

Brain Tumor Analysis Using Multi-Scale CNN and Gated DenseNet-169

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ABSTRACT

Brain tumors refer to the uncontrolled growth of cells in the human brain, posing a significant risk to human health. Therefore, early detection of these tumors are crucial. However, existing feature extraction approaches often fail to capture the intricate characteristics of tumors, leading to suboptimal classification performance. To address this limitation, a Multi-scale Convolutional Neural Network and Gated Channel Transformation unit-based DenseNet-169 model (MC-GCT-DenseNet-169) is proposed for efficient brain tumor classification. The multi-scale convolutional neural network captures the nonlinear relationships between texture, shape, and intensity in magnetic resonance images (MRI). The GCT function in the DenseNet-169 model enhances the ability to learn subtle variations in MRI such as tumor texture and boundary features, which are essential for accurate classification. Experimental results show that the MC-GCT-DenseNet-169 method attains accuracy of 98.97% on the Figshare dataset, surpassing previous approaches such as Cross-prior Bayesian attention mechanism with a Correlated Inception and Residual Learning Network (CB-CIRL Net).

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1. INTRODUCTION

Brain tumors are deadly diseases caused by irregular cell growth in the human brain, resulting significant changes in brain behavior and function. Therefore, the early detection of brain tumors is vital for accurate diagnosis and effective treatment [1–3]. Brain tumors are classified into two types: those consists of cancerous cells, referred to as malignant tumors, and those without cancerous cells, known as benign tumors, which are considered less harmful [4], [5]. The risk level associates with brain tumors is determined by factors such as tumor size, behavior, and growth rate, which contribute to the accurate differentiation of malignant, glioma, and benign tumors [6]. Various imaging techniques are employed to detect brain tumors, including X-ray, Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Ultrasound, Positron Emission Tomography (PET), and Single-Photon Emission Computed Tomography (SPECT) [7], [8]. Among these, MRI is widely used for brain tumor classification because of its excellent contrast, high spatial resolution, and detailed cross-sectional imaging of brain tumor tissues [9], [10]. MRI-based imaging enables the early detection and classification of brain tumors, enabling effective treatment and reduced risks to patients. Consequently, researchers have extensively utilized MRI images to detect tumors in brain tissue, as they provide comprehensive structural information about the brain [11].

However, manual brain tumor detection and classification are time-consuming and often fail to produce accurate results [12]. To address this drawback, automatic classification using artificial intelligence techniques is essential to reduce inaccuracies when classifying various brain tumors from MRI data. Machine learning (ML) approaches, utilize training data to detect brain tumors, offer significant advantages in the fields

of medical diagnosis and image processing [13–15]. However, traditional ML approaches have limitations such as lower accuracy, high susceptibility to errors, and the need for a separate algorithm for tuning and selection [16]. Thus, Deep Learning (DL) architectures are employed to focus on complex image features and for comprehensive learning of brain tumors. However, many existing approaches incorporate irrelevant features and lack adequate information on the tumor shapes, texture, and size, making accurate classification of tumor types challenging.

Khan et al. [17] presented a DL method for the classification of brain tumors using MRI. A classification model based on a residual skip block-based MobileNet (RSB-MobileNet) was employed to enhance brain tumor classification by preserving relevant information generated by the model. Swish activation was replaced with a rectified linear unit to improve the information retention during feature extraction. However, the RSB-MobileNet model failed to capture details related to the texture, shape, and size of the tumor, which affected the classification performance. Agarwal et al. [18] designed a Multi-Scale Feature-Scaling Network (MultiFeNet) for efficient brain tumor classification using MRI. The MultiFeNet model combined a multi-scale technique with a Convolutional Neural Network (CNN) to capture important features and to classify various types of tumors. An advantage of the MultiFeNet model was its ability to enhance feature representation in MRI images. However, it failed to classify tumors accurately due to variations in tumor size, texture, and shape, which were not properly segmented. Vijayalakshmi and Anand [19] explored a Cross-prior Bayesian attention mechanism with a Correlated Inception and Residual Learning Network (CB-CIRL Net) to classify brain tumors. The CB-CIRL Net model was employed to classify various tumor types using MRI-based data. Its main advantage was the integration of correlated learning, which helped to focus on both channel and spatial features. However, the explored classification approach failed to capture the subtle differences between tumors, resulting in inaccurate segmentation outcomes.

Sachdeva et al. [20] presented various Deep CNN (DCNN) models to classify brain tumors using MRI. The DCNN models included XceptionNet, DenseNet, EfficientNetV21, EfficientNet-B0, and ResNet-50, which were pretrained models employed for the classification of brain tumors. The main advantage of these DCNN models was used different activation functions and pooling layers to extract relevant features for efficient classification. However, these models faced limitations in distinguishing between tumor types, owing to the extraction of inappropriate or redundant features, which negatively impacted the detection performance. Kaur and Mahajan [21] presented a brain tumor detection and classification approach using a transfer learning model, namely a Residual Network (ResNet). The ResNet-152 model was used in combined with GoogleNet to capture meaningful features from the MRI. ResNet-based classification was performed using traditional ML methods that relied on relevant features with informative values. However, the proposed transfer learning and ML-based classification model was limited by its inability to detect and classify tumors accurately due to low-quality image processing. Preetha et al. [22] suggested a hybrid DL approach that combined MobileNet V1 and DenseNet for the classification of brain tumors based on MRI data. The hybrid model integrated hyperparameter fine-tuning and feature fusion ensemble techniques in the feature extraction phase, which improved the classification efficiency. Dense connections and regularization techniques were incorporated to mitigate the overfitting. However, the model performance relied heavily on the quality of the MRI, which directly affected the classification accuracy.

Wang et al. [23] designed an improved brain tumor categorization model that fused various pretrained models. The classification model combined multiple CNN models, including Visual Geometry Group-16 (VGG-16), ResNet-50, and MobileNet-V2, to enhance feature extraction and mitigate overfitting issues. The deep fusion strategy enabled the model to detect subtle variations in MRI images, which was crucial to identify various types of tumors and grades. However, the fusion model performance varied across different datasets due to domain shifts, which reduced its generalizability as a result of inappropriate preprocessing techniques. Gull et al. [24] explored a multi-class classification model using a DL-based algorithm to classify brain tumors. A hybrid approach integrating a three-branch CNN (3B-CNN) with the EfficientNet-B2 model was utilized to categorize brain tumors efficiently. The combination of these models captured fine-grained contextual information from MRI images. However, the model failed to classify tumors effectively owing to the different sizes, shapes, and textures of the tumors. Abd El-Wahab BS et al. [25] developed a DL-based segmentation and classification model to detect brain tumors. U-Net and You Only Look Once (YOLOv5) were utilized due to their ability to learn complex spatial patterns from segmented images that helped in identification of tumor regions. However, the U-Net-based segmentation model failed to accurately delineate tumor regions due to irregular boundaries and overlapping tissue intensities, which degraded the overall detection performance.

Afroj et al. [26] introduced an attention-based segmentation model to enhance brain tumor detection. A multi-view coupled cross-modal attention-based SegNet (MSegNet) integrated with a transformer approach was utilized for the segmentation and detection of brain tumors. It effectively fused information across different

MRI modalities, allowing the model to focus on the related features for tumor identification and classification. However, the complexity of the MSegNet with the transformer model led to overfitting, particularly on small or imbalanced datasets. Mostafa AM et al. [27] presented a DL-based multi-class classification method to categorize brain tumors using MRI. A transfer learning approach with a modified EfficientNet-B2 was employed on MRI sequences to classify tumors. The modified EfficientNet-B2 model distinguished between the multiple tumor types. However, it faced challenges in accurate classification due to the presence of artifacts or noise in MRI scans. Ahsan et al. [28] presented a segmentation and feature fusion method for brain tumor detection using an MRI. A three-dimensional segmentation model was employed to localize the tumor, followed by a Deep CNN-based DarkNet19 approach for feature extraction. The integration of multiple features enabled the classification method to learn variations in tumor size, shape, and intensity across different MRI scans. However, fusion techniques increased the model complexity, requiring significant computational resources.

Jaspin et al. [29] introduced a DL-based CNN method for the multi-stage classification of brain tumors using MRI. The CNN-based tumor detection model utilized a fast box-bounding technique for segmentation to efficiently localize tumor regions in the brain. The CNN method sequentially focused on specific tasks by segmenting the classification process into multiple stages. However, the introduced model resulted in misclassifications during the early stages of tumor progression. Kaya [30] designed a Multi-Class CNN (MCCNN)-based brain tumor classification model using MRI scans. The MCCNN was employed to distinguish between healthy and diseased MRI by learning full-region feature information. An advantage of the MCCNN model was that it learned hierarchical feature representations from raw MRI automatically, enabling it to capture complex patterns of different tumor types. However, the model faced difficulties in accurate classification due to the presence of noise and poor image quality, which affected overall performance. El- Zulficar et al. [31] presented a multiclass brain tumor classification model based on the Faster CNN (FCNN) approach. The FCNN model was employed to efficiently categorize brain tumors on MRI according to their respective labels. The integration of average pooling layers in the FCNN helped mitigate overfitting. However, the model lacked a segmentation component to accurately segment tumors of varying sizes, which degraded its detection performance. Brain tumor classification depended on both the network architecture and the characteristics of the MRI modality, which were used for image acquisition. T1-weighted contrast-enhanced (T1CE) MRI primarily highlighted contrast-enhanced tumor regions, whereas T2-weighted MRI provides information related to edema and surrounding tissues. These MRI modalities differ in terms of image appearance, intensity distribution, and tissue contrast. The datasets used in this research were acquired using a consistent MRI modality and evaluated under the same imaging protocol. Accordingly, the proposed framework was developed and validated for a single-modality MRI setting. The application of the proposed framework to multiple MRI modalities and cross-modality learning will be considered in future work.

From the literature review, existing methods utilized for brain tumor classification showed several limitations, which are summarized as follows: variations in tumor size, shape, and texture; poor image quality; irregular boundaries; and overlapping tissue intensities. These models are also sensitive to domain shifts and noisy MRI data, and suffer from overfitting on small or imbalanced datasets, which limit their generalizability. To overcome these limitations, a Multi-Scale Convolutional Neural Network and Gated Channel Transformation unit-based DenseNet-169 model (MC-GCT-DenseNet-169) is proposed to classify the types of tumors from MRI. The proposed MC-GCT-DenseNet-169 framework incorporates a structurally organized, end-to-end architecture for brain tumor classification. A Multi-Scale CNN is employed as the initial feature extraction stage to capture complementary local and global tumor representations through parallel convolutional branches with different receptive fields. The extracted feature maps are subsequently processed by a DenseNet-169 backbone, in which lightweight GCT units are positioned after each Dense Block and immediately before the corresponding Transition layer. This placement enables channel-wise feature recalibration before dimensionality reduction, preserving the tumor-related texture, boundary, and intensity information during feature propagation. The Multi-Scale CNN and the GCT-enhanced DenseNet-169 are jointly optimized through end-to-end training, enabling the learning of multi-scale spatial representations together with channel-wise contextual dependencies. The resulting framework combines multi-scale feature extraction and adaptive channel transformation within a unified architecture that are designed for MRI-based brain tumor classification. The significant contributions of this work are,

- MRI brain images are preprocessed using resizing and noise removal techniques to convert raw images into enhanced noise-free data for subsequent classification.
- The proposed multi-scale CNN is used to extract diverse sets of features based on different tumor types, capturing texture, size, and shape information to enhance classification accuracy.
- The proposed GCT-DenseNet-169 model is employed to classify brain tumors by learning inter-class relationships from brain images and assigning precise labels to each tumor type.

This manuscript is structured as follows: Section 2 explains the proposed MC-GCT-DenseNet-169 methodology. The experimental results and discussion of the proposed classification approach with existing models are represented in Section 3. Section 4 provides the conclusion.

2. METHODOLOGY

The proposed brain tumor classification system using the MRI framework involves four phases: dataset acquisition, preprocessing, feature extraction, and classification. Figure 1 represents the overall architecture of the proposed brain tumor classification system. First, brain tumor MRI images are acquired and preprocessed using resizing and Gaussian filtering techniques to improve the image quality. Next, a multi-scale CNN approach is used to extract significant features from the preprocessed images. Finally, the proposed GCT-DenseNet-169 model efficiently classifies tumors based on the selected features.

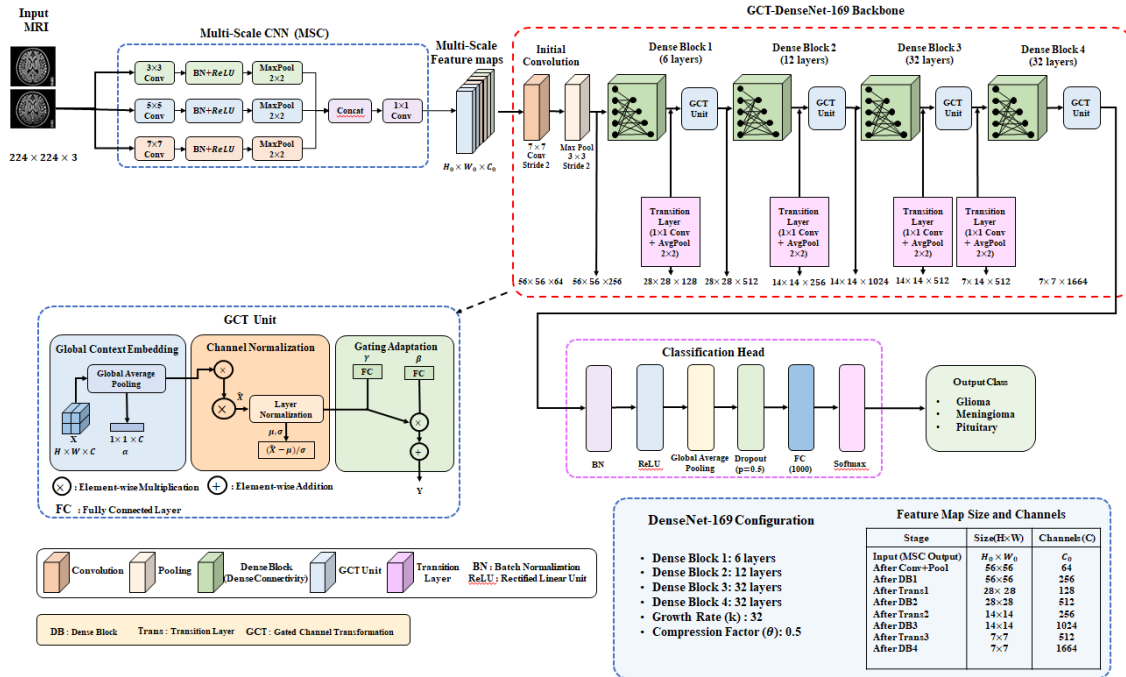


Figure 1. Overall architecture of the proposed MC-GCT-DenseNet-169 based brain tumor classification framework. The framework consists of a Multi-Scale CNN for feature extraction, a GCT-enhanced DenseNet-169 backbone for hierarchical feature learning, the internal structure of the GCT unit, the classification head, and the feature map dimensions across different network stages.

2.1. Dataset Acquisition

To train and validate the proposed brain tumor classification model, two benchmark datasets known as Figshare and Kaggle, are utilized in this research.

- Figshare dataset is a publicly available dataset [32], categorized into multiple classes for various tumour classes. These data are divided based on the Sagittal, Coronal, and Axial perspectives. To minimize data leakage, patient-wise partitioning is applied. This dataset comprises of 930 samples taken from 62 patients diagnosed with pituitary tumors, alongside 1,426 data from 89 patients diagnosed with glioma tumors, and 708 samples from 82 patients diagnosed with meningioma tumors.
- The Kaggle dataset is an open-access dataset [33] that includes 7,200 human brain MR images, which are verified data from the Figshare brain MRI dataset and uses an image-level split. The 7,200 images are uniformly divided into four balanced classes as 1,800 images per class, 1,800 glioma, 1,800 meningioma, 1,800 pituitary tumor, and 1,800 normal (no tumor). Table 1 represents the patient-wise and slice partition breakdown for the Figshare dataset, in Figshare dataset slice counts deviate slightly because splitting is performed at patient level. The images in both the Figshare and Kaggle datasets are T1-weighted contrast-enhanced (T1-CE) MRI scans, the sole modality used with no T2 or FLAIR images included.

Table 1. Patient-Wise and Slice Partition Breakdown for the Figshare and Kaggle dataset

Tumor Category	Total Slices (Patients)	Training Set (70%) Slices (Patients)	Validation Set (10%) Slices (Patients)	Testing Set (20%) Slices (Patients)
Glioma	1,426 (89)	994 (62)	144 (9)	288 (18)
Pituitary Tumor	930 (62)	645 (43)	90 (6)	195 (13)
Meningioma	708 (82)	501 (58)	69 (8)	138 (16)
Total Figshare	3,064 (233)	2,140 (163)	303 (23)	621 (47)
Kaggle Dataset				
Image Classification Class (Image wise split)	Total Images	Training Set (70%)	Validation Set (10%)	Testing Set (20%)
Glioma	1,800	1,260	180	360
Meningioma	1,800	1,260	180	360
Pituitary Tumor	1,800	1,260	180	360
No Tumor (Normal)	1,800	1,260	180	360
Total Curated Kaggle	7,200	5,040	720	1,440

The Figshare dataset serves as the primary benchmark dataset to evaluate the proposed framework. The Kaggle dataset is considered as a related secondary dataset obtained from publicly available brain MRI images. However, both datasets contain images representing the same tumor categories and are evaluated independently using their respective data partitions to validate the classification performance of the proposed framework across different publicly available datasets.

2.2. Preprocessing

The acquired brain images are fed as input for preprocessing to enhance them into a suitable form for subsequent classification. The MRI images in the dataset vary in dimensions and may contain noise, which is introduced during the acquisition process that can degrade the performance in tumor identification and negatively impact classification accuracy. In the preprocessing phase, resizing, augmentation, and Gaussian filtering techniques are applied to normalize image dimensions and reduce noise in the brain images.

- **Resizing:** The resizing technique reduces the dimensions of all images to a uniform size to prevent inconsistent feature extraction performance. The input images from the Figshare dataset, originally structured with 3D spatial dimensions of $240 \times 240 \times 155$, which are decomposed along with their respective anatomical axes to extract independent 2D structural slices. Then, to standardize the dimensions for subsequent Multi-Scale CNN, these individual 2D images from Kaggle and Figshare dataset are resized from 240×240 pixels to 224×224 pixels [34].
- **Noise Removal:** The resized images are then smoothed by a Gaussian filter, which mitigates random noise and preserves the edges as well as important information during training. The Gaussian filter improves brain images by filtering out unnecessary noise, which helps focus on features with meaningful information. The mathematical expression of the Gaussian kernel with radial basis function is represented in (1):

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

Where x and y denote the locations of image pixels, $G(x, y)$ refers to the Gaussian kernel function, and σ indicates the standard deviation. Kernel window size of 3×3 is used with a fixed standard deviation of $\sigma = 1.0$. Data augmentation is applied to the training set to improve the ability of the model to generalize, by randomly rotating and scaling the images to rotation range of -15° to $+15^\circ$, scale range of 0.90 to 1.10, horizontal flip probability 0.50, and vertical flip probability 0.50. In the final experimental configuration, vertical flipping is disabled (probability = 0.00) because vertical inversion may alter the anatomical orientation of brain MRI images and introduce unrealistic samples. The anatomically plausible augmentations such as small rotations, translation, and intensity perturbations are applied. The MRI images are resized to 224×224 pixels to satisfy the input dimensions that are required by the DenseNet-169 architecture. The same preprocessing procedure is applied to all comparative models to maintain a consistent experimental protocol. Following resizing, the proposed Multi-Scale CNN extracts feature representations using multiple receptive fields before feature learning by the DenseNet-169 backbone. This processing sequence allows image information in different spatial scales to be represented within the standardized input size. The evaluation of higher-resolution MRI images and their impact on tumor classification performance remains an area for future investigation.

2.3. Multi-scale Feature Extraction

The preprocessed images are fed into a multi-scale CNN model [35] to extract features at various tumor scales, enabling the efficient classification of different tumor types. Various brain tumor types share

similar characteristics such as shape, intensity, size, and texture; thus, extracting these features helps distinguish tumor types and improves classification accuracy. The convolutional operations are followed by batch normalization and an activation function. Finally, stride and max pooling operations are applied to the normalized feature maps. Similarly, the subsequent layers extract detailed features, and for training, a Adam optimizer is utilized in the CNN feature extractor. This multi-scale CNN architecture effectively extracts local and global tumor features from preprocessed images, which helps enable accurate tumor analysis. The lower layers extract features such as shapes, textures, and edges, whereas deeper layers extract abstract and complex features. This aids brain tumor classification, and these extracted tumor features are transferred to the proposed classification phase.

2.4. Classification

The extracted features with information related to brain tumors are fed as the inputs for feature selection. In this research, a DenseNet-169 model is utilized for brain tumor classification, consisting of two primary components: Dense Blocks and Transition layers. The dense block in the DenseNet-169 architecture enables inter layer connectivity and feature learning, whereas the transition layer minimizes the feature map dimensions to ensure the efficiency of the model. The key advantage of the DenseNet-169 method is its dense connectivity mechanism, which connects each layer to the prior layer to generate a feature map as an input in each layer, as shown in (2).

$$x_l = H_l([x_0, x_1, \dots, x_{l-1}]) \quad (2)$$

Where x_l denotes the output layer l , and $H(.)$ indicates a non-linear transformation function that integrates the Rectified Linear Unit (ReLU) with 3×3 convolution operations and Batch Normalization (BN). The non-linear transformation in DenseNet-169 not only reduces feature dimensionality but also improves model non-linearity and addresses overfitting issues. This non-linear function aids in achieving fine-grained distinctions between various tumor types during brain tumor classification. The transition layers are positioned between dense blocks to efficiently control the feature-map dimensions to optimize the overall model capacity. However, while the DenseNet-169 model achieves dimensionality reduction and tumor detection, it has limitations that affect the precise classification of brain tumors. Brain tumors in MRI images vary in terms of contrast and intensity, which are subtle that the DenseNet model fail to capture them, resulting in misclassification. In order to overcome this limitation, this research a proposes a GCT unit, which is incorporated into the DenseNet-169 network for enhanced brain tumor classification. The proposed framework incorporates GCT units into the DenseNet-169 architecture through a predefined network arrangement. The GCT units are positioned after each Dense Block and before the corresponding Transition Layer to perform channel-wise feature recalibration before feature-map dimensionality reduction. This arrangement enables the extracted feature maps to adaptively weighted based on the channel responses prior to the transition-layer processing. The Multi-Scale CNN provides local and global feature representations that are subsequently processed by the GCT-enhanced DenseNet-169. The entire network is trained through an end-to-end optimization process, enabling the learning of multi-scale spatial representations together with channel-wise contextual information for brain tumor classification.

2.4.1. Gated Channel Transformation–DenseNet-169

The proposed GCT is a lightweight module that enhances the recognition of tumor regions by enabling dynamic interactions among various channels in the DenseNet-169 model. The proposed GCT unit comprises three components: global context embedding, channel normalization, and a gating mechanism, which effectively captures the interactions between distinct channels. Additionally, the proposed GCT unit trains the inherent parameters of the DenseNet model, thereby conforming an optimally consistent classification framework. Figure 2 illustrates the architecture of the GCT unit.

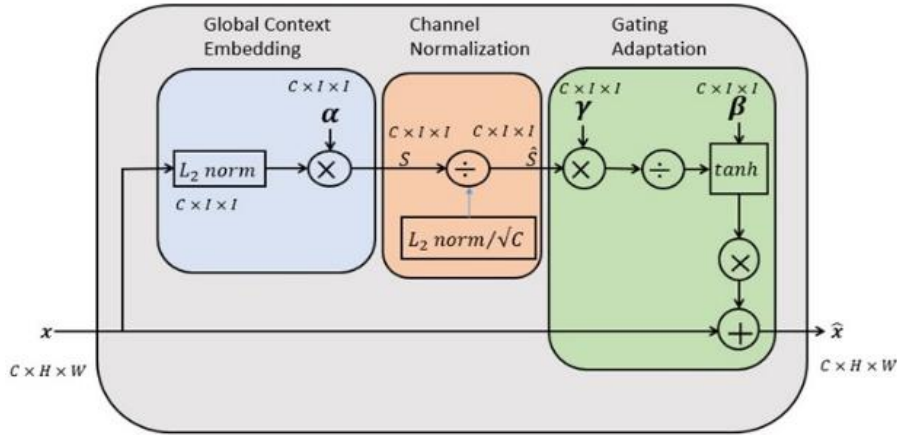


Figure 2. Architecture of the proposed Gated Channel Transformation Unit

Let x denotes the activation feature in the DenseNet model with C channels. Then, the proposed GCT unit performs as mathematically denoted in (3).

$$\hat{x} = F(x|\alpha, \gamma, \beta), \quad \text{where } \alpha, \gamma, \beta \in R^C \quad (3)$$

Where α represents the trainable parameters that contribute adaptively when designing a global context module, γ and β denote the trainable parameters that control the gating activation within each channel that impacts feature interactions, which are captured by the GCT unit. An advantage of the proposed GCT unit is its efficient integration of the normalization technique with an attention mechanism for learning interrelations between channels of the DenseNet-169. It is assumed that $x = [x_1, x_2, \dots, x_C]$, where, x_C indicates a channel of x . The three primary components of the proposed GCT unit is integrated with a DenseNet-169, which are briefly explained below.

2.4.2. Global Context Embedding

According to the L2 regularization norm, this module integrates global context information within each channel in the DenseNet-169 model. The global context embedding module in the GCT unit is mathematically expressed in (4). Where ε denotes the small constant to prevent issues that correspond to differentiation at zero.

$$s_c = \alpha_c \|x_c\|_2 = \alpha_c \left\{ \left[\sum_{i=1}^H \sum_{j=1}^W (x_c^{i,j})^2 \right] + \varepsilon \right\}^{\frac{1}{2}} \quad (4)$$

2.4.3. Channel Normalization

Generally, normalization techniques help the model to balance the activity across neurons and channels by enhancing the influence of strongly responsive channels while reducing the impact of weaker one. L2 normalization is used in cross-channel feature normalization, which is mathematically represented in (5). Where $\sqrt{C}$ denotes a scale factor to ensure the scale of $\hat{s}_c$, which is not exceptionally small.

$$\hat{s}_c = \frac{\sqrt{C} s_c}{\|s_c\|_2} = \frac{\sqrt{C} s_c}{\left[\left(\sum_{c=1}^C s_c^2 \right) + \varepsilon \right]^{\frac{1}{2}}} \quad (5)$$

2.4.4. Gating Adaptation

The gating adaptation module dynamically adjusts feature activation using weights, such as γ and bias β to permit the activation of channels adaptively. This gating mechanism is mathematically presented in (6). When the channel feature weights are positively activated, the GCT unit requires a channel competition relationship; whereas when the weights are negatively activated, the GCT unit requires a synergy relationship. The global context embedding captures long-range dependencies from the features, aiding in the tumors recognition across various contrasts. The gating mechanism in GCT focuses exclusively on tumor-relevant features, facilitating differentiation between various tumor types and enhancing classification accuracy. Algorithm 1 presents the overall process of brain tumor classification using the MC-GCT-DenseNet-169 model.

$$\hat{x}_c = x_c[1 + \tanh(\gamma_c \hat{s}_c + \beta_c)] \quad (6)$$

When the channel feature weights are positively activated, the GCT unit promotes a competitive relationship among channels. In contrast, when the weights are negatively activated, the GCT unit encourages a synergistic relationship between the channels. The global context embedding captures long-range dependencies from the features, aiding in the tumors recognition across various contrasts. The gating mechanism in GCT focuses exclusively on tumor-relevant features, which facilitates differentiation between various tumor types and enhances classification accuracy. Algorithm 1 presents the overall process of brain tumor classification using the MC-GCT-DenseNet-169 model, where the Figshare output = 3 classes; Kaggle output = 4 classes.

The advantages of the proposed model significantly improve brain tumor classification by enabling focused attention on fine-grained tumor features that are critical for accurate diagnosis. The adaptive channel weighting of the GCT ensures that subtle variations in texture and boundaries are not overlooked. Dense connectivity promotes efficient learning even with limited data, thereby reducing overfitting. The GCT module enhances the DenseNet-169 model's ability to distinguish between similar tumor variants, resulting in enhanced classification performance.

Algorithm 1:

Begin

PHASE 1: ACQUISITION, DETERMINISTIC STATE LOCKING, AND BALANCED SPLITTING

- Step 1: Load raw brain MR datasets (Figshare and Curated Kaggle repositories).
- Step 2: Seed the global pseudorandom number generator for execution stability: random seed (42).
- Step 3: Apply 70:10:20 patient-wise partitioning to the Figshare dataset cohort (233 total patients):
 - Confine 163 patient files to the Training Set (2,140 slices).
 - Confine 23 patient files to the Validation Set (303 slices).
 - Confine 47 patient files to the Testing Set (621 slices).
- Step 4: Execute a stratified 70:10:20 image-wise split for the 7,200 curated Kaggle images:
 - Assign 5,040 balanced images to Training (1,260 images per class).
 - Assign 720 balanced images to Validation (180 images per class).
 - Assign 1,440 balanced images to Testing (360 images per class).
- Step 5: Define the ground-truth target categorical class encoding vectors:
 - Figshare Target Map: {1: 'Glioma', 2: 'Pituitary Tumor', 3: 'Meningioma'}
 - Kaggle Target Map: {1: 'Glioma', 2: 'Pituitary Tumor', 3: 'Meningioma', 4: 'No Tumor'}

PHASE 2: STANDARDISED IMAGE PREPROCESSING

- Step 6: for each image within the assigned data partitions do
 - Slice extraction: Decompose 3D volumes into discrete 2D spatial planes.
 - Dimension normalization: Spatial resize from native grid to uniform 224×224 pixels.
 - Denoising: Pass matrices through a 2D Gaussian filter kernel to mitigate background noise.
 - if current image belongs to the Training Set partition then
 - Apply runtime affine data augmentations (random rotations, spatial scaling).
 - end if
- end for

PHASE 3: NETWORK MODEL OPTIMIZATION (TRAINING LOOP)

- Step 7: Initialize Multi-Scale CNN filter weights and core DenseNet-169 layer arrays.
- Step 8: Set hyperparameters: MaxEpochs = 50, MiniBatchSize = 32, Initial Learning Rate (η) = $1e - 4$.
- Step 9: Initialize Tracking Variables
- Step 10: for Epoch = 1 to MaxEpochs do
 - Shuffle the training set instance queue randomly.
 - for each MiniBatch batch execution sequence do
 - Forward Pass 1: Feed 2D inputs into parallel Multi-Scale CNN layers to extract local structural variances and global abstract complex feature maps.
 - Forward Pass 2: Transfer combined feature configurations into DenseNet Dense Blocks for inter-layer connectivity learning, followed by Transition Layers.
 - Gated Channel Transformation (GCT) Unit Processing:
 - * Calculate global context embeddings via channel-wise L2 regularization.
 - * Apply cross-channel normalization scaling.
 - * Dynamically rescale feature map channels using gating weights (γ) and bias parameters (β).

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- Loss Computation: Calculate Multi-Class Categorical Cross-Entropy objective loss.
- Backward Pass: Compute model parameter error gradient tensors via backpropagation.
- Parameter Tuning: Optimize architectural layer weights with the Adam Optimizer.
end for

- Epoch Evaluation & Validation Monitoring Checkpoints:
  Feed the complete Validation Set through the current processing pipeline.
  Compute current Validation Loss and Validation Accuracy metrics.
  if Validation_Loss < Best_Val_Loss then
    Best_Val_Loss = Validation_Loss
    Patience_Counter = 0
    Save current network weights layout as 'Best_Model_Checkpoint'.
  else
    Patience_Counter = Patience_Counter + 1
  end if
  Stopping Criterion: if Patience_Counter ≥ Early_Stopping_Threshold then
    Terminate network training iteration loop immediately (Early Stopping Triggered).
  end if
  Scheduled Decoupling: if Epoch matches an integer multiple of 10 then
    Decay active optimizer learning policy threshold step rate
  end if
end for

```

PHASE 4: EXTRACTIVE TESTING INFERENCE AND LABELLING

Step 11: Load the optimized model parameters from the saved 'Best_Model_Checkpoint'.

Step 12: Route the unseen test image dataset matrix through the trained network pipeline.

Step 13: Compute soft multi-class classification confidence scores using the output Softmax activation layer.

Step 14: Isolate maximum response indices and map them to their matching target class string labels.

Return: Predicted target class soft probabilities vector and categorical brain tumor classification labels.

End

3. EXPERIMENTAL RESULTS

The performance evaluation of the proposed MC-GCT-DenseNet-169 is employed in brain tumor classification, which utilizes Figshare and Kaggle datasets, which are depicted in this section. The proposed MC-GCT-DenseNet-169 method is implemented and simulated using MATLAB R2024b on a system running Windows 10 OS equipped with an Intel i9 processor and 64 GB of RAM. The performance of the MC-GCT-DenseNet-169 method is estimated using different performance metrics such as accuracy, precision, sensitivity, specificity, and recall. The mathematical representation of the performance metrics is presented in (7)–(11):

$$Accuracy = \frac{TP+FN}{TP+TN+FP+FN} \times 100 \quad (7)$$

$$Precision = \frac{TP}{TP+FP} \times 100 \quad (8)$$

$$Sensitivity = \frac{TP}{TP+FP} \times 100 \quad (9)$$

$$Specificity = \frac{TN}{TN+FP} \times 100 \quad (10)$$

$$F1 - Score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \times 100 \quad (11)$$

Where TP is true positive, TN is True negative, FP is the false positive, and FN is the false negative.

3.1. Hyperparameter settings and System Configuration

The proposed MC-GCT-DenseNet-169 method is implemented and simulated using MATLAB R2024b on a system running Windows 10 OS equipped with an Intel Core i9-13900K @ 3.00 GHz. Tables 2 and 3 explain the comprehensive hyperparameter settings of the proposed MC-GCT-DenseNet-169 and

baseline models. To ensure the evaluation fairness, all baseline architectures are re-implemented and optimized under the identical hyperparameter configurations, dataset partitions, and hardware conditions of the proposed MC-GCT-DenseNet-169 technique. The two benchmark datasets are split into 70% of the data for training, 10% for hyperparameter validation, and 20% for final performance evaluation. The patient-wise splitting strategy is used in the Figshare dataset to confirm that the MRI images from the same patient are not distributed across multiple subsets. This data split helps prevent the overlap of patient data between the training and testing phases. The Kaggle dataset is an adapted subset derived from the primary Figshare source repository, to maintain strict scientific integrity no cross-dataset pre-training or mixed-domain evaluation is performed. The Kaggle dataset is used only to evaluate various image formats and not treated as a separate test baseline. The experimental evaluation is conducted separately on the Figshare and Kaggle datasets. The results obtained from each dataset are reported independently and are not combined during model training or performance evaluation. To ensure absolute statistical rigor, the 70:10:20 split and the 5-fold cross-validation are executed as entirely separate validation tracks. In cross validation of 5×8 is used exclusively for the final statistical validation framework. The dataset is split into 5 mutually exclusive folds, which is repeated over 8 unique random permutations to produce 40 independent data splits. No test or validation images from any fold leaked into the active optimization loops. Subsequently, a thorough structural overlap audit is performed because the Kaggle dataset is a secondary repository, which curates the adaptation of the primary Figshare source.

Table 2. Comprehensive hyperparameter settings and System Configuration of proposed MC-GCT-DenseNet-169 technique

Category	Parameter Specification	Configured Baseline Value
Optimization Core	Base Model Optimizer	Adam Optimizer
Batch Management	Mini-batch Training Size	32 Samples
Epoch Duration	Maximum Training Epochs	50 Epochs
Learning Policy	Initial Learning Rate (η)	0.001
Scheduler Settings	Learning Rate Drop Period	Piecewise step decay (every 10 epochs)
Scheduler Scale	Learning Rate Drop Factor	0.5 multiplication step
Regularization	Network Dropout Coefficient	0.2 rate (applied at Transition Layers)
Environment Locking	Random Seed	42
Optimization Core	Early-Stopping Patience Threshold	10 Epochs without Validation Loss drop
	Terminal Learning Rate Boundary	1×10^{-6} (minimum floor threshold)
Inference Controls	Evaluation Execution Batch Size	1 Sample per batch (Strict sequential processing)
Baseline Fairness	Memory Tracking Metric	Peak Hardware GPU VRAM Footprint Allocation
	Fine-Tuning Optimizers (ViT/MobileNet)	Adam Optimizer, Initial $LR = 5 \times 10^{-5}$
Data Augmentation	Rotation Range	-15° to +15°
	Scale Range	0.90 to 1.10 ($\pm 10\%$ zooming)
	Horizontal Flip Probability	0.50 (50% chance)
	Vertical Flip Probability	0.50 (50% chance) (Disabled during final experimental configuration)
Execution Environment	Augmentation Mode	Training-Only Execution (Disabled for validation/testing)
	Development Platform	MATLAB R2024b (Deep Learning Toolbox)
	Training Execution Environment	GPU Engine ('gpu')
	Precision Configuration	Single-precision floating-point (fp32)
Hardware Specifications	Graphics Processing Unit (GPU)	1× NVIDIA RTX 3090 (24GB VRAM)
	Host Processor (CPU)	Intel Core i9-13900K @ 3.00 GHz
	System Memory (RAM)	B DDR5

Table 3. Hyperparameter settings for all baseline models used for comparison with proposed model technique

Hyperparameter	VGG16	ResNet-50	InceptionV3	MobileNetV2	EfficientNet-B0	DenseNet-169
Input Size	$224 \times 224 \times 3$	$224 \times 224 \times 3$	$224 \times 224 \times 3$	$224 \times 224 \times 3$	$224 \times 224 \times 3$	$224 \times 224 \times 3$
Optimizer	Adam	Adam	Adam	Adam	Adam	Adam
Initial Learning Rate	0.001	0.001	0.001	0.001	0.001	0.001
Batch Size	32	32	32	32	32	32
Epochs	50	50	50	50	50	50
Loss Function	Categorical Cross-Entropy	Categorical Cross-Entropy	Categorical Cross-Entropy	Categorical Cross-Entropy	Categorical Cross-Entropy	Categorical Cross-Entropy
Activation Function	ReLU, Softmax	ReLU, Softmax	ReLU, Softmax	ReLU, Softmax	ReLU, Softmax	ReLU, Softmax
Dropout Rate	0.5	0.5	0.5	0.5	0.5	0.5
Early Stopping	Yes	Yes	Yes	Yes	Yes	Yes
Weight Initialization	ImageNet Pre-trained	ImageNet Pre-trained	ImageNet Pre-trained	ImageNet Pre-trained	ImageNet Pre-trained	ImageNet Pre-trained

To ensure a fair comparison, all baseline models are implemented and evaluated using the same experimental protocol as the proposed MC-GCT-DenseNet-169 framework. The identical training, validation, and testing partitions are used for all methods, together with the same image preprocessing procedure and evaluation metrics. Each model is trained using the Adam optimizer with an initial learning rate of 0.001, a batch size of 32, and 50 training epochs under the same hardware and software environment. This standardized experimental setup minimizes variations resulting from training configurations, thereby allowing the comparison to isolate the architectural characteristics of the evaluated models.

3.2. Quantitative Analysis

The performance evaluation of the MC-GCT-DenseNet-169 method is carried out on Figshare and Kaggle datasets, with the results presented in this section. The feature extraction and classification models are utilized in this research are evaluated against DL-based state-of-the-art methods on both datasets. To mitigate evaluation bias, all baseline techniques and the proposed model are evaluated under an identical benchmarking protocol. A standardized resolution of 224×224 , mutually exclusive patient-wise dataset splits of 70:10:20, and unified MATLAB execution settings were utilized to ensure a fair and robust evaluation process. To ensure a fair evaluation, the proposed GCT-DenseNet-169 and standard CNN baselines are trained from scratch using random uniform weight initialization. Conversely, the MobileNet-V2 and Vision Transformer (ViT) baselines are fine-tuned using pre-trained ImageNet weights, with their core feature extraction blocks. Tables 4–10 present the quantitative analysis of the proposed MC-GCT-DenseNet-169. The Transformer baseline evaluated in Tables 5 and 7 is a standard Vision Transformer (ViT-B/16) architecture, which uses 16×16 patch embedding, 12 attention heads, a hidden dimension of 768, and is fine-tuned using pre-trained ImageNet-1k weights. Table 4 presents the performance outcomes of the feature extraction method on the Figshare dataset. The multi-scale CNN method attains a higher classification accuracy of 98.97%, outperforming existing optimization algorithms. The identical metrics reported for the proposed model in Table 4 is attained due to the unified end-to-end framework layout. The multi-scale CNN feature extractor and GCT-DenseNet-169 classifier blocks are optimized simultaneously through backpropagation. The global classification performance metrics are applied equally to both operational domains when analyzing the integrated performance metrics.

Table 4. Feature extraction performance with various feature extraction backbones on the Figshare dataset

Methods	Accuracy (%)	Sensitivity (%)	Precision (%)	F1-score (%)	Specificity (%)
CNN	92.38	92.17	92.37	92.03	91.96
DCNN	93.68	93.67	93.66	93.66	93.65
EfficientNet	95.57	95.56	95.55	95.55	95.54
ResNet	96.84	96.81	96.83	96.81	96.82
Multi scale CNN	98.97	98.96	98.98	98.95	98.95

Table 5 illustrates the performance analysis of the MC-GCT-DenseNet-169-based classification method on the Figshare dataset. The performance of MC-GCT-DenseNet-169 method is evaluated with various DL classifiers such as MobileNet, CNN, Transformers, and conventional DenseNet-169 models, which are employed for brain tumor classification. The MC-GCT-DenseNet-169 model achieves an accuracy 98.97%, which is greater than that of existing DL-based classifier approaches.

Table 5. Performance analysis of MC-GCT-DenseNet-169 method using Figshare dataset

Classifiers	Accuracy (%)	Sensitivity (%)	Precision (%)	F1-score (%)	Specificity (%)
CNN	90.81	90.78	90.80	90.78	90.79
MobileNet-V2	92.79	92.76	92.78	92.77	92.77
Transformer	94.62	94.60	94.61	94.60	94.59
DenseNet-169	95.46	95.46	95.45	95.44	95.43
Proposed MC-GCT-DenseNet-169	98.97	98.96	98.98	98.975	98.95

Table 6 presents performance analysis of multi-scale CNN-based feature extraction techniques on Kaggle dataset by utilizing the proposed MC-GCT-DenseNet-169 model to generate the final classification metrics. Performance of multi-scale CNN is evaluated with various DL models CNN, DCNN, EfficientNet, and ResNet, which are employed for feature extraction process. The presented feature extraction method

achieves an accuracy of 99.16%, proving competitive performance to the existing DL-based feature extraction methods.

Table 6. Performance analysis of feature extraction methods using Kaggle dataset

Method	Accuracy (%)	Sensitivity (%)	Precision (%)	F1-score (%)	Specificity (%)
CNN	93.44	93.41	93.43	93.42	93.42
DCNN	94.55	94.53	94.54	94.52	94.51
EfficientNet	97.93	97.93	97.94	97.93	97.92
ResNet	96.68	96.66	96.67	96.64	96.65
Multi scale CNN	99.16	99.17	99.18	99.16	99.16

Table 7 presents the performance analysis of the MC-GCT-DenseNet-169-based classification method on the Kaggle dataset. The performance of MC-GCT-DenseNet-169 model performance is evaluated against various existing DL classifier models such as MobileNet, CNN, Transformers, and conventional DenseNet-169. The proposed MC-GCT-DenseNet-169 method achieves an accuracy of 99.16%, demonstrating refined outcomes than existing DL-based classifier methods for brain tumor classification.

Table 7. Performance analysis MC-GCT-DenseNet-169 method using Kaggle dataset

Methods	Accuracy (%)	Sensitivity (%)	Precision (%)	F1-score (%)	Specificity (%)
CNN	91.57	91.55	91.56	91.55	91.54
MobileNet-V2	95.90	95.88	95.89	95.87	95.87
Transformer	96.71	96.73	96.72	96.72	96.74
DenseNet-169	97.66	97.64	97.65	97.65	97.93
Proposed MC-GCT-DenseNet-169	99.16	99.17	99.18	99.16	99.16

Tables 8 and 9 explain the class-wise diagnostic performance of the proposed MC-GCT-DenseNet-169 on both the datasets. On the Figshare dataset, the proposed model scores a higher 98.97% macro F1-score, and 99.17% macro F1-score on the Kaggle dataset, which represents the efficiency of handling in rare classes. The computational and statistical analysis of the proposed MC-GCT-DenseNet-169 model are represented in Tables 10 and 11. The proposed MC-GCT-DenseNet-169 model uses a strict 5-fold cross-validation ($K = 5$) protocol, and the complete 5-fold validation cycle is repeated eight times using unique random permutations. This combination uses exactly 40 independent training and testing runs. To ensure absolute integrity, Cohen's d effect sizes are calculated directly from this 40-run performance matrix. Table 12 represents the ablation and baseline structural analysis of the proposed MC-GCT-DenseNet-169 technique. The parameter counts and FLOPs are programmatically verified using the MATLAB Deep Learning Toolbox Profiler. The GCT module adds exactly 0.06M parameters due to the trainable vector arrays. The statistical significance of the proposed technique is evaluated using a two-tailed paired Student's t -test across the 40 individual cross-validation execution runs, and a 95% confidence level ($\alpha = 0.5$). The p -values are dynamically scaled by utilizing Holm's step-down Bonferroni correction, the sequential Holm correction ranked the baseline tests from lowest to highest p -value, which verifies each step against the adjusted alpha threshold $\alpha_{adjusted} = \frac{\alpha}{k-i+1}$.

Table 8. Detailed class-wise diagnostic performance of the proposed MC-GCT-DenseNet-169 on the Figshare

Tumor Category	Support (Slices)	Precision (%)	Sensitivity / Recall (%)	F1-score (%)
Glioma	288	98.97	99.31	99.14
Meningioma	138	98.48	97.83	98.15
Pituitary	195	99.49	99.74	99.62
Macro Average	621	98.98	98.96	98.97

Table 9. Detailed class-wise diagnostic performance of the proposed MC-GCT-DenseNet-169 on the Kaggle dataset

Diagnostic Tumor Category	Support (Slices)	Precision (%)	Sensitivity / Recall (%)	F1-score (%)	Specificity (%)
Glioma	360	98.89	99.17	99.03	99.63
Meningioma	360	98.61	98.33	98.47	99.54
Pituitary	360	99.44	99.17	99.31	97.56
No Tumor (Healthy Control)	360	99.78	100.00	99.89	99.91
Macro Average	1,440	99.18	99.17	99.17	99.16

Table 10. Computational analysis of the proposed MC-GCT-DenseNet-169 model with state-of-the-art models

Method	Dataset	Training time/ epoch (ms)	Memory usage (MB)	Inference time/image (ms)	Parameters (M)	Flops (G)
CNN	Figshare	32,400	1,843	1.12	4.20	1.85
	Kaggle	54,100	1,843	1.15		
MobileNet-V2	Figshare	24,100	1,433	0.85	3.58	0.31
	Kaggle	38,900	1,433	0.88		
Transformer	Figshare	115,400	5,120	3.84	45.21	8.92
	Kaggle	168,200	5,120	3.98		
DenseNet-169	Figshare	78,500	3,891	2.15	14.32	3.42
	Kaggle	112,400	3,891	2.22		
P	Figshare	84,200	4,198	2.38	15.10	3.68
Proposed Method MC-GCT-DenseNet-169	Kaggle	118,500	4,198	2.45		

Table 11. Statistical analysis of the proposed MC-GCT-DenseNet-169 model with state-of-the-art models

Comparison	Dataset	N	Mean Accuracy (%)	SD	SE	95% Confidence Interval	t-value	df	p-value	Wilcoxon W	Z-value	Wilcoxon p-value	Holm-adjusted p	Rank-bise (rrb)	Cohen's d	Decision
CNN vs Proposed	Figshare	40	90.81	1.26	0.199	(90.42, 91.20)	15.84	39	<0.001	5	-5.42	<0.001	<0.001	0.95	2.51	Significant
CNN vs Proposed	Kaggle	40	93.44	1.29	0.204	(93.04, 93.84)	17.36	39	<0.001	4	-5.51	<0.001	<0.001	0.96	2.74	Significant
MobileNetV2 vs Proposed	Figshare	40	92.79	1.29	0.204	(92.39, 93.19)	11.72	39	<0.001	11	-4.96	<0.001	0.002	0.91	1.85	Significant
MobileNetV2 vs Proposed	Kaggle	40	95.90	1.31	0.207	(95.49, 96.31)	10.26	39	<0.001	15	-4.52	0.0002	0.0003	0.88	1.62	Significant
Transformer vs Proposed	Figshare	40	94.62	1.34	0.212	(94.20, 95.04)	8.64	39	0.0001	22	-4.08	0.0004	0.0006	0.82	1.37	Significant
Transformer vs Proposed	Kaggle	40	96.71	1.37	0.217	(96.28, 97.14)	7.53	39	0.0002	26	-3.76	0.0008	0.0008	0.78	1.19	Significant
DenseNet-169 vs Proposed	Figshare	40	95.46	0.70	0.111	(95.24, 95.68)	5.82	39	0.0007	34	-3.21	0.0020	0.0014	0.69	0.92	Significant
DenseNet-169 vs Proposed	Kaggle	40	97.69	0.73	0.115	(97.46, 97.92)	4.37	39	0.00021	41	-2.71	0.0065	0.0032	0.58	0.69	Significant

Table 12. Ablation and Baseline Structural Analysis of proposed MC-GCT-DenseNet-169 technique

Model Configuration	Parameters (M)	FLOPs (G)	Figshare Accuracy (%)	Kaggle Accuracy (%)
Standard DenseNet-169 (Baseline)	14.32	3.42	95.46	97.66
DenseNet-169 + GCT (Ours)	14.38	3.44	96.88	98.12
Multi-Scale CNN + DenseNet-169	15.04	3.66	97.12	98.45

The ablation study further demonstrates the contribution of each architectural component. The Multi-Scale CNN improves feature diversity by extracting representations at multiple spatial scales, whereas the GCT module further processes these representations through channel selection based on contextual information. The complete MC-GCT-DenseNet-169 framework integrates these components within a unified network, resulting in improved feature representation and classification performance compared with configurations that employ only one of the two components.

The results of the performance analysis are associated with the complementary functions of the two principal components of the proposed framework. The Multi-Scale CNN extracts feature representations using convolutional branches with different receptive fields, enabling the network to capture both localized tumor characteristics, such as texture and boundary information, and broader structural patterns within the MRI images. These multi-scale feature maps are subsequently processed by the GCT units, which are integrated into the DenseNet-169 backbone. The GCT module selectively adjusts the contribution of feature channels according to the extracted contextual information before feature-map dimensionality reduction. This operation modifies the contribution of individual feature channels based on the learned contextual information, producing feature representations for the tumor classification. The combination of multi-scale spatial feature extraction and channel selection contributes to improved discrimination between tumor categories across the evaluated datasets.

3.3. Qualitative Analysis

Figures 3 and 4 represent the confusion matrices of Figshare and Kaggle datasets to validate the performance of the proposed model in brain tumor classification. The confusion matrices indicate that the proposed MC-GCT-DenseNet-169 framework correctly classifies the majority of MRI images across all tumor categories, with only a limited number of misclassified samples. For the Figshare dataset, nearly all samples are assigned to their corresponding classes, with only a few misclassifications observed between glioma, meningioma, and pituitary tumor images. These results indicate that the proposed framework effectively distinguishes tumor classes with similar imaging characteristics. Similarly, in Kaggle dataset, the confusion matrix shows accurate classification performance of proposed model across all four categories with only a few off-diagonal entries. The limited misclassification between tumor and non-tumor classes indicate that the extracted feature representations provide effective class separation. The Multi-Scale CNN captures image features at different receptive fields, whereas the GCT units selectively adjust the contribution of feature channels before each transition layer in the DenseNet-169 backbone. The integration of these components are contributed to consistent class-wise prediction performance across both datasets.

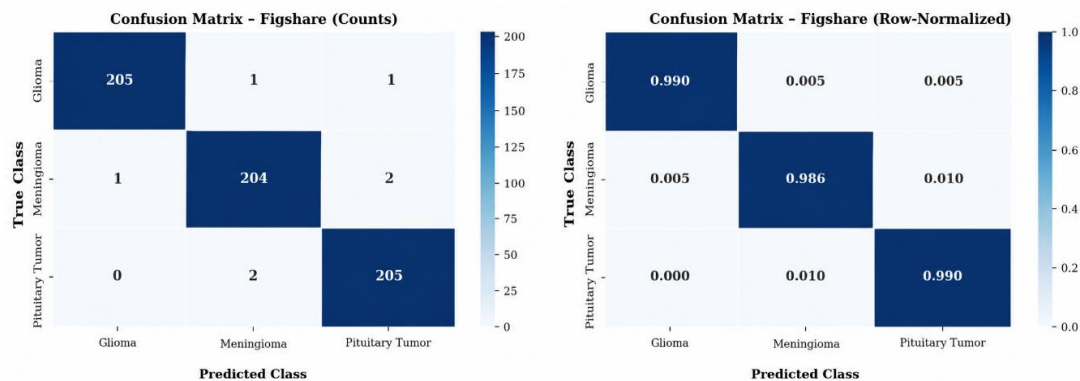


Figure 3. Confusion matrix of Proposed MC-GCT-DenseNet-169 for Figshare dataset

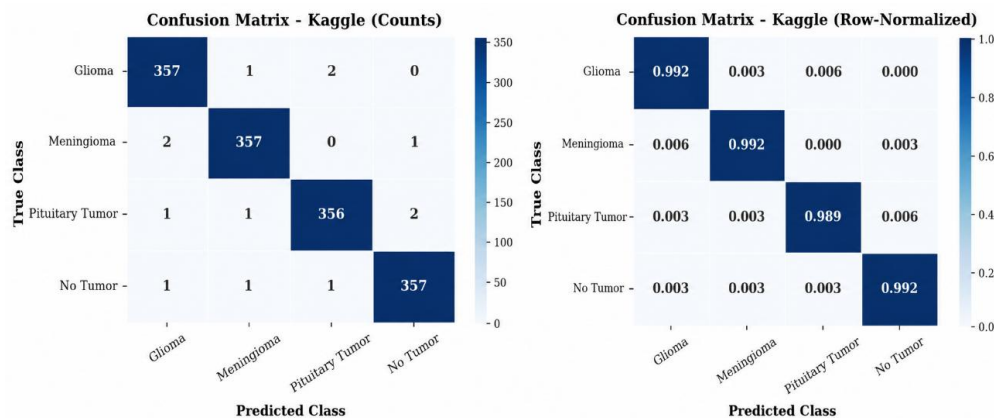


Figure 4. Confusion matrix of Proposed MC-GCT-DenseNet-169 for Kaggle dataset

Figure 5 a) and b) illustrates the ROC curves of the proposed MC-GCT-DenseNet-169 framework for the Figshare and Kaggle datasets. The ROC curves for both the Figshare and Kaggle datasets show that the proposed MC-GCT-DenseNet-169 framework achieves high true positive rates with low false positive rates across all tumor categories. The curves remain close to the upper-left corner of the Receiver Operating Curve (ROC) space, indicating effective class discrimination. The high AUC values are obtained for individual tumor classes and the macro-average further demonstrate consistent classification performance across the evaluated datasets. The Multi-Scale CNN extracts feature representations at different receptive fields, allowing the framework to capture both local and global image characteristics. These feature representations are subsequently processed by the GCT units within the DenseNet-169 backbone, where feature channels are selectively adjusted according to the contextual information before transition-layer processing. The integration of these components produce discriminative feature representations that contribute to the observed ROC characteristics.

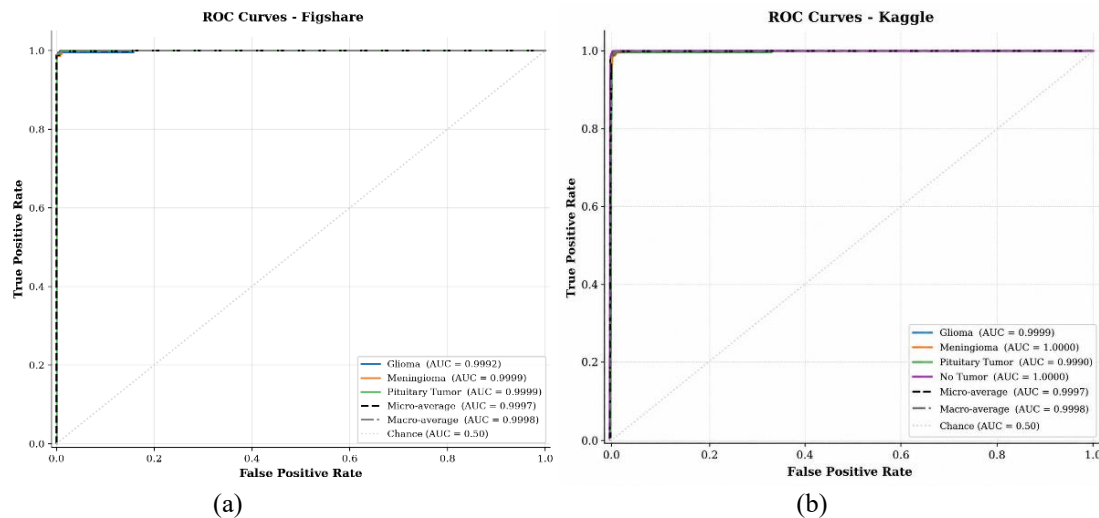


Figure 5 a) and b) ROC curves of the proposed MC-GCT-DenseNet-169 framework for the Figshare and Kaggle datasets. The corresponding AUC values for each tumor category and the macro-average AUC

Figure 6 a) and b) presents the training and validation accuracy curves of the proposed MC-GCT-DenseNet-169 framework, demonstrating stable convergence and consistent classification performance on both datasets. The training and validation accuracy curves demonstrate the stable convergence of the proposed MC-GCT-DenseNet-169 framework on both the Figshare and Kaggle datasets. The training and validation accuracies increase steadily during the initial training epochs and gradually converge as training progresses, with only a small difference between the two curves. This convergence pattern indicates stable optimization under the selected training configuration. The Multi-Scale CNN provides diverse feature representations from multiple receptive fields, whereas the GCT-enhanced DenseNet-169 backbone processes these features through dense feature propagation and selective channel processing. The resulting feature representations contribute to stable learning behaviour throughout the training process, leading to a consistent classification performance on both datasets.

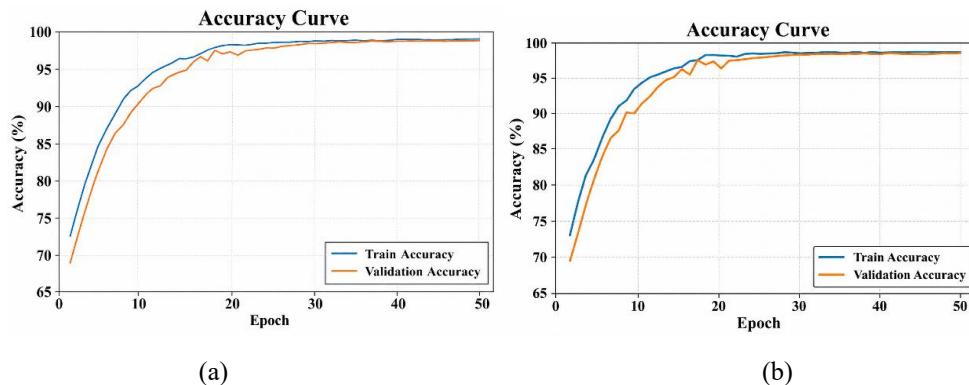


Figure 6. a) and b) Training and Validation Accuracy Curve of Proposed MC-GCT-DenseNet-169 for Figshare and Kaggle datasets

Figure 7 a) and b) presents the training and validation loss curves of the proposed MC-GCT-DenseNet-169 framework for the Figshare and Kaggle datasets. The loss curves demonstrate consistent convergence for both the Figshare and Kaggle datasets. The training and validation losses decrease rapidly during the initial epochs and gradually stabilize as training progresses. The small difference between the two curves indicates that the learned model parameters remain consistent across the training and validation datasets. The smooth convergence pattern without oscillations indicates stable optimization throughout the training process. These observations demonstrate that the proposed framework achieves consistent convergence under the selected training configuration.

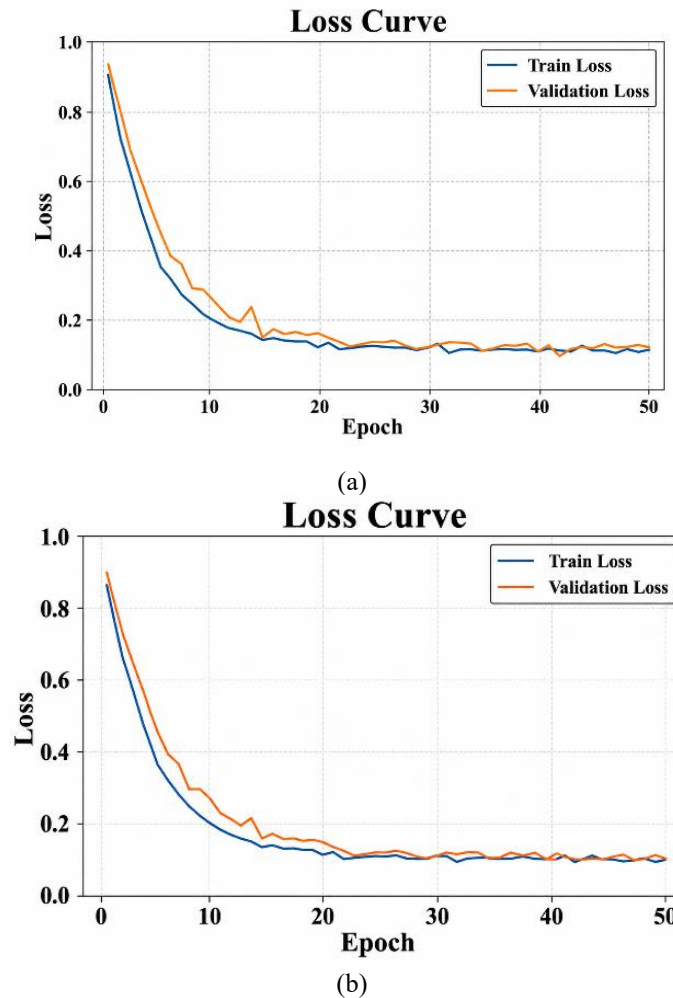


Figure 7. a) and b) Training and Validation Loss Curve of Proposed MC-GCT-DenseNet-169 for Figshare and Kaggle datasets

Figure 8 presents the Grad-CAM visualizations of the proposed MC-GCT-DenseNet-169 framework for representative input MRI images. The highlighted activation regions are primarily concentrated within the tumor structures, whereas comparatively limited activation is observed in the surrounding brain tissues. These visualizations indicate that the proposed framework utilizes tumor-related image characteristics during classification. The Grad-CAM analysis complements the quantitative evaluation by providing visual evidence of the regions contributing to the classification decisions across different tumor categories.

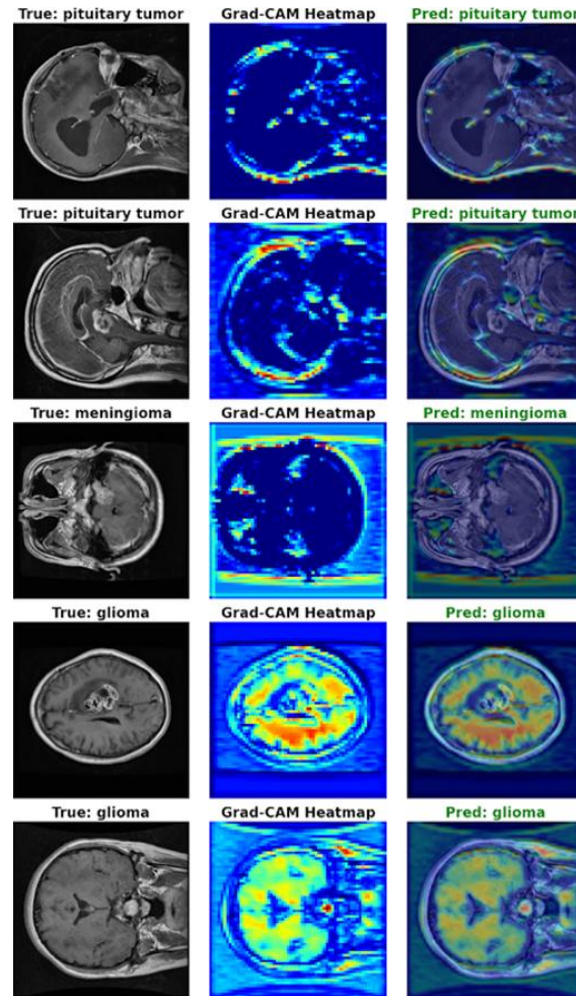


Figure 8. Grad-CAM visualizations of the proposed MC-GCT-DenseNet-169 for brain tumor classification

3.4. Comparative Analysis

A comparative analysis of the proposed MC-GCT-DenseNet-169 with existing detection approaches using the Figshare and Kaggle datasets is presented in this section. All state-of-the-art baselines are re-implemented and evaluated under an identical, seed-locked 5-fold cross-validation technique is repeated over 8 runs to ensure fair benchmark conditions. Tables 13 and 14 present a comparative evaluation of MC-GCT-DenseNet-169 model using the Figshare and Kaggle datasets. The method is compared with existing classification approaches, such as [17], [18], [19] and [20]. The model achieved an accuracy of 98.97%, precision of 98.98%, on the Figshare dataset. All baseline values from the Tables 13 and 14 are compiled directly from the local re-implementation and verification under identical runtime seeds.

Table 13. Comparative study of MC-GCT-DenseNet-169 model in Figshare dataset with existing models

Methods	Accuracy (%)	Sensitivity (%)	Precision (%)	F1-score (%)	Specificity (%)
RSB-MobileNet [17]	96.95	95.13	96.33	95.73	96.84
CB-CIRL Net [18]	97.06	96.88	97.02	96.95	97.11
Proposed method MC-GCT-DenseNet-169	98.97	98.96	98.98	98.97	98.95

Table 14. Comparative study of MC-GCT-DenseNet-169 model in the Kaggle dataset with existing models

Methods	Accuracy (%)	Sensitivity (%)	Precision (%)	F1-score (%)	Specificity (%)
EfficientNet-B0 [19]	96.25	96.18	96.22	96.20	96.31
ResNet-152 [20]	98.53	97.80	98.06	97.93	98.45
Proposed method MC-GCT-DenseNet-169	99.16	99.17	99.18	99.17	99.16

3.5. Discussion

The proposed MC-GCT-DenseNet-169 classification model achieves improved results in brain tumor classification using MR images. Existing detection approaches exhibit several limitations in accurately classifying brain tumors. For instance, the RSB-MobileNet [17] model fails to capture essential details regarding the texture, shape, and size of tumors, which directly affects classification performance. The CB-CIRL Net [18] model faces challenges in classifying tumors accurately because of variations in tumor size, texture, and shape, which are not properly segmented. EfficientNet-B0 [19] and other DCNN models face challenges in differentiating between various tumors owing to the presence of inappropriate or redundant features that impact detection performance. The ResNet-152 [20] model, when used with conventional machine learning methods struggle with a drawback of being unable to correctly detect and classify tumors due to low-quality image processing. To overcome these limitations, the MC-GCT-DenseNet-169 model is proposed for the accurate classification of brain tumors using a selectively optimized set of features.

The GCT-DenseNet-169 model enhances brain tumor classification by combining dense feature propagation with dynamic channel interactions. DenseNet-169 efficiently reuses features across layers, promoting improved learning of complex tumor characteristics. The integrated GCT module enables adaptive feature selection by emphasizing tumor-relevant channels and suppressing irrelevant channels. This improves sensitivity to subtle variations in tumor texture, shape, and intensity. As a result, the model achieves higher accuracy and robustness traditional deep learning classifiers.

3.6. Limitation and Future Work

However, the proposed tumor classification model achieves competitive results in terms of sensitivity, the MC-GCT-DenseNet-169 model still heavily depends on high-quality pre-processed input. This enhances tumor-specific pattern learning and significantly improves the classification accuracy by reducing interference from nontumorous tissues. Additionally, the current framework performed only image-level classification. The proposed framework is evaluated using MRI images resized to a resolution of 224×224 pixels to satisfy the input requirements of the DenseNet-169 architecture. The effect of higher-resolution MRI images on feature representation and the characterization of fine anatomical structures is not analyzed in the current research. The proposed framework is evaluated using publicly available MRI datasets that provide tumor class labels but do not include detailed annotations describing tumor characteristics, such as tumor size, edema volume, or anatomical location. The present research evaluates the proposed framework using MRI datasets, which are acquired under a consistent imaging modality. Consequently, the effect of these tumor characteristics on classification performance is not analyzed in the current research. Future work will evaluate the proposed framework using MRI datasets containing annotations for tumor size, edema volume, and anatomical location to examine the classification performance under varying tumor characteristics. Additionally, the future work will investigate the generalization of the proposed architecture across multiple MRI sequences, including T1-weighted contrast-enhanced and T2-weighted images, using domain adaptation and cross-modality learning strategies.

4. CONCLUSION

The MC-GCT-DenseNet-169 model is employed to classify brain tumors using MRI data. Brain tumor features have complex relationships between texture, shape, and intensity in MRI; thus, a multi-scale CNN model is employed to capture these nonlinear relationships effectively. The integration of the GCT module enables adaptive channel-wise feature modulation within the DenseNet-169 backbone, improving the representation of discriminative tumor features during feature propagation. This is beneficial for brain tumor classification, where subtle variations in MRI images, such as tumor texture or boundary features, are crucial for accurate classification. Experimental results of the proposed MC-GCT-DenseNet-169 method attains accuracies of 98.97% and 99.16% for the Figshare and Kaggle datasets, respectively, which are higher when compared to existing brain tumor classification approaches such as CB-CIRL Net and EfficientNet-B0. The key points of this research are as follows: the MRI brain images are preprocessed using resizing and noise removal techniques, which enhance image quality by eliminating noise and ensuring enhanced input for subsequent classification processes. The multi-scale convolutional neural network effectively extracts diverse features such as texture, size, and shape relevant to different tumor types, which helps improve the accuracy of tumor classification. The integration of the proposed GCT module with DenseNet-169 enables the model to learn the inter-class relationships within brain tumor data, leading to precise classification based on tumor labels. The proposed model demonstrates a high image-level classification performance on the evaluated benchmark datasets. However, external validation and lesion-level evaluation using independent MRI datasets are required before practical application in real-world settings.

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