

Innovative Deep Learning Strategies for Early Detection of Brain Tumours in MRI Scans with a Modified ResNet50V2 Approach

Rashadul Islam Sumon¹, Md Ariful Islam Mazumder¹, Salma Akter¹, Shah Muhammad Imtiyaj Uddin¹,
Hee-Cheol Kim^{1,2*}

¹ Digital Anti-Aging Health Care, Inje University, Gimhae-si, Republic of Korea

² Department of Computer Engineering, Inje University, Gimhae-si, Republic of Korea

sumon39.cst@gmail.com, arifislamro@gmail.com, salma05.eu@gmail.com, imtiyaj.dream@gmail.com,
heeki@inje.ac.kr

Abstract— Classifying brain tumors is vital to medical diagnosis since early identification and the distinction between benign and malignant tumors can greatly enhance patient outcomes. In this work, we use magnetic resonance imaging (MRI) scans to categorize brain cancers into four groups: pituitary, meningioma, glioma, and no tumor. Our model was trained and evaluated using a dataset of 18230 MRI pictures of the human brain. To optimize feature extraction and model performance, we suggest a modified ResNet50V2 architecture that is improved with numerous Squeeze-and-Excitation (SE) modules. The model attained a stunning 99.97% training accuracy and 97.98% validation accuracy. These findings show how our method may help improve the precision and consistency of brain tumor diagnosis, which would be a significant advancement for neurology and medical research.

Keywords— Brain Tumor, Squeeze-and-Excitation, ResNet50V2, Medical diagnosis, MRI

I. INTRODUCTION

This Brain tumors, whether benign or malignant, are a major issue in neurology because they can cause significant neurological impairment and potentially catastrophic outcomes. As they grow, these tumors can increase intracranial pressure, which can lead to brain injury, neurological disabilities, and even death. Early detection and precise classification of brain tumors are essential for effective treatment planning and improved patient outcomes [1]. For non-invasive tumor diagnosis, magnetic resonance imaging (MRI), which provides fine-grained images of brain anatomy and makes anomaly detection easier, is crucial. Because manual MRI scan interpretation is time-consuming and prone to human error, automated solutions that assist radiologists in making accurate diagnoses must be developed [2]. Deep learning (DL) and machine learning (ML) have demonstrated great promise in medical image analysis in recent years, especially in the categorization of cancers [3-5].

These methods have been used extensively to improve diagnosis accuracy because they enable the automatic extraction of characteristics from MRI images. In image classification tasks, deep learning models, particularly convolutional neural networks (CNNs), have emerged as the cutting edge, providing strong instruments to aid in clinical decision-making [6]. These models can differentiate between various tumor kinds and healthy brain tissues in the context of brain tumor classification, which could increase diagnosis speed and accuracy. Glioma, Meningioma, No Tumor, and Pituitary tumors are the four categories into which brain tumors are divided in this work. Because of their aggressive nature, gliomas—malignant tumors that originate from the brain's glial cells—frequently require prompt and accurate treatment. Conversely, meningiomas, which arise from the meninges, the protective coverings encircling the brain and spinal cord, are usually benign. Although pituitary tumors can be benign or malignant, they can cause serious hormonal imbalances and neurological symptoms if they are located close to important brain regions [7].

We used a dataset of 18230 MRI images, with samples from each of the four previously listed categories. The difficulty of distinguishing between these classes between benign and malignant tumors calls for a sophisticated model that can pick up on minute changes in the image [8]. In order to enhance feature extraction, we used a modified ResNet50V2 model that included Squeeze-and-Excitation (SE) module [9]. By recalibrating channel-wise feature responses, SE Module improve CNNs' representational capability by enabling the model to suppress less pertinent features and concentrate on more useful ones adding security [10-16].

Our updated ResNet50V2 model performed exceptionally well, achieving 99.97% training accuracy and 97.98% validation accuracy. These outcomes show that the proposed method has the potential to be used practically in clinical

settings, where patient care depends on high precision. Additionally, the model's generalizability is enhanced by the use of SE blocks, which guarantee that it works well on both unseen validation data and training data. In this study, we describe our method for classifying brain tumors, emphasizing the architecture of the improved ResNet50V2 model and the performance impact of the Squeeze-and-Excitation modules. The remainder of the document is structured as follows: dataset and the preparation methods used are described in Section II. The architecture and training of the improved ResNet50V2 model are described in detail in Section III. The experimental results and their importance are presented in Section IV. The paper's conclusion, Section V, offers suggestions for further research in this area.

II. DATASET

We use a publicly available dataset for this experiment, available in Kaggle [11]. The 7023 human brain MRI images that comprise the dataset used in this study are divided into four classes: pituitary, meningioma, glioma, and no tumor, as shown in Figure 1. The classification of brain tumors and a thorough depiction of malignant and non-cancerous brain disorders are the specific goals of this dataset's curation. The definitions of the four classes are as follows:

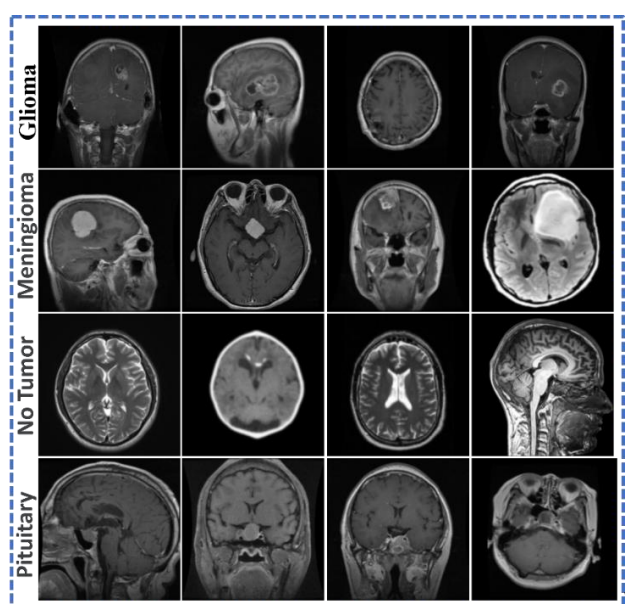


Figure 1. A sample brain MRI image shows glioma in row 1, meningioma in row 2, no tumor in row 3, and pituitary tumors in row 4.

Gliomas are malignant brain tumors that start in the glial cells that nourish and shield the brain's neurons. A type of non-cancerous tumour called a meningioma develops from the meninges, which are the brain and spinal cord's protective coverings. No tumor: This class serves as a control group for

the classification task and consists of normal brain scans devoid of discernible anomalies or tumours. Pituitary: Because the pituitary gland is close to important brain areas, tumors affecting it, whether malignant or non-cancerous, frequently influence hormone balance. The sample photos from each class shown in **Figure 1** show various tumor types and normal brain scans. Glioma images are shown in the first row, meningioma images in the second row, no tumor images in the third, and pituitary tumor images in the fourth row.

III. METHOD

In this study, we used MRI scans to classify brain tumors using a modified ResNet50V2-based model architecture. To categorize MRI images into four different groups glioma, meningioma, no cancer, and pituitary tumors the model was created. The Squeeze-and-Excitation (SE) module, integrated into the design, enhances the model's capacity to concentrate on pertinent features by recalibrating channel-wise feature responses. The model uses three parallel routes to capture various spatial and channel-wise information from the MRI images, each of which uniquely processes the extracted features. The detailed architecture of the suggested model is shown in Figure 2. The backbone of our design was a pre-trained ResNet50V2 model show in Figure 2. When the ResNet50V2 model was loaded without its top layers, the first convolutional layers' potent feature extraction capabilities were preserved. With an input size of $224 \times 224 \times 3$, this pre-trained backbone was refined using our brain MRI dataset, and its output was used as the input for further parallel routes.

Three parallel routes are included in our redesigned architecture, each of which is intended to process the feature maps from the ResNet50V2 base uniquely: A Global Average Pooling (GAP) layer is applied immediately to the SE block output in the first path. This is followed by a thick layer of 512 units with ReLU activation. Before sending the output to the concatenation layer, a dropout layer with a rate of 0.3 is added to avoid overfitting. Second Route: Convolution Using MaxPooling and SE Block. The second route starts with a MaxPooling operation with a 2×2 pool size after a 3×3 convolutional layer with 256 filters. A second SE block is used to recalibrate the feature maps following MaxPooling. After that, the output is flattened and run through a dense layer that has ReLU activation and 512 units. Regularization is achieved by applying a dropout layer (0.3). Third Route: Minimal Convolution Using MaxPooling and SE Block Like the second approach, the third path uses MaxPooling with a 2×2 pool size after a convolutional layer with 128 filters and a

3×3 kernel. An SE module is added after the pooling layer to improve feature selection.

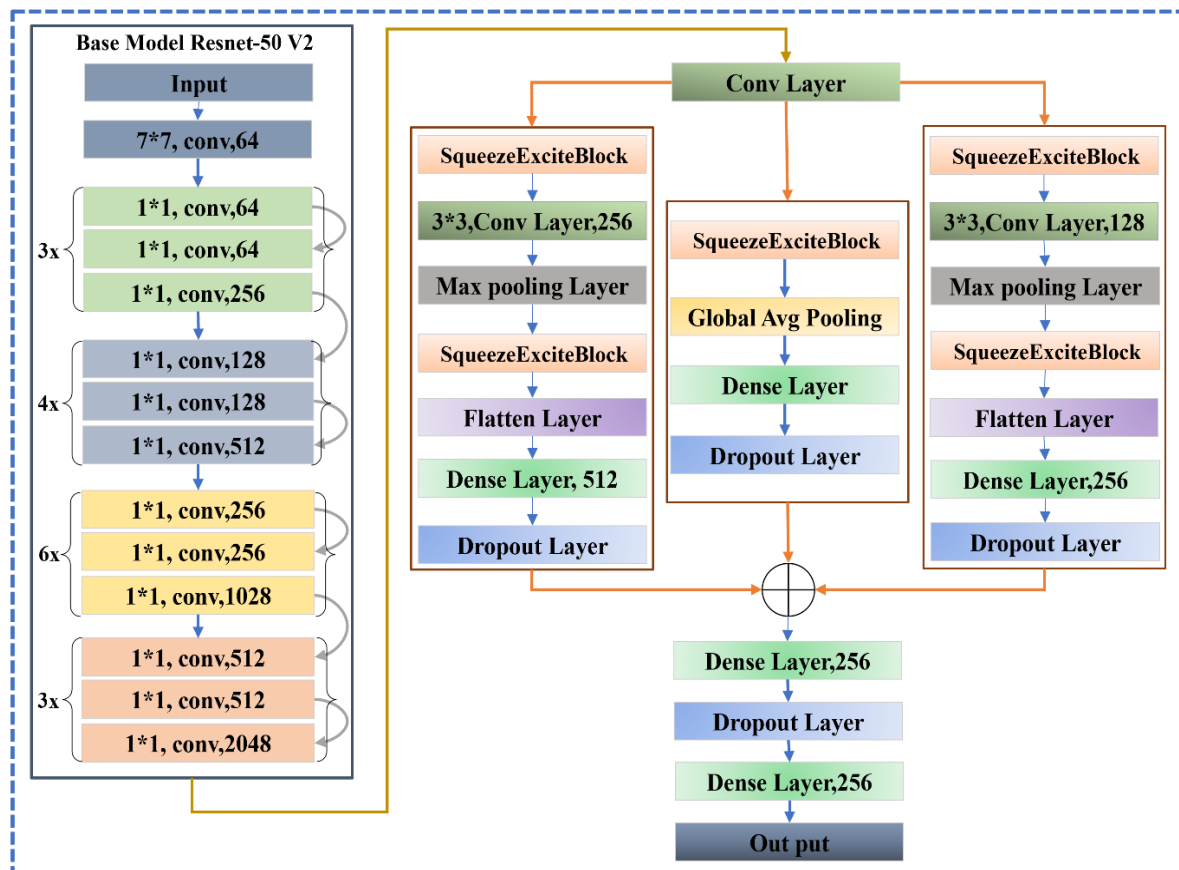


Figure 2. Backbone Architecture of our proposed architecture.

After that, the feature maps are flattened and run through a 256-unit dense layer and a 0.3-unit dropout layer. The outputs of the three parallel routes are concatenated to create a single representation of the MRI scans. A fully linked dense layer with 1024 units and a dropout layer with a rate of 0.5 are then applied to this concatenated vector. The four units in the final output layer—glioma, meningioma, no tumor, and pituitary—are activated using SoftMax to calculate the class probabilities.

Squeeze-and-Excitation: To recalibrate feature maps and improve the model's emphasis on more crucial channels, the Squeeze-and-Excitation (SE) module adds a channel-wise attention mechanism as shown in Figure 3. Squeeze and excitation are their two primary functions. Global Average Pooling compiles spatial data into a channel description during the squeeze phase. Subsequently, the excitation phase generates channel significance weights using two Dense layers: sigmoid activation and ReLU activation to minimize dimensions. These weights are then multiplied by the input feature maps to emphasize important channels and suppress less important ones. By emphasizing important

features, this enhances model performance, particularly for tasks like medical image categorization.

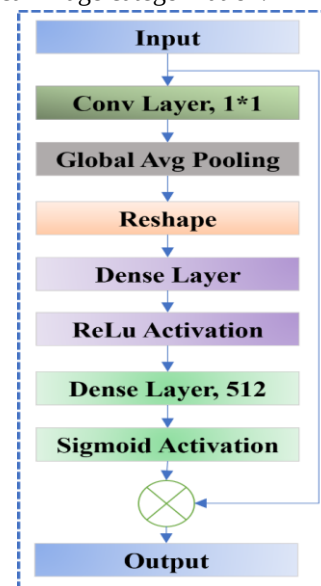


Figure 3. Squeeze-and-Excitation architecture

IV. EXPERIMENT RESULT

To assess our model's performance during the experimental phase, we used confusion matrices together with a number of related metric parameters, including accuracy (Acc), precision (Pre), recall (Rec), f-score (F-Scr), and Cohen Kappa Score (Ckp). To compute these metrics, we employed the true positive (TP), false positive (FP), true negative (TN), and false negative (FN) parameters that were derived from the confusion matrix. The following formulas were used to determine the confusion metrics.

$$Acc = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Pre = \frac{TP}{TP + FP}$$

$$Rec = \frac{TP}{TP + FN}$$

$$F1 - Scr = \frac{2 * (Rec * Pre)}{(Rec + Pre)}$$

$$Ckp = \frac{P_o - P_e}{1 - P_e}$$

P_o represents a high observed agreement rate between classifiers and raters.

P_e The fictitious likelihood of random agreement.

The model is successfully learning the training data when the training accuracy steadily increases and eventually approaches 99.97%. After some early swings, the validation accuracy stabilizes 97.98%, indicating a significant improvement as well as show in Figure 4. The model appears to generalize well with unseen data, as seen by the close convergence of training and validation accuracy and the absence of notable overfitting. The validation loss eventually levels off between 0.1 and 0.2, suggesting that there is little overfitting and that the model continues to perform well in terms of generalization even on the validation set.

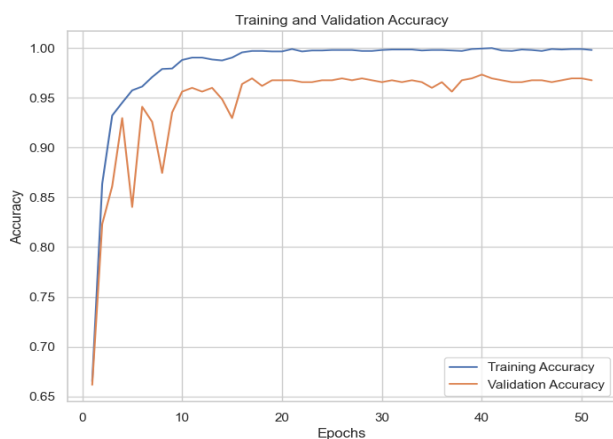


Figure 4 (a). Training and validation accuracy graph



Figure 4(b). Training and validation loss curve

The suggested model's outstanding predictive performance, which included high accuracy and little validation loss, indicated strong learning and generalization skills. In particular, the model achieved a Cohen Kappa score of 97.85%, an F1 score of 98.3%, a precision of 98.14%, and a recall of 97.78%. With a balanced performance across all evaluation criteria, these measures highlight the model's efficacy in correctly identifying the data.

The classification performance across four categories—glioma, meningioma, no tumor, and pituitary—is depicted in the confusion matrix as shown in Figure 5. With only 4 samples incorrectly identified as Meningioma, the model accurately predicted 1052 samples for Glioma, demonstrating a good classification accuracy in this category.

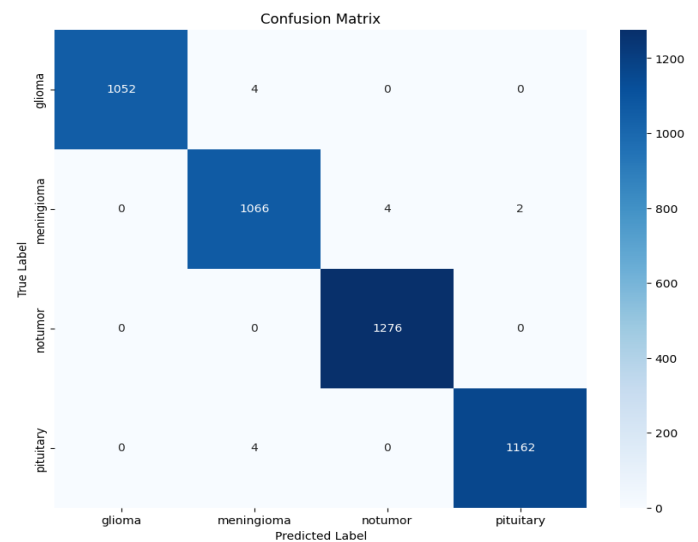


Figure 5. Confusion matrix

A total of 1066 valid predictions were made for meningioma; however, there were a few misclassifications: two samples were predicted to be pituitary, and four samples were reported to be no tumor, suggesting a little more confusion in this class. With all 1276 samples correctly predicted, No tumour's perfect classification indicates good model performance in differentiating this class from others. The difficulty in distinguishing between these two groups is demonstrated by the fact that, whereas 1162 samples were accurately categorized as pituitary, four samples were incorrectly labelled as meningioma. With slight errors, mostly between Meningioma and Pituitary, the confusion matrix shows a strong classification performance overall.

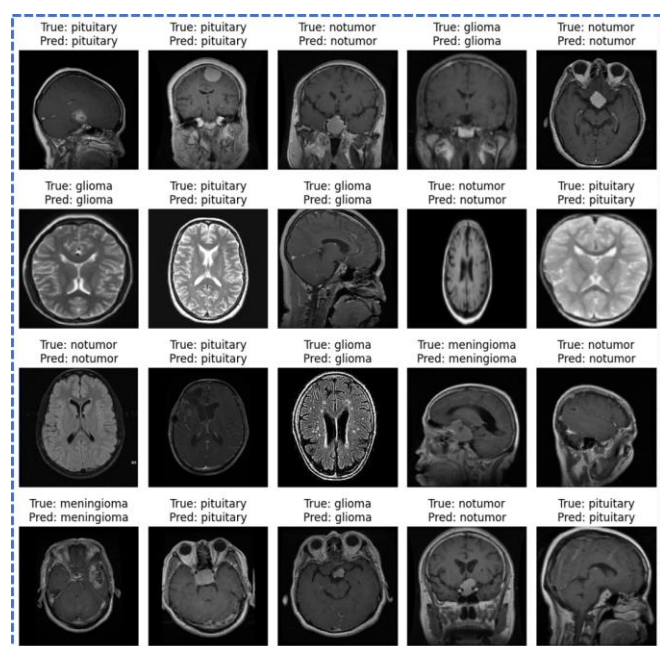


Figure 6. proposed model prediction result.

Figure 6 shows MRI scans that were chosen at random from the test set and weren't utilized to train the suggested model. Our model accurately predicted the categories of these samples. The pictures show various brain tumors, such as meningioma, no tumor, and pituitary tumor, which are consistent with the model's classification findings. This illustrates how the model can generalize new data.

V. CONCLUSIONS

In summary, the suggested model for classifying brain tumors, which uses a modified ResNet50V2 architecture with Squeeze-and-Excitation (SE) blocks, performed exceptionally well in classifying MRI images into four groups: pituitary, meningioma, glioma, and no tumor. With a stunning 99.97% training accuracy and a 99.20% validation accuracy, Cohen Kappa score of 97.85%, an F1 score of 98.3%, a precision of

98.14%, and a recall of 97.78%, the model demonstrated its high efficacy in generalizing to new data. No tumor received a flawless classification, but glioma and pituitary showed minor errors, according to the confusion matrix analysis. The model's emphasis on informative traits was strengthened by adding SE blocks, which increased classification accuracy. These findings demonstrate the model's potential for practical use, supporting patients with brain tumors in their early diagnosis and treatment planning. Future research will investigate additional architectural improvements and sophisticated data augmentation to improve generalization and resilience further.

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Rashedul Islam Sumon is pursuing his Ph.D. in the Institute of Digital Anti-Aging Healthcare at Inje University. His research interest aligns with Computer Vision, Medical Image Processing, Metaverse, Artificial Intelligence, and Bio Signal Processing.



Md Ariful Islam Mozumder is pursuing his Ph.D. in the Institute of Digital Anti-Aging Healthcare & Computer Science at Inje University. His research interest aligns with Deep Learning, Computer Vision, Medical Image Processing, Digital Pathology Images, Sensor Data Analysis, Bio Signal Processing, NLP, and Blockchain.



Salma Akter is pursuing his master's degree in the Institute of Digital Anti-Aging Healthcare at Inje University. Her research interests include Computer Vision.



Shah Muhammad Imtiyaz Uddin is pursuing his Ph.D. in the Institute of Digital Anti-Aging Healthcare at Inje University, he received his BSc in Computer Science and engineering from the World University of Bangladesh in 2017. His research interests include Computer Vision, Machine Learning, and Deep Learning.



Hee-Cheol Kim Ph.D. at Numerical Analysis and Computing Science, at Stockholm University in Sweden. He is a professor and Head of Institute of the Digital Anti-aging Healthcare, Inje University, South Korea. His research interests include Machine learning, Computer Vision, Text mining, Bioinformatics, Blockchain, Metaverse, and XAI.