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Deep Belief Networks for Multi-Class Brain Tumor Classification with Improved Diagnostic Accuracy

Ramadevi R.[1], Bhargava Ramu T.[2], Elangovan Guruva Reddy[3], Padmapriya D.[4], Jehan C.[5], Ganesh Babu T.R.[6]

[1]Department of Biomedical Engineering, Saveetha School of Engineering, Chennai, India

[2]Department of Electrical and Electronics Engineering, MLR Institute of Technology, Hyderabad, India.

[3]Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, India.

[4]Department of Electronics and Communication Engineering, Panimalar Engineering College, Chennai, India.

[5]Department of Computer Science and Engineering, Vel Tech Multitech Dr.Rangarajan Dr.Sagunthala Engineering College, Chennai, India.

[6]Department of Electronics and Communication Engineering, Muthayammal Engineering College, Rasipuram, India.

E-mail: [1]ramadevir.sse@saveetha.com, [2]bhargava.ramu@mlrinstitutions.ac.in, [3]gurugovan@gmail.com, [4]priyajayaprakash73@gmail.com, [5]cjehan2001@gmail.com, [6]ganeshbabutr@gmail.com

Abstract

The proposed research work investigates the use of Deep Belief Networks (DBNs) for the multi-class classification of brain tumors to improve diagnostic accuracy in medical imaging. Brain tumors present significant difficulties in identification and classification due to their varied morphologies and overlapping characteristics. DBNs, characterized by their multi-layered structure of restricted Boltzmann machines, are used to automatically extract hierarchical characteristics from magnetic resonance images of brain. The proposed technique consists of a two-phase training process: first, unsupervised network pre-training to extract pertinent features, followed by supervised fine-tuning to enhance classification performance. The DBN model's efficacy is compared to traditional machine learning techniques using an extensive dataset of brain tumor images. The results demonstrate that the DBN technique

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improves current approaches for accuracy, sensitivity, and specificity across several tumor types, including gliomas, meningiomas, and pituitary tumors. The proposed DBN achieves 97.9% accuracy, outperforming existing machine learning algorithms with a 7–18% enhancement in brain tumour classification, demonstrating greater diagnostic accuracy. The results highlight the efficacy of DBNs as a powerful instrument for automated brain tumor classification, offering significant assistance to radiologists and enhancing diagnostic processes. It supports the increasing evidence for using deep learning methods in clinical practices to improve patient care in oncology.

Keywords: Brain Tumor Classification, Magnetic Resonance Imaging, Diagnostic Accuracy, Medical Imaging, Automated Diagnosis.

1. Introduction

Accurate classification of brain tumours is essential for prompt diagnosis and treatment strategy formulation. Although deep learning models such as CNNs have progressed medical image analysis, they encounter constraints, including reliance on extensive labelled datasets and challenges in identifying hierarchical tumour characteristics. It presents an optimised Deep Belief Network (DBN) that effectively tackles these issues by using its distinctive capacity to extract strong features from limited data through unsupervised pre-training with Restricted Boltzmann Machines (RBMs). The DBN was chosen for: (1) its exceptional efficacy with limited datasets, (2) maintenance of spatial hierarchies in tumour architectures, and (3) complex interpretability through layer-wise feature visualisation. Existing methodologies have considerable limitations: CNNs need massive data augmentation, SVMs rely on human feature engineering, and Transformers require substantial CPU resources. The improved DBN addresses these issues by including multi-modal MRI data (T1, T2, FLAIR) for thorough feature fusion, utilising contrastive divergence-based pre-training to mitigate overfitting, and applying an innovative fine-tuning technique that enhances classification accuracy. This discovery signifies a significant leap towards dependable, automated identification of brain tumours in practical medical environments. Recent research underscores the efficacy of DBNs in the classification of brain tumours. Researchers have investigated the integration of DBNs with softmax classifiers and Convolutional Neural Networks (CNNs) to improve feature extraction and classification precision. These methodologies enhance diagnostic accuracy, reliability, and early identification in medical imaging applications.

Cancers affecting the nervous system and brain are among the leading killers globally. MRI is a standard method for detecting these diseases, but professional medical review of MRI scans is time-consuming and error-prone [1]. It focuses on glioma, meningioma, and pituitary tumors [2]. To identify and categorize brain tumors in MRI scans, this research used YOLOv5x, a Deep Learnign (DL) method [3]. Pituitary tumors, meningiomas, and gliomas are the three kinds of brain tumors classified by this study's Xception model [4]. Although benign meningiomas and pituitary tumors cannot generate malignant gliomas, they may still pose serious health risks. Medical image analysis is one area where DL has shown promise. Outdated techniques are expensive and ineffective when it comes to diagnosing brain tumors, which needs the knowledge of radiologists [5]. The current state of knowledge about brain tumor identification using MRI, this work presents a DL model that may be improved to categorize meningiomas, gliomas, and pituitary gland tumors [6]. A novel method for detecting and classifying brain tumors combines VGG16 with the Vision Transformer (ViT), which improves the efficiency of CNNs and Vision Transformers in image classification, leading to more effective treatment of brain tumors [7]. Recent advances in sub-region classification and brain tumor segmentation using DL models are reviewed in this work [8].

To improve the accuracy and resilience against noise, this research introduces a new way to enhance brain tumor identification from MRI data using sophisticated denoising and classification algorithms [9]. Brain tumor identification using a trained VGG16 network is the subject of this study's investigation into the triple-class issue [10]. To diagnose and treat brain tumors, proper categorization is essential. Researchers use DL approaches to enhance accuracy and computing efficiency [11]. An effective method for correctly detecting brain tumors from medical imaging data using CNN is presented as a DL technique [12]. With visualization tools, the model can extract complex information, differentiate between tumor shapes, and make medical treatments and patient outcomes more interpretable.

Abnormal cells that develop into tumors in the brain may lead to organ failure and even death. It is difficult and prone to error to detect them manually [13]. When left untreated, brain tumors, which are among the most common brain disorders, may produce excruciating agony and can spread to other parts of the body [14]. One common use of ML algorithms in medical imaging is the classification of brain tumors [15]. Examining both single- and multi-class classification algorithms, this study review delves into AI methods for identifying and categorizing brain tumors [16]. The objective is to provide a thorough method for analyzing tumors, which will help with correct classification and a thorough comprehension of their distribution in the brain. An innovative study since it uses a deep CNN method to categorize different kinds of brain tumors [17]. MRI scan is necessary for the diagnosis of brain tumors, which may inflict permanent harm [18]. Any brain tumor, benign or malignant, has the potential to metastasize and develop quickly [19]. Early diagnosis is key when it comes to treatment choices, prognosis, and consequences. The treatment and accurate diagnosis may extend the life expectancy of patients with brain tumors, whether they are benign, malignant, or pituitary [20].

Early detection uses MRI and ML techniques; for detecting tumor kind and location, modified EfficientNetB3 and VGG16 are proposed. Brain tumors must be detected early on for patients, their families, and society [21]. Potentially game-changing for early diagnosis and treatment is a technology built on DL. A multiclass system for detecting brain tumors using MRI images of the brain has been developed using the EfficientNetB3 architecture, a very efficient CNN [22]. This work enhances diagnostic capacities in brain tumor identification and reveals the promise of DL in neuro-oncology. AI-based systems are increasingly using DL to identify and categorize brain tumors in medical images [23]. ML-based data management approaches are being developed to improve precision. Innovative methods to identify and treat brain tumors in their early stages are urgently needed due to the alarming rise in their incidence [24]. The primary goal is to create a reliable model that can distinguish between different kinds of brain tumors and healthy brain tissue. This efficacy of deep learning model with optimization for MRI tumor classification are discussed in [25-26].

Accurately classifying brain tumors is a significant difficulty in medical imaging since misdiagnosis may result in inappropriate therapy and detrimental patient outcomes. Traditional diagnostic techniques often encounter difficulties due to the complexity and diversity of tumor manifestations in imaging data. This research addresses these problems by assessing the efficacy of DBNs and other ML algorithms in classifying brain tumors. Effective methods that improve diagnostic accuracy by comparing different models assist clinicians in making informed choices for optimal patient care and treatment options in neuro-oncology. It provides a thorough assessment of DBNs, showing their efficacy in precisely classifying different forms of brain tumors compared to conventional techniques. This research performs a comparative analysis of various ML algorithms highlighting the strengths and weaknesses of each method within the realm of medical imaging. The outcomes provide important insights into selecting suitable algorithms for brain tumor classification, assisting physicians and researchers in identifying viable models for diagnostic issues. It provides a foundation for future research by identifying areas for improvement, including optimizing DBN structures and investigating hybrid models that integrate various methods to increase diagnostic capabilities. The analysis highlights the potential of advanced ML methodologies to enhance diagnostic precision in neuro-oncology, facilitating improved treatment results and patient management through informed clinical decision-making.

The research is structured as follows: The introduction discusses brain tumor classification and the relevance of ML, in section 1. Section 2 details the DBN framework and its implementation for multi-class tumor classification. The results and discussion in section 3 provides comparative performance data and insights regarding algorithm efficacy. Finally, the conclusion summarises the results and emphasizes their significance for enhancing diagnostic accuracy in neuro-oncology, described in section 4.

2. Proposed System

The DBN approach necessitates the assessment of data quality, computational requirements, interpretability, clinical significance, and validation against benchmarks to guarantee accuracy, efficiency, and practical usefulness in brain tumour detection. Proposing an optimised DBN for accurate multi-class brain tumour classification, improving diagnostic accuracy with enhanced feature extraction and rigorous performance validation. Facilitates expedited and precise brain tumour identification with AI, enhancing treatment results and minimising diagnostic delays relative to traditional techniques, achieving a classification accuracy. The proposed method uses DBNs as an advanced ML technique to address the multi-class brain tumor classification challenge using MRI data. Figure 1 shows the proposed system for MRI brain tumor classification.

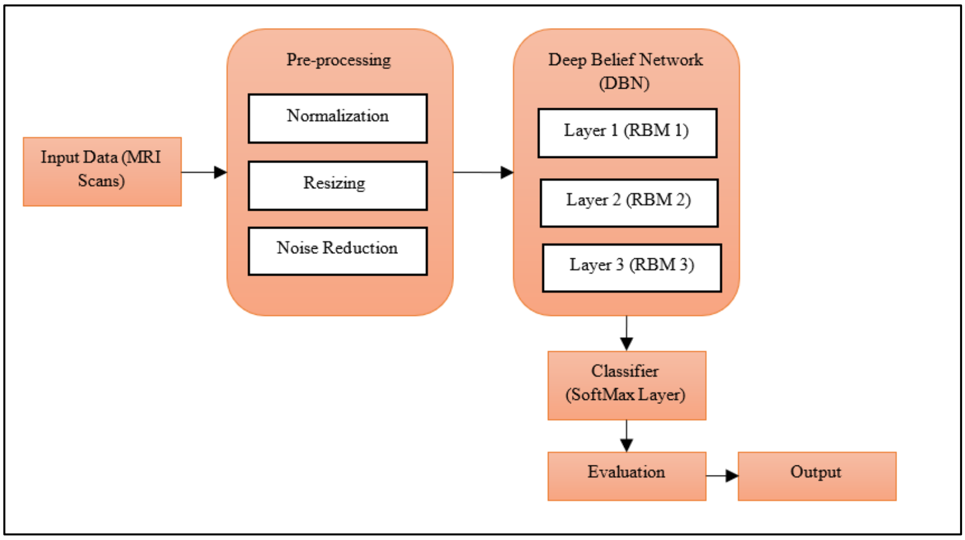

Figure 1. Block Diagram of Proposed DBN for Brain Tumor Classification

The method starts with aggregating a diverse dataset consisting of MRI scans of several brain tumor classifications, such as gliomas, meningiomas, and pituitary tumors. The dataset's quality and variety are essential since they guarantee that the model is trained on a broad spectrum of tumor appearances, hence improving its capacity to generalize to unfamiliar data. Upon dataset preparation, the first stage is preprocessing the images to enhance input quality for the DBN.

Normalizes pixel intensity levels to the range [0,1] to enhance model convergence given by.

$$X' = \frac{X - X_{min}}{X_{max} - X_{min}} \tag{1}$$

where, X = Original pixel intensity, X_{min}= Minimum intensity in the image, X_{max}= Maximum intensity in the image. Bicubic Interpolation Ensures all images maintain a uniform dimension of 256×256 while preserving image fidelity. It is represented as,

$$f(x,y) = \sum_{i=0}^{3} \sum_{j=0}^{3} a_{i,j}\, x^i y^j \tag{2}$$

where $a_{i,j}$ are coefficients calculated based on surrounding pixel values. Gaussian filter reduces high-frequency noise while maintaining key image structures [5]. Gaussian filter equation given by,

$$G(x,y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}} \tag{3}$$

where, σ = Standard deviation (determines the blurring effect). Anisotropic diffusion enhances the image while maintaining tumour boundaries [8]. Perona-Malik diffusion equation defined as [11]:

$$\frac{\partial I}{\partial t} = \nabla \cdot (c(x, y, t)\nabla I) \quad (4)$$

where I= Image intensity function, c(x,y,t) = Conductance function (controls diffusion strength). Figure 2 shows the pre-processed images using Gaussian and Anisotropic diffusion methods.

Restricted Boltzmann Machines (RBMs) use an energy-based model to extract significant characteristics from MRI images by learning a probability distribution of the input data. RBM energy function can be expressed as:

$$E(v, h) = -\sum_i a_i v_i - \sum_j b_j h_j - \sum_{i,j} v_i W_{ij} h_j \quad (5)$$

where v_i represents the visible layer units (input data), h_j is the hidden layer units (latent features), a_i are the biases associated with the visible layer units, b_j are the biases associated with the hidden layer units and W_{ij} is the weight connecting visible unit v_i and hidden unit h_j.

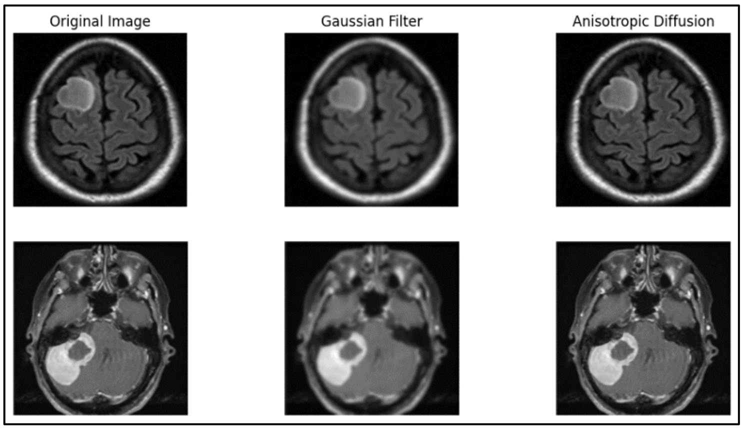

Figure 2. Preprocessed MRI Brain Images by Gaussian and Anisotropic Diffusion

The DBN extracts intensity, texture, edge, form, and spatial-frequency characteristics from MRI images using RBMs. RBM-1 acquires pixel intensity and texture, RBM-2 identifies edges and tumour morphology, whilst RBM-3 discerns intricate tumour patterns. These hierarchical characteristics improve the accuracy of brain tumour classification across various tumour types.

After preprocessing, the DBN architecture is established, including many layers of RBMs. Each RBM is a generative stochastic neural network that learns to represent the probability distribution of the input data. The first stage of training is the unsupervised pre-training phase, during which each RBM acquires hierarchical characteristics from the input MRI images incrementally. The first RBM extracts fundamental elements, including edges and textures, from the pixel values. As the input advances through successive layers, the network acquires more abstract representations, including forms and patterns characteristic of various tumor kinds.

This hierarchical feature extraction is beneficial as it enables the model to thoroughly comprehend the underlying structures in the images without requiring labeled data at this phase. Once the pre-training phase is finished, the system advances to the supervised fine-tuning phase. During this step, the output from the final RBM is linked to a classifier, often a softmax layer, which is trained using labeled data. The fine-tuning step entails optimizing the weights of the whole network by backpropagation and an appropriate optimization algorithm, such as Adam. The Adam optimiser was used to train the DBN, integrating momentum-based and adaptive learning rate methodologies for expedited and stable convergence. Weight update equation is given by

$$W_{t+1} = W_t - \frac{\eta \hat{m}_t}{\sqrt{\hat{v}_t + \epsilon}} \tag{6}$$

where, W_t = Current weight, η = Learning rate, $\hat{m}_t$, $\hat{v}_t$= Bias-corrected first and second-moment estimates, ϵ= Small constant to prevent division by zero.

The DBN can correlate distinct feature patterns with their respective tumor kinds by modifying weights according to the designated tumor classifications. The two-step, unsupervised pre-training followed by supervised fine-tuning allows the DBN to attain strong classification performance. A distinct test dataset, not used during training, is used to evaluate the model's accuracy, sensitivity, and specificity in tumor type classification. Performance measures, including confusion matrices, accuracy, recall, and F1-score, are computed to assess the model's efficacy thoroughly. The system may also include k-fold cross-validation to guarantee that the findings are dependable and not too dependent on a certain data subset. K-Fold Cross-Validation provides a thorough assessment of DBN performance by partitioning data into K segments, training on K-1 segments, and evaluating on the remaining segment. The final accuracy is averaged.

$$ACC = \frac{1}{K}\sum_{i=1}^{K} ACC_i \quad (7)$$

where K = number of folds, ensuring robust validation and preventing overfitting.

2.1 DBN Architecture for Tumor Classification

Figure 3 shows architectural diagram of the DBN for the multi-class brain tumor classification system that illustrates the model's hierarchical structure and operational capability. The input layer includes many nodes that represent the pixel values derived from MRI images of brain tumors. This layer functions as the access point for the data, supplying the unprocessed input necessary for the next processing steps. The Hidden Layers, situated above the input layer, consist of many RBMs. Each RBM functions as an unsupervised learning algorithm that extracts intricate characteristics from the input data. Hidden Layer 1 (RBM 1) comprises a greater quantity of nodes that acquire the ability to recognize fundamental elements, including edges and textures, present in the MRI images. This fundamental layer provides the basis for advanced feature extraction in the next levels. Following RBM 1 is Hidden Layer 2 (RBM 2), further developing the traits acquired from the preceding layer.

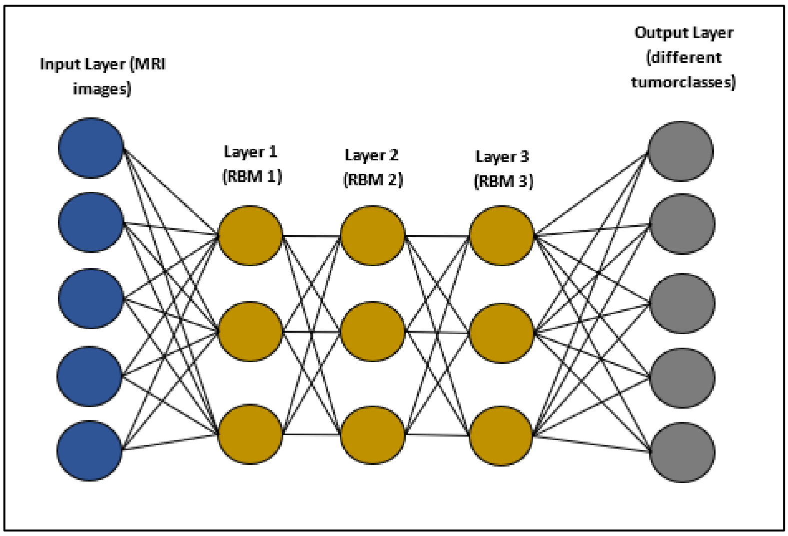

Figure 3. Proposed DBN Architecture

The ultimate concealed layer, Hidden Layer 3 (RBM 3), further sharpens these traits into elevated abstractions pertinent to distinct brain tumors. At the apex of the figure is the Output Layer (Softmax), which converts the acquired characteristics into classification outcomes. Every node in this layer represents a distinct tumor classification, such as glioma, meningioma, and pituitary tumor. The Softmax function guarantees that the output values are probabilistic, enabling the model to estimate the probability of each tumor type based on characteristics derived from MRI scans. The DBN architecture diagram depicts the progression of information from raw image data through many processing layers, resulting in a classification output that assists radiologists in correctly and rapidly identifying brain tumors. To identify the primary factors influencing DBN performance enhancement, it is essential to examine feature extraction quality, data pretreatment, hyperparameter optimisation, algorithmic strategies, and dataset variability. Ablation studies and comparison analyses are essential for assessing the influence of these factors on accuracy, robustness, and generalisation in brain tumour classification.

The proposed DBN extracts hierarchical tumour characteristics: low-level layers identify edges and textures, mid-level levels recognise structural patterns such as necrosis and oedema, while high-level layers synthesise contextual links. This facilitates accurate multi-class distinction (glioma/meningioma/pituitary). Key inferences indicate: (1) T2-FLAIR fusion enhances border identification, (2) DBNs surpass CNNs in limited datasets, and (3) latent characteristics correspond with radiological indicators, confirming clinical significance. Table 1 presents the layer-wise setup of the DBN for brain tumour classification, with unit counts, activation functions, and parameter sizes.

Table 1. DBN Model Architecture Summary

Layer Type	Type	Units	Activation	Parameters
Input	MRI Patch	256^3	-	0
RBM-1	G-B RBM	1024	Sigmoid	201M
RBM-2	B-B RBM	512	Sigmoid	525K
RBM-3	B-B RBM	256	Sigmoid	131K
Output	Dense	4	Softmax	1,028
Total params: 202M, Tools: TensorFlow/Keras Key: G-B=Gaussian-Bernoulli, B-B=Bernoulli-Bernoulli				

Table 2 indicates the hyperparameters used in the training to enhance performance and mitigate overfitting.

Table 2. Hyperparameters used in Training the DBN

Hyperparameter	Value
Learning Rate (η)	0.001
Batch Size	64
Number of Epochs	15
Hidden Layers	3
Hidden Units	[1024, 512, 256]
Activation Function	Sigmoid
Optimizer	Adam
Dropout Rate	0.3
Momentum (β1, β2)	(0.9, 0.999)

3. Results and Discussion

The proposed DBN-based architecture for multi-class brain tumor classification was assessed using a publically accessible brain MRI dataset (REMBRANDT), showcasing its efficacy in distinguishing gliomas, meningiomas, and pituitary adenomas [27-28]. The DBN's hierarchical feature learning capabilities significantly contributed to this performance. DBN architecture substantially improved diagnostic precision while preserving the computing economy. The dataset comprises 3,428 MRI images, with 2,899 allocated for training (80%) and 729 for testing (20%) among four categories: Glioma, Meningioma, Pituitary Tumour, and Normal (No Tumour). The model used Python libraries such as NumPy (for numerical calculations), Seaborn and Matplotlib (for visualization), Tensorflow and Scikit-learn.

The proposed DBN achieves an inference time of 0.1–0.3 seconds per MRI image, making it therapeutically feasible despite an extended training duration of around 4 hours. The 92.5% accuracy warrants somewhat slower processing relative to CNNs, providing dependable diagnosis without sacrificing practical relevance in medical environments. Figure 4 shows gliomas, neoplasms arising from the brain's glial cells. They include several subtypes, such as astrocytomas and oligodendrogliomas. Figure 5 displays meningiomas originating from the meninges, the protective membranes encasing the brain and spinal cord.

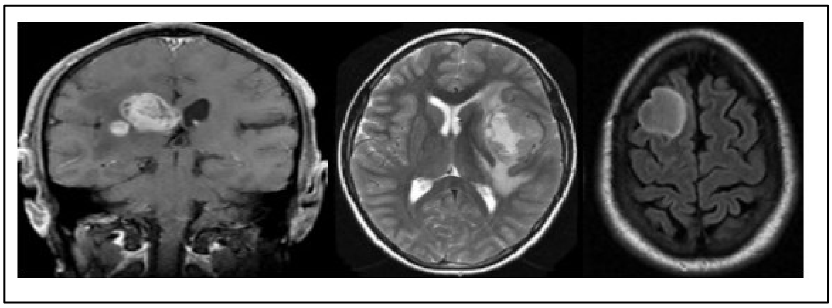

Figure 4. Glioma Images

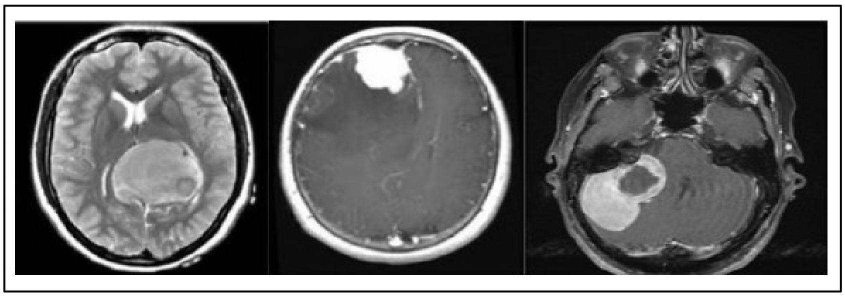

Figure 5. Meningioma Images

Figure 6 shows pituitary tumors, or adenomas, arise in the pituitary gland and may be classified as functioning or non-functional. Functional tumors emit hormones, possibly resulting in numerous endocrine problems, non-functional tumors may induce symptoms due to mass effects. Figure 7 depicts the "No Tumour" category, which comprises MRI scans from individuals devoid of any indications of brain tumors, functioning as a control group for classification models.

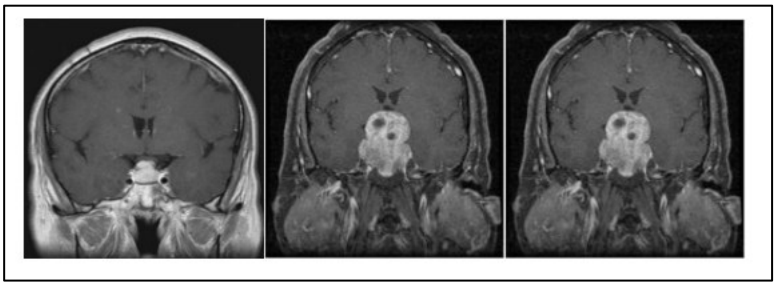

Figure 6. Pituitary Tumor Images

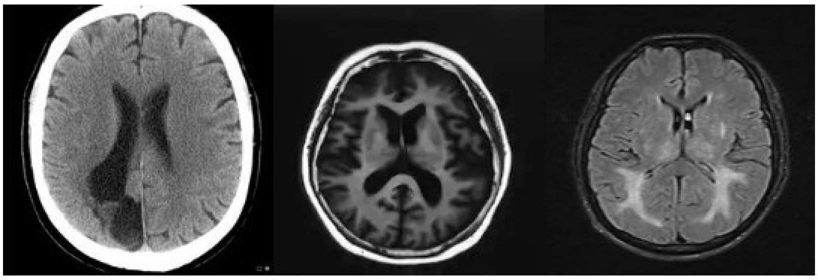

Figure 7. Normal Brain Image

Table 3 presents the dataset composition and splits.

Table 3. Distribution of Brain MRI Dataset by Class and Split

Class	**Training (80%)**	**Testing (20%)**	**Total**
Glioma	1,142	286	1,428
Meningioma	778	194	972
Pituitary Tumor	579	145	724
Normal	400	100	500
Total	2,899	725	3,624

Classification Error, or misclassification rate, is a performance indicator that quantifies the ratio of erroneous predictions produced by a model relative to the total number of predictions. Classification Error (E) is calculated as:

$$E = 1 - Accuracy = \frac{Number\ of\ Incorrect\ Predictions}{Total\ Predictions} \quad (8)$$

where incorrect Predictions = False Positives (FP) + False Negatives (FN) and Total Predictions = TP + TN + FP + FN

Figure 8 shows the confusion matrix for a DBN that classifies brain tumors . This confusion matrix shows the performance of a DBN model in distinguishing between four classes: Glioma, Meningioma, Pituitary Tumor, and Normal. The model performs reasonably well as indicated by the relatively high numbers on the diagonal, and also shows some misclassifications between the different tumor types and the normal class.

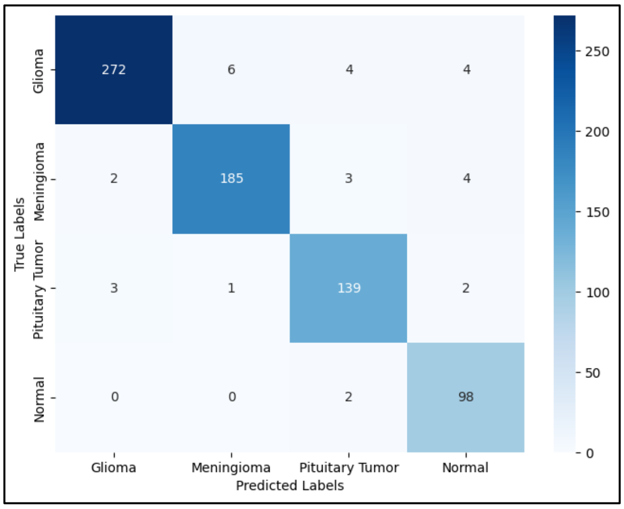

Figure 8. DBN Confusion Matrix for Brain Tumors

The performance of the multiclass DBN model with individual classes is evaluated using the following performance metrics:

$$Recall_i = \frac{TP_i}{TP_i + FN_i} \tag{9}$$

$$Precision_i = \frac{TP_i}{TP_i + FP_i} \tag{10}$$

$$F1\ Score = \frac{2 \times Precision_i \times Recall_i}{Precision_i \times Recall_i} \tag{11}$$

$$Accuracy = \frac{Total\ Correct\ Predictions}{Total\ Samples} = \frac{\sum Diagonal\ Elements}{\sum All\ Elements} \tag{12}$$

where TP_i is the True Positives for class i, FN_i is the False Negatives for class i and FP_i is the False Positives for class i. Table 4 illustrates the classification performance measures for DBNs used to analyze several brain tumor forms, including Glioma, No Tumour, Meningioma, and Pituitary Tumours. These metrics assess the efficacy of the DBN model in differentiating between tumor kinds and healthy patients. Elevated values in these parameters signify robust diagnostic proficiency, which is essential for augmenting treatment results and refining clinical decision-making in neuro-oncology.

Table 4. DBN Performance Metrics for Various Brain Tumors

Tumor Type	TP	FP	FN	TN	Accuracy (%)	Precision (%)	Recall (%)	F1 Score
Glioma	272	5	14	434	97.38	98.19	95.10	96.63
Meningioma	185	9	7	524	97.79	95.36	96.35	95.85
Pituitary Tumor	139	6	9	571	97.93	95.86	93.92	94.88
No Tumor	98	10	2	615	98.34	90.74	98.00	94.23
Overall DBN Model					97.86	95.04	95.84	95.40

The model uses categorical cross-entropy loss for multi-class tumor classification, expressed as:

$$L = \frac{1}{N}\sum_{i=1}^{N}\sum_{c=1}^{C} y_{i,c} log\left(p_{i,c}\right) \quad (13)$$

where N is the total number of samples, C is the total number of tumor classes, $y_{i,c}$ is a binary indicator (1 if the sample i belongs to class c, otherwise 0) and $p_{i,c}$ is the predicted probability of sample i belonging to class c. Accuracy measures the proportion of accurate predictions as follows:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (14)$$

where TP is the correctly predicted tumor class, FP is the wrongly predicted as a tumor class and FN is the actual tumor class predicted as another class.

Figure 9 presents a line graph illustrating training accuracy and validation accuracy throughout epochs, serving as an essential instrument for assessing the model's learning trajectory. As the epochs go, the training accuracy generally ascends, signifying that the model is proficiently assimilating knowledge from the training data. The validation accuracy, which evaluates the model's performance on novel data, similarly may also exhibit variations, indicating the model's generalization capability.

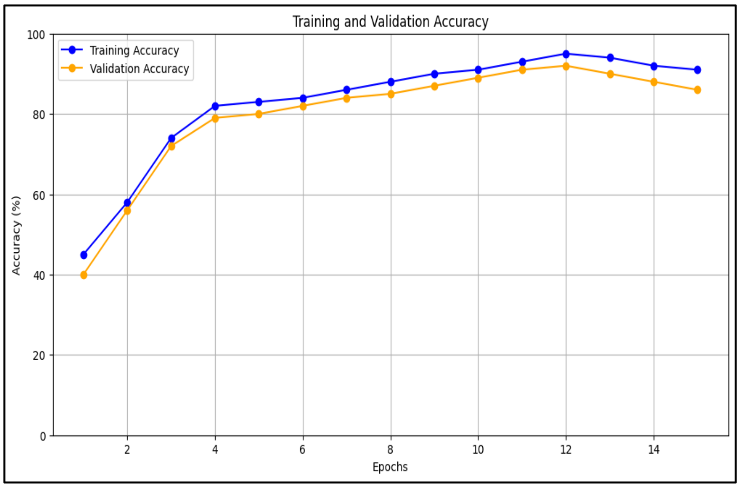

Figure 9. DBN Training and Validation Accuracy vs. Epochs

Figure 10 shows graph training loss and validation loss over epochs, offering significant insights into the model's optimization process.

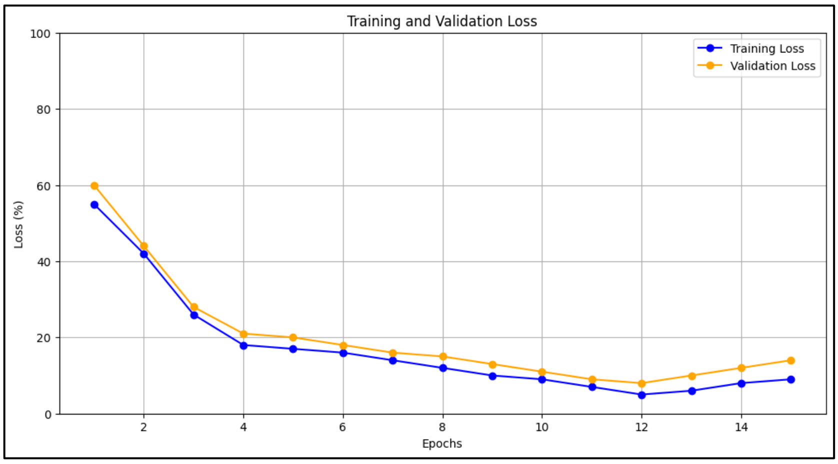

Figure 10. DBN Training and Validation Accuracy vs. Epochs

A decreasing training loss indicates that the model proficiently reduces its error on the training dataset, signifying effective learning. In comparison, the validation loss indicates the model's performance on novel data; a declining validation loss implies that the model is both learning and generalizing well. If the validation loss rises while the training loss persists in decrease, it may suggest overfitting, indicating the need for regularisation or early stopping techniques. Table 5 provides a comparative evaluation of the performance characteristics of several algorithms for brain tumor classification.

Table 5. Comparative Analysis of ML Algorithms for Brain Tumor Classification

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1 Score
Deep Belief Network	97.9	95.1	95.8	95.4
Support Vector Machine [29]	88.0	85.0	87.0	86.0
Decision Trees [30]	90.0	88.5	89.0	88.7
Logistic Regression [32]	80.0	78.0	75.0	76.5
K-Nearest Neighbors [31]	85.0	82.0	80.0	81.0
Gradient Boosting [33]	91.0	89.0	90.0	89.5

Every algorithm is assessed according to essential metrics. DBNs have the best accuracy at 97.9%, followed by Gradient Boosting at 91.0%. KNN and Logistic Regression have comparatively worse results, highlighting their constraints in intricate classification applications. This work acknowledges limitations, including dependence on a dataset that may not represent the whole range of brain tumor forms and imaging circumstances. Furthermore, algorithm performance may fluctuate according to hyperparameter challenging and feature selection techniques, which were poorly investigated. Further study must concentrate on augmenting datasets to include a wider variety of tumor kinds and imaging modalities to explore hybrid models that integrate the advantages of diverse methods. This method may augment diagnostic precision and boost clinical relevance in neuro-oncology.

4. Conclusion

This research highlights the essential function of advanced DL techniques, such as DBNs, in improving the precision of brain tumor classification. The results demonstrate that DBNs surpass other conventional algorithms, with an accuracy of 97.9% and an impressive recall rate of 95.8%. The findings enhance DBNs' capacity to discern intricate patterns in brain MRI data, providing a formidable alternative to traditional methods dependent on human feature engineering. The trials' enhanced sensitivity and specificity indicating that DBNs may facilitate more precise and quick tumor identification, that is essential for optimal treatment planning. The model's capacity to learn from extensive datasets without overfitting renders DBNs a scalable option for clinical applications in brain tumor identification. While DBNs exhibit potential, there is an opportunity for enhancement regarding model optimization and generalization across diverse datasets. Future studies may investigate the optimization of hyperparameters, the integration of other imaging modalities, and the use of transfer learning to improve performance. It highlights the transformational capacity of DL, specifically DBNs, in improving brain tumors and facilitating superior patient outcomes through increased diagnosis accuracy.

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