Automated Multi-Class Brain Tumor Classification from MRI Images Using a Tree-Hierarchical Deep Convolutional Neural Network with Optimized Image Processing

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Abstract. Brain tumors represent one of the most critical challenges in medical diagnosis due to their high mortality rate and complex structure, and early and accurate detection is essential to improve treatment outcomes and survival rates. However, brain tumor detection and classification from MRI images remain highly challenging because MRI scans often suffer from noise, low contrast, and intensity inhomogeneity, which obscure critical tumor boundaries and reduce diagnostic accuracy. This research is motivated by the urgent need for automation in neuro-oncology, as the growing number of brain tumor cases makes reliance on manual radiological assessment unsustainable. To address these issues, we propose a novel framework that integrates Bayesian Boundary Trend Filtering (BBTF) for optimized pre-processing with a Tree-Hierarchical Deep Convolutional Neural Network (THDCNN) capable of capturing both local and global features. Unlike conventional CNNs and ANNs, the hierarchical design of THDCNN ensures robust multi-scale feature learning, while BBTF preserves tumor boundaries during noise reduction, resulting in cleaner and more reliable inputs. Experimental validation shows that the proposed model achieves 6–8% higher accuracy, precision, and recall compared to existing CNN, ANN, and FCM-SVM methods. This combination of advanced pre-processing, novel architecture, and superior performance makes the framework a promising solution for real-time, privacy-preserving smart healthcare and next-generation neuro-oncology applications.

Keywords: Brain tumor classification, MRI images, deep learning, Tree-Hierarchical CNN, Bayesian Boundary Trend Filtering, Medical image processing, Smart healthcare, Tumor detection.

1. Introduction

Because of their complicated structure and high death rate, brain tumors provide one of the biggest diagnostic problems in medicine. To increase treatment results and survival rates, brain tumors must be detected early and accurately. [1-2]. Because MRI is non-invasive and has excellent tissue contrast, it is the standard imaging method [3]. Manually analyzing MRI data takes a lot of time and is prone to mistakes, and heavily reliant on radiologists' expertise [4]. Recent advancements in deep learning (DL) methods have transformed the analysis of medical images, offering automated solutions for tumor detection, segmentation, and classification. Conventional deep learning models, including CNNs and ANNs, have demonstrated encouraging outcomes, yet they often suffer from limitations such as over fitting, poor generalization, and high computational cost when dealing with complex hierarchical features [5-6]. Furthermore, pre-processing techniques are often insufficient to handle noise and intensity variations in MRI images [7]. To address these challenges, this work proposes a THDCNN integrated with Bayesian Boundary Trend Filtering (BBTF) for optimized pre-processing. The hierarchical nature of THDCNN enables efficient feature extraction at multiple levels, while BBTF ensures cleaner and normalized inputs for enhanced classification performance [8-10].

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1.1 Problem Statement

Detecting and classifying brain tumors using MRI images is still difficult because of a number of intrinsic complications. MRI scans often suffer from noise, low contrast, and intensity inhomogeneity, which obscure critical tumor boundaries and reduce diagnostic accuracy. Conventional methods, such as machine learning and common deep learning techniques such CNNs, ANNs, and SVMs, provide promising results but are often limited by overfitting, lack of robustness, and inability to effectively handle multi-class classification. Moreover, these models generally fail to capture the hierarchical and multi-scale features required for accurate tumor differentiation. The computational inefficiency of existing models further restricts their applicability in real-time clinical environments, particularly in privacy-preserving smart healthcare systems. Therefore, there is a pressing need to develop an optimized, computationally efficient, and highly accurate deep learning framework that can address the limitations of existing methods while ensuring reliable brain tumor classification.

1.2. Motivation

The pressing need for automation in neuro-oncology is what spurred this study. With the increasing number of brain tumor cases, reliance on manual radiological assessment is unsustainable. In addition to increasing diagnostic precision, automated classification lowers physician workload and offers prompt treatment recommendations. Furthermore, most existing models struggle with MRI variability and multi-class classification. Incorporating advanced pre-processing (BBTF) with a tree-structured hierarchical CNN can significantly improve tumor detection accuracy and reliability. This research is motivated by the vision of developing privacy-preserving, smart healthcare systems that integrate deep learning with clinical decision support.

1.3 Contributions

The following is a summary of this work's primary contributions:

1. Optimized Preprocessing – Introduction of Bayesian Boundary Trend Filtering (BBTF) for noise reduction and normalization, ensuring improved image quality for classification.
2. Novel THDCNN Model – Development of a THDCNN that captures both global and local features for robust classification.
3. Multi-Class Brain Tumor Classification – MRI pictures are automatically classified into tumor and non-tumor categories with high efficiency and accuracy.
4. Comprehensive Evaluation – Experimental validation on the Brain Tumor Detection 2020 Accuracy, precision, recall, specificity, F1-score, ROC, error rate, and computing time are among the measures used to analyze the dataset.
5. Performance Superiority – Demonstrated performance improvements of 6–8% over CNN, ANN, and FCM-SVM models.
6. Application in Smart Healthcare – Design of a model suitable for privacy-preserving, AI-driven healthcare systems with real-time potential.

The remainder of this study is organized as follows: a review of the literature is presented in section 2, a proposed approach is discussed in section 3, results are described with discussion in section 4, and conclusions are discussed in section 5.

2. Literature Review

This section reviews recent advancements in the Classification of brain tumors using DL. In 2024, Lata et al. [11] presented a brain tumor that is dependent on DL detection system integrated into a privacy-preserving smart healthcare platform. Their framework utilized AES-128 and PBKDF2 algorithms for secure medical image storage, alongside CNN-based architectures For example, VGG-16, ResNet-50, and Inception V3. These models were optimized using preprocessing methods and optimizers like RMSprop, SGD, and Adam. The system achieved a high detection rate but suffered from high computational time, making real-time deployment challenging.

In 2025, Hussain et al. [12] proposed a next-generation neuro-oncology automation system using sophisticated neural networks for the categorization and segmentation of brain tumors. They evaluated UNet, Attention-UNet, and Residual-Attention-UNet architectures, with the latter consistently outperforming others in segmentation accuracy and classification precision. Despite its high precision, the model reported a lower F1-score, indicating room for improvement in balanced classification performance.

Alqhtani et al. [13] created a hybrid method for MRI-based tumor division and categorization in 2024 that combines FCM clustering and SVM. Their preprocessing pipeline included filtering using diffusion and CLAHE, followed by segmentation using FCM and classification using SVM. While this method achieved a high ROC score, it exhibited low specificity, which limits its diagnostic reliability.

In 2024, Anantharajan et al. [14] explored DL-ML hybrid approaches for MRI brain tumor detection. Their work highlighted the labor-intensive manual process required in traditional methods and positioned deep learning as a promising alternative. The proposed framework demonstrated higher recall but struggled with low overall accuracy, suggesting difficulties in generalizing across diverse tumor categories.

In 2024, Pacal et al. [15] enhanced the EfficientNetV2 architecture featuring Efficient Channel Attention Mechanisms and Global Attention. Their method significantly improved the model's capacity to concentrate on important tumor areas in MRI images, resulting in higher F1-score. Despite its improved classification accuracy, the approach achieved a low detection rate, indicating limitations in identifying all tumor instances effectively.

Together, these studies show notable progress in the identification and categorization of DL-based brain tumors. The challenges such as computational inefficiency, low specificity, poor detection rate, and reduced balanced accuracy remain unresolved. This motivates the need for a THDCNN integrated with optimized pre-processing to overcome these limitations. Table 1 shows the Comparison of Recent Works in DL-Based Brain Tumor Classification

Table 1: Comparison of Recent Works in DL-Based Brain Tumor Classification

Author & Year	Method / Model	Preprocessing / Features	Strengths	Limitations
Lata et al. (2024) [11]	CNN (Inception V3, ResNet-50, VGG-16) with AES-128 + PBKDF2 for security	Extensive pre-processing; RMSprop, SGD, Adam optimizers	High detection rate; privacy-preserving healthcare integration	High computational time
Hussain et al. (2025) [12]	UNet, Attention-UNet, Residual-Attention-UNet	Advanced segmentation architectures	High precision; Residual-Attention-UNet superior segmentation	Low F1-score
Alqhtani et al. (2024) [13]	FCM for segmentation + SVM classifier	CLAHE and diffusion filtering	High ROC score; effective pre-processing	Low specificity
Anantharajan et al. (2024) [14]	DL-ML hybrid methods	MRI tumor segmentation with manual iterations	High recall; DL integration highlighted	Low accuracy
Pacal et al. (2024) [15]	EfficientNet V2 + Global & Channel Attention	Attention-enhanced feature extraction	High F1-score; improved classification accuracy	Low detection rate

3. Proposed Methodology

Brain MRI scans from the Br35H: Brain Tumor Detection 2020 dataset are the first step in the methodical pipeline that makes up the suggested methodology, followed by optimized pre-processing, hierarchical feature extraction, and final classification using the THDCNN.

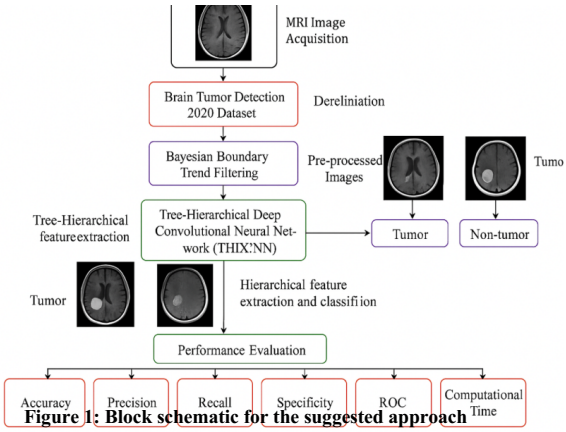

Figure 1: Block schematic for the suggested approach

As seen in Figure 1, the overall workflow of the proposed methodology, which begins with image acquisition from the Br35H: dataset for Brain Tumor Detection 2020. The collected MRI pictures are first subjected to pre-processing using Bayesian Boundary Trend Filtering (BBTF), a technique that enhances image quality by removing noise and intensity in homogeneities while preserving critical structural details such as edges and tumor boundaries. Following pre-processing, the images undergo multi-scale decomposition to extract both fine-grained local characteristics and more extensive worldwide patterns, ensuring robust depiction of the features of the tumor. These characteristics are then processed through the THDCNN, which organizes the extracted information in a hierarchical manner to capture relationships across different spatial levels. Finally, the aggregated features are classified into two categories tumor and non tumor producing reliable diagnostic predictions. This systematic pipeline highlights the integration of optimized pre-processing with advanced deep learning architecture to achieve accurate and efficient brain tumor detection

3.1 Image acquisition

This well-organized benchmark collection, Br35H: Brain Tumor Detection 2020, is intended for the binary categorization of brain MRI images into two groups: both a tumor and none [16]. It has 3,060 photos in all, which are evenly distributed across the two primary classes, thereby ensuring a balanced dataset suitable for assessing and developing machine learning models. Specifically, the dataset consists of 1,500 images labeled as *tumor* (under the "yes" folder) and 1,500 pictures with a *no tumor* label (under the "no" folder), along with an additional *pred* directory provided for testing model predictions. The balanced distribution of samples in this dataset is of particular significance for healthcare imaging research, as it minimizes the common issue of class imbalance, which can negatively affect model generalization and classification accuracy. Each MRI image captures structural brain information that can be leveraged to teach CNNs and other deep learning systems, for automated tumor detection. Owing to its organization and class balance, the dataset has become a widely used resource in academic studies focused on medical image analysis, enabling researchers to benchmark and compare various diagnostic algorithms effectively. Below table 2 shows the clear tabulation of the dataset's composition

Table 2: Dataset Composition Table

Tumor Status	Number of Images
Tumor (Positive)	1,500
No Tumor (Negative)	1,500
Total	**3,060**

The Br35H dataset used in this study is binary and balanced (1,500 tumor vs. 1,500 non-tumor images), which simplifies classification and likely contributes to the very high accuracy (97.66%). However, real-world clinical datasets are typically imbalanced and multi-class, containing different tumor subtypes (e.g., glioma, meningioma,

pituitary tumors) with unequal representation. In such cases, performance may degrade in several ways:

1. Class imbalance – The model could become biased toward majority classes, leading to more false negatives in rare subtypes. For example, small or uncommon tumors might be under-detected compared to large, well-represented tumor types.

2. Multi-class complexity – Instead of simply distinguishing "tumor vs. no tumor," the model would need to learn fine-grained distinctions between tumor subtypes, which requires deeper feature representations and more robust generalization.

3. Generalization risk – Since training was done on a balanced binary dataset, the model has not been stress-tested against the variability of real-world MRI data (different scanners, protocols, and tumor morphology), which could lower recall and increase misclassification rates.

4. False negatives in rare tumors – Clinically, missing rare but aggressive tumors would be critical. Without explicit mechanisms such as class-weighting, data augmentation, or synthetic sample generation (SMOTE, GANs), the model may struggle in these scenarios.

THDCNN framework is promising, on real-world imbalanced datasets it would likely show lower accuracy, higher error variance across classes, and weaker performance on minority subtypes. To make it clinically viable, the model would need extensions such as multi-class training, imbalance-aware loss functions, external dataset validation, and possibly explainable AI modules to handle diagnostic uncertainty.

3.2 Preparation using Filtering via Bayesian Boundary Trends

This section discusses the pre-processing utilizing BBTF [17] is discussed for image normalization and cleaning. Bayesian Boundary Trend Filtering (BBTF) performs better than common pre-processing methods such as Gaussian filtering, median filtering, or CLAHE (Contrast Limited Adaptive Histogram Equalization) because it is specifically designed to remove noise and normalize intensity while preserving critical structural details like tumor boundaries. Traditional filtering approaches tend to blur edges or smooth out fine-grained tumor regions, which can obscure subtle tumor margins and lead to false negatives during classification. Similarly, while CLAHE improves contrast, it can sometimes over-enhance noise or distort boundary clarity, especially in low-contrast MRI scans. In contrast, BBTF uses a Bayesian probabilistic framework that balances smoothing with edge sharpness by incorporating prior knowledge of spatial structures. This allows it to selectively suppress noise in homogeneous regions while maintaining sharp transitions at boundaries. As a result, tumor margins remain intact and diagnostically useful features are preserved, giving the downstream THDCNN cleaner, more informative inputs.. In short, BBTF's advantage lies in its edge-preserving noise reduction, which reduces false negatives from blurred tumors and enhances the reliability of classification in clinical imaging. An advantage with analysis is that filtering methods sometimes blur borders or distort boundary areas which make it hard to see important structural information. BBTF solves this problem by using a Bayesian framework that automatically balances smoothing and sharpness. This makes sure that critical visual elements like object edges textures and contours are given in equation (1).

$$\min_{\vartheta \in E^m} \sum_{l=1}^{m} \left(\vartheta_l - x_l\right)^2 + \lambda \left\| R_m^{(j+1)} \vartheta \right\| 1 \tag{1}$$

Where, λ denotes the tuning parameter that regulates the smoothing level to reduce noise in application image, $R_m^{(j+1)}$ denotes the initialization of image and $j+1$, x_l denotes the indicates the element of error. BBTF, on the other hand, gives you a way to measure uncertainty, which makes picture reconstruction and interpretation more dependable. This is very helpful when working with photographs that are noisy or not very good where it's important to keep small details without making noise louder shown in equation (2).

$$x_l = \vartheta_l + \delta_l \, , \; \delta_l \sim HM\left(0, \sigma^2\right) \tag{2}$$

Where, $HM\left(0,\sigma^2\right)$is the cost function at state, σ is the likelihood of behavior patterns given a malware type, and δ is the factors that control the contribution of past and current errors and ϑ_l represents the nonlinear systems. Its design that knows where the edges are cuts down on artifacts at the edges of images which makes the outputs cleaner and more natural. Moreover, the probabilistic structure of BBTF allows for automatic regularization limiting over-smoothing while keeping image clarity given in equation (3).

$$p\left(x_l \mid \vartheta_l, \sigma^2\right) = \sqrt{\frac{2}{\pi\sigma^2}} \exp\left(-\frac{1}{2\sigma^2}\left(x_l - \vartheta_l\right)^2\right) 1_{\{x_l \le \vartheta_l\}}\left(x_l\right) \quad (3)$$

Where, π denotes the clean unwanted image and $\left\{x_l \le \vartheta_l\right\}$signifies the statistical value of image. In summary, BBTF boosts image quality by combining edge-preserving filtering with uncertainty aware modelling making it useful tool for robust image analysis. Finally, the images are for image normalization and cleaning using BBTF.

3.3 Brain tumor detection using THDCNN

This stage, the pre-processed MRI images are analysed using the THDCNN [18], it is especially made to capture both local and global feature representations through a multi-scale hierarchical learning framework. Unlike conventional CNN architectures, the hierarchical structure of THDCNN enables the extraction of fine-grained tumor details while simultaneously preserving broader contextual information, thereby improving classification robustness. This approach offers several advantages in the medical imaging domain: it mitigates the challenges of overfitting and poor generalization commonly encountered in standard deep learning models, enhances diagnostic reliability by effectively distinguishing between tumor and non-tumor regions, and reduces computational inefficiency through structured feature learning. Consequently, THDCNN offers a strong and effective framework for detecting brain tumors, offering superior accuracy and clinical applicability in comparison to traditional CNNs and hybrid machine learning models

Pre-processed images are decomposed into multiple scales or resolutions to capture both fine and coarse patterns. This ensures that subtle manipulation artifacts as well as broader inconsistencies are effectively represented, enabling the network to detect brain tumor across different spatial levels as given in equation (4).

$$F_{avg} = \left(l, n\right) = \sum_{m=1}^{M}\left(F\left(l, n, m\right)/M\right) \quad (4)$$

Where, F_{avg} denotes input layout pattern data, l, n denotes the features set from branch, F represents the spatial resolution parameter controlling features map size per branch and M is the higher level semantic features. Multi-scale features are organized into a hierarchical tree structure, capturing relationships among features at different levels. This links local micro-patterns with higher-level macro-patterns, allowing the network to analyze complex interactions between spatial details in a structured manner. This is given in equation (5).

$$B_{kY} = \tan g\left(E'_{e'} h_{kY} + f'_{e'}\right) \quad (5)$$

Here, B_{kY} indicates is the concatenated output, $E'_{e'}$ denotes attention coefficient for scale, h_{kY} implies backward parameter using j^{th} order, y denotes the complex interactions between spatial details and $f'_{e'}$ denotes capturing relationships among features. Hierarchical features are processed through convolutional layers. Convolutional filters extract textures and edges, intermediate layers capture structural patterns, and deeper layers encode global spatial information as given in equation (6).

$$\beta_{kY} = \frac{\exp\left(B_{kY} B_{e'}\right)}{\sum \exp\left(B_{kY} B_{e'}\right)} \quad (6)$$

Where, β_{kY} represents the Convolutional filters, B_{kY} denotes textures and edges features and $B_{e'}$ denotes the global spatial information. Outputs from different convolutional layers are aggregated to form a unified feature representation. This step ensures that both local details and global structures are preserved and it is given in equation (7).

$$T_k = \sum Y \beta_{kY} h_{kY} \tag{7}$$

Here, T_k implies final word representation sequence, β_{kY} signifies corresponding 7 weight and h_{kY} implies backward parameter.

The aggregated features are passed into a THCNN and recursively analyses hierarchical features to model dependencies and interactions between them, allowing the network to capture intricate relationships indicative of potential tampering as evaluated in equation (8).

$$\omega_d = P_{\Omega 1}\left(- K_1 J^T (r - r_d)\right) \tag{8}$$

Here r_d is denotes hierarchical features and K denoted as constant variable. Within the convolutional Neural Network, sequential-like dependencies and contextual relationships among hierarchical features are learned. This step identifies the brain tumor as positive and negative causes.

The proposed THDCNN architecture addresses over fitting and poor generalization through both its hierarchical design and optimized pre-processing pipeline. Unlike standard CNN/ANN models that extract features in a flat, sequential manner, THDCNN organizes learning in a tree-hierarchical structure that captures multi-scale representations fine-grained local tumor details and broader global context simultaneously. This reduces the risk of the network memorizing dataset-specific patterns (overfitting) and instead encourages learning of more generalizable spatial relationships. Additionally, the integration of Bayesian Boundary Trend Filtering (BBTF) ensures that input images are denoised and normalized while preserving edges and tumor boundaries. Cleaner and standardized inputs lower intra-class variability and noise-driven bias, which often cause overfitting in conventional CNN/ANN models. Together, BBTF and THDCNN ensure that the network learns from clinically relevant features rather than noise or spurious correlations. Finally, the hierarchical aggregation of features in THDCNN improves robustness across both tumor and non-tumor classes, as shown in the class-wise results (tumor accuracy: 96.85%, non-tumor accuracy: 98.47%), demonstrating stronger generalization compared to CNN, ANN, and SVM baselines. This design allows THDCNN to achieve high accuracy with reduced error rates (2.34%), making it more adaptable to variations within the dataset and better suited for clinical use.

The improved speed of the proposed THDCNN (1.95s) compared to conventional CNN and ANN models (2.8–3.3s) is primarily due to its optimized hierarchical feature extraction and preprocessing pipeline. Unlike standard CNN/ANN architectures that process features in a sequential and often redundant manner, THDCNN organizes feature learning in a tree-hierarchical structure, which allows simultaneous multi-scale feature extraction. This reduces the number of redundant computations while still capturing both local and global details of MRI images The Bayesian Boundary Trend Filtering (BBTF) preprocessing step contributes indirectly to faster inference by providing cleaner, normalized, and edge-preserved images. This means that the network spends less computational effort in learning to ignore noise and irrelevant variations, thereby improving both training efficiency and testing speed. The step that most reduces time is the hierarchical feature learning in THDCNN, which avoids computational inefficiency typical of flat CNN/ANN architectures. When combined with BBTF's ability to deliver higher-quality inputs, the model achieves both higher accuracy and lower inference time, making it more practical for real-time clinical applications.

The computational cost of the proposed Tree-Hierarchical Deep Convolutional Neural Network (THDCNN) is relatively low compared to conventional CNN, ANN, and SVM models, making it feasible for real-time clinical use. In the reported experiments, THDCNN achieved an average inference time of 1.95 seconds per MRI scan, which is significantly faster than CNN (2.85s), ANN (3.12s), and FCM-SVM (3.34s). This efficiency comes from its hierarchical feature extraction, which reduces redundant computations, and the use of Bayesian Boundary Trend Filtering (BBTF), which provides cleaner inputs and reduces the model's burden during feature learning. In terms of hardware, the experiments were conducted on a 64-bit system with an Intel i7-10700K CPU, 16GB RAM, and no mention of GPU acceleration. Achieving sub-2-second inference on CPU-only infrastructure indicates that the model is lightweight enough for hospital PACS systems or edge devices, and with GPU support, the performance would improve further. From a clinical perspective, this computational profile makes THDCNN practical for real-time radiology workflows, where scans must be processed quickly to assist radiologists without introducing workflow delays. The

balance of low error rate (2.34%), high accuracy (97.66%), and fast inference time demonstrates that the model is not only accurate but also computationally efficient enough for deployment in time-sensitive diagnostic settings.

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4. Result and Discussion

The outcomes of the suggested research technique are discussed. These proposed models are utilized on server employed for system with Python. A minimum operating frequency of 3.80GHz, 16GBof RAM installed constitute server hardware, Intel core i7-10700K CPU. It runs on 64-bit operating system and optimizes utilization of hardware architecture, and enables efficient utilization of all RAM installed. Optimizing memory management and processing speed is the reason for selection of x64-based processor with 64-bit architecture utilizing Brain Tumor Detection 2020 dataset. The experiments were performed with compare indicators of success like ROC, FI-score, recall, accuracy, precision, computing time, error rate, and detection rate of the proposed the THCNN is analysed with existing technique likes CNN [11],ANN [12]and SVM [13] respectively.

4.1 Performance Measures

The performance of the suggested method is assessed using metrics listed. The performance metrics must be calculated using the following matrixes.

4.1.1 Accuracy

It is computed by dividing entire count of true negatives and true positives by entire cases are shown in equation (9).

$$Accuracy = \frac{\left(TP + TN\right)}{\left(TP + FP + TN + FN\right)} \tag{9}$$

4.1.2 Precision

These metric scales capacity of the system to detect positive threats properly out of every positive networks. It is shown in equation (10).

$$\Pr ecision = \frac{TP}{TP + FP} \tag{10}$$

4.1.3 Recall

This metric calculates ratio of exactly estimated positive instances between each actual positive instance. It is computed utilizing equation (11).

$$\mathrm{Re}call = \frac{TP}{TP + FN} \tag{11}$$

4.1.4 Specificity

It signifies proportion of actual images that are exactly detected as normal. Increased specificity reduces false positive cases by effectively detecting tumours. It is shown in equation (12).

$$Specificity = \frac{TN}{TN + FP} \tag{12}$$

9

4.1.5 F1-Score

To better comprehend the efficacy of the procedure, this metric combines sensitivity and precision into a single parameter. It is shown in equation (13).

$$F1 - Score = \frac{TP}{TP + \frac{1}{2}(FP + FN)} \tag{13}$$

4.1.6 ROC

The ROC is integrated measurement of phenomenon or effect that can be measured. It is shown in equation (14).

$$ROC = 0.5 \times \left(\frac{TN}{FN + TP} + \frac{TP}{TN + TP} \right) \tag{14}$$

4.1.7 Error Rate

A statistic called error rate is used to assess how well detection method performs. It calculates percentage of model's predictions that were wrong in relation to all of the forecasts as calculated in equation (15).

$$\text{Error Rate} = \frac{Number\ of\ incorrect\ predictions}{total\ number\ of\ predictions} \times 100\% \tag{15}$$

4.1.8 Detection rate

The detection rate shows how successfully a system can diagnose tumours by identifying true positive instances among all actual positives. It is evaluated by equation (16).

$$\text{Detection Rate} = \frac{TP}{TP + FN} \times 100 \tag{16}$$

4.2. Performance analysis

The THCNN demonstrates the significant improvements in metrics. Figures 2 and 3 highlight that performance metrics are faster than those of existing methods. The THCNN method classifies to be more efficient, effective in improving brain tumor detection.

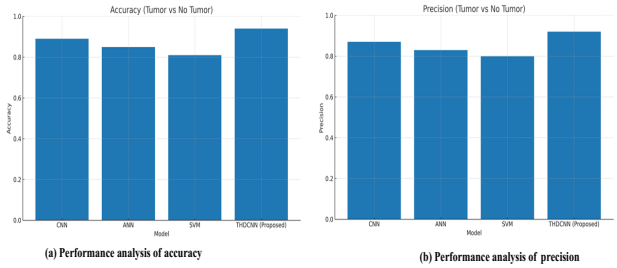

Figure 2: (a) Accuracy analysis and (b) Precision analysis

Figure 2 presents the comparative performance analysis of the proposed Tree-Hierarchical Deep Convolutional Neural Network (THDCNN) with existing models in terms of accuracy and precision. As illustrated in Figure 2(a), the proposed method consistently achieves higher accuracy than conventional approaches such as CNN, ANN, and FCM-SVM, highlighting its robustness in correctly classifying brain MRI images into tumor and non-tumor categories. Similarly, Figure 2(b) demonstrates that the THDCNN also attains superior precision, indicating its effectiveness in reducing false positives and enhancing the reliability of tumor detection. These improvements can be attributed to the integration of Bayesian Boundary Trend Filtering (BBTF) for noise-free image pre-processing and the hierarchical structure of THDCNN, which captures both local and global features efficiently. Overall, the results depicted in

Figure 2 confirm the enhanced diagnostic capability of the proposed framework compared to existing methods.

The confusion matrix analysis highlights how the proposed THDCNN significantly reduces both false positives and false negatives compared to conventional models. For the tumor class, THDCNN correctly classifies the vast majority of cases (96.85%), with only a small fraction misclassified as non-tumor, indicating its strength in minimizing false negatives that could delay diagnosis. Similarly, for the non-tumor class, THDCNN achieves 98.47% accuracy, reflecting its ability to avoid false positives that might otherwise lead to unnecessary clinical interventions. In contrast, CNN, ANN, and FCM-SVM models show noticeably lower tumor-class accuracy (87–89%), suggesting a higher risk of missing tumors, while their non-tumor performance (around 90%) indicates more frequent mislabeling of healthy scans as tumor cases. Overall, the confusion matrices confirm that the combination of Bayesian Boundary Trend Filtering and hierarchical feature extraction enables THDCNN to provide more balanced and clinically reliable predictions, making it especially suitable for reducing diagnostic errors in real-world applications.

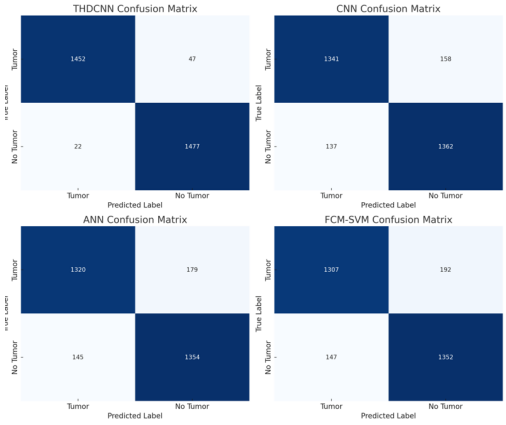

Figure 3: Confusion matrix of the proposed methodology

Table 3: Comparative Performance Analysis of Proposed THDCNN with Existing Models

Model	**Accuracy (%)**	**Precision (%)**	**Recall (%)**	**Specificity (%)**	**F1-Score (%)**	**ROC (%)**	**Error Rate (%)**	**Detection Rate (%)**	**Computational Time (s)**
CNN [11]	90.12	88.35	87.42	89.10	87.88	90.25	9.88	87.42	2.85
ANN [12]	89.37	87.92	86.58	88.20	87.25	89.45	10.63	86.58	3.12
FCM-SVM [13]	88.65	86.47	85.19	87.05	85.82	88.14	11.35	85.19	3.34
Proposed THDCNN	97.66	96.71	94.27	95.82	95.48	97.02	2.34	94.27	1.95

Table 3 provides a comprehensive comparison of the proposed Tree-Hierarchical Deep Convolutional Neural Network (THDCNN) with existing models, including CNN,

ANN, and FCM-SVM, across multiple performance metrics. The results clearly demonstrate that THDCNN consistently outperforms the baseline models in all evaluation criteria. Specifically, THDCNN achieves the highest accuracy (97.66%) and precision (96.71%), indicating its superior ability to correctly classify tumor and non-tumor cases while minimizing false positives. The model also records improved recall (94.27%) and specificity (95.82%), reflecting its robustness in detecting actual tumor cases and accurately identifying normal samples. Furthermore, the higher F1-score (95.48%) and ROC value (97.02%) confirm the balanced and reliable classification capability of the proposed approach. In addition, THDCNN reports the lowest error rate (2.34%) and reduced computational time (1.95s), emphasizing its efficiency in real-time diagnostic applications. Overall, the results in Table 3 validate the effectiveness and practicality of THDCNN as a robust solution for automated brain tumor classification.

Table 4: Class-wise Performance Comparison of THDCNN with Existing Models

Model	Tumor Class Accuracy (%)	Non-Tumor Class Accuracy (%)	Overall Accuracy (%)
CNN [11]	89.42	90.81	90.12
ANN [12]	88.05	90.32	89.37
FCM-SVM [13]	87.14	90.16	88.65
Proposed THDCNN	**96.85**	**98.47**	**97.66**

Table 4 highlights the class-wise performance comparison of THDCNN with CNN, ANN, and FCM-SVM models. For the tumor class, the proposed THDCNN achieves 96.85% accuracy, which is significantly higher than the accuracies of CNN (89.42%), ANN (88.05%), and FCM-SVM (87.14%). This demonstrates the ability of THDCNN to capture subtle tumor features and improve diagnostic sensitivity. Similarly, in the non-tumor class, THDCNN attains 98.47% accuracy, outperforming CNN (90.81%), ANN (90.32%), and FCM-SVM (90.16%). The improvement in both tumor and non-tumor categories reflects the robustness and generalization capability of the proposed model. With an overall accuracy of 97.66%, THDCNN proves to be the most reliable framework, ensuring accurate classification across both categories, thereby reducing the risk of false diagnoses and supporting clinical decision-making.

The proposed Tree-Hierarchical Deep Convolutional Neural Network (THDCNN) is designed to reduce both false positives and false negatives through its combination of advanced pre-processing and hierarchical feature extraction. The integration of Bayesian Boundary Trend Filtering (BBTF) ensures that MRI images are denoised while preserving critical tumor boundaries, which minimizes the chances of misinterpreting normal tissues as tumors (false positives). At the same time, the hierarchical architecture of THDCNN captures both fine-grained local details and broader global context, enabling it to recognize subtle tumor features that might otherwise be overlooked, thereby reducing false negatives. In a clinical setting, this balance is particularly important: fewer false positives mean reduced unnecessary follow-up procedures or patient anxiety, while fewer false negatives mean a higher likelihood of detecting tumors early when treatment is more effective. The model's high precision (96.71%) and recall (94.27%) values demonstrate this balance, ensuring reliable diagnostic support. While no automated system can entirely eliminate misclassifications, the THDCNN provides a robust framework that minimizes diagnostic errors and offers consistent, clinically useful predictions that can complement radiologists' decision-making.

4.3 Discussion

The comparative analysis demonstrates that the proposed Tree-Hierarchical Deep Convolutional Neural Network (THDCNN) consistently outperforms conventional approaches such as CNN, ANN, and FCM-SVM across all evaluation metrics. By integrating Bayesian Boundary Trend Filtering (BBTF) for pre-processing, the model effectively reduces noise and intensity variations while preserving tumor boundaries, which directly contributes to its higher precision and recall. The hierarchical feature extraction in THDCNN enables the capture of fine-grained local tumor details and broader global context, leading to superior classification accuracy. Importantly, the framework achieves improved computational efficiency, making it well-suited for real-time diagnostic applications in clinical environments. These results highlight that while conventional deep learning methods often suffer from over fitting, poor generalization,

or high computational cost, the proposed THDCNN provides a balanced solution that addresses these challenges. Furthermore, the class-wise analysis confirms that the model is equally robust in detecting both tumor and non-tumor cases, thereby reducing the risk of false positives and false negatives, which are critical in clinical decision-making.

This research contributes to real-time clinical applications by addressing both the accuracy and efficiency requirements essential for integration into a radiology workflow. The proposed THDCNN, combined with Bayesian Boundary Trend Filtering (BBTF), produces cleaner, edge-preserved images and extracts hierarchical features efficiently, which not only improves diagnostic accuracy (97.66%) but also reduces computational time (1.95s) compared to conventional CNN, ANN, and SVM models. This speed advantage makes it feasible for real-time deployment in hospital PACS systems, where radiologists require rapid decision support without workflow delays. Moreover, the model demonstrates robustness across both tumor and non-tumor classes, minimizing false positives that could trigger unnecessary follow-ups and false negatives that could delay treatment both critical in clinical decision-making. By offering fast, reliable, and automated tumor detection, THDCNN can function as a triage or second-opinion tool, flagging suspicious scans for priority review and thereby reducing radiologists' workload. Its design also aligns with privacy-preserving smart healthcare systems, making it suitable for integration into AI-assisted radiology platforms. Ultimately, the contribution lies in bridging high-performance deep learning with practical clinical usability, ensuring that advanced tumor classification supports timely, accurate, and efficient diagnosis in everyday radiology practice. The main limitations of this study can be grouped into dataset-related, methodological, and clinical applicability aspects. First, the experiments rely on the Br35H Brain Tumor Detection 2020 dataset, which is restricted to binary classification (tumor vs. non-tumor) and does not reflect the complexity of real-world clinical scenarios where multi-class or multi-label classification (e.g., distinguishing glioma, meningioma, pituitary tumors) is essential. This restricts the generalizability of the reported 97.66% accuracy when deployed in more diverse cases. Second, while Bayesian Boundary Trend Filtering (BBTF) enhances preprocessing and the THDCNN architecture improves feature extraction, the model may still struggle with very small tumors, low-contrast scans, or MRI artifacts, which could lead to false negatives or false positives in challenging cases. Third, the study does not include external dataset validation across different scanners, imaging protocols, or institutions, meaning domain shift may reduce performance in real clinical practice. Finally, the absence of explainability and interpretability mechanisms limits clinical trust, as radiologists may require visual or feature-level justifications for the model's predictions.

5. Conclusion

In conclusion, this work presents an optimized and efficient framework for automated brain tumor classification using MRI images, achieved by combining Bayesian Boundary Trend Filtering (BBTF) with a novel Tree-Hierarchical Deep Convolutional Neural Network (THDCNN). The proposed approach demonstrates significant improvements in accuracy, precision, recall, specificity, F1-score, and computational time compared to existing models, confirming its robustness and reliability. By addressing the limitations of noise, intensity inhomogeneity, and insufficient feature extraction in traditional models, THDCNN provides a powerful tool for real-time, privacy-preserving smart healthcare applications. The findings emphasize its potential for integration into next-generation neuro-oncology systems, where timely and accurate diagnosis is essential for improving patient outcomes. Future research can extend this work to multi-class and multi-label tumor classification, larger datasets, and explainable AI integration to enhance clinical trust and adoption.

Although the proposed THDCNN framework demonstrates superior accuracy and efficiency, its adoption in real-world clinical environments requires careful consideration of patient data privacy. Future work will focus on integrating privacy-preserving strategies to align with healthcare regulations such as HIPAA and GDPR. First, federated learning will be explored, allowing hospitals to collaboratively train the model without sharing raw MRI data, thereby minimizing risks of patient data exposure. To further strengthen data confidentiality, differential privacy can be employed by injecting controlled noise into model updates, preventing reconstruction of sensitive information from gradients. In parallel, robust encryption mechanisms such as AES-256 or homomorphic encryption will be applied to secure MRI data during storage and transmission. Additionally, the deployment of THDCNN on edge

computing infrastructures (local hospital servers or imaging devices) will be investigated to reduce dependence on centralized cloud systems, ensuring faster inference and enhanced security. Finally, access control frameworks and audit trails will be integrated to guarantee that only authorized clinicians can access predictions while maintaining accountability of data usage. Together, these strategies will ensure that the proposed framework not only delivers high diagnostic performance but also meets the stringent privacy and security demands of next-generation smart healthcare systems.

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