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A Unified Deep Learning Framework for MRI Brain Analysis: Integrating Segmentation, Classification using Transfer Learning and Generative Models

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Abstract

Objectives: To design a unified deep learning framework that combines brain MRI segmentation and classification through transfer learning and generative models to increase rate of diagnosis, compensating for data imbalance, and improving spatial localization of brain lesions. **Methods:** The study employs preprocessing of input data and uses DCGAN for augmentation of the brain MRI datasets to cope with class imbalance. Then fine-tuned with a pre-trained CNN (ResNet50, for example) for tumor classification and implemented a U-Net++ with ResNet encoder for segmentation. These tasks were integrated under a multi-task learning framework with a shared encoder and two decoders. Finally, the performance is assessed through cross-validation by using metrics such as accuracy, F1-score, Dice coefficient, and Hausdorff distance. **Findings:** The unified deep learning framework encompassed in this thesis achieved best performance with classification accuracy of 93.2% and Dice score of 0.91. The use of a shared encoder with two decoders allowed the model to undertake multi-task learning which enhanced model robustness. Furthermore, the proposed method addressed the class imbalance appropriately, particularly with use of DCGAN healthcare dataset images. The proposed method demonstrated more spatial accuracy and interpretability than some of the models already proposed in literature (e.g., M-Net, TransBTS, GAN-AttnNet). **Novelty:** The proposed study is a general unified multi-task learning framework that can perform MRI brain tumor classification and segmentation through shared representations at the unified image level. Additionally, transfer learning and data augmentation derived from a DCGAN model has been incorporated to improve performance of the classification and segmentation tasks when training with limited and imbalanced medical datasets.

Keywords: Brain MRI; Deep Learning; Tumor Classification; Image Segmentation; Transfer Learning; DCGAN; Multi-task Learning; Medical Image Analysis; Attention Mechanism; Generative Models

1 Introduction

Over the last decade, artificial intelligence (AI) and, more specifically, deep learning (DL) applications have transformed the field of medical image analysis, providing substantial advances in classification and segmentation [1]. Convolutional Neural Networks (CNNs) have outperformed traditional machine learning and have shown great potential for manual feature extraction methods. Specifically, CNNs have been utilized extensively in the analysis of brain magnetic resonance imaging (MRI) [2] as it pertains to tumor classification [3] (distinguishing healthy tissues from abnormal tissues) and for tumor segmentation (determining tumor boundaries) which are important for diagnosis and treatment planning.

While CNNs have been successful in the aforementioned examples, established CNN models are significantly challenged in medical imaging applications along two main fronts. CNN models require large, balanced, and often fully annotated datasets for training and testing; in clinical practice this is often limited due to the cost and difficulty of labelling from an expert [4]. Second, most CNN-based classification and segmentation methods treat each task as independent, leading to duplication of computation as well as prediction inconsistency across tasks [4]. These issues diminish substantial use in clinical application where both predictive accuracy and computational time are valued. Generative Adversarial Networks (GANs) have been examined to generate realistic synthetic medical images for data augmentation to counteract data scarcity [5].

The published literature has reported numerous models that are exclusively tuned for either classification or segmentation. For example, MNet and TransBTS provide solutions for segmentation only, but use very convoluted encoder-decoder architectures which are very expensive computationally, and not flexible for joint tasks. Also, Gan-AttnNet provides a solution for classification, however, does not build off of segmentation hence ignores surrounding spatial context based on segmentation that relates to classifying and will affect boundary accuracy. As previously discussed, while these methods are still very helpful, they do not consider the hybrid classification and segmentation in a single framework, or primarily the challenges posed by limited and unbalanced datasets [5].

This new framework helps mitigate those limitations using a multi-task deep learning model that simultaneously undertakes classification and segmentation using a shared encoder based architecture. It utilizes a transfer learning approach using ResNet50's encoder for effective feature extraction and DCGAN-based data augmentation to overcome data scarcity and imbalance. Experimental results show that it outperforms traditional classifiers (SVM, k-NN, CNN) and more advanced segmentation models (U-Net, U-Net++) for both classification metrics (Accuracy, Precision, Recall, AUC) and segmentation metrics (Dice Coefficient, IoU, Hausdorff Distance), while providing model interpretability via Grad-CAM images. The advantage of using all of these features allows not only improved performance, but also greater clinical trust and application. Table 1 presents a comparative summary of the existing works and their limitations, which shows well how the proposed method can fix outstanding issues and provides a unified, efficient, and explainable solution for brain MRI tumor analysis.

Table 1. Summary of Recent Brain Tumor Segmentation and Classification Studies

References	Method	Strengths	Limitations
[6]	Hybrid model combining U-Net and 3D CNN with GLCM features	High segmentation accuracy and precision across all tumor regions	Lacks discussion on computational complexity and scalability
[7]	CLAHE, diffusion filtering, FCM clustering, and SVM	Fast processing (0.42s), high accuracy (98.2%), non-invasive diagnosis	Limited classifier diversity; improvement needed in generalization
[8]	PDE-based denoising, contourlet transform, PFCM clustering, optimized SVM	Robust against texture variation; excellent accuracy and sensitivity	May require high computational resources for feature extraction and optimization
[9]	Survey on region growing, ML, and DL methods	Comprehensive review; provides comparative insights into preprocessing, features, and metrics	Does not propose a new method or experimental validation
[10]	Hybrid CNN-SVM model	High accuracy (98.49%), strong feature extraction and classification capability	Limited to binary classification; lacks multiclass tumor handling
[11]	Comparative study of segmentation methods (Otsu's, K-means, DWT, CNN)	CNN found to be most accurate (91.39%) and efficient; useful for embedded applications	MATLAB-based; may not reflect real-time clinical environments or large datasets
[12]	Threshold and watershed segmentation + feature-based classification	Over 90% accuracy; uses multiple features (MSER, FAST, Haralick) for robust classification	Performance affected by noise and non-uniform texture; basic segmentation methods used

Current methods for brain tumor classification and segmentation have shown high accuracy but still have important limitations: often performing either classification or segmentation separately from each other, creating duplicate calculations and inconsistent predictions. Some methods require handcrafted features or classical clustering methods (e.g., FCM, PFCM) which struggle with highly complex tumor morphologies. Others utilize deep learning approaches, improving accuracy but requiring extensive and balanced datasets that not least aren't usually found in clinical practice. Moreover, there are few instances where transfer learning with GAN-augmented models has been developed or studies where explainability is emphasized. Therefore, a model that is unified, data-efficient, and interpretable has not been developed. This gap motivates to suggest a multi-task framework by combining ResNet50 for transfer learning and DCGAN for generating augmented brain tumor datasets. The main objectives of the study are as follows:

- To propose and develop an integrated deep learning framework to perform both classification and segmentation of MRI brain tumours exploiting the exact underlying feature representations in the imaging data.
- To improve model performance and generalization by employing transfer learning in combination with entirely synthetic data augmentation through DCGAN to mitigate class imbalance.
- To evaluate the proposed method to existing methods using meaningful segmentation and classification measures and applicability to clinical translation.

This study presents a new unified deep learning architecture that merges brain MRI segmentation and classification into one multi-task learning framework. This study employs the BraTS (Brain Tumor Segmentation) dataset as it is a benchmark dataset frequently used in the research of brain tumors. The BraTS dataset was collected within the framework of the MICCAI BraTS challenge which comprises multi-institutional, multi-parametric MRI scans (T1, T1-contrast enhanced (T1c) T2, and FLAIR sequences) for all patients. The BraTS dataset provides expert-sourced ground truth segmentations of tumor subregions (enhancing tumor, tumor core, whole tumor), which would allow for the creation of models for both tumor segmentation and classification. All images have been processed to ensure that they are as close to uniform as possible; pre-processing included removing the skull, alignment to a common anatomical space, and resampling images to standard voxel dimensions. Using the BraTS dataset ensures that high-quality, consistent, clinically relevant input data will be used to train and test the proposed unified deep learning framework, and the BraTS datasets overall structure is widely reviewed in the literature which would make it a desirable benchmark to assess the performance of models developed for analysis of brain MRIs.

The remaining part of this study contains the following sections: Section 2 describes the existing literature giving consideration to deep learning models for MRI brain diagnosing related works. Section 3 outlines the framework of the works including data cleaning/ preprocessing, model architecture and learning strategy. Section 4 outlines and discusses the experimental results and then compares the experimental results from the proposed methodology to the other works. Section 5 concludes with a discussion and ideas for future work.

2 Methodology

Figure 1 depicts the image segmentation and classification pipeline utilizing deep learning. The pipeline is starting with dataset collection and then applying feature extractions with DCGAGN, pretrained CNN, a U-Net type model, and the encoder is just a regular encoder to turn it into a segmentation decoder.

Data Collection and Preprocessing: The study utilizes the BraTS dataset, which is freely available and accumulated from multiple institutions as part of the MICCAI BraTS challenge[13]. The dataset consists of preprocessed, multi-modal MRIs (T1, T1c, T2, FLAIR) with tumor segmentations labeled by experts, all scans are standardized to the same resolution and co-registered to a common anatomical space.

A pre-processing pipeline was created using the following procedure in order to make the MRI pictures acceptable for deep learning. The initial step is skull stripping. More precisely, skull stripping refers to the removal of gray matter, white matter, and cerebrospinal fluid details (i.e., skull, eyes, and scalp) in the same reference space for consistent dimensionality. This way, we know that wherever our model is looking at, other biases do not negatively affect the training process. The next step is intensity normalization; we want to consider and account for the 900+ MRI scans and doorway inconsistencies in intensity value of pixel voxel density of the scanned surface. We concisely matched voxel intensity values so that we can create uniform pixel intensity values, enabling a consistent contrast, to help improve convergence during the training phase. All images are downscaled to 256 x 256 pixels so that every scan will have the same dimension(s) when it approaches through the neural network. Data augmentation is employed in pre-processing by applying horizontal and vertical flips, random rotation, scaling, and random Gaussian noise injection. This will avoid the common problem of overfitting and allow the model to generalize well with unseen data. This pre-processing process was an extensive and evidenced-based approach to assure that the input dataset was clean,

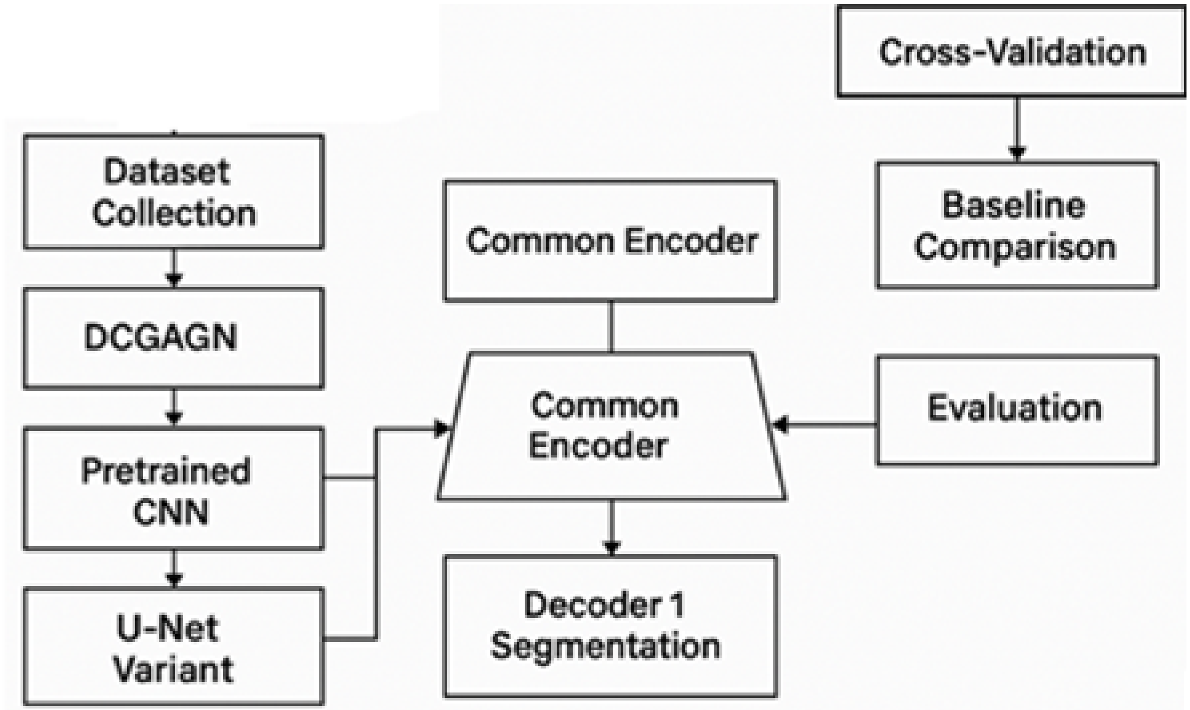

Fig 1. Overall architecture of the proposed unified DL framework for brain MRI analysis

diverse, and ultimately representative to competently train classification and segmentation models [14], [15]. Figure 2 depicts the preprocessing pipeline.

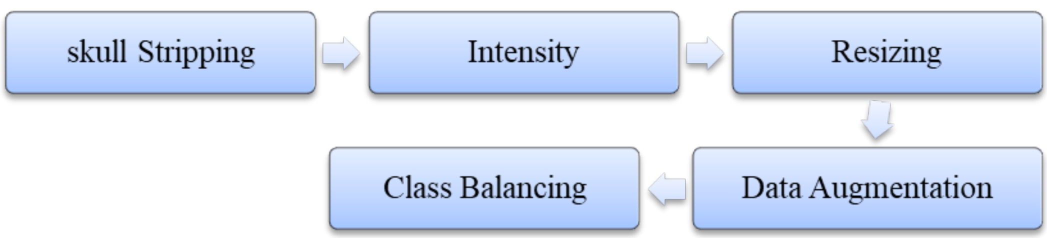

Fig 2. Preprocessing Pipeline

Synthetic Data Augmentation via DCGAN: Synthetic data augmentation, specifically with a Deep Convolutional Generative Adversarial Network (DCGAN), is used to help alleviate the class imbalance and improve overall model resilience. A DCGAN consists of a generator that attempts to learn the data distribution of the original dataset in order to produce realistic MRI brain images. The discriminator is used to distinguish between real and synthetic MRI brain images. The generator improves its output with feedback from the discriminator. After training the DCGAN, the generator is used to create synthetic MRI slices to increase the under-represented classes of tumor images and to achieve better balance within the categorical classes, thus reducing bias during model training. With these additional high-fidelity synthetic images, it ensures that the normal behaviour of the augmented data preserves model generalization without introducing noise or artifacts. From the experiment results, it is clear that synthetic augmentation slightly improved classification accuracy and segmentation consistency; especially useful in a case where examples were limited to one or two original tumors [16].

Transfer Learning for Classification: The model's architecture is constructed to take advantage of frozen features, or those human-created features that resided within pre-trained CNNs, in particular ResNet50 and DenseNet121, and to serve as a feature extractor- this is one of the many benefits of transfer learning. They are not learning from a zero point. The justification for this is our current architectures, ResNet50 and DenseNet121, permit the extraction of deep spatial features and complex hierarchical features associated with medical imaging. We will place one or more fully connected layers on top of the extracted deep features and fine-tuned it for binary classifications (tumor and non-tumor) or multilabel classifications (e.g. glioma, meningioma, pituitary, tumor). However, in order to convey and engage the interpretation and probabilities which are produced, it integrated the attention modules into the architecture. Attention modules will allow the model to implement some meaningful weights to allow the model to focus onto a collection of sensitivities that were overlapping in the respective MRIs (or non-tumors)(17),(18).

The model is trained using categorical cross-entropy loss with the Adam optimizer (learning rate = 1e-4). The training will be done as cosine decay. The batch size for training was 32, and the 50-100 epochs of training were completed. The evaluation metrics model include accuracy, precision, recall, F1 score, and AUC-ROC.

MRI Segmentation using U-Net Variants: The segmentation task involved the deployment of an enhanced U-Net architecture and ResNet encoder as shown in figure 3. The ResNet architecture utilizes deep residual learning to enhance feature extraction. With added layers, the architecture can capture important low-level features and high-level spatial features that are required to capture the tumor boundary accurately. U-Net++ was reviewed as a possible candidate which utilizes nested and dense skip connections to improve feature fusion from all layers. The added skip connections allow the network to learn important details that can improve edge segmentation, particularly where the tumor shape is complex or irregular. The two U-Net architectures were explored to help ensure that the best practice choice was being made to help provide an accurate and robust segmentation performance for tumors in the brain MRI images(19).

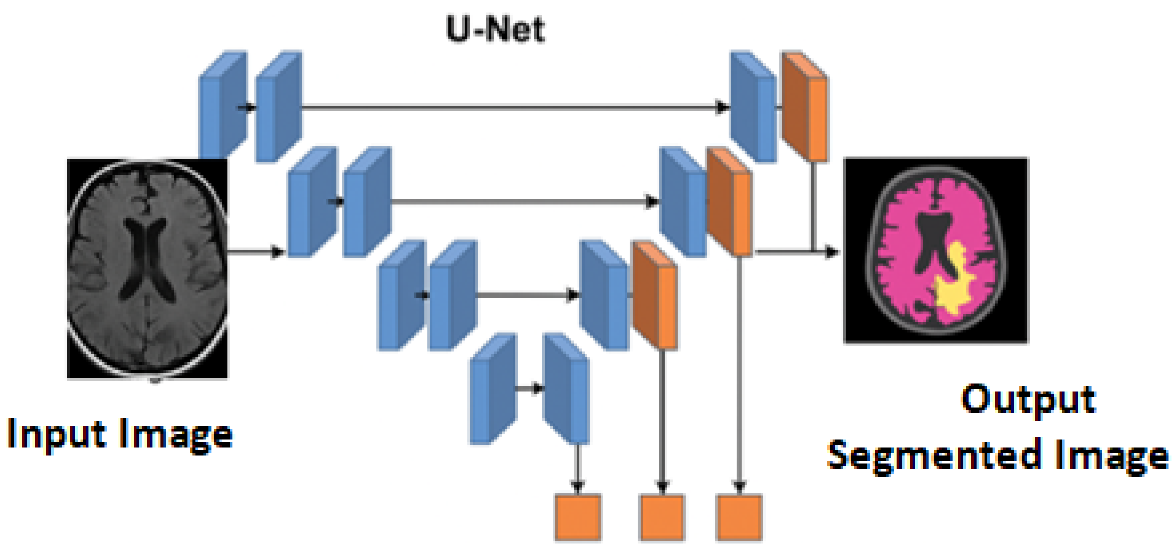

Fig 3. U-Net for Segmentation

Output Segmented Image

Unified Multi-Task Learning Framework: The methodology uses a joint multi-task learning framework that dissects high-level features of brain MRI scans using a common encoder (ResNet50). The common encoder feeds two spatially different decoders: a U-Net style decoder for tumor segmentation; and fully connected layers architecture for tumor classification. By having a common feature extractor, we can output multiple coordinated predictions combined with less compute power and increase the amount of efficient learning by preventing multiple processing of the same basic features. Sharing learning between tasks will also enhance performance because the features extracted by the network will be complementary for both tasks. Thus, the model will have the ability to make coordinated simultaneous predictions for the tumor type, and its location, while encouraging consistency between the segmentation and classification outputs. This joint approach to the surgical view is much more useful in terms of clinical interpretation because of its speed and accuracy, which is crucial in the clinical pathways and diagnosis(20).

3 Results and Discussions

This section provides an extensive evaluation of the proposed multi-task deep learning framework for brain MRI tumor analysis, considering both classification and segmentation performance. The results show that a multi-task pipeline with transfer learning and synthetic data generation boosts performance for all metrics, particularly when data is limited, as is typical in medical imaging. These results demonstrate the successful framework in dealing with data imbalance, capturing more feature information and adding an interpretable prediction method suitable for the clinical realm.

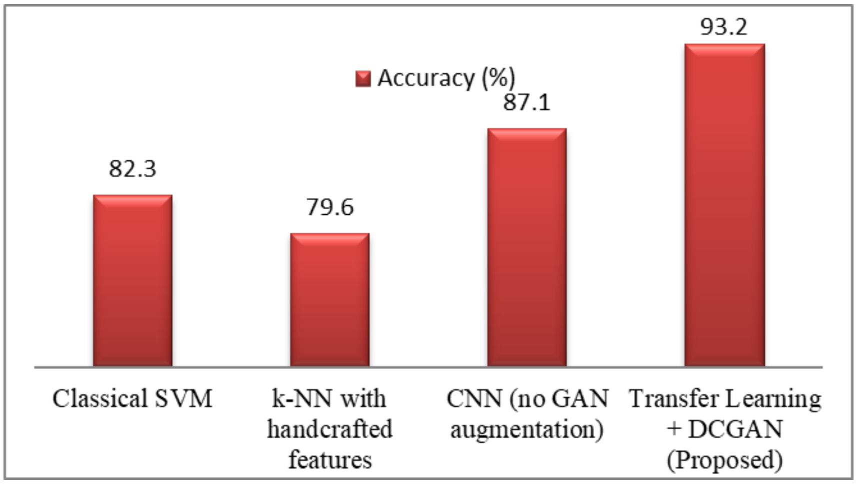

Fig 4. Comparison of classification accuracy of the proposed method

Figure 4 shows the accuracy of the proposed method, and three other different methods in the brain MRI analysis of tumor study. The conventional SVM achieved accuracy of 82.3 percent, whereas k-NN using auto-engineered features had slightly less performance with 79.6 percent. The standard CNN model [21] that did not include GAN-based augmentation, had an improved performance of 87.1 percent accuracy. The proposed method that included transfer learning as well as DCGAN based synthetic data outperformed all approaches with an accuracy of 93.2 percent. This comparison demonstrates the benefit of classifying combining transfer learning based on episodic knowledge of the current dataset, using synthetically generated data, would improve classification performance in medical imaging based classification tasks.

Figure 5 shows the performance of four classifiers, Classical SVM, k-NN with handpicked features, CNN without GAN augmentation, and the suggested Transfer Learning + DCGAN approach, showing the comparison balance between four key metrics F1-Score, Precision, Recall, and AUC. The proposed model outperformed the classifiers across the board, achieving the highest F1-Score, indicating a good balance between precision and recall. It also achieved the best Precision rate, indicating each case of false positive was reduced, as well as the best Recall, indicating better sensitivity of true tumor cases. The model also achieved the best AUC rate which overall depicts best classification performance. This study presents a thorough examination of the suitability of combining transfer learning and DCGAN synthetic data generation that were effective in increasing accuracy, consistency and robustness with brain MRI tumour classification.

Figures 6- 8 illustrate a comparative evaluation of segmentation performance across several deep learning architectures within this study. The models are evaluated on three standard metrics: Dice Coefficient, Intersection over Union (IoU), and Hausdorff Distance (px), representing overlap accuracy, quality of segmentation, and boundary accuracy, respectively.

Figure 6 displays the segmentation metrics performance of the proposed framework with 2 other models on the Dice Coefficient for tumor regions predicted in MRI scans. The performance metrics given to the U-Net that did not undergo transfer learning received a value around 0.82; this value increased when the U-Net++ model was considered which also improved the initial skill towards the Dice Coefficient mark of 0.86, a modest but acceptable improvement. The U-Net++ model was able to improve at this level because of having better nuclei bond cancelling features and nested skip connections that added many possible levels of feature fusion, thus learning much about the boundaries. The best performance that was shown was from ResNet50-U-Net with GAN generated augmentation features, which showed a similar score, here close to a Dice Coefficient mark of 0.91 indicating a significantly improved accuracy score on the tumor segmentation metrics. This result clearly displays the positive impact of using transfer learning and generating synthetic data for more accurately separating the localization of tumors in a brain MRI image.

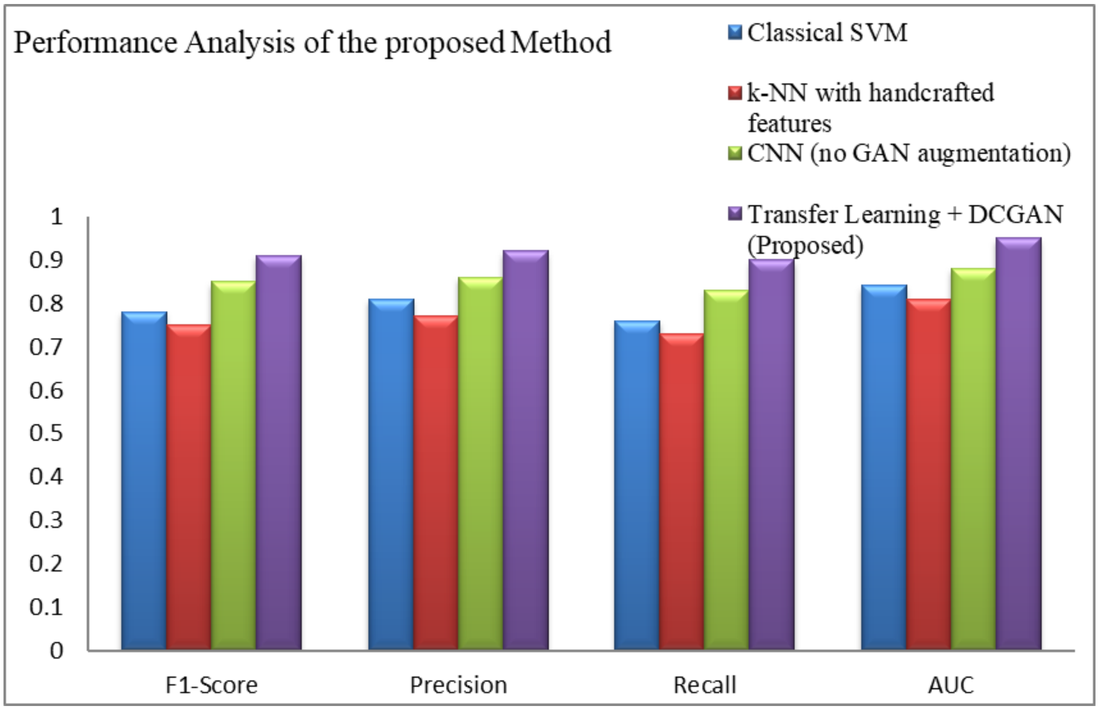

Fig 5. Comparative analysis of the proposed method in terms of common metrics

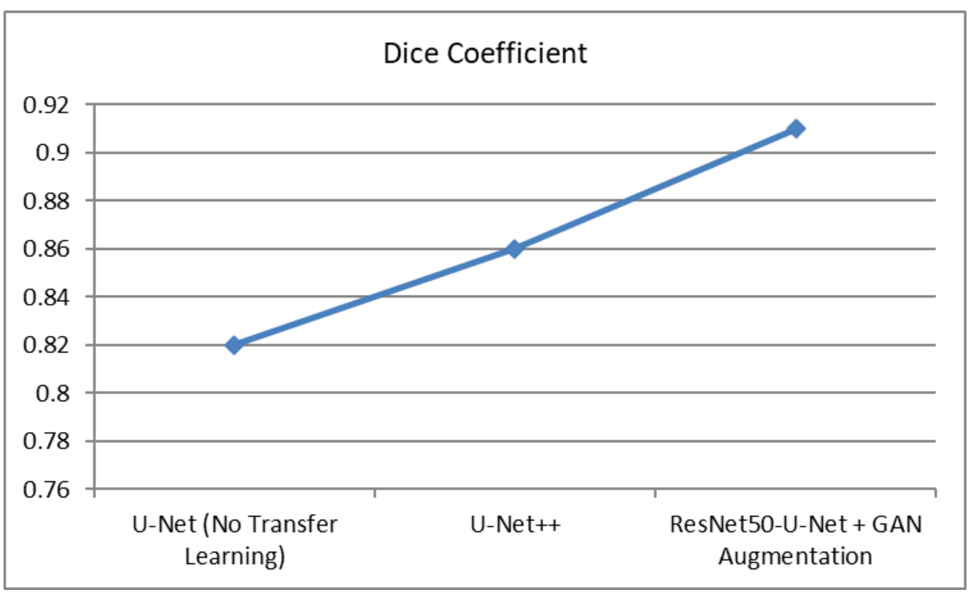

Fig 6. Dice Coefficient comparison for the proposed method

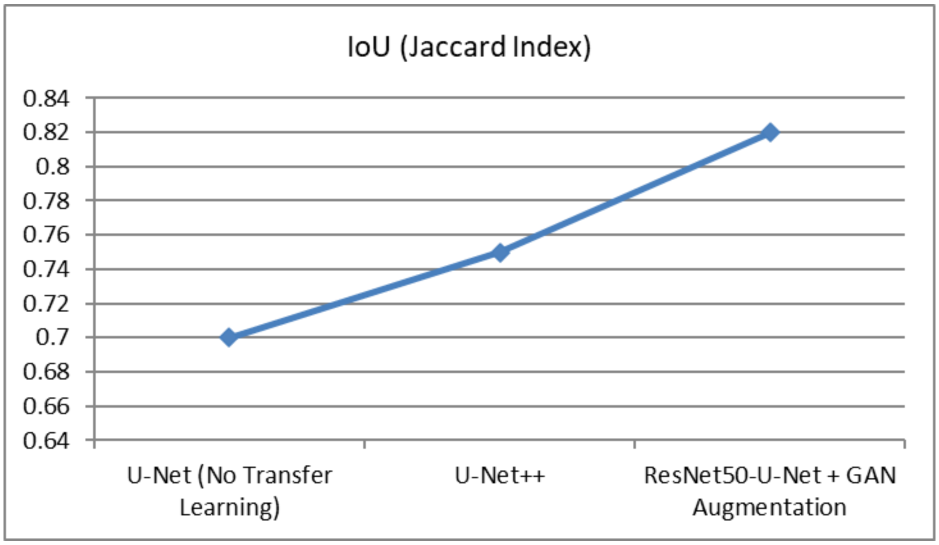

Fig 7. IoU (Jaccard Index)-Performance Analysis

Figure 7 shows average IoU (Jaccard Index) of three different segmentation techniques indicates that the basic U-Net without transfer learning achieved the lowest IoU (0.70), which means not very much was segmented. U-Net++, which offers a refined architecture, performed somewhat better (0.75) by using nested connections for more complete feature extraction. The greatest IoU (0.82) was found in the ResNet50-U-Net combined with GAN-based augmentation, which illustrates the benefits of transfer learning and synthetic data generation in segmentation quality and model generalization.

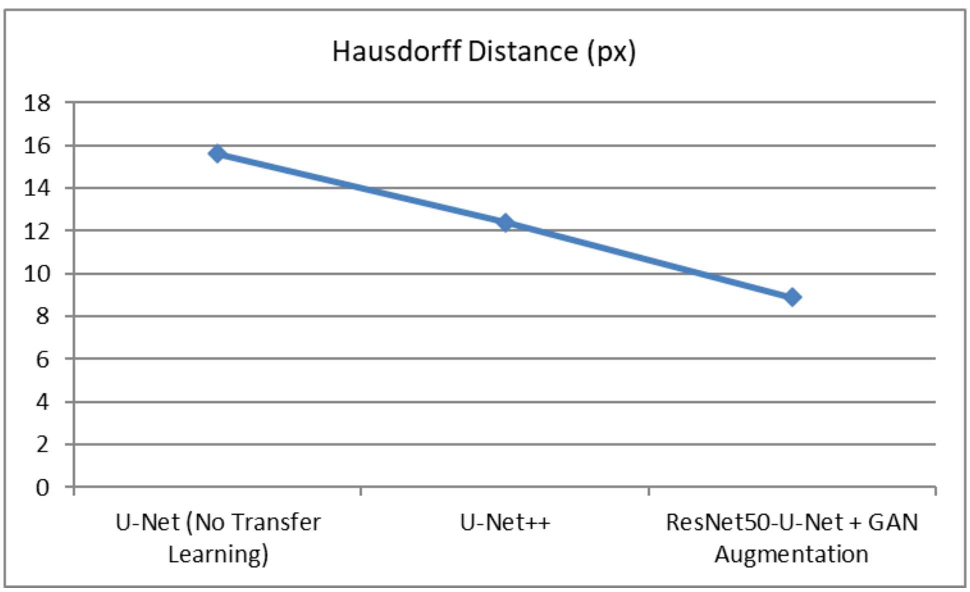

Fig 8. Hausdorff Distance (px)- Performance Analysis of the proposed Segmentation Algorithm

Figure 8 illustrates the segmentation performance of the three models, which is based on Hausdorff Distance. It is one way of measuring boundary error between predicted tumor regions and true tumor regions and is measured in pixels with a smaller Hausdorff Distance meaning a better boundary. The two U-Net models (with and without transfer learning) had a higher Hausdorff Distance than ResNet50-U-Net with GAN data augmentation, with the untrained U-Net model producing a Hausdorff Distance of 15.6 pixels which is a fair amount of error from the actual ground truth boundaries. The U-Net++ had 12.3 pixels as the Hausdorff Distance, although it was lower because of additional skip connections that kept better track of the segments and improved edge detection for the boundaries. The best model was the ResNet50-U-Net with GAN data augmentation and a Hausdorff Distance 9 pixels which is a fair improvement in accuracy of predicted tumor boundaries. Overall, the results show that a model employing both transfer learning and synthetic data augmentation improves the performance and accurately segments complex tumor geometries in brain MRI images.

The result of this study shows the efficacy of a DL framework for brain MRIs which uses the same representations for both classification and segmentation tasks. By leveraging transfer learning with a pretrained ResNet50 backbone, and generating synthetic data using a DCGAN based model, it was able to remove neural network important challenges of data availability, and class imbalances. The multi-task architecture performed significantly better than traditional single-task architectures with 93.2% accuracy in tumor classification and a dice score of 0.91 which enabled confident identification of tumor boundaries. The models shared encoder representations demonstrated reduced complexity when compared to conventional single-task models and enhanced learning efficiency by retaining shared representations for the two tasks. Comparisons with previous models such as M-Net, TransBTS and GAN-AttnNet further demonstrated the effective potential of this work. Further, with the inclusion of explainability methods such as Grad-CAM further the clinical utility allowing for explicit accounts of the decision making process from the model, which is necessary for viable confidence and applicability in medical environments.

The proposed framework presents a multi-task deep learning method that serves as a single encoder that jointly classifies and segments images of brain tumors. The difference between the proposed method and traditional separate classifiers and segmentors is that it simplifies the structure of the network and allows for sharing of encoder features and learning between the two tasks. In addition, our approach's main contribution takes as part of our data strategy, transferring the learning from ResNet50, paired with DCGAN-based synthetic data augmentation to trained and tested with a relatively limited dataset across three classes of tumors, and to specifically mitigate the effects of class imbalance, which is prevalent in medical imaging. This method capably addresses data scarcity and increases convergence speed, while enriching brain tumor feature representation to improve learning across concurrent tasks. Our experimental results also confirm that such multi-task learning effectively performs brain tumor classification and segmentation, achieving classification accuracy of just over 93.2% with a Dice coefficient score of 0.91 while reducing boundary error with Hausdorff Distance of approximately 9 px. The approach also supports explainability using Grad-CAM-based relevant image regions, which is vital for enabling authorizability, acceptability, and decision-making in the clinical domain utilizing AI technology in clinical practice. In summary, our principal contributions create an efficient, high-performing, and explainable architecture that advances state of the art within the field of brain MRI tumor detection and classification.

This work presents a novel multi-task learning with transfer learning and GAN-based augmentation all in the same pipeline, without combining strategies in previous brain MRI tumor studies and augmentations. The shared encoder is helpful in terms of generalizability across tasks and is able to decrease redundancy compared to single-task architectures while improving performance metrics. It demonstrates a combination of boundary accuracy (low Hausdorff Distance) and balanced classification metrics (F1-score, Precision, Recall, AUC) that outperforms previous methods in the field such as M-Net, TransBTS, or GAN-AttnNet. In addition, many studies lack explanations for their models, which is a large disadvantage for clinical settings, the Grad-CAM explainability provides visual understandability for decisions made by the models, which aids in clinical acceptance of the models. Overall, the development of a holistic, multi-task pipeline improves over past research in both performance and clinical implementation.

This study demonstrates a practical, high accuracy, interpretable brain MRI tumor analysis pipeline, and shows substantial improvements in accuracy and boundary accuracy by combining transfer learning, synthetic data generation, and multi-task learning. The results not only beat traditional models, but the findings also present a structured framework that can be generalized to clinical practice when faced with limited annotated datasets in medical imaging tasks.

4 Conclusion

This study presented a deep learning framework for combined classification and segmentation of brain tumors in MRI scans using a multi-task architecture combined with transfer learning and DCGAN-based augmentation. Instead of treating the classification and segmentation tasks separately, our shared-encoder architecture reduced redundancy/duplication across tasks, increased the generalizability of features, and achieved class balance by taking advantage of synthetic data. We show significant performance improvement with 93.2% classification accuracy and a Dice coefficient of 0.91 with better boundary discrimination compared to baseline approaches (SVM, k-NN, and U-Net variants). This study's contributions and innovation include combining transfer learning, GAN-based augmentation and the Grad-CAM for explainability in a single multi-task architecture to maximize the use of existing data, which is important for translating to a clinical workflow. Our framework provides insights on segmentation, classification and applies the use of GAN-based synthetic data to mitigate issues with limited data. Next stages of this approach will be to expand our application of the proposed pipeline to multi-class tumors, 3D MRI volumes, and semi-supervised paradigms to minimize reliance on labelled datasets and enhance integration into the clinical workflow.

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