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Advances in Brain Tumor Detection and Localization: A Comprehensive Survey

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Abstract
Brain tumors present a formidable challenge in modern medicine. These diverse growths require early detection and precise localization for effective treatment. Recent medical imaging innovations, including magnetic resonance images (MRI) and computed tomography scan (CT) scans, offer detailed insights into the tumor characteristics. Various algorithms, such as K-means and convolutional neural networks (CNNs), enhance the detection and localization accuracy. Support vector machine (SVM) have emerged as effective classifiers and innovative approaches such as the Fractional Harley transformation show promise. Multi-CNN architectures improve accuracy, while combining algorithms such as K-means and Fuzzy K-means enhance segmentation. Moreover, Convolutional Neural Networks consistently excel in brain tumor detection. Deep learning, particularly CNNs, offers superior performance, although complexities and resource constraints should be considered. This survey highlights the evolving landscape of brain tumor detection and localization, highlighting the power of deep learning in improving diagnostics and treatment planning.

***Keywords*:** MRI, CT scans, K-Means, CNNs, SVM, fractional harley transformation, fuzzy K-Means, segmentation

8.1 Introduction

Brain tumors represent a complex and formidable challenge in modern medicine [18]. According to the American Cancer Society, approximately

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24,810 malignant tumors of the brain or spinal cord have been recorded for the year 2023 [19]. The abnormal growth of cells within the brain can manifest in various forms, each posing unique diagnostic and therapeutic dilemmas. Brain tumors exhibit remarkable diversity in terms of their histology, location, and clinical presentation. Understanding the nature of glioblastomas [1, 2], the most aggressive form of brain cancer, to benign tumors like meningiomas is crucial for effective management. These tumors can cause cognitive deficits and motor impairments, further emphasizing the need for their early detection and localization [3–5]. Timely and accurate detection, as well as precise localization, are paramount for ensuring optimal patient outcomes. The last decade has witnessed a notable surge in research and technological innovations aimed at enhancing brain tumor detection and localization. This introduction sets the stage for a comprehensive exploration of this critical area, underscored by the analysis of several recent brain tumor cases. Recent advancements in medical imaging technologies have played a pivotal role in transforming the landscape of brain tumor diagnosis. MRI and CT have become indispensable tools, that enable clinicians to visualize the brain in detail. These high-resolution images not only aid in identifying the presence of tumors but also provide vital information about their size, shape, and closeness to vital structures of the brain. Over the decades, several methods have been developed to detect brain tumors [6]. The segmentation process begins by employing the k-means algorithm to partition the image based on its gray-level intensity. Subsequently, the distance between the cluster data points and the cluster centroid is computed using the Fuzzy C-means algorithm.

In [7], the authors demonstrated enhancements in image quality using contrast enhancement techniques. Subsequently, they applied an optimized Fuzzy C-means algorithm with a genetic algorithm to perform feature extraction using the GLRLM and GLCM. The classification task involved distinguishing between images of normal brains and those with tumors, achieving an accuracy rate of 94.8%. Due to the inherent complexities in the analysis of medical images, an elaborate methodology combining CNN and SVM was extensively discussed in [8]. In [9], the authors conducted a comparative analysis of various machine learning classifiers to distinguish between benign and malignant brain cancer MRIs. The evaluated classification algorithms included support SVM, neural network, naive Bayes, and K-nearest neighbors. The findings of this study indicate that the SVM model is the most efficient approach for tumor detection. Nagabushanam *et al.* [10] proposed a study of the two-phased approach. After enhancing the image contrast, they used the fractional Harley transformation method to pre-process the MRI scans. The coefficients of the transformation were classified into normal and abnormal based on adaptive neuro fuzzy inference (ANFIS) approach. The accuracy without the clinical dataset was 99.3%; however, with the Brain Tumor Image Segmentation (BRAT) 2015 clinical dataset, the accuracy was 97.54%. However, the entire process was evaluated using several metrics, such as sensitivity, specificity, classification rate, and accuracy. An article focusing on the low accuracy of traditional brain tumor detection has shown the use of multi-CNN as an effective measure [11]. The normalization layer added between the convolutional layers and pooling layers reduces the problem of overfitting. The accuracy improved significantly compared to 2D detection networks. Moreover, the accuracy improved significantly in comparison to the single-mode brain tumor detection methods.

In [12], a combination of four algorithms, i.e., K-means, Fuzzy K-means, Gaussian Hidden Markov Random Field (GHMRF), and Gaussian Mixture Model (GMM), has been proposed for brain tumor segmentation. Although various methods have been explored for brain tumor detection and localization, Convolutional Neural Networks (CNNs) have been widely acknowledged as the most effective and accurate approach. In [13], a Convolutional Neural Network (CNN) was used to segment tumors in seven types of brain diseases: glioma, Alzheimer's disease, Alzheimer's plus, meningioma, pick, Huntington, and sarcoma. In [14], Abd-Ellah *et al.* introduced a two-phase approach in which the first phase showed how CNN was used for feature extraction, and Error-correcting Outputs (ECO-SVM) were used for feature classification. This phase focuses on detecting and classifying MRI images into normal and abnormal images. The next phase focused on localization within abnormal MRIs using a region-based Convolutional Neural Network. In [15], an automatic segmentation method based on a CNN was proposed by the second-place holder of the onsite BRATs 2015 challenge. It explores small kernels, as they provide a deeper architecture and have positive results for overfitting. They also focused on the use of intensity normalization during preprocessing, resulting in the enhancement of the regions. In [16], a methodology using deep convolutional activation features was proposed, where the challenge of limited data for training and the large dimensions of the image were tackled by transferring the features extracted from CNNs activations trained using ImageNet.

Machine Learning algorithms continue to serve as effective tools for brain tumor detection and localization. However, Deep Learning algorithms, such as CNNs, have significantly narrowed the gap by delivering superior performance. This was achieved through automatic feature learning and their ability to process extensive datasets. Nonetheless, DL's heightened complexity, computational demands, and interpretability challenges should be thoughtfully considered, particularly in medical contexts with resource constraints. A detailed overview of the various ML and DL models used was presented in [17]. The choice between ML and DL depends on specific task requirements, available resources, and desired accuracy levels. Although ML remains relevant, DL, exemplified by CNNs, has become a powerful ally in the quest for precise brain tumor detection and localization, offering a pathway to improve diagnostic capabilities and treatment planning.

8.2 Background Study on Various Methods

To enhance brain tumor detection and precise localization, several cutting-edge methods, including machine learning and deep learning techniques, have emerged as powerful contenders. This comparative analysis delves into the effectiveness of these methods, shedding light on their strengths, limitations, and real-world applications.

8.2.1 SVM [24]

Support Vector Machines belong to the category of supervised learning algorithms. It was used for classification and regression. The SVM helps us to find a hyperplane that separates the data into different classes. The mathematical formulation for a linear SVM in a binary classification can be summarized as a minimization problem, i.e.,

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$$\textit{minimize } \|w_1\|^2 \quad \textit{subject to } y_i'(w_1.x_i' - b') \geq 1\,;\, i \in \{1,2,\ldots,n\}$$

where $(x_i', y_i')\,(i = 1,2,\ldots,n)$ represents the training dataset and w represents the normal vector to the hyperplane $w_1{}^T\, x_i - b' = 0$. Moreover, the classifier is based on the values of w_1 and b'.

8.2.1.1 Advantages

SVMs effectively handle both linear and non-linear classification in complex medical image data. They are ideal for high-dimensional medical images (e.g., MRI with thousands of pixels). SVMs minimize overfitting, which is crucial for small, noisy datasets. They maximize class separation by finding optimal hyperplanes, making them suitable for moderately sized datasets, which is essential when obtaining large labeled data is challenging.

8.2.1.2 Limitations

Traditional SVMs are binary classifiers suited for tasks such as binary brain tumor detection (present/absent). For complex tasks such as tumor type or grading, SVMs may require extensions. They handle nonlinearity but struggle with highly complex data, where deep learning, such as CNNs, may perform better. Imbalanced datasets can bias SVMs toward the majority class, requiring techniques such as class weight adjustment or resampling. Tuning the SVM hyperparameters for peak performance can be computationally expensive, e.g., with grid search or cross-validation.

8.2.2 KNN [24]

K-Nearest Neighbors (KNN) is a simple and intuitive supervised machine-learning algorithm. It has also been used for classification and regression. We use KNN to predict the assignment of the label of an unknown data point. More specifically, based on the training data, an unknown data point is assigned a label that is either assigned or most common to its k-nearest neighbors.

8.2.2.1 Advantages

KNN is predicted by a majority vote of K-nearest neighbors, making it user friendly. It handles nonlinear data, which are vital for complex tasks such as brain tumor detection. The KNN relies on the local context for predictions and is valuable for medical imaging. This is a lazy learning algorithm that does not build an explicit training model. Furthermore, it stores the entire dataset for predictions, is useful with limited labeled data and avoids complex model building.

8.2.2.2 Limitations

KNN's computational demands increase with larger datasets and high-dimensional spaces. K parameter choice is vital. Small K values yield noise, and large K values yield overly smooth boundaries. Distance metric selection impacts performance and often requires experimentation. KNN is sensitive to class imbalance, which is common in the medical imaging of rare tumor samples. This is addressed through resampling or class-weight adjustment.

8.2.3 Logistic Regression [24]

Logistic Regression is a popular statistical method used for binary classification in data analytics. The logistic function (also known as the sigmoid function) is a key component of the logistic regression equation. Logistic regression is primarily used for binary classifications. Moreover, a logistic function (sigmoid function) transforms the input variables into values between 0 and 1. The Sigmoid function is represented mathematically in the following manner: $f(z)=\frac{1}{1-e^{-z}}$. An important observation of the sigmoid function is that $f(z)\rightarrow 1$ whenever $z\rightarrow\infty$ and $f(z)\rightarrow 0$ whenever $z\rightarrow -\infty$.

8.2.3.1 Advantages

Logistic regression is well-suited for binary brain tumor detection (present or absent) and can be adapted for multiclass classification. It has a lower risk of overfitting, which is crucial in medical imaging for the generalization to new data. Logistic regression provides probabilities, aiding medical decision-making and confidence assessment. L1 or L2 regularization can be applied to prevent overfitting and enhance the model generalization.

8.2.3.2 Limitations

Logistic regression assumes a linear decision boundary, limiting its ability to capture complex nonlinear patterns in the imaging features. Medical imaging datasets can be high-dimensional, posing efficiency challenges for logistic regression. Feature selection or dimensionality reduction is required. Logistic regression is sensitive to outliers, which are common in medical imaging data and potentially lead to biased model results. Logistic regression may not harness the full potential of deep learning techniques such as CNNs, which have excelled in image-based tasks, including medical imaging.

8.2.4 CNN [24]

Convolutional Neural Networks (CNNs) are well-known deep learning architectures. It is can process structured grid data, i.e., images.

The components of the CNNs are (1) convolutional layers, (2) pooling layers, and (3) fully connected layers.

8.2.4.1 Advantages

CNNs are ideal for grid-like data, which are crucial for identifying structures in brain scans by effectively capturing the spatial relationships. They learn features at different levels of detail by adapting to various tumor characteristics. Transfer learning from ResNet-trained models enhances the performance by leveraging prior knowledge. CNNs are robust to tumor position and orientation variations and recognize patterns across images. CNNs require less sequential data, which is crucial in situations where labeled sequences are scarce and expensive. They benefit from parallel processing, accelerated training, and inference for large medical image datasets.

8.2.4.2 Limitations

To achieve high performance, a large amount of labeled data is required by CNNs for training. In medical imaging, collecting extensive and accurately labeled datasets is challenging and time consuming. CNNs are often considered as *"black-box"* models. It is challenging to interpret how CNNs perform predictions. This lack of interpretability can be a drawback in medical contexts, where understanding the reasoning behind a diagnosis is important.

8.3 Methodology

Convolutional Neural Networks (CNNs) have demonstrated exceptional capabilities for the detection and localization of brain tumors. Unlike traditional machine learning methods, such as SVM, KNN, and Logistic Regression, CNNs excel at automatically extracting intricate features and patterns from medical images, particularly MRI scans. This inherent ability to discern subtle distinctions between tumor and non-tumor regions enables CNNs to precisely localize tumors within the brain. By leveraging CNN-based models, healthcare professionals can expedite the diagnosis process, aid in timely treatment planning, and improve patient outcomes. In summary, CNNs have emerged as a transformative tool, surpassing conventional machine learning techniques in the realm of brain tumor detection and localization. In this study, we provide a detailed methodology for

Q4 **Table 8.1** Comparison of machine learning algorithms.

Method	Advantage	Limitations	References
SVM	Nonlinearity Handling High Dimensionality Robustness to Overfitting Clear Margin and Decision Boundary Effective on Small Datasets	Limited to Binary Classification Limited Handling of Imbalanced Data Handling Complex Data Computationally Intensive Parameter Tuning	[20]
KNN	Nonlinearity Handling Local-context Consideration No need for model training	Computational intensity Sensitivity to the Value of K Sensitivity to Distance Metric Data Imbalance	[21]
Logistic Regression	Low Overfitting Risk Probabilistic Output Regularization	Linear Assumption High-Dimensional Data Limited Deep Learning Use	[22]
CNN	Hierarchical Feature Extraction Spatial Information Pretrained Models Translation Invariance Data Efficiency	Requires a large amount of training data. Complex model architecture may lead to longer training times. Model interpretability can be challenging.	[23]

tumor detection and localization using a CNN. CNNs, or Convolutional Neural Networks, are deep learning models specifically designed for image-related tasks. They excel at learning hierarchical features from images and have been highly successful in several computer vision tasks, including medical image analysis.

Transfer learning is a technique in which a pretrained neural network, usually trained on a large dataset for a different task, is fine-tuned for a specific problem or domain. In the context of brain tumor detection and localization, transfer learning can be beneficial due to the limited availability of medical imaging data. The ResNet-50 model is a deep CNN architecture with 50 layers. ResNet-50 is primarily used for image-classification tasks. This model can classify an input image into one or several predefined classes or categories. It has been pretrained on large datasets, such as ImageNet, which makes it particularly useful for a wide range of image classification problems. ResBlock is a fundamental component of ResNet-based architecture. It comprises multiple convolutional layers with skip connections. Skip connections allow gradients to flow more effectively during training, making it easier to train deep networks. In ResBlock, the main path consists of convolutional layers, whereas the short path is a direct connection from the input to the output. This direct connection facilitates the gradient flow during training. The kernel-size parameter specifies the size of the convolutional kernel (filter). In this case, the matrix is 1×1. The stride parameter determines how the convolutional filter moves across input data. Here, a 1×1 matrix indicates that the filter moves one pixel at a time, both horizontally and vertically. In this configuration, there was no downsampling of the input. The kernel initializer parameter specifies the setting of the initial values of the convolutional filter weights. It is designed to work well with Rectified Linear Unit (ReLU) activation functions and helps train deep neural networks. A Conv2D layer that performs 2D convolution with 16 filters of size 3 × 3 applies the ReLU activation function to the output, uses uniform padding to maintain spatial dimensions, and initializes the filter weights with the kernel initializer. This layer is applied to the input tensor in the neural network architecture. To downsample the spatial dimensions of the input data, we used a max-pooling layer. More specifically, MaxPool2D was used, which worked as a 2D max-pooling layer. Max-pooling is a type of operation that selects the maximum value from a group of values within a defined region of the input feature map. The pool size determines the size of the pooling window. In this case, (2, 2) indicates that the pooling window is a 2 × 2 matrix. During the max-pooling operation, this 2 × 2 window slides over the input feature map and selects the maximum value from each 2 × 2 block. Next, we add the Output from the Main Path and Short Path Together. In ResBlock, we combined the output from the main path and the short path by element-wise addition. This combination enhances the feature learning. Depending on the architecture, particularly in U-Net-like models for image segmentation, we need to upscale and concatenate feature maps from earlier layers to capture both high- and low-level details, such as the part with an anomaly in the image and the rest of the image. To build our CNN model, we referred to the ResBlock function and Conv2D layers in stages. The Conv2D layers perform convolution operations, whereas ResBlocks introduce residual connections. To address the challenge of data imbalance in medical image segmentation during the compilation process, we employed a custom loss function derived from the Tversky index. This tailored loss function effectively balances the trade-off between precision and recall, particularly when dealing with small structures such as lesions. In our evaluation, we enhanced the attention U-Net model by integrating an image pyramid approach to retain important contextual features. Kernel convolution is a fundamental image-processing technique that involves the application of a small numerical matrix, referred to as a kernel or filter, across an input image. This process transforms the image based on values within the filter. To compute the values of the resulting feature map, we utilized the following formula, where x_1 represents the input image and y_1 is the kernel. The indices for rows and columns in the resulting matrix are denoted as 'b' and 'c,' while the function's boundaries are indicated by 'I' and 'j.'

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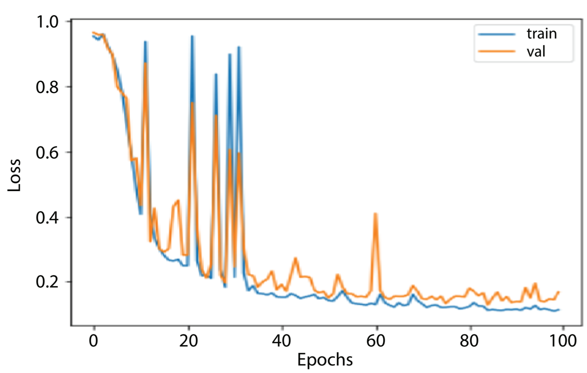
$$A_1[b,c] = (x_1.y_1)[b.c] \sum_i^{\square} \square \sum_j^{\square} y_1[i,j] x_1[b-i, c-j] \tag{8.1}$$

To create a generative tumor localization model, we used a custom loss function based on the Tversky Loss index. It addresses the class imbalance issues in segmentation tasks. Tversky loss allows us to balance precision and recall by adjusting hyperparameters. This corresponds to the Dice coefficient, which is a common segmentation metric. The Tversky index is defined as:

$$X(A_1, B_1; \alpha_1, \beta_1) = |A_1 B_1| / [|A_1 B_1| + \alpha_1 |A_1 / B_1| + \beta_1 |B_1 / A_1|] \tag{8.2}$$

Let A_1 and B_1 be the sets of predicted and ground-truth binary labels, respectively. The magnitude of the penalties for false positives (FPs) is



Q5 **Figure 8.1** Graph of validation loss vs. iterations.

controlled by α_1, and similarly, the magnitude of penalties for false negatives (FNs) is controlled by β_1.

8.4 Experimentation

8.4.1 Dataset

The dataset used in this paper is available at https://www.kaggle.com/datasets/mateuszbuda/lgg-mrisegmentation. This dataset comprises magnetic resonance (MR) brain images and the accompanying manual segmentation masks for FLAIR abnormalities. These image data were sourced from The Cancer Imaging Archive (TCIA). The archive contains data from 110 patients who were part of The Cancer Genome Atlas (TCGA) collection for lower-grade gliomas. To be included in this dataset, patients were required to have available fluid-attenuated inversion recovery (FLAIR) sequence data as well as genomic cluster information. Additional information about the tumor genomic clusters and the data collected from the patients can be found in the data.csv file.

8.4.2 Results Achieved

The CNN model had the highest average accuracy (98.1%), indicating its suitability for image classification tasks. It excels in automatically learning intricate features from data. Logistic Regression, while simple and interpretable, achieved lower accuracy (85%) compared to CNN, suggesting limitations in capturing complex patterns. Thus, it may be more suitable for straightforward binary-classification tasks. KNN offers simplicity and adaptability, but it falls behind both CNN and Logistic Regression in terms of its accuracy (80%). Its performance is reasonable for some tasks but may struggle with high-dimensional or complex data. SVM, with an average accuracy of 71%, performed least effectively in this comparison. SVM's strengths lie in handling high-dimensional data, but its performance may benefit from further tuning or considering other model options. The choice of the most suitable model depends on the specific problem, dataset size, and data complexity. In this context, for image classification tasks, the CNN model appears to be the preferred choice due to its superior performance. However, for simpler tasks, or when interpretability is crucial, Logistic Regression may still be a viable option. Careful consideration of the problem's requirements and data characteristics is essential when selecting a machine learning model and collaborating with such esteemed professionals.

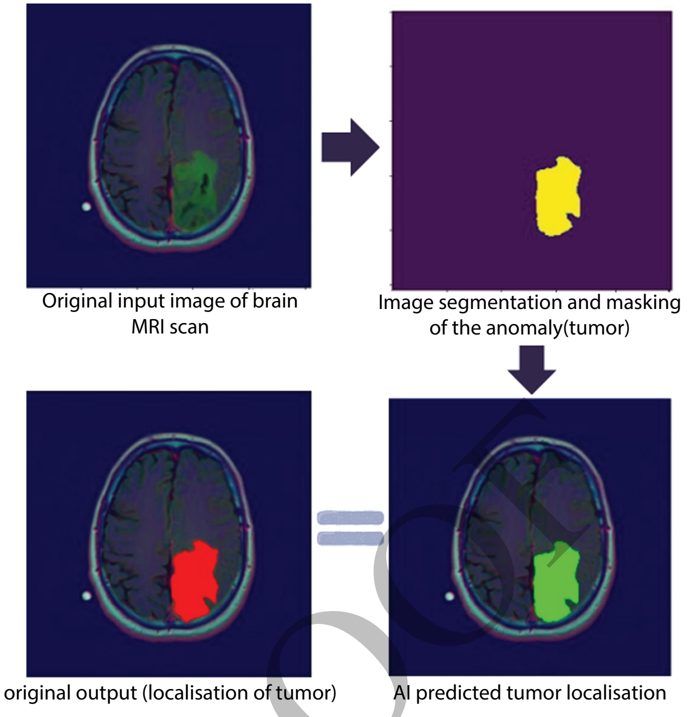


Figure 8.2 Working overview of tumor detection and localization.

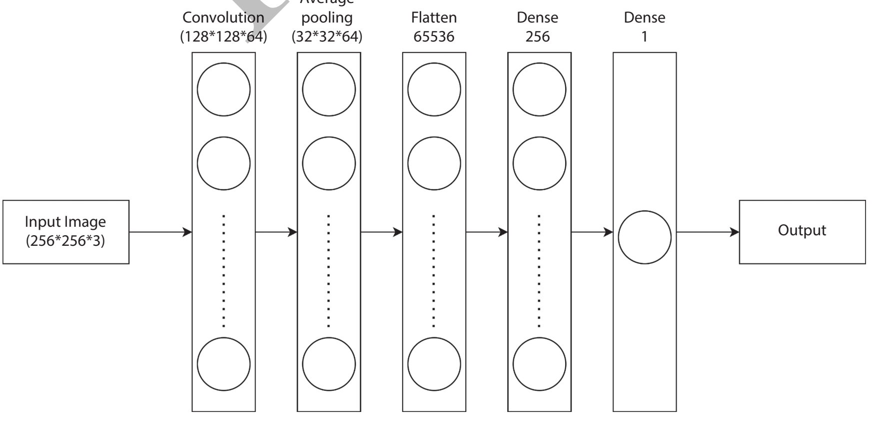


Figure 8.3 CNN model for tumor detection.

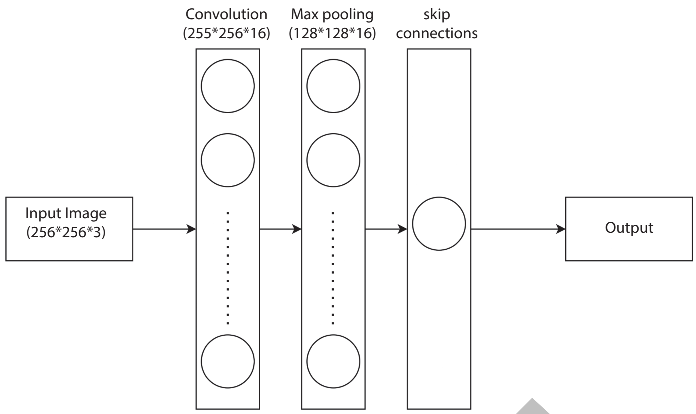


Figure 8.4 CNN model for tumor localization.

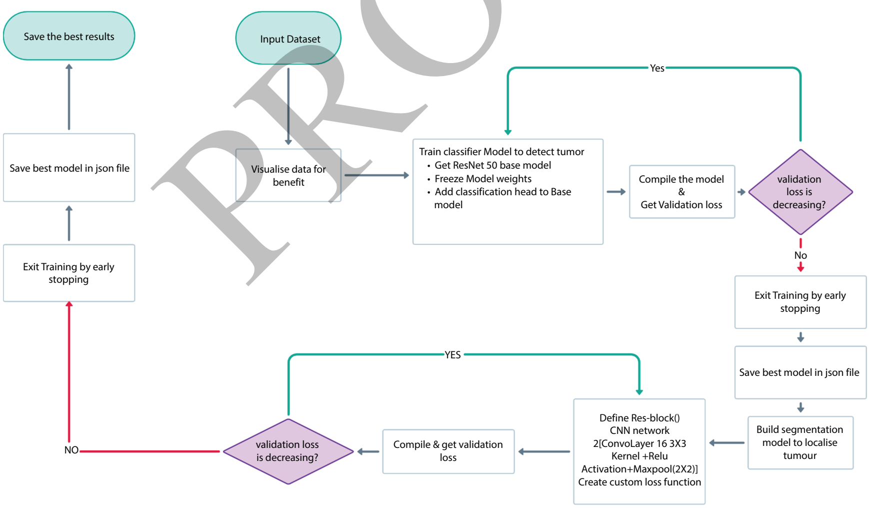


Figure 8.5 Flowchart on the overview for the tumor detection and localization using CNN.

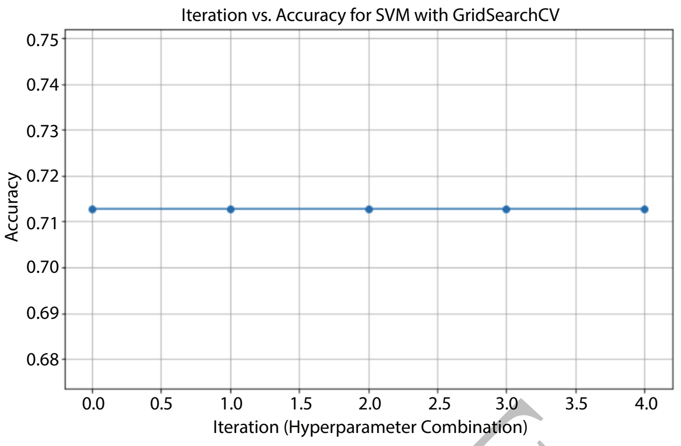


Figure 8.6 Accuracy through GridSearchCV.

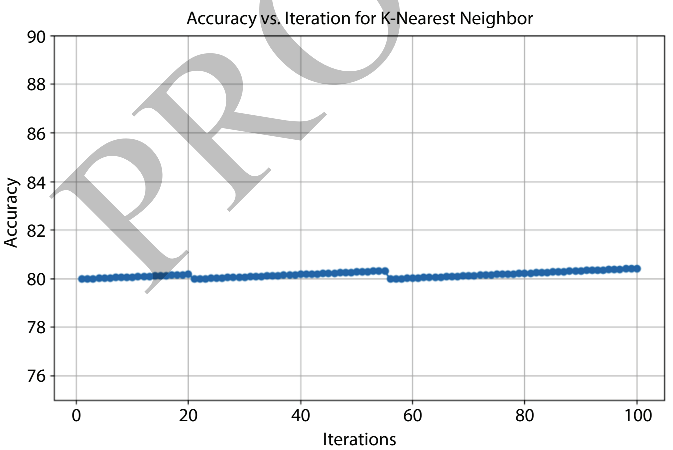


Figure 8.7 Accuracy through K-nearest neighbor.

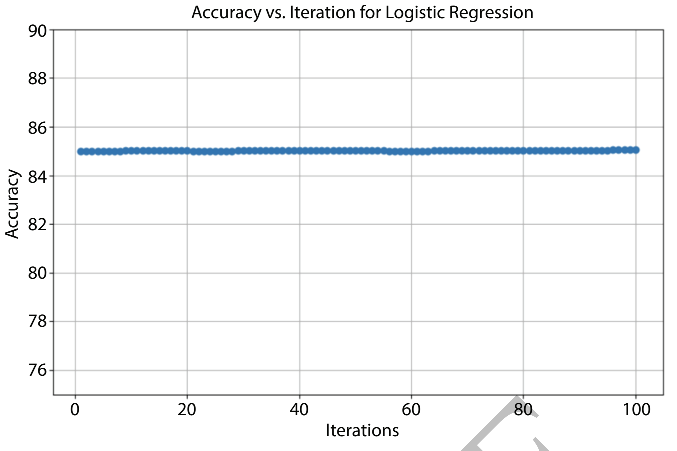


Figure 8.8 Accuracy through logistic regression.

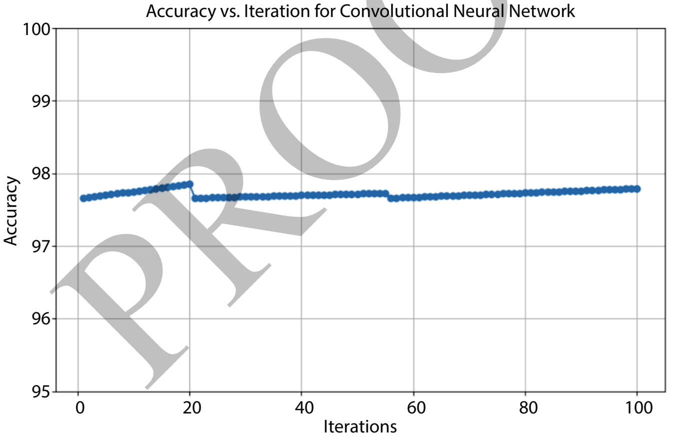


Figure 8.9 Accuracy through CNN.

Table 8.2 Comparison of evaluation metrics.

Algorithm	*Algorithm*	*Precision*	*Recall*	*F1-score*
SVM	*71.28*	*0.67*	*0.67*	*0.66*
KNN	*80.32*	*0.6*	*0.66*	*0.63*
Logistic Regression	*85.19*	*0.7*	*0.63*	*0.61*
CNN	*98.09*	*0.97*	*0.99*	*0.98*

8.5 Discussion

From the table of evaluation metrics, it can be observed that the Convolutional Neural Network, when applied with the Transfer Learning Technique, yields the highest precision and accuracy for tumor detection and localization. These findings underscore the significance of CNN in medical image segmentation tasks, emphasizing their potential to enhance accuracy and efficiency and ultimately improve patient diagnosis and treatment planning.

8.6 Conclusion

Image segmentation is a crucial component of medical image processing, particularly in the context of MRI. In this study, we explored and compared several classification methods such as SVM, KNN, and Logistic Regression. However, the spotlight lies in Convolutional Neural Networks (CNN) as they exhibit the most promising results. The superiority of CNN can be attributed to its innate ability to automatically learn complex features and patterns from medical images, making it well-suited for the intricacies of medical image segmentation. In this study, we delve into the methodology behind CNN, detailing its architectural design and training procedures that contribute to its exceptional performance. Hence, it can be concluded that applying Deep Learning and Neural Networks is highly efficient and accurate compared with traditional Machine Learning Algorithms.

8.6.1 Future Scope

Continuous improvement and expansion of the dataset can lead to better model performance. Collecting more diverse MRI images, including different tumor types, stages, and patient demographics, can help improve the model generalization. Advanced data augmentation techniques can artificially increase the size and diversity of datasets. Moreover, it can improve the robustness and generalization of the model. In addition, fine-tuning the hyperparameters, such as the learning rate, batch size, and optimizer choice, will optimize the performance of the model. Exploring different pre-trained models and architectures for transfer learning, such as EfficientNet, Inception, and NASNet, may capture different features and improve performance.

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