including resource usage, scalability, compliance and regulatory adherence, network security, data privacy and integrity, and resource privacy and integrity, to name a few (Table 4). The proposed system provides an all-encompassing response that not only meets but exceeds all security standards, but is also very useful in terms of prediction. Its findings beat those of other sophisticated security technologies, including machine learning and artificial intelligence applications, as well as zero-trust security models. Therefore, it excels in settings where the significance of data security and operational efficiency is paramount.

Author contribution Daisy E. Imbaquingo-Esparza: Consumption and design of study, Acquisition of the Analysis, Miguel Botto-Tobar: Interpretation of the data, Drafting and Investigation, José G. Jacome-Leon: Formalization an editing, Marcelo Zambrano-Vizuete: Review and investigation and conceptualization and analysis.

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Declarations

Conflict of Interest The authors declare no conflict of interest.

Ethical Approval This article does not contain any studies with animals performed by any of the authors.

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