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Gastrointestinal Tract Lesion Classification Using Deep Involution Neural Networks

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Abstract

Classification of gastrointestinal (GI) tract lesions from endoscopic images is one of the challenging medical image analysis. Conventionally, the automation techniques that leverage very large and complex deep learning methods, that are very difficult to be deployed. This study proposes a lightweight four-layer Deep Involution Neural Network for automated classification of GI tract lesions into four classes: Normal, Ulcerative Colitis, Polyps, and Esophagitis. The proposed model uses involution operations to efficiently extract essential features while reducing computational complexity. The model has been evaluated on a publicly available dataset that consists of 6000 endoscopic images. After training the model on the dataset, it achieves an overall accuracy of 91.13%. These results validate that the proposed model is an effective and computationally efficient approach for computer-aided GI tract lesion classification.

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INTRODUCTION

Endoscopic imaging for GI tract is a gold standard for the diagnosis of a number of lesion [1]. Usually, human experts known as gastroenterologist examine the images manually and determine the possible presence of a lesion. However, the availability and expertise of gastroenterologists is always a challenge, especially in developing countries. Recently, automated methods for GI tract lesion detection have gained a lot of attention [2]. The automated techniques use computation methods to determine the health of the GI tract of human on the basis of histological images acquired using endoscopy methods. These automated methods rely solely on the computation mechanism used for the diagnosis. If a suitable computational mechanism is not used, there is huge chance of erroneous results [3].

The emergence of deep learning methods in medical image analysis, especially for GI tract lesion detection and classification have drastically improved the results [4]. There are a number of works which report a tremendous results. For instance, Raza et al. [5] use a novel deep learning method for the GI tract lesion detection. Similarly, Majid et al. [6] use attention based deep learning method to detection GI tract lesions, they report a high accuracy in their work. Despite these excellent works, there is still a huge room for improvement. Current methods, either use a very complex model with a very large underlying architecture or the presented results are far from the results produced by gastroenterologists [7].

To use the capabilities of automated systems and gastroenterologists combined in a hybrid setup, some the studies have attempted incorporate such approaches [8]. Although, this hybrid setup is more accurate but it carries the pros and cons of both automated systems and human experts [9]. Apparently, this looks an ideal method in current times but in long run it is again a technique that has similar challenges [10]. Those challenges can only be mitigated if there is a fully automated mechanism [11]. Other than being a fully automated mechanism, the system needs to be lightweight and less complex so that it can be deployed on machines having moderate computational capabilities [12].

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This study is focused to use lightweight four layer deep involution network for detection of GI tract lesions, especially, ulcerative colitis, polyps and esophagitis. The study automates the detection of these lesions by producing deployable capabilities without losing the accuracy. The intended accuracy is not only competitive to the state-of-the-art methods but it is almost comparable to the accuracy of a gastroenterologist.

2. Methodology

The proposed method used a deep involution neural network architecture [13]. Compared to convention convolution, the weights of an involution kernel are dynamically generated based on the input feature maps at a particular spatial location of the input image. Figure 1 depicts the conceptual block diagram of the proposed four layer deep involution neural network.

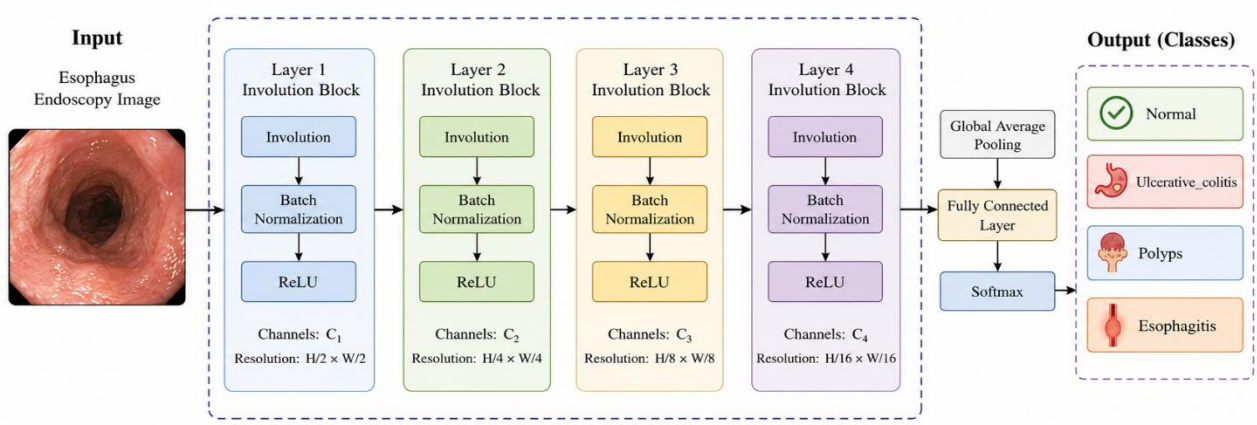

Figure 1: Block diagram of four-layer deep involution Network

The network uses input of the size $224 \times 224 \times 3$, the output produces probabilities of the four expected output classes. The inner layers are based on involution step, batch normalization and ReLU activation function.

2.1 Mathematical Formulation of Involution

One of the main steps in the proposed network is the process of involution. This process uses a sophisticated mechanism to learn discriminative features at different spatial locations in an input image. To understand the process thoroughly, let's suppose $X \in \mathbb{R}^{H \times W \times C}$ be the input feature

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map, where H, W and C represent the height, width and the number of channels. Similarly, let's assume $Y \in \mathbb{R}^{H \times W \times C}$ is the output feature map. The involution kernel at a particular spatial position (i, j) is dynamically generated by a kernel generation $\emptyset$, which maps the local neighborhood of $X_{i,j}$ to a reduced space [13]. The mathematical formulation for the involution operation at a location (i, j) for a specific channel group δ is defined as follows:

$$Y_{i,j,c} = \sum_{(u,v) \in N(i,j)} \mathcal{H}_{i,j,u+\frac{K}{2},v+\frac{k}{2},\delta} \cdot H_{u,v,c} \quad (1)$$

Where:

- $N(i, j)$ represents the local neighborhood of spatial size $K \times K$ centered at coordinate (i, j).
- $\mathcal{H}_{i,j} \times \mathbb{R}^{K \times K \times G}$ is the dynamic involution kernel, shared across channels within the same group $\delta \times \{1, \ldots, G\}$.

Along with algorithmic and mathematical procedure the size and the type of input significantly impacts the feature maps quality. Therefore, training parameters and training data is also very essential for better results [14].

2.2 Dataset Composition

This study uses a public dataset [15] that comprises of 6000 images, each class has 1500 samples and Table 1 shows the class-wise detail.

Table 1: Number of samples in the dataset for each class

Class	Number of Samples
Normal	1500
Ulcerative Colitis	1500
Polyps	1500
Esophagitis	1500

The dataset is distributed for training and testing portions. The training part has 5200 images (1300 samples for each class) and 800 samples for testing (200 samples for each class).

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3. Results and Discussion

The proposed model demonstrates potentially results on the dataset used in this study. Proposed model has been trained on the following hyper-parameters:

- Learning rate: 0.001
- Optimizer: Adam
- Batch size: 32
- Loss function: Cross Entropy Loss
- Number of Epochs: 20

On the basis of these hyper-parameters the proposed model converged successfully. Figure 2 depicts the training accuracy, validation accuracy, training loss and validation loss. Figure 3 shows the training and validation AUC.

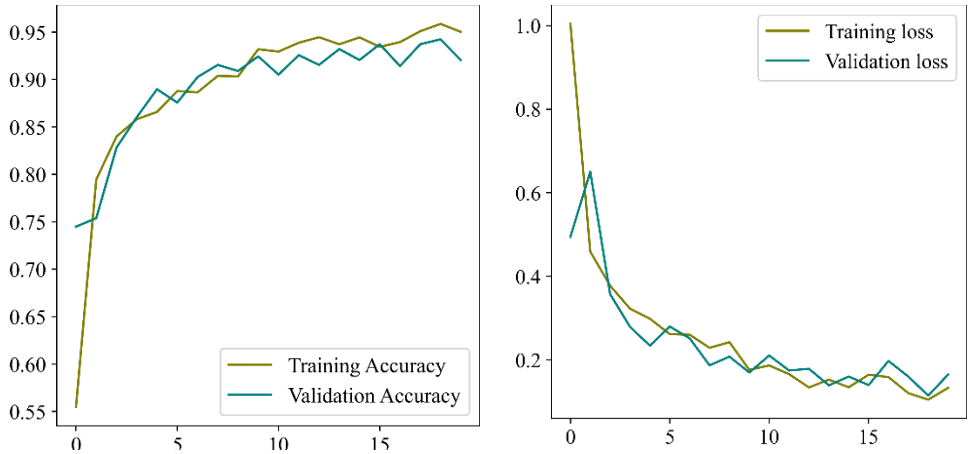

Figure 2: Training accuracy, validation accuracy, training loss and validation loss

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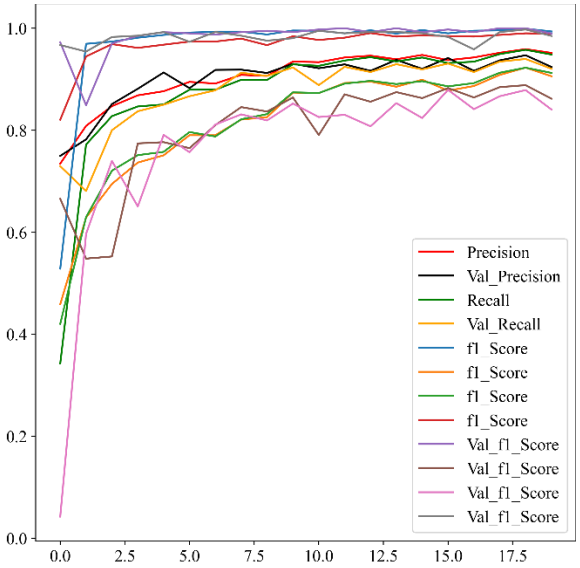

Figure 3: Training AUC and validation AUC

3.1 Mathematical Formulation of Performance Metrics

After the process of the training, the trained model have been evaluated on test data. The model have been tested for 200 samples of each class. Equation 1-5 show formulas for precision, recall, f1-score, and accuracy respectively [16].

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (4)$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (5)$$

3.2 Evaluation and Error Analysis

The trained model produced excellent results on the test data. Figure 4 depicts the confusion matrix generated on test data.

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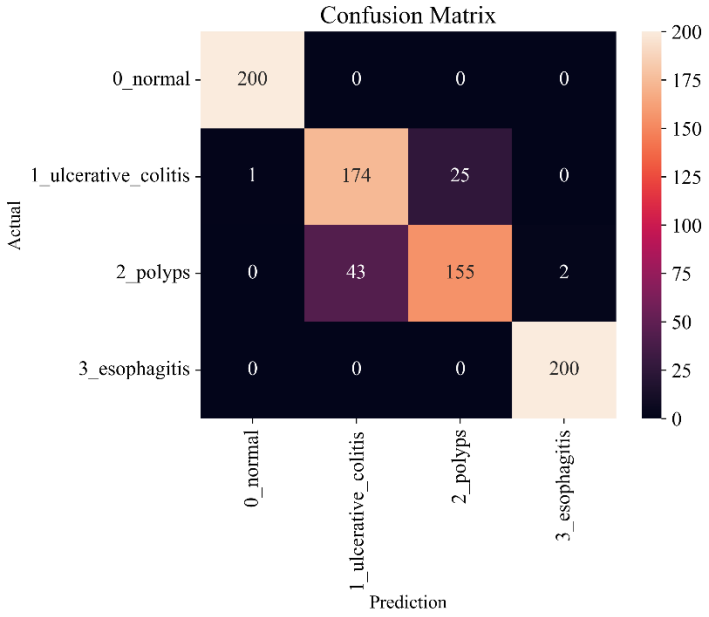

Figure 4: Confusion matrix generated on test data

The confusion matrix helped to determine the values of accuracy, precision, recall and f1-score. These score are illustrated in Table 2. It can be clearly determined that model very clearly identifies the normal cases with a very high confidence.

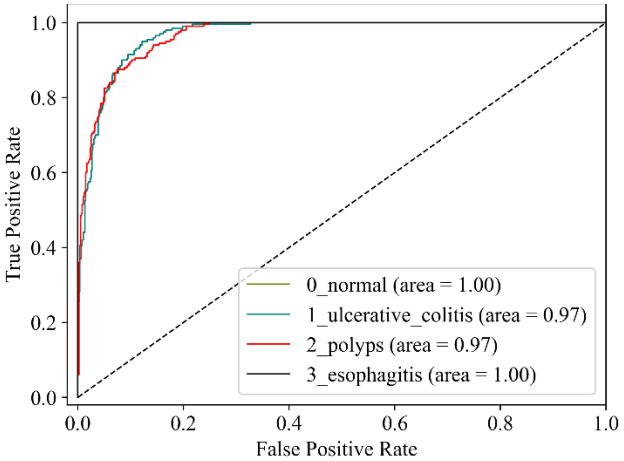

Figure 5: AUC produced by the model on test data for all the four classes

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Other than normal cases the model has significantly high accuracy to identify Esophagitis almost equivalent to the normal cases. Figure 5 depicts the AUC for each class that further validates the effectiveness of the proposed method.

Table 2: Results produced by the model on test data

Class	Precision	Recall	F1-score
Normal	0.9950	1.0000	0.9975
Ulcerative Colitis	0.8018	0.8700	0.8345
Polyps	0.8611	0.7750	0.8158
Esophagitis	0.9901	1.0000	0.9950

Hence, the proposed deep involution network has demonstrated its effectiveness in accurately classifying gastrointestinal (GI) tract lesions from endoscopic images. The experimental results show that the model achieves high classification performance on all the classes, including normal, ulcerative colitis, polyps and esophagitis, with an overall accuracy of more than 91% and strong precision, recall, and F1-score values. By incorporating the adaptive spatial feature extraction capability of involution operations, the proposed architecture effectively captures both local and contextual lesion features, resulting in improved classification. These results suggest that the proposed model is a reliable for the early detection and classification of GI tract lesion.

4. Conclusion

This study proposed a lightweight four-layer Deep Involution Neural Network for automated classification of gastrointestinal tract lesions from endoscopic images. The model effectively classified four lesion categories with an overall accuracy of 91.13% and achieved high precision, recall, and F1-score values. The use of involution operations enabled efficient extraction of features while maintaining low computational complexity. The results demonstrate that the proposed model is a reliable computer-aided diagnostic tool for GI lesion classification. Future work will focus on evaluating the model on larger multicenter datasets, incorporating explainable AI techniques, and extending the framework to additional gastrointestinal diseases.

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