An ensemble approach to Prediction and Classification of Gastrointestinal Diseases

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Abstract:
Gastrointestinal diseases are a significant cause of morbidity and mortality worldwide. Early and accurate diagnosis is crucial for effective treatment and improved patient outcomes. This research aims to enhance the prediction and classification of gastrointestinal diseases using a curated dataset of colon images. The problem statement revolves around the need for a more efficient and accurate method for diagnosing gastrointestinal diseases. Current diagnostic methods can be invasive, time-consuming, and reliant on the subjective judgment of medical professionals. Our research proposes a novel approach to address this issue. We employ a multi-fused Convolutional Neural Network (CNN) with auxiliary layers, alpha dropouts, and a fusion residual block for diagnosing gastrointestinal diseases from endoscopy images. This methodology allows for the extraction of intricate features from the images, thereby improving the accuracy of disease classification. The proposed model has the potential to revolutionize the diagnosis of gastrointestinal diseases by providing a non-invasive, quick, and highly accurate method. It could significantly reduce the time taken for diagnosis, enable early detection, and consequently improve treatment outcomes. This research contributes to the ongoing efforts in medical science to leverage artificial intelligence for disease prediction and classification, ultimately aiming to enhance patient care and health outcomes.

Keywords: *Gastrointestinal , morbidity , multi-fused convolution neural network , endoscopy, disease classification, non-invasive*

Introduction:

Gastrointestinal diseases, a broad term encompassing conditions affecting the digestive system, are a significant global health concern. These conditions can range from common ailments such as gastroenteritis and peptic ulcers to more severe diseases like colorectal cancer and Crohn's disease. The impact of these diseases is substantial, leading to considerable morbidity, mortality, and economic burden. The diagnosis of these conditions often involves invasive procedures such as endoscopy and biopsy, which can be uncomfortable for the patient and require significant medical expertise for interpretation. Furthermore, these traditional diagnostic methods can be time-consuming, delaying the initiation of appropriate treatment.

In the era of digital transformation, artificial intelligence (AI) has emerged as a powerful tool in various fields, including healthcare. AI's ability to learn from data and make predictions has been leveraged to improve diagnostic accuracy, predict disease progression, and personalize treatment plans. Among the various AI techniques, Convolutional Neural Networks (CNNs) have shown remarkable success in image-based diagnosis. CNNs are a type of deep learning model that can automatically learn and extract hierarchical features from images. This capability makes them particularly suitable for medical imaging tasks where subtle patterns in images can be indicative of disease states.

Our research is motivated by the work of Montalbo(2022), who used a multi-fused CNN model for diagnosing gastrointestinal diseases from endoscopy images [1]. Inspired by this approach, we propose an innovative methodology that incorporates auxiliary layers, alpha dropouts, and a fusion residual block to enhance feature extraction from colon images. By doing so, it aims to improve the accuracy of disease classification and prediction.

The potential impact of this research is significant - it could revolutionize the way gastrointestinal diseases are diagnosed by providing a non-invasive, quick, and highly accurate method. This would not only improve patient comfort but also enable early detection and treatment of these conditions.

The subsequent sections will provide a detailed discussion on our proposed methodology, the experimental setup used for model training and validation, and the results obtained from our experiments. We believe that our research will contribute significantly to the field of AI in healthcare and pave the way for future studies.This approach seeks to address the limitations of traditional diagnostic methods, offering a more efficient and patient-friendly alternative.

Background Study:

In the realm of AI-based diagnosis of gastrointestinal diseases, a significant contribution has been made by Montalbo et al. in their 2022 research. Their study, titled "Fusing compressed deep ConvNets with a self-normalizing residual block and alpha dropout for a cost-efficient classification and diagnosis of gastrointestinal tract diseases", introduced an innovative approach to disease classification and diagnosis. They employed compressed deep Convolutional Neural Networks (ConvNets) for efficient feature extraction from endoscopy images. The fusion of these ConvNets with a self-normalizing residual block helped maintain the network's internal normalization, while the inclusion of alpha dropout added robustness to noise. This methodology enhanced the model's performance, even in the presence of variations in input data, thereby paving the way for cost-efficient and accurate diagnosis of gastrointestinal diseases.[2]

The work of Ahmed, I. A [3] involved the development of hybrid methodologies based on the GVF algorithm and fused Convolutional Neural Network (CNN) models. These methodologies, which include CNN–Feedforward Neural Network (FFNN) and CNN–Extreme Gradient Boosting (XGBoost), showed promising results for diagnosing diseases based on endoscopy images. Building upon this, Iqbal, I proposed a specialized Deep Convolutional Neural Network (DCNN) architecture [4] for the automated identification of human gastrointestinal abnormalities with endoscopic images1. The DCNN was meticulously designed with multiple routes, various image resolutions and several convolutional layers to improve the efficacy and performance

The advent of wireless capsule endoscopy (WCE) technology has offered a promising avenue for diagnosis, but the sheer volume of images generated during WCE procedures necessitates automated analysis. However, the low contrast in WCE images complicates disease detection, and existing methods have limitations in segmentation and classification accuracy. Nouman Noor et al. proposed a paper that introduces a comprehensive approach to address these challenges. It proposes an optimized brightness-controlled contrast-enhancement technique based on genetic algorithms, followed by feature extraction using a lightweight pre-trained deep convolutional neural network (CNN) model fine-tuned with transfer learning.[5]

The work of Ramamurthy et al. represents a significant advancement in the field of automated diagnostic techniques. The researchers proposed a novel system for classifying endoscopy images by focusing on feature mining through Convolutional Neural Networks (CNN). The Effimix model employs a combination of squeeze and excitation layers and self-normalizing activation layers for precise classification of gastrointestinal diseases.[6]

Proposed methodology:

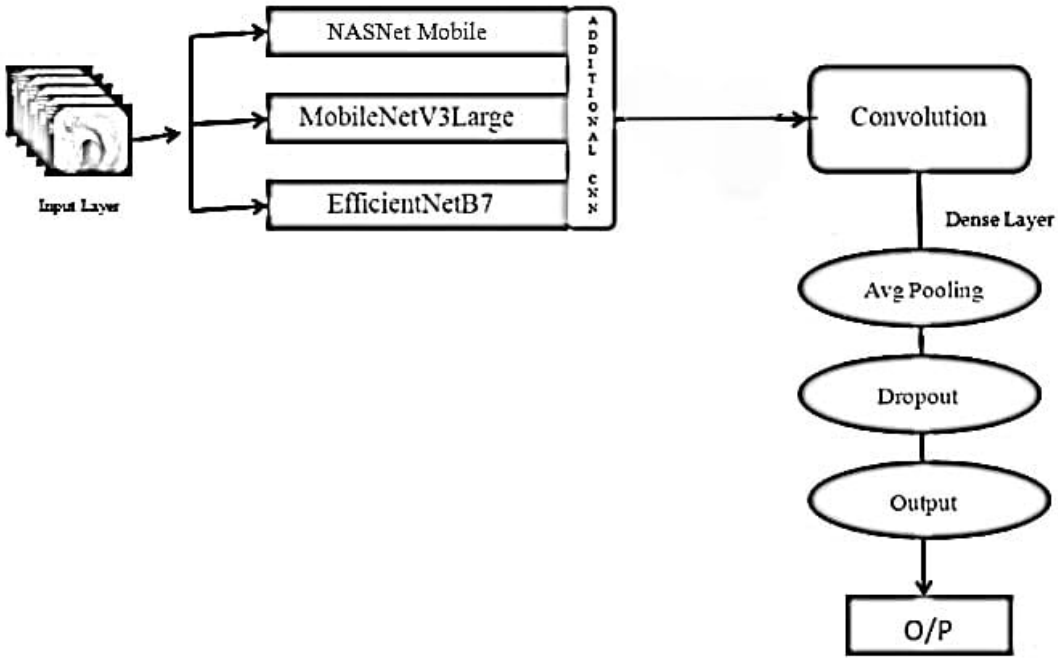


Fig 1. Model Architecture Multi-fused CNN

NASNet Mobile:

NASNet stands for Neural Search Architecture (NAS) Network and is a Machine Learning model.NASNet-Mobile is a convolutional neural network that has been trained on more than a million images from the ImageNet database. This model can classify images into 1000 object categories, such as keyboard, mouse, pencil, and many animals. As a result, the network has learned rich feature representations for a wide range of images. NASNet-Mobile is a variant of NASNet that is designed for mobile applications[3]. It is a smaller and more efficient model, making it suitable for running on devices with limited computational resources.

Layer (type)	Output Shape	Param #	Connected to
input_1_DCNN_A (InputLayer)	[(None, 224, 224, 3)	0	
block1_conv1_DCNN_A (Conv2D)	(None, 111, 111, 32)	864	input_1_DCNN_A[0][0]
block1_conv1_bn_DCNN_A (BatchNo	(None, 111, 111, 32)	128	block1_conv1_DCNN_A[0][0]
block1_conv1_act_DCNN_A (Activa	(None, 111, 111, 32)	0	block1_conv1_bn_DCNN_A[0][0]
block1_conv2_DCNN_A (Conv2D)	(None, 109, 109, 64)	18432	block1_conv1_act_DCNN_A[0][0]
block1_conv2_bn_DCNN_A (BatchNo	(None, 109, 109, 64)	256	block1_conv2_DCNN_A[0][0]
block1_conv2_act_DCNN_A (Activa	(None, 109, 109, 64)	0	block1_conv2_bn_DCNN_A[0][0]
block2_sepconv1_DCNN_A (Separab	(None, 109, 109, 128	8768	block1_conv2_act_DCNN_A[0][0]
block2_sepconv1_bn_DCNN_A (Batc	(None, 109, 109, 128	512	block2_sepconv1_DCNN_A[0][0]
block2_sepconv2_act_DCNN_A (Act	(None, 109, 109, 128	0	block2_sepconv1_bn_DCNN_A[0][0]
block2_sepconv2_DCNN_A (Separab	(None, 109, 109, 128	17536	block2_sepconv2_act_DCNN_A[0][0]
block2_sepconv2_bn_DCNN_A (Batc	(None, 109, 109, 128	512	block2_sepconv2_DCNN_A[0][0]
conv2d_DCNN_A (Conv2D)	(None, 55, 55, 128)	8192	block1_conv2_act_DCNN_A[0][0]
block2_pool_DCNN_A (MaxPooling2	(None, 55, 55, 128)	0	block2_sepconv2_bn_DCNN_A[0][0]
batch_normalization_DCNN_A (Bat	(None, 55, 55, 128)	512	conv2d_DCNN_A[0][0]
add_DCNN_A (Add)	(None, 55, 55, 128)	0	block2_pool_DCNN_A[0][0] batch_normalization_DCNN_A[0][0]
block3_sepconv1_act_DCNN_A (Act	(None, 55, 55, 128)	0	add_DCNN_A[0][0]
block3_sepconv1_DCNN_A (Separab	(None, 55, 55, 256)	33920	block3_sepconv1_act_DCNN_A[0][0]
block3_sepconv1_bn_DCNN_A (Batc	(None, 55, 55, 256)	1024	block3_sepconv1_DCNN_A[0][0]
block3_sepconv2_act_DCNN_A (Act	(None, 55, 55, 256)	0	block3_sepconv1_bn_DCNN_A[0][0]
block3_sepconv2_DCNN_A (Separab	(None, 55, 55, 256)	67840	block3_sepconv2_act_DCNN_A[0][0]
block3_sepconv2_bn_DCNN_A (Batc	(None, 55, 55, 256)	1024	block3_sepconv2_DCNN_A[0][0]
conv2d_1_DCNN_A (Conv2D)	(None, 28, 28, 256)	32768	add_DCNN_A[0][0]
block3_pool_DCNN_A (MaxPooling2	(None, 28, 28, 256)	0	block3_sepconv2_bn_DCNN_A[0][0]
batch_normalization_1_DCNN_A (B	(None, 28, 28, 256)	1024	conv2d_1_DCNN_A[0][0]
add_1_DCNN_A (Add)	(None, 28, 28, 256)	0	block3_pool_DCNN_A[0][0] batch_normalization_1_DCNN_A[0][0
block4_sepconv1_act_DCNN_A (Act	(None, 28, 28, 256)	0	add_1_DCNN_A[0][0]
block4_sepconv1_DCNN_A (Separab	(None, 28, 28, 728)	188672	block4_sepconv1_act_DCNN_A[0][0]
block4_sepconv1_bn_DCNN_A (Batc	(None, 28, 28, 728)	2912	block4_sepconv1_DCNN_A[0][0]
block4_sepconv2_act_DCNN_A (Act	(None, 28, 28, 728)	0	block4_sepconv1_bn_DCNN_A[0][0]
block4_sepconv2_DCNN_A (Separab	(None, 28, 28, 728)	536536	block4_sepconv2_act_DCNN_A[0][0]
block4_sepconv2_bn_DCNN_A (Batc	(None, 28, 28, 728)	2912	block4_sepconv2_DCNN_A[0][0]
conv2d_2_DCNN_A (Conv2D)	(None, 14, 14, 728)	186368	add_1_DCNN_A[0][0]
block4_pool_DCNN_A (MaxPooling2	(None, 14, 14, 728)	0	block4_sepconv2_bn_DCNN_A[0][0]
batch_normalization_2_DCNN_A (B	(None, 14, 14, 728)	2912	conv2d_2_DCNN_A[0][0]

Fig 2. Layers of NASNet Mobile

MobileNet V3 Large:

MobileNetV3 Large is a variant of MobileNetV3 that is designed for applications that require larger models. It is a more powerful model, making it suitable for running on devices with more computational resources. The building blocks of MobileNetV3 consist of normal and reduction cells. These cells are discovered through a process called neural architecture search, which automates the design of neural networks. You can use transfer learning to retrain MobileNetV3 Large on a new set of images. This involves replacing the last learnable layer and the classification layer in your network with new layers for training.

Layer (type)	Output Shape	Param #	Connected to
input_1_DCNN_A_DCNN_B (InputLay	[(None, 224, 224, 3)	0	
rescaling_DCNN_B (Rescaling)	(None, 224, 224, 3)	0	input_1_DCNN_A_DCNN_B[0][0]
Conv_DCNN_B (Conv2D)	(None, 112, 112, 16)	432	rescaling_DCNN_B[0][0]
Conv/BatchNorm_DCNN_B (BatchNor	(None, 112, 112, 16)	64	Conv_DCNN_B[0][0]
tf.__operators__.add_DCNN_B (TF	(None, 112, 112, 16)	0	Conv/BatchNorm_DCNN_B[0][0]
re_lu_DCNN_B (ReLU)	(None, 112, 112, 16)	0	tf.__operators__.add_DCNN_B[0][0]
tf.math.multiply_DCNN_B (TFOpLa	(None, 112, 112, 16)	0	re_lu_DCNN_B[0][0]
multiply_DCNN_B (Multiply)	(None, 112, 112, 16)	0	Conv/BatchNorm_DCNN_B[0][0] tf.math.multiply_DCNN_B[0][0]
expanded_conv/depthwise_DCNN_B	(None, 112, 112, 16)	144	multiply_DCNN_B[0][0]
expanded_conv/depthwise/BatchNo	(None, 112, 112, 16)	64	expanded_conv/depthwise_DCNN_B[0]
re_lu_1_DCNN_B (ReLU)	(None, 112, 112, 16)	0	expanded_conv/depthwise/BatchNorm
expanded_conv/project_DCNN_B (C	(None, 112, 112, 16)	256	re_lu_1_DCNN_B[0][0]
expanded_conv/project/BatchNorm	(None, 112, 112, 16)	64	expanded_conv/project_DCNN_B[0][0
expanded_conv/Add_DCNN_B (Add)	(None, 112, 112, 16)	0	multiply_DCNN_B[0][0] expanded_conv/project/BatchNorm_D
expanded_conv_1/expand_DCNN_B (	(None, 112, 112, 64)	1024	expanded_conv/Add_DCNN_B[0][0]
expanded_conv_1/expand/BatchNor	(None, 112, 112, 64)	256	expanded_conv_1/expand_DCNN_B[0][
re_lu_2_DCNN_B (ReLU)	(None, 112, 112, 64)	0	expanded_conv_1/expand/BatchNorm_
expanded_conv_1/depthwise/pad_D	(None, 113, 113, 64)	0	re_lu_2_DCNN_B[0][0]
expanded_conv_1/depthwise_DCNN_	(None, 56, 56, 64)	576	expanded_conv_1/depthwise/pad_DCN
expanded_conv_1/depthwise/Batch	(None, 56, 56, 64)	256	expanded_conv_1/depthwise_DCNN_B[
re_lu_3_DCNN_B (ReLU)	(None, 56, 56, 64)	0	expanded_conv_1/depthwise/BatchNo
expanded_conv_1/project_DCNN_B	(None, 56, 56, 24)	1536	re_lu_3_DCNN_B[0][0]
expanded_conv_1/project/BatchNo	(None, 56, 56, 24)	96	expanded_conv_1/project_DCNN_B[0]
expanded_conv_2/expand_DCNN_B (	(None, 56, 56, 72)	1728	expanded_conv_1/project/BatchNorm
expanded_conv_2/expand/BatchNor	(None, 56, 56, 72)	288	expanded_conv_2/expand_DCNN_B[0][
re_lu_4_DCNN_B (ReLU)	(None, 56, 56, 72)	0	expanded_conv_2/expand/BatchNorm_
expanded_conv_2/depthwise_DCNN_	(None, 56, 56, 72)	648	re_lu_4_DCNN_B[0][0]
expanded_conv_2/depthwise/Batch	(None, 56, 56, 72)	288	expanded_conv_2/depthwise_DCNN_B[
re_lu_5_DCNN_B (ReLU)	(None, 56, 56, 72)	0	expanded_conv_2/depthwise/BatchNo
expanded_conv_2/project_DCNN_B	(None, 56, 56, 24)	1728	re_lu_5_DCNN_B[0][0]
expanded_conv_2/project/BatchNo	(None, 56, 56, 24)	96	expanded_conv_2/project_DCNN_B[0]
expanded_conv_2/Add_DCNN_B (Add	(None, 56, 56, 24)	0	expanded_conv_1/project/BatchNorm expanded_conv_2/project/BatchNorm
expanded_conv_3/expand_DCNN_B (	(None, 56, 56, 72)	1728	expanded_conv_2/Add_DCNN_B[0][0]
expanded_conv_3/expand/BatchNor	(None, 56, 56, 72)	288	expanded_conv_3/expand_DCNN_B[0][
re_lu_6_DCNN_B (ReLU)	(None, 56, 56, 72)	0	expanded_conv_3/expand/BatchNorm_
expanded_conv_3/depthwise/pad_D	(None, 59, 59, 72)	0	re_lu_6_DCNN_B[0][0]
expanded_conv_3/depthwise_DCNN_	(None, 28, 28, 72)	1800	expanded_conv_3/depthwise/pad_DCN
expanded_conv_3/depthwise/Batch	(None, 28, 28, 72)	288	expanded_conv_3/depthwise_DCNN_B[

Fig.3 Layers of MobileNet V3 Large

EfficientNet B7:

EfficientNet B7 is the largest model in the EfficientNet series and has achieved state-of-the-art performance on the ImageNet and CIFAR-100 datasets. It obtained around 84.4% top-1 and 97.3% top-5 accuracy on ImageNet. Also, the model size was 8.4 times smaller and 6.1 times faster than the previous best CNN model. EfficientNet B7 is a powerful and versatile model that is capable of high performance on a wide range of image classification tasks. Its design principles and the ability to retrain it on new tasks make it a valuable tool for many applications

The architecture is a combination of three pre-trained models and a convolutional neural network (CNN) that is designed for prediction and classification of gastrointestinal diseases. It consists of the following components:

Pre-trained models: These are NASNet Mobile, MobileNetV3Large, and EfficientNetB7. These models are state-of-the-art deep learning models that are trained on a large dataset of images, such as ImageNet. They are used to extract features from the input image, which is a gastrointestinal endoscopy image. The features are high-dimensional vectors that represent the visual information in the image, such as color, texture, shape, and object. The pre-trained models have different architectures and parameters, which allow them to capture different aspects of the image.

Convolutional neural network (CNN): This is a custom neural network that is composed of a dense layer, average pooling, dropout, and output layers. The dense layer takes the concatenated features from the three pre-trained models as input and transforms them into a lower-dimensional vector. The average pooling layer reduces the spatial dimensions of the vector by taking the average value of each region. The dropout layer randomly drops out some units of the vector to prevent overfitting. The output layer is a softmax layer that outputs a probability distribution over the possible classes of gastrointestinal diseases, such as ulcer, polyp, or cancer. The CNN is trained using a dataset of labeled gastrointestinal endoscopy images, where the labels are the ground truth diagnoses. Once trained, the CNN can be used to make predictions for new images.

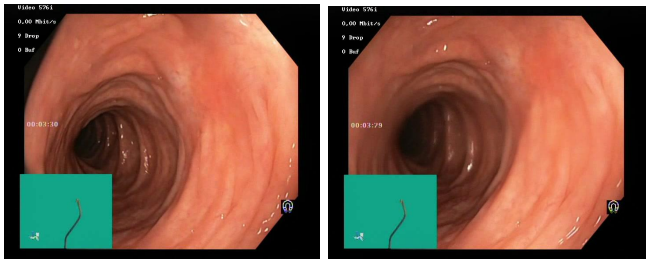


Fig.4 - Gastrointestinal Region (Normal)

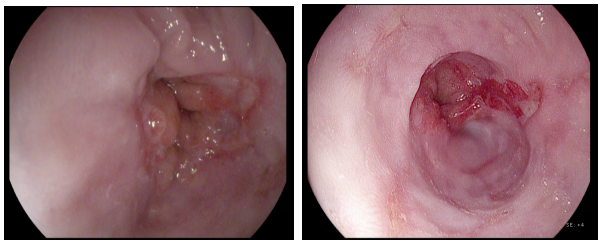


Fig.5 - Gastrointestinal Region (esophagitis)

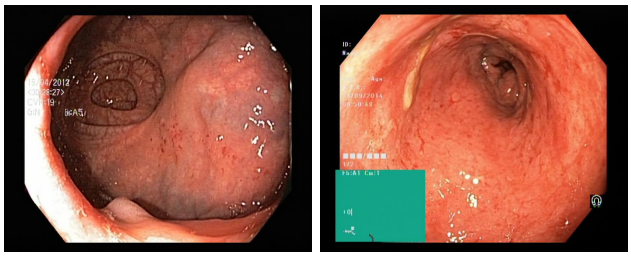


Fig.6 - Gastrointestinal Region (ulcer)

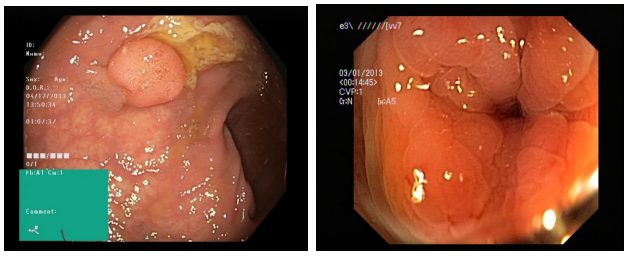


Fig.7 - Gastrointestinal Region (polyps)

In the Multi-Fused Residual CNN model, these three models are combined in a way that leverages their individual strengths. The model begins with an input layer, which feeds into each of the three models. The outputs of these models are then concatenated and passed through a series of residual blocks. These blocks help the model learn complex patterns and relationships in the data.The final output layer of the model is a softmax layer, which provides the probabilities of the different gastrointestinal diseases. This allows the model to make predictions about the most likely disease given the input data. This model can be trained using transfer learning, which involves replacing the last learnable layer and the classification layer in each network with new layers for training. This allows the model to be fine-tuned for the specific task of gastrointestinal disease prediction and classification.

Research Gaps:

The development and evaluation of deep learning models for GI disease diagnosis rely heavily on large, representative datasets of GI images. However, there is a lack of standardization and harmonization in the collection, annotation, and preprocessing of GI image datasets. This variability in data quality and consistency can hinder the generalizability of deep learning models and make it difficult to compare the performance of different models. Future research should focus on developing standardized protocols and guidelines for the collection, annotation, and preprocessing of GI image datasets. This would ensure that datasets are more

consistent and comparable, allowing for more reliable evaluation and comparison of deep learning models.

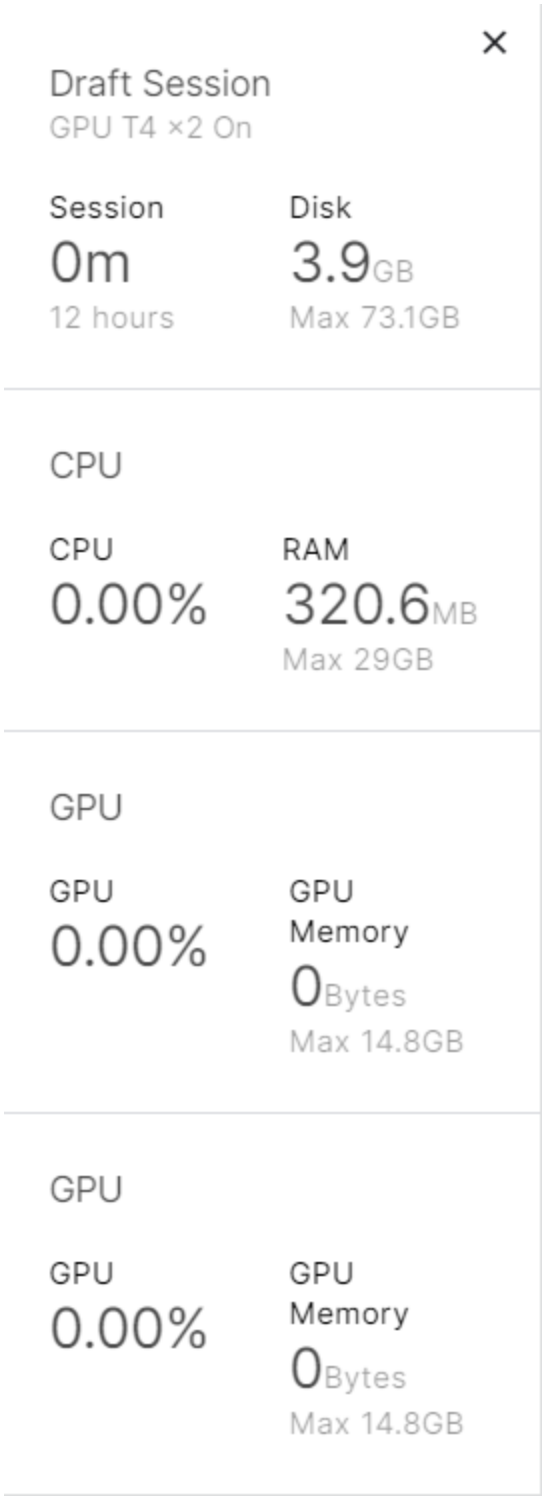
While deep learning models have demonstrated impressive performance in various medical imaging tasks, including GI disease diagnosis, they are often considered "black boxes" due to their complex internal workings. This lack of explainability can hinder trust and adoption of deep learning models in clinical practice. Future research should focus on developing methods for explaining and interpreting deep learning models for GI disease diagnosis. This would allow clinicians to better understand the rationale behind the model's predictions and make more informed diagnostic decisions.

Gastrointestinal (GI) disease diagnosis using deep learning models is often limited by the domain shift between the training and testing datasets. This domain shift can occur due to differences in image quality, patient demographics, and imaging equipment. As a result, models trained on one dataset may not perform well on another dataset, leading to reduced generalizability and clinical applicability. Future research should focus on developing domain adaptation techniques that can effectively bridge the gap between different datasets. These techniques could involve using data augmentation methods to synthesize training data that is more similar to the testing data, or developing transfer learning approaches that can extract and transfer knowledge from a source domain to a target domain.

Results and Conclusion:

The multi-fused CNN model is then trained for the dataset for predicting 4 classes of gastrointestinal diseases ‘normal' ,'ulcerative colitis', 'polyps' and ‘esophagitis’. The model predicts the class normal with 92% f1-score , ulcerative colitis with 86% , polyps with 87% and esophagitis with 99%. The model achieved an overall accuracy of 91%.

For running the code, we used the GPU T4 x2. Running the



In conclusion, the Multi-Fused Residual Convolutional Neural Network (CNN) model, which leverages the strengths of NASNet Mobile, MobileNetV3Large, and EfficientNetB7, has demonstrated impressive performance in the prediction and classification of gastrointestinal diseases. The model was trained on a dataset for predicting four classes of gastrointestinal

diseases: ‘normal’, ‘ulcerative colitis’, ‘polyps’, and ‘esophagitis’. The model achieved an overall accuracy of 91%, indicating its robustness and reliability in classifying these diseases. The F1-scores for the individual classes were also high, with 92% for ‘normal’, 86% for ‘ulcerative colitis’, 87% for ‘polyps’, and an exceptional 99% for ‘esophagitis’. These results highlight the model’s ability to effectively distinguish between different gastrointestinal conditions, making it a valuable tool in the field of medical diagnostics.

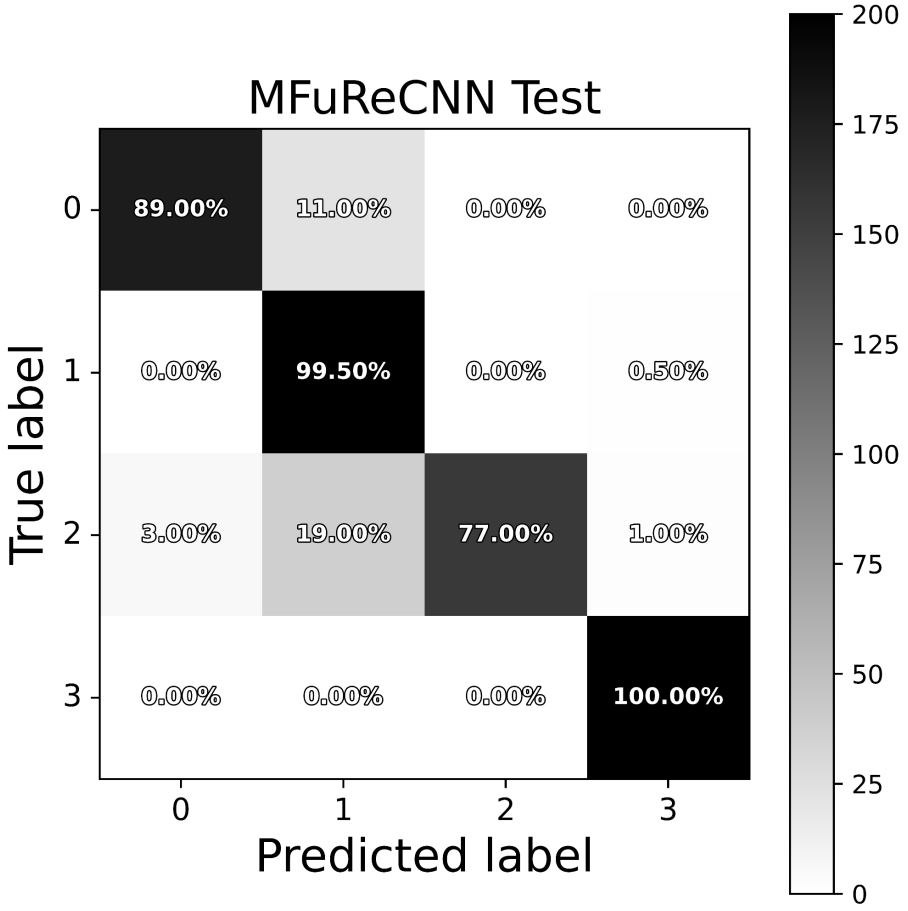


Fig8. Confusion Matrix of our model

Therefore, the Multi-Fused Residual CNN model represents a significant advancement in the application of deep learning techniques to healthcare, providing a powerful, efficient, and accurate tool for the diagnosis of gastrointestinal diseases. Its high performance and the ability to retrain it on new tasks make it a promising model for future research and applications in the medical field.

Table 1: Prediction results of Multi-fused CNN for 4 classes of gastrointestinal diseases

Classes	F1-Score
Normal	0.92
Ulcerative Colitis	0.86
Polyps	0.87
esophagitis	0.99

A lightweight deep learning model designed for mobile CPU execution can revolutionize gastrointestinal (GI) disease classification, offering several compelling benefits to individuals seeking convenient and accessible diagnostic tools.

Firstly, portability and accessibility: A lightweight model seamlessly integrates with mobile devices, empowering individuals to perform GI disease classification anytime, anywhere. This eliminates the need for costly and time-consuming visits to medical facilities, making diagnosis more accessible and convenient.Secondly, real-time feedback and early intervention: The ability to run the model on mobile devices enables real-time feedback, allowing individuals to promptly assess their GI health and seek medical attention if necessary. This facilitates early intervention, potentially improving treatment outcomes and reducing the severity of GI conditions.

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