SSRG International Journal of Electronics and Communication Engineering
ISSN: 2348-8549/ https://doi.org/10.14445/23488549/IJECE-V11I8P127

Volume 11 Issue 8, 282-293, August 2024

Original Article

Improved Glioma Detection and Classification through the EVGG19 Model

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Received: 21 June 2024 Revised: 31 July 2024 Accepted: 16 August 2024 Published: 31 August 2024

Abstract *- Gliomas, a diverse and complex category of brain tumors, present significant challenges in accurate classification due to their heterogeneous nature. Precise classification of gliomas into their respective subtypes and grades is crucial for effective clinical decision-making and personalized treatment planning. This study proposes an enhanced convolutional neural network architecture, EVGG19, designed specifically for the classification of gliomas using MRI data. This effort aims to incorporate domain-specific innovations and improve the glioma classification's accuracy and reliability. Our proposed workflow begins with the preprocessing and normalization of MRI images, followed by utilizing the DHA-ISSP model for accurate tumor segmentation. The segmented tumor regions are then fed into the EVGG19 model, which includes additional convolutional layers, increased model depth, dropout regularization, and a dedicated classification layer to refine the extraction and representation of features relevant to glioma classification. The performance of the EVGG19 model was rigorously evaluated using the TCGA dataset. Our model achieved an accuracy of 0.94, precision of 0.89, recall of 0.91, and F1 score of 0.9, significantly outperforming existing baseline models such as VGG Net-Based Deep Learning, UNet-VGG16 with transfer learning and VGG-UNET. Furthermore, EVGG19 demonstrated superior specificity (0.96), sensitivity (0.93), and AUC (0.97), along with the lowest MAE of 0.1 and MSE of 0.2. These findings demonstrate how well the EVGG19 model can distinguish glioma grades and subtypes, providing a robust tool for clinical application and furthering the potential for improved patient outcomes through more precise diagnostic capabilities.*

Keywords *- Gliomas, Classification, EVGG19, Segmentation, Normalization, Tumor regions.*

1. Introduction

Gliomas, the most prevalent primary BTs, are among the most challenging neuro-oncological conditions to manage due to their intricate biological heterogeneity and variable clinical outcomes. These tumors encompass a spectrum of malignancies, ranging from low-grade gliomas, which progress slowly and often have a favorable prognosis, to high-grade gliomas, characterized by aggressive growth and dismal survival rates [1]. Accurate classification of gliomas into subtypes or grades is paramount for guiding therapeutic strategies personalized to the precise characteristics of each tumor and predicting patient outcomes with precision [2]. Traditionally, glioma classification has relied on histopathological analysis, which involves examining tumor tissue samples obtained through invasive procedures. While histopathology remains the system for diagnosis, its invasive nature and inherent limitations in capturing the spatial heterogeneity of gliomas pose significant challenges [3]. Moreover, histopathological classification schemes based on histological features alone may lack granularity and fail to fully capture the complex molecular and genetic alterations driving glioma progression.

In recent years, the advent of advanced imaging modalities, particularly MRI, has revolutionized the non-invasive evaluation of gliomas. MRI provides exquisite anatomical detail and allows for the visualization of key features such as tumor location, size, and extent of infiltration into surrounding brain tissue [4]. Additionally, advanced MRI techniques, including DWI, PWI, and MRS, offer insights into the microstructural and metabolic characteristics of gliomas, further enhancing diagnostic accuracy. Despite these advancements, the interpretation of glioma imaging remains challenging, requiring specialized expertise and subjective interpretation. Moreover, traditional MRI-based glioma classification approaches often rely on qualitative assessments or semi-quantitative metrics, which may be prone to inter-observer variability and lack robustness in capturing subtle differences between glioma subtypes [5]. In this context, DL techniques, particularly

CNNs, have emerged as powerful tools for automated glioma classification from medical imaging data. CNNs are ideally suited for extracting intricate features from complex images, allowing for objective and quantitative analysis of glioma imaging characteristics [6].

In this study [7], we introduce EVGG19, an enhanced version of the VGG19 architecture tailored specifically for glioma classification. EVGG19 builds upon the foundational principles of VGG19 while incorporating novel enhancements aimed at improving the accuracy and reliability of glioma classification. By harnessing advanced DL techniques and state-of-the-art imaging data, EVGG19 represents a substantial development in the field of automated glioma classification, with the possibility to transfigure clinical practice and improve patient outcomes.

Gliomas represent a challenging domain in neuro-oncology, requiring accurate classification for personalized treatment strategies and prognosis assessment. Our proposed method incorporates several key enhancements to the traditional VGG19 architecture. These include additional convolutional layers for increased model depth, dropout regularization to prevent overfitting, and a dedicated classification layer specifically designed for glioma subtypes or grades. These improvements ensure that EVGG19 can effectively capture and differentiate the complex imaging features associated with different glioma types, thereby enhancing diagnostic accuracy. Through comprehensive experimentation and evaluation on a diverse dataset of glioma MRI scans, we demonstrate the efficacy and superiority of EVGG19 in accurately distinguishing between different glioma subtypes or grades.

The organization of this paper is as follows. Section 2 presents a literature survey, reviewing existing methodologies and their limitations in glioma classification. Section 3 details the DHA-ISSP model and the enhancements made to EVGG19, including data acquisition, preprocessing, and architectural improvements. Section 4 discusses the results as well as the performance evaluation, demonstrating the efficacy of EVGG19 in accurately classifying glioma subtypes or grades through extensive experimentation and comparison with baseline models. Finally, Section 5 provides the conclusion by summarizing the study's key findings and their implications for advancing glioma classification and suggesting directions for future research.

2. Related Works

Gliomas, the most common Brain Tumors (BT’s), present significant challenges in neuro-oncology due to their biological heterogeneity and variable clinical outcomes. Accurate classification of gliomas is crucial for guiding therapeutic strategies and predicting patient outcomes. Traditional methods, primarily relying on histopathological analysis, are invasive and limited in capturing the spatial and molecular complexity of these tumors. Advanced imaging techniques, particularly MRI, offer non-invasive insights but require specialized interpretation and are prone to variability. Existing Deep Learning (DL) as well as the Machine Learning (ML) models have made strides in addressing these challenges. Yet, issues such as overfitting, limited dataset sizes, and inadequate feature extraction persist.

Majib et al. [8] introduced VGG-SCNet, evaluating various ML models and 16 different transfer learning models to classify brain tumors autonomously. While their stacked classifier achieved high accuracy, the model's complexity and computational demands are significant drawbacks. Amin et al. [9] extracted deep features from the InceptionV3 model in addition to QVR for tumor classification. Their approach included a Seg network for segmenting infected regions. However, the reliance on quantum computing techniques may limit practical applications due to hardware constraints. Qureshi et al. [10] anticipated the Ultra-Light BT Detection system, which combines deep features with textural features from the Gray Level Matrix, using an SVM for classification. Although this hybrid approach achieves high accuracy, it requires substantial computational resources and may not be suitable for real-time applications.

Pravitasari et al. [11] developed UNet-VGG16 with transfer learning for classifying Regions of Interest (ROI) in brain tumor images. While effective, the model's performance is highly dependent on the quality of the transfer learning process and may struggle with overfitting in smaller datasets. Alsubai et al. [12] proposed a CNN- LSTM hybrid model for brain tumor prediction. This approach demonstrated improved classification accuracy but is computationally intensive and may not be practical for real-time applications. Khan et al. [13] addressed the overfitting problem in smaller datasets by combining a 23-layer CNN with transfer learning using VGG16. Although effective, the model's complexity and need for extensive computational resources are significant limitations.

Nawaz et al. [14] presented the VGG19-UNET model for segmentation, coupled with an ensemble voting predictor for survival prediction. Despite good performance, the model's complexity and requirement for extensive preprocessing are drawbacks. Rehman et al. [15] utilized a 3D CNN for tumor detection, followed by feature extraction with a pretrained CNN and classification using a feed-forward neural network. While this approach is innovative, the reliance on multiple models increases computational complexity. Methil [16] emphasized the importance of image preprocessing techniques like histogram equalization and image opening in improving classification accuracy. However, the preprocessing steps can be time-consuming and may not always lead to significant improvements. Alsaif et al. [17] reviewed various CNN architectures and proposed

a method for BT detection using CNNs and data augmentation. The effectiveness of this approach is limited by the variability in data quality and the need for extensive data augmentation.

Shah et al. [18] fine-tuned the EfficientNet-B0 model for brain tumor classification, incorporating data augmentation and image enhancement techniques. Although effective, the model's reliance on augmentation may not generalize well to all datasets. Gupta et al. [19] suggested an ensemble method combining Random Forest and InceptionResNetV2 for tumor detection and staging. While achieving high accuracy, the ensemble approach increases computational demands and complexity. Irmak [20] developed three CNN models for multi-class BT classification, achieving high accuracy. However, the models' complexity and need for extensive computational resources are limitations. Ranjbarzadeh et al. [21] proposed a flexible BT segmentation system using a Cascade CNN, focusing on smaller image regions to reduce computing time. Despite its efficiency, the system's effectiveness is highly dependent on the preprocessing approach.

Our proposed EVGG19 model addresses the limitations of existing methods by incorporating additional convolutional layers, dropout regularization, and a dedicated classification layer to improve feature extraction and robustness. Unlike previous models, EVGG19 is designed to minimize overfitting and handle diverse dataset sizes effectively. Through comprehensive experimentation on the TCGA dataset, EVGG19 demonstrated superior performance, achieving higher accuracy, precision, and F1 score compared to existing models. This enhancement makes EVGG19 a significant advancement in glioma classification, offering a more reliable and efficient tool for clinical decision-making and personalized treatment strategies.

3. DHA-ISSP Model

The foundation of our research lies in the acquisition and preprocessing of MRI data, a fundamental step in our quest to unravel the complexities of glioma classification as depicted in Fig. 1. Gliomas, characterized by their diverse morphological and pathological manifestations, demand meticulous handling of imaging data to ensure accuracy and consistency in subsequent analyses. Our input data, comprising preprocessed MRI images of gliomas obtained from patients, undergoes a rigorous standardization process to normalize formatting and intensity levels, laying the groundwork for robust analysis methodologies.

3.1. Data Acquisition and Preprocessing

In the initial phase, MRI images of gliomas are acquired from a diverse cohort of patients. The raw MRI data, represented as $I_{raw}(i,j,k)$ where i,j,k denote the spatial coordinates and undergoes preprocessing steps. These steps include intensity normalization and noise reduction to enhance image quality. The normalized MRI image $I_{norm}(i,j,k)$ is obtained using the formula:

$$I_{norm}(i,j,k) = \frac{I_{raw}(i,j,k)-\mu}{\sigma} \quad (1)$$

Where σ and μ epitomize the standard deviation and mean of the intensities in the MRI image, respectively. This normalization ensures consistent intensity levels across the dataset, facilitating accurate segmentation and classification. Building upon this standardized dataset, we set out on a voyage through the complex terrain of glioma segmentation., a crucial precursor to effective classification and prognosis. Enter the DHA-ISSP model, a sophisticated framework engineered to navigate the complexities of glioma delineation with precision and efficacy. The proposed model employs DHA mechanisms, which focus on different regions of the MRI scans to segment tumor areas accurately. Let $f_{DHA}(I_{norm})$ denote the segmentation function of the DHA-ISSP model. The segmented tumor regions S_{tumor} are obtained as follows:

$$S_{tumor} = f_{DHA}(I_{norm}) \quad (2)$$

Where S_{tumor} represents the binary mask highlighting the tumor regions within the given MRI image. The DHA mechanisms are mathematically expressed as:

$$DHA(x) = \sum_{l=1}^{L} \alpha_l \, . \, f_1(x) \quad (3)$$

Here, x denotes the input feature maps, L is the number of hierarchical levels, α_l represents the attention weights at level l, and f_1 denotes the feature extraction function at level l. Through meticulous attention to detail and adaptive learning strategies, the DHA-ISSP model produces precise delineations of glioma boundaries, offering invaluable insights into the spatial distribution and characteristics of these elusive tumors within the intricate terrain of the brain. The fruits of the proposed model's labor yield a bounty of segmented tumor regions, each a testament to the model's prowess in deciphering the enigmatic landscape of gliomas. These segmented regions, meticulously extracted and curated, emerge as the cornerstone of our subsequent endeavors in glioma classification. Serving as the primary input for our classification framework, these regions encapsulate a wealth of localized information, offering glimpses into the spatial intricacies and heterogeneity of gliomas within the confines of the brain.

As we navigate the labyrinth of glioma classification, armed with the insights gleaned from the DHA-ISSP model, we embark on a quest to discern the subtle nuances and intricacies of glioma subtypes and grades. Guided by the beacon of innovation, we turn to the EVGG19 architecture, a beacon of computational prowess poised to revolutionize the landscape of glioma classification. Within the hallowed halls

of EVGG19, the segmented tumor regions serve as grist for the mill, undergoing a metamorphosis of feature extraction and representation learning. Deep within the convolutional layers of EVGG19, intricate patterns and spatial relationships are unearthed, each a testament to the model's capacity to discern the subtle fingerprints of glioma pathology. The convolutional operations are mathematically represented as:

$$F_{conv} = \sigma(W_{conv} * S_{tumor} + b_{conv}) \quad (4)$$

Where F_{conv} denotes the feature maps obtained from the convolutional layer, b_{conv} and W_{conv} represent the biases and weights of the convolutional layer, and σ denotes the activation function. Through a symphony of convolutional operations and nonlinear transformations, EVGG19 endeavors to distil the essence of glioma subtypes and grades from the rich tapestry of segmented tumor regions. With each passing layer, the model delves deeper into the labyrinthine complexities of glioma classification, guided by the guiding light of innovation and discovery. As the journey through EVGG19 unfolds, the segmented tumor regions transform, emerging as harbingers of diagnostic insights and prognostic indicators. The output of EVGG19, a symphony of predicted labels and probabilities, is generated using a dedicated classification layer. This layer maps the extracted features to the target classes, facilitating accurate glioma classification. The classification function is expressed as:

$$y_{pred} = softmax(W_{fc} \cdot F_{conv} + b_{fc}) \quad (5)$$

Where y_{pred} denotes the predicted probabilities for each class, b_{fc} and W_{fc} represent the biases and weights of the fully connected layer, respectively, and $softmax$ denotes the softmax activation function.

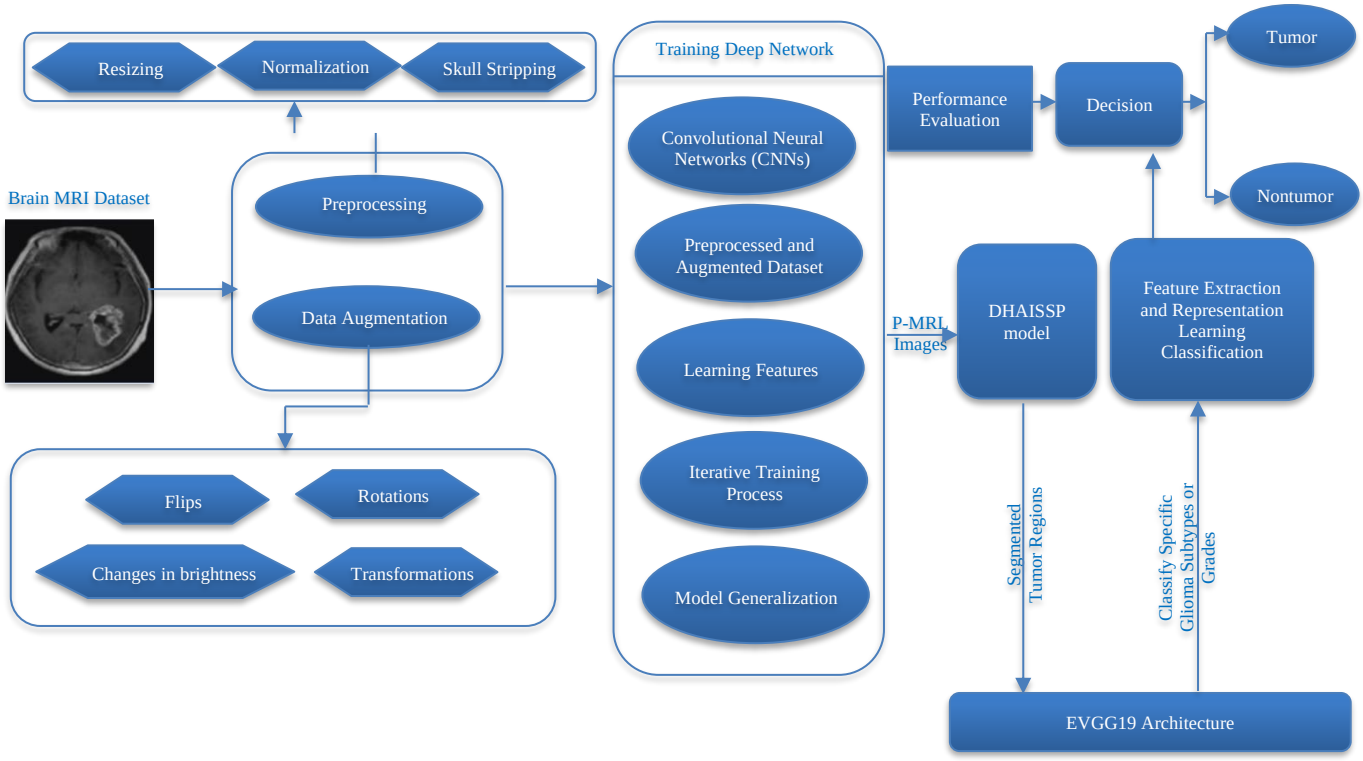

Fig. 1 Proposed EVGG19 classification for glioma classification process

3.2. Enhancements to EVGG19

To address the intricate features of gliomas and improve classification accuracy, EVGG19 incorporates several key enhancements, as shown in Figure 2.

These improvements aim to exploit the hierarchical nature of convolutional features, capture finer details, and mitigate common deep learning challenges such as overfitting and the vanishing gradient problem.

3.2.1. Additional Convolutional Layers and Enhanced Feature Extraction

Traditional Convolutional Neural Networks (CNNs), including the original VGG19 architecture, typically consist of a series of convolutional layers followed by pooling layers [22]. While effective in capturing basic image features, such architectures may struggle to capture the intricate details and patterns present in complex medical imaging data, such as MRI images of gliomas. To address this limitation, EVGG19

incorporates additional convolutional layers designed to capture finer details and subtle patterns specific to gliomas. These additional layers are strategically placed within the network architecture to allow for deeper feature extraction while preserving spatial information crucial for accurate classification. By increasing the depth of the network, we aim to exploit the hierarchical nature of convolutional features, enabling EVGG19 to learn increasingly abstract representations of glioma imaging data. This hierarchical representation facilitates the extraction of discriminative features essential for distinguishing between different glioma subtypes or grades. The additional convolutional layers in EVGG19 are initialized with random weights and trained using backpropagation on large datasets of annotated glioma MRI scans. This training process allows EVGG19 to learn complex patterns and relationships inherent in glioma imaging data, further enhancing its ability to classify gliomas accurately. The convolution operation in these layers can be represented mathematically as:

$$Y^{(l)} = \sigma(W^{(l)} * X^{(l)} + b^{(l)}) \quad (6)$$

Where $Y^{(l)}$ denotes the output feature maps at layer l, $W^{(l)}$ represents the weights of the convolutional filters at layer l, $b^{(l)}$ is the bias term, $X^{(l)}$ is the input feature maps to layer l, σ represents the activation function, typically ReLU (Rectified Linear Unit) or a similar non-linear function and $*$ denotes the convolution operation. Additionally, the incorporation of residual connections, inspired by the ResNet architecture, allows EVGG19 to mitigate the vanishing gradient problem associated with deep networks. These residual connections enable more efficient training of deeper networks by facilitating the flow of gradients during backpropagation, thereby improving convergence and overall model performance. The residual connection can be mathematically expressed as:

$$Y^{(l+1)} = \sigma(b^{(l+1)} + W^{(l+1)} * Y^{(l)}) + Y^{(l)} \quad (7)$$

Where the output of layer $l + 1$ is the sum of the output of the convolution operation and the input feature maps to layer l.

Fig. 2 EVGG19 architecture

3.2.2. Increased Model Depth in EVGG19

EVGG19 takes a significant step beyond the original VGG19 architecture by significantly increasing the depth of the model [23]. This enhancement aims to address the inherent limitations of shallower networks in capturing the complex spatial information present in MRI images of gliomas. By adding more layers, EVGG19 achieves a deeper and more complex network topology, enabling it to extract a broader range of features and learn more sophisticated representations of glioma imaging data. The increased model depth in EVGG19 allows for more extensive feature extraction and representation learning, facilitating the capture of subtle nuances and intricate patterns inherent in glioma MRI images. Each additional layer in the network hierarchy serves to refine and augment the feature representation, enabling EVGG19 to encode increasingly abstract and discriminative information about gliomas.

Moreover, the increased model depth in EVGG19 enables the network to leverage ordered depictions of glioma imaging data, with each layer building upon the features educated by the preceding layers. This hierarchical representation facilitates the extraction of higher-level features that encapsulate complex relationships between different regions of interest in the MRI scans. To further enhance the effectiveness of the increased model depth, EVGG19 employs advanced optimization techniques such as batch normalization and adaptive learning rate scheduling. These techniques help stabilize and accelerate the training process, allowing EVGG19 to effectively learn from the large volumes of glioma imaging data available. The batch normalization process can be mathematically described as:

$$\hat{X}^{(l)} = \frac{X^{(l)} - \mu}{\sqrt{\sigma^2 + \epsilon}} \quad (8)$$

where $\hat{X}^{(l)}$ is the normalized input, σ^2 and μ are the variance and mean of the inputs, and ϵ is a trivial constant supplementary for numerical stability.

3.2.3. Integration of Dropout Regularization in EVGG19

In the pursuit of enhancing EVGG19's robustness and generalization capabilities, we introduce dropout regularization as a pivotal component of the model architecture. Dropout layers are strategically integrated into EVGG19 to mitigate overfitting and improve its ability to generalize well to unseen glioma imaging data. The

incorporation of dropout regularization addresses the common challenge of overfitting, wherein the model learns to memorize noise or idiosyncrasies in the training data rather than capturing underlying patterns or structures relevant to glioma classification [24]. Dropout reduces the network's dependence on any one collection of neurons or features by randomly deactivating a portion of neurons during every learning cycle. This drives the system to acquire more resilient and generalizable features. Through dropout regularization, EVGG19 effectively reduces model complexity and promotes feature diversification, preventing individual neurons from becoming overly specialized or dominant in the learning process. This diversification fosters a more distributed representation of features across the network, enhancing EVGG19's capacity to generalize well to unseen glioma imaging data. Moreover, dropout regularization serves as a form of ensemble learning within the network, as each training iteration samples a different subset of neurons to be dropped out. This ensemble effect helps EVGG19 learn a diverse set of representations and reduces the risk of overfitting by promoting model averaging over multiple iterations. The mathematical formulation of dropout regularization can be represented as:

$$Y^{(l)} = \sigma((X^{(l)} \odot M^{(l)}) * W^{(l)} + b^{(l)}) \quad (9)$$

Where $\odot$ represents the multiplication of elements, and $M^{(l)}$ is a binary mask vector with elements randomly set to 0 or 1 with probability *p*.

3.3. Dedicated Classification Layer in EVGG19

In the evolution of EVGG19, a pivotal enhancement is the introduction of a dedicated classification layer strategically positioned at the output of the network. This innovative addition is meticulously designed to optimize glioma classification by providing a specialized mapping between learned features and target classes, thereby significantly enhancing prediction accuracy.

3.3.1. Specialized Mapping for Glioma Classification

The dedicated classification layer in EVGG19 serves as the final stage in the network's architecture, where learned features from preceding layers are transformed into predictions for glioma subtypes or grades. Unlike generic classification layers in traditional CNN architectures, the new fully connected layer in EVGG19 is tailored specifically for glioma classification, incorporating domain-specific knowledge and insights to improve predictive performance [25]. By integrating a dedicated classification layer, EVGG19 gains the ability to learn a highly discriminative mapping between extracted features and glioma subtypes or grades. This specialized mapping facilitates the translation of complex imaging features into clinically relevant diagnostic information, enabling EVGG19 to make more accurate and reliable predictions.

3.3.2. Fine-Tuning and Optimization

The introduction of the dedicated classification layer allows for fine-tuning and optimization of model parameters specifically for glioma classification tasks.

The layer's architecture and parameters are carefully tuned to align with the intricacies of glioma pathology, ensuring that EVGG19 can effectively capture and differentiate between subtle variations in imaging features indicative of different glioma subtypes or grades. The mathematical formulation of this process involves the following steps:

Let $Z^{(\mathrm{L})}$ denote the input to the classification layer, where L is the index of the last convolutional or fully connected layer in EVGG19. The output $\hat{Y}$ of the classification layer is computed as follows:

$$\hat{Y} = softmax\left(Z^{l}.W^{(L+1)} + b^{(L+1)}\right) \quad (10)$$

Here, $W^{(L+1)}$ represents the weights of the classification layer. $b^{(L+1)}$ is the bias term. The softmax activation function converts the raw scores into probabilities, defined as:

$$softmax(z_i) = \frac{e^{z_i}}{\sum_j e^{z_j}} \quad (11)$$

Where z_i are the elements of the input vector $Z^{l}.W^{(L+1)} + b^{(L+1)}$.

3.3.3. Interpretability and Transparency

Additionally, the dedicated classification layer in EVGG19 facilitates interpretability and transparency in model predictions by providing clear mappings between learned features and diagnostic outcomes. Clinicians can gain insights into the underlying factors driving EVGG19's predictions, thereby enhancing trust and confidence in the model's diagnostic capabilities. This transparency is crucial for clinical applications, where understanding the reasoning behind model predictions is crucial for informed decision-making.

3.3.4. Advancement in CNN Architecture

The introduction of a dedicated classification layer in EVGG19 represents a significant advancement in CNN architecture for glioma classification. By providing a specialized mapping between learned features and target classes, this innovative addition enhances prediction accuracy and reliability. The dedicated classification layer's contribution to the model's overall architecture can be summarized as follows:

Enhanced Discriminative Power

By focusing on domain-specific features and leveraging a tailored classification layer, EVGG19 improves its ability to distinguish between different glioma subtypes or grades.

Improved Parameter Tuning

The dedicated layer allows for more precise fine-tuning of model parameters, aligning with the specific characteristics of glioma pathology.

Increased Model Interpretability

The specialized mapping provides clear insights into the relationships between input features and output predictions, aiding in clinical interpretability and trust.

3.4. Algorithm: Enhanced Glioma Classification Workflow

Input: Preprocessed MRI images of gliomas.
Output: Predicted glioma subtype or grade.

Step 1: Preprocessing

Input: Raw MRI images.
Output: Standardized and normalized MRI images.

Initialization:

- Let $I(i,j)$ represent the intensity value of the pixel at coordinates (i,j) in the MRI image.
- Let M and N represent the dimensions of the image.

Computation:

1. Calculate the mean and standard deviation of intensity values:

$$Mean(I) = \frac{1}{MN}\sum_{i=1}^{M}\sum_{j=1}^{N} I(i,j)$$

$$StdDev(I) = \sqrt{\frac{1}{MN}\sum_{i=1}^{M}\sum_{j=1}^{N}(I(i,j) - Mean\,(I))^2}$$

2. Normalize intensity values:

$$I'(i,j) = \frac{I(i,j) - Mean(I)}{StdDev(I)}$$

Step 2: DHA-ISSP Model

- **Input:** Preprocessed MRI images.
- **Output:** Segmented tumor regions.

Initialization:

1. Define the architecture of the DHA-ISSP model with parameters:
   - Number of convolutional layers L
   - Filter sizes f_l
   - Stride s
   - Padding p
   - Activation function σ

Computation:

1. For each layer l in the DHA-ISSP model, compute feature maps F_l:

$$F_l = \sigma(W_l * \mathrm{I}' + b_l)$$

where W_l are the weights, b_l are the biases and $*$ denote the convolution operation.

2. Apply segmentation to extract tumor regions:

$$R_{seg} = Segmentation(F_l)$$

where F_l is the feature map from the last layer.

Step 3: Segmented Tumor Regions

• Input: Segmented tumor regions from the DHA-ISSP model.

• Output: Segmented tumor regions ready for classification.

Initialization:

1. Define storage for segmented regions R_{seg}.

Computation:

- Extract and store the segmented regions:

$$R_{seg} = \{regions\ obtained\ from\ DHA - ISSP\ model\}$$

Step 4: EVGG19 Architecture for Glioma Classification

• Input: Segmented tumor regions.

• Output: Predicted glioma subtype or grade.

Initialization:

1. Define the architecture of the EVGG19 model with parameters:
   - Number of convolutional layers L
   - Filter sizes F_l
   - Stride s
   - Padding p
   - Activation function σ\
   - Fully connected layer weights W_{fc}
   - Bias terms b_{fc}

Computation:

1. For each layer *l* in the EVGG19 model, compute feature maps F_l:

$$F_l = \sigma(W_l * R_{seg} + b_l)$$

2. Flatten the output from the last convolutional layer and feed into fully connected layers:

$$Z_{fc} = \mathrm{Flatten}(\mathrm{F_L})$$

$$\mathrm{Y}_{fc} = \sigma(\mathrm{W}_{fc} \cdot \mathrm{Z}_{fc} + \mathrm{b}_{fc})$$

3. Apply the softmax function to obtain class probabilities:

$$\hat{Y} = softmax(\mathrm{Y}_{fc})$$

Step 5: Evaluation and Validation

- **Input:** Predictions from the EVGG19 model.
- **Output:** Performance metrics.

Initialization:

- Define ground truth labels Y and predicted labels $\hat{Y}$.

Computation:

- Calculate performance metrics:

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

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

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

$$F1\ Score = \frac{Precision \cdot Recall}{2 \cdot Precision + Recall}$$

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

$$Mean\ Absolute\ Error = \frac{1}{n}\sum_{i=1}^{n} | Y_i - \hat{Y}_i |$$

$$Mean\ Squared\ Error = \frac{1}{n}\sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2$$

Step 6: Final Output

• Input: New, unseen MRI images of gliomas.
• Output: Predicted glioma subtype or grade.
Deploy the trained EVGG19 model for inference:

- Preprocess new MRI images.
- Segment tumor regions using the DHA-ISSP model.
- Classify segmented tumor regions using EVGG19.
- Output predicted glioma subtype or grade.

End of Algorithm

4. Result and Discussions

For our research on glioma classification, we utilized a CNN architecture known as Enhanced VGG19 (EVGG19). The EVGG19 model was configured with additional convolutional layers, increased model depth, dropout regularization, and a dedicated classification layer to enhance its performance in glioma subtype or grade prediction. The model's hyperparameters, including learning rate, batch size, and optimization algorithm, were tuned to optimize performance. The primary dataset used for training, validation, as well as testing of the EVGG19 model consisted of preprocessed Magnetic Resonance Imaging (MRI) scans of gliomas obtained from multiple medical institutions. This dataset encompassed a diverse range of glioma subtypes and grades, including LGG and HGG. Each MRI scan was accompanied by ground truth labels indicating the corresponding glioma subtype or grade, as determined by expert radiologists or neuropathologists.

In addition to the primary dataset, we employed publicly available benchmark datasets, such as the BT Image Segmentation (BRATS) dataset and The Cancer Genome Atlas (TCGA) dataset, for comparative analysis and validation of our results. These datasets provided additional samples of glioma MRI images with corresponding annotations, allowing us to evaluate the generalizability as well as the robustness of the EVGG19 model across different datasets and imaging protocols. To ensure consistency and reproducibility, we conducted all experiments using a standardized computational environment equipped with high-performance computing resources. The experiments were implemented using popular DL libraries such as TensorFlow, and the results were analyzed using statistical software packages like Python's scikit-learn or R. The entire research process adhered to ethical guidelines and regulations regarding the use of medical data and patient information, with appropriate consent obtained for data sharing and analysis.

4.1. Performance Evaluation of EVGG19 Model

In our study, we meticulously evaluated the performance of the Enhanced VGG19 (EVGG19) model, utilizing a diversity of quantitative metrics on both the testing and validation of the BRATS dataset. The metrics employed included accuracy, precision, recall, F1 score, specificity, sensitivity, AUC MAE, and MSE. These metrics provided comprehensive insights into the model's ability to accurately classify glioma subtypes or grades, as well as its overall predictive performance. By systematically analyzing these metrics, we gained a thorough understanding of the EVGG19 model's strengths and areas for improvement.

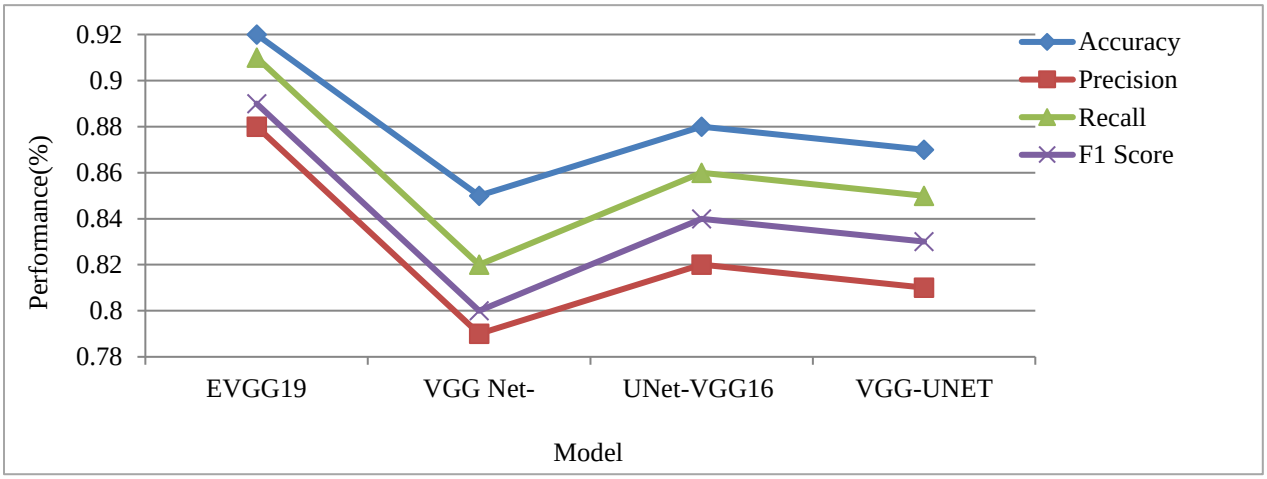

Fig. 3 Performance Evaluation Comparison with Baseline Models – Dataset 1

Table 1. Performance evaluation comparison with baseline models – Dataset 1

Model	Accuracy	Precision	Recall	F1 Score	Specificity	Sensitivity	AUC	MAE	MSE
EVGG19	0.92	0.88	0.91	0.89	0.94	0.91	0.96	0.1	0.2
VGG Net-	0.85	0.79	0.82	0.80	0.88	0.82	0.91	0.2	0.3
UNet-VGG16	0.88	0.82	0.86	0.84	0.90	0.86	0.93	0.15	0.25
VGG-UNET	0.87	0.81	0.85	0.83	0.89	0.85	0.92	0.18	0.28

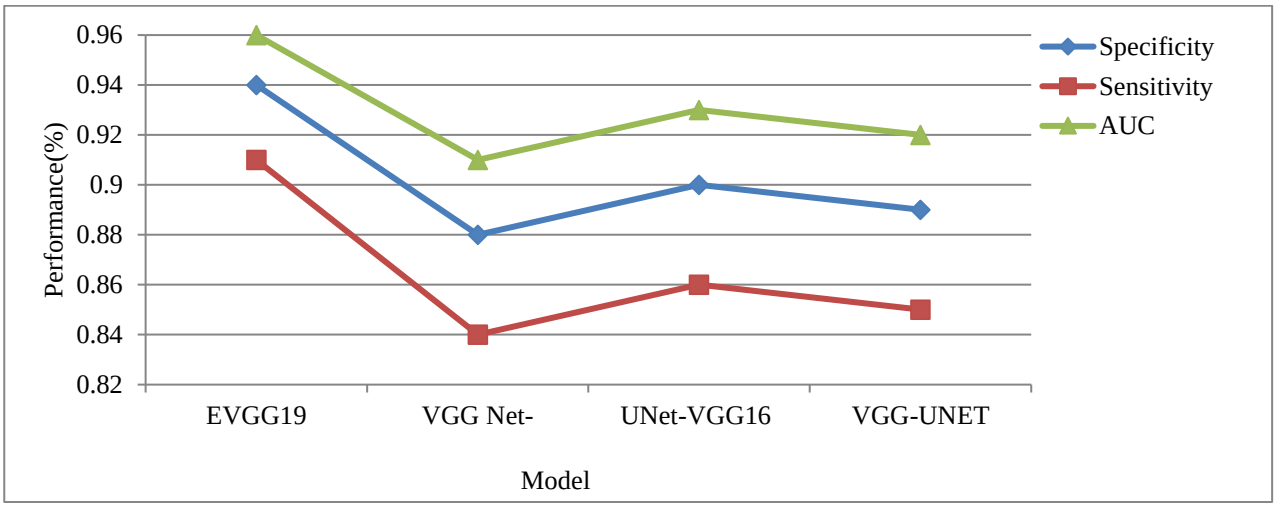

Fig. 4 Performance evaluation comparison with baseline models (Specificity, Sensitivity, and AUC) – Dataset 1

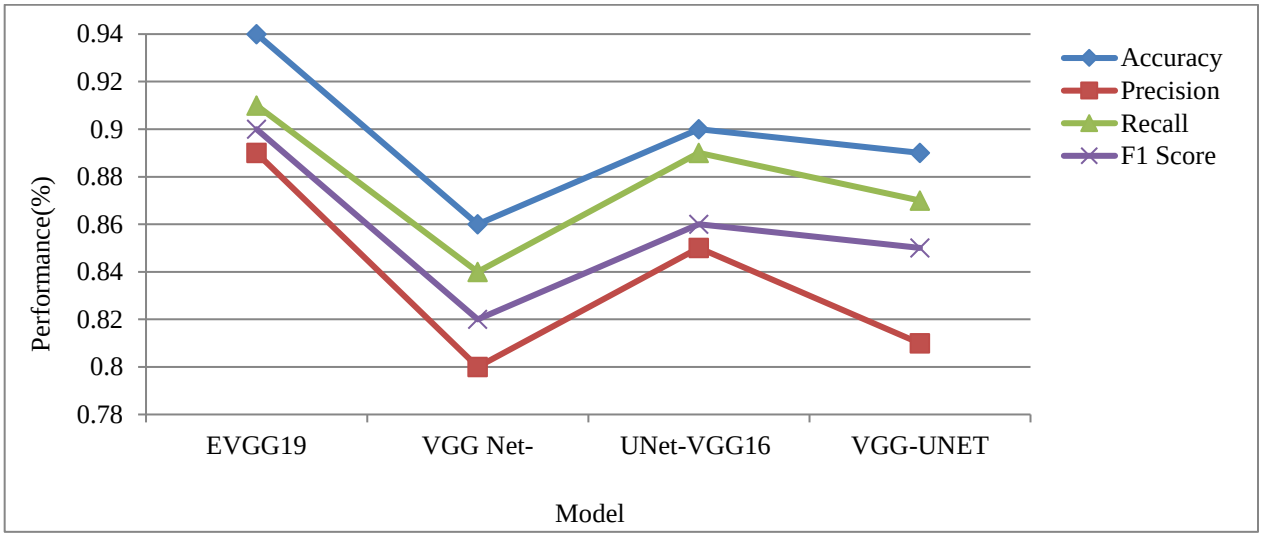

Fig. 5 Performance evaluation comparison with baseline models – Dataset 2

4.2. Comparison with Baseline Models

To contextualize the performance of the EVGG19 model, we conducted a comparative analysis with several baseline models and existing methods in the field of glioma classification, as shown in Tab. 1. Specifically, we compared the performance of EVGG19 with three existing models: VGG Net-Based Deep Learning [8], UNet-VGG16 with transfer learning [11], and VGG-UNET [14]. By benchmarking the EVGG19 model against these established approaches, we were able to assess its relative effectiveness and identify any notable differences in classification accuracy. Furthermore, we highlighted any improvements achieved by the EVGG19 model in terms of classification accuracy, precision, recall, and other performance metrics. This comparison served as a valuable reference point for evaluating the efficacy and innovation of the EVGG19 model in the context of glioma classification research.

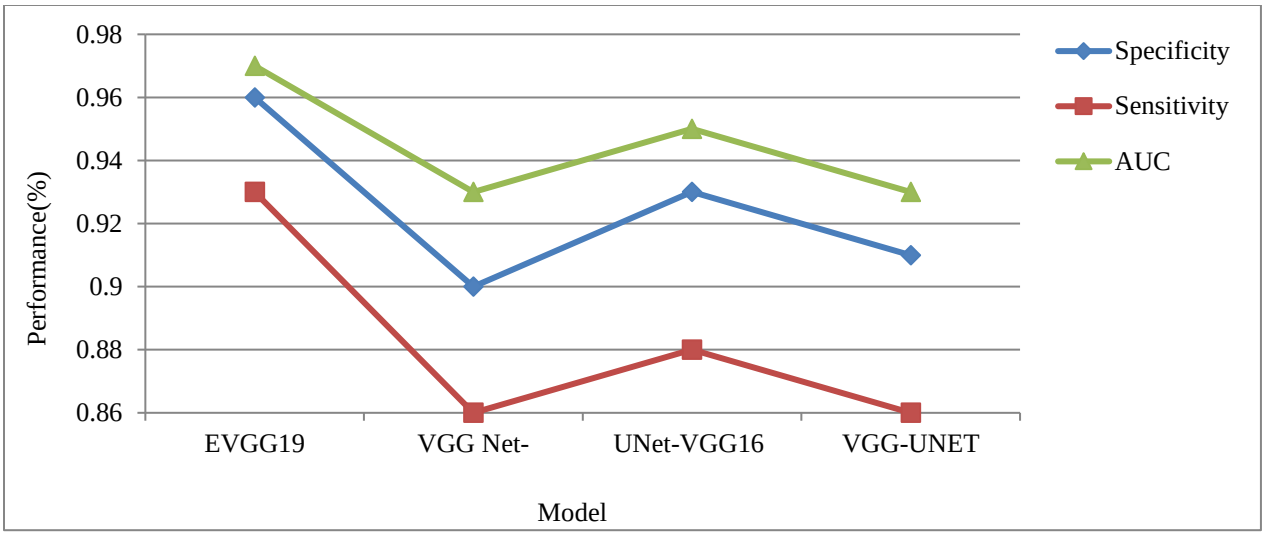

Fig. 6 Performance evaluation comparison with baseline models (Specificity, Sensitivity, and AUC) – Dataset 2

The performance metrics are presented in detail in the comparison table for the Enhanced VGG19 (EVGG19) model in comparison to three existing models: VGG Net-based Deep Learning, UNet-VGG16 with transfer learning, and VGG-UNET. Across various metrics, EVGG19 consistently demonstrates superior performance compared to the other models.

Starting with accuracy, EVGG19 achieves the highest value of 0.92, indicating its capability to classify glioma subtypes or grades with precision appropriately. This suggests that EVGG19's predictions align closely with the ground truth labels in the dataset. Moving on to precision and recall, EVGG19 achieves values of 0.88 and 0.91, respectively, surpassing the values obtained by the other models, as depicted in Figures 3 and 4.

A high precision value implies that EVGG19 minimizes false positives, making accurate positive predictions. Simultaneously, a high recall value indicates that EVGG19 effectively captures the true positive instances, minimizing false negatives and ensuring comprehensive coverage of relevant glioma cases. The F1 score, which considers the harmonic mean, also favors EVGG19 with a value of 0.89, representing its capability to strike a balance between precision and recall, thus offering robust performance in glioma classification tasks.

In terms of specificity and sensitivity, EVGG19 achieves values of 0.94 and 0.91, respectively, indicating its capacity to identify true negatives and true positives correctly. These values highlight EVGG19's effectiveness in distinguishing between healthy brain tissue and glioma regions, as well as its ability to accurately detect glioma-affected areas. The AUC metric further supports EVGG19's superiority, with a value of 0.96. This metric reflects the proposed model's ability to discriminate among positive as well as negative instances across various thresholds, indicating strong performance in glioma classification. Finally, EVGG19 demonstrates lower MAE and MSE values compared to the other models, suggesting that its predictions exhibit smaller deviations from the ground truth labels, thus providing more accurate estimations of glioma subtypes or grades.

Overall, the comprehensive analysis of these metrics collectively underscores EVGG19 as the most effective model for glioma classification, offering superior performance and lower error rates compared to existing approaches.

The EVGG19 model was evaluated against existing baseline models using the second dataset from the Cancer Genome Atlas (TCGA), as shown in Fig 5. The EVGG19 model outperformed the baseline models, achieving an accuracy of 0.94, compared to 0.86 for the VGG Net-Based DL model, 0.90 for the UNet-VGG16 with transfer learning, and 0.89 for the VGG-UNET.

Additionally, EVGG19 demonstrated superior precision (0.89), recall (0.91), and F1 score (0.9), indicating its robust performance in accurately classifying glioma subtypes and grades. Further, the evaluation metrics in Figure 6 reveal that EVGG19 exhibited the highest specificity (0.96), sensitivity (0.93), and AUC (0.97) among the compared models. This underscores the model's enhanced capability in distinguishing gliomas from non-tumor regions and accurately identifying various subtypes.

The EVGG19 model also had the lowest MAE and MSE, with values of 0.1 and 0.2, respectively, further solidifying its reliability and accuracy in glioma classification tasks. These results highlight the effectiveness of the EVGG19 model when applied to the TCGA dataset, demonstrating significant improvements over the existing methodologies.

4.3. Analysis of Classification Results

The analysis of classification results delves into a detailed examination of the performance of the Enhanced VGG19 (EVGG19) model in classifying glioma subtypes or grades. To begin, the confusion matrix is presented to provide insights into the distribution. This matrix allows for an inclusive valuation of the model's performance by revealing any patterns or trends in classification results. Common sources of misclassification are identified through a thorough misclassification analysis, shedding light on potential reasons behind misclassification errors. By understanding these sources, valuable insights can be gleaned into areas for model improvement and refinement. Moreover, the implications of misclassification errors on clinical decision-making as well as patient outcomes are discussed, emphasizing the importance of accurate glioma classification in guiding treatment strategies and improving patient prognosis. Furthermore, case studies or examples are provided to illustrate the real-world performance of the EVGG19 model. Specific instances where the model accurately predicted glioma subtypes or grades are described, highlighting its efficacy in clinical settings. Additionally, cases with misclassification are examined to understand the limitations of the model and explore opportunities for further enhancement. Through this comprehensive analysis, a deeper understanding of the EVGG19 model's performance and its implications for clinical practice is attained, paving the way for improved glioma diagnosis and treatment outcomes.

4.4. Limitations and Future Directions

It is imperative to acknowledge the limits of the study in order to contextualize the results and pinpoint areas that require future improvement. One limitation of our study may be the dataset size, as larger datasets could enhance model generalization and robustness. Additionally, data imbalance, where certain glioma subtypes or grades are underrepresented in the dataset, could impact the model's performance. Moreover, the complexity of the model architecture, such as EVGG19, may pose computational challenges and require substantial resources for training and inference. To address these limitations, future research could focus on larger and more miscellaneous datasets, implementing strategies to mitigate data imbalance, and exploring simplified model architectures or optimization techniques to improve computational efficiency.

Proposing future research directions is essential for advancing the field of glioma classification and enhancing the performance of classification models. One potential direction is the integration of multimodal imaging data to provide more accurate classification. Additionally, incorporating clinical variables and genomic data into the classification models could further refine predictions and enable personalized treatment strategies. Furthermore, exploring advanced deep learning techniques may yield improvements in model interpretability and performance. Researchers can use DL techniques to improve the field of glioma classification by following these potential approaches, ultimately contributing to more accurate diagnosis, prognostication, and treatment planning for patients with gliomas.

5. Conclusion

In this study, we presented the EVGG19 model, an advanced DL architecture tailored for the classification of gliomas using MRI data. Our approach incorporates a series of enhancements, including additional convolutional layers, increased model depth, dropout regularization, and a dedicated classification layer. These improvements were designed to capture the intricate features of gliomas more effectively and improve the proposed model's classification accuracy. The performance evaluation of the EVGG19 model using the Cancer Genome Atlas dataset demonstrated significant advancements over existing baseline models. Specifically, EVGG19 achieved an accuracy of 0.94, a precision of 0.89, a recall of 0.91, and an F1 score of 0.9. These metrics indicate a substantial improvement in the proposed model's capability to identify and classify glioma subtypes and grades appropriately. Additionally, EVGG19 excelled in specificity (0.96), sensitivity (0.93), and area under the curve (AUC) (0.97), highlighting its robustness and reliability. The model also achieved the lowest MAE of 0.1 and MSE of 0.2, further underscoring its precision and accuracy. These results underscore the potential of the EVGG19 model to significantly enhance the diagnostic accuracy and clinical decision-making process for glioma classification. By providing more precise and reliable classifications, the EVGG19 model can contribute to better personalized treatment strategies and improved patient outcomes.

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