

Ensemble Convolutional Layers and Modified Wild Horse Optimized Learning Framework for Kidney Tumor Classification from CT Images

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ABSTRACT

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Our society is affected by the most common disease Kidney Tumor (KT) in humans. The early diagnosis of KT may reduce the risk of death rates. Preventive measures can be taken to reduce the severe effects and overcome the tumor progression. Traditional methods consume time and tedious task. Deep Learning (DL) methods are emerging now to save time for diagnosis, to improve the accuracy of detection and reduce the physician's manpower. In this research work, detection system is developed to detect KT in Computed Tomography (CT) images. Convolutional Neural Networks (CNNs) integrated with Modified Wild Horse Optimization (MWHO) is developed to test and train the network. The images from the Kaggle dataset are taken for the experiment. The dataset is divided into two as 80% is for training and 20% is for testing purpose. The accuracy values provided by CNN, CNN combined with particle swarm optimization (PSO) and CNN combined with genetic algorithm (GA) models are 86.6%, 86.8%, and 96%, respectively. The accuracy value provided by the proposed classification method is 100%. The proposed model achieved promising results when the number of classes able to be predicted (K) is equal to 5.

Keywords: Kidney Tumor, Wild Horse Optimized Learning Framework, Deep Learning.

INTRODUCTION

The kidneys extract the undesired products from the human body [1,2]. The undesirable growth of cells develops the cancers. This may affect the human differently depending on the extent and causes various symptoms. Early detection of KT is important for reducing the risk of severity of the disease. This may reduce the human's life threat [2,3]. When the persons are treated for some kind of diseases, accidentally the KT came to appear in CT or different radiography. Actually the signs may not do anything to kidneys [4,5]. But KT causes symptoms such as vomiting, less haemoglobin, anemia or stomach pain in patients [6,7]. The tumors present inside the kidney will become as cancer. Therefore, the recovery rate depends on the early detection of the KT from CT image of abdomen and tumor diagnosis [8,9]. Without human involvement, DL network learns the features of KT [10-12]. DL proves to be better than machine learning methods in providing the accurate results in detecting KT [13-15]. In dealing with the computer stored images DL methods are preferred [16,17]. Radiology is useful in getting the information about the diseases from the images in medical field.

METHODOLOGY

In this research, computer –assisted kidney tumor diagnosis system based on CT Images has been proposed. The method is framed by the combination of customised U-NET segmentation with heuristic based deep training network. The proposed model consists of efficient convolutional structure integrated the MWHO for tuning the hyper-parameters for the achieving the better classification process. To validate the proposed model, classification

performance parameters, namely, accuracy, precision, recall, F1-score are calculated. Moreover the statistical analysis of the proposed system has been calculated and analysed in Figure 1.

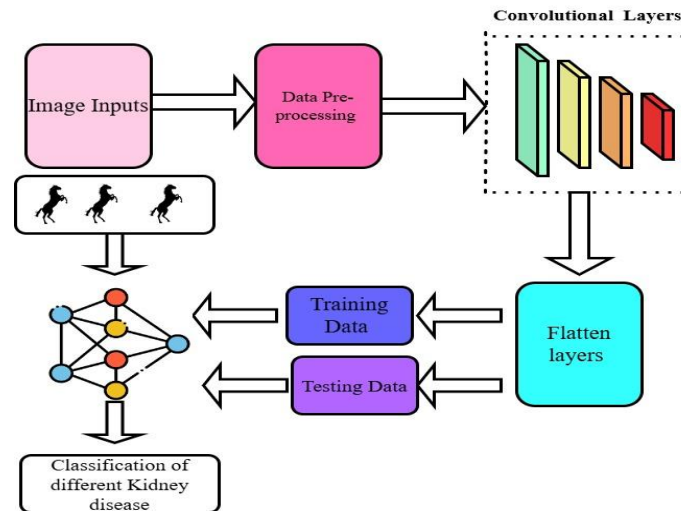


Figure 1: Statistical Analysis of the Proposed System

Ensemble convolutional layers represent an advanced architecture design in CNNs, combining the strengths of multiple convolutional layers or sub-networks to improve performance, generalization, and robustness. The ensemble approach leverages diversity in feature extraction to create a more comprehensive representation of input data.

By using ensemble convolutional layers, the model can provide multiple parallel convolutional paths on the same input. Each path may have different kernel sizes, strides, or architectural designs, allowing the model to capture a wider range of features. Ensemble layers learn features at different scales. Layers may specialize in low level features like edges or high level features like shapes. The outputs from parallel paths are combined. The features are passed to successive layers.

Figure 2 shows the ensemble convolutional layers. The input image is the input layer. 1,2, and 3 shows the path1, path 2 and path 3. They are the convolutional paths with a small kernel, large kernel and depth wise convolution respectively. In the output stage features are added.

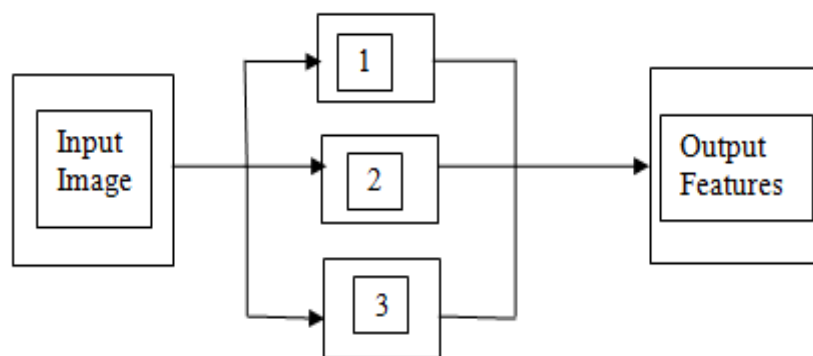


Figure 2: Ensemble convolutional layers

The MWHO learning framework could be an enhanced model that integrates principles inspired by natural processes, specifically the behavior and strategies of wild horses, into a learning framework. It might be useful in various deep learning methods. The MWHO is known for its ability to thrive in varied and challenging environments. MWHO leads to the optimized outcomes. It ensures continuous learning and development based on environmental changes using neural networks. MWHO also minimizes redundancy.

EXPERIMENTAL RESULTS

The model framed in this paper was done by Keras with tensorflow as backend. Table 1 explains the hyperparameters utilized for training the method.

Table 1: Hyperparameters utilized for training the proposed method

Hyper parameters used	Specifications
Initial learning rate	0.001
No of Epochs used	10
Batch Size	32
Optimizer	MWHO
Momentum	0.02

In the training stage, early stopping method was undertaken to end the training in advance to avoid the overfitting challenge. Several augmented images were adopted to improve the training process. The final algorithm was experimented in the personal computer workstation with 16GB RAM, 2TB SSD, Intel i7, NVIDIA Geforce RTX and 3.4 GHZ operating frequency.

Evaluation Parameters

The evaluation of the proposed research is analyzed by classification metrics. The segmentation model evaluates the difference between the model prediction results and the ground truth. The classification performance parameters, namely, accuracy, precision, recall and F1-score are utilized to analyze the performance of the algorithm in classifying the different levels of kidney tumors. Table 2 explains the expression for the determining the classification metrics.

Table 2: Expression for evaluating the classification metrics

Performance Metrics	Mathematical Expression
Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$
Sensitivity or recall	$\frac{TP}{TP + FN} \times 100$
Precision	$\frac{TP}{TP + FP} \times 100$
F1-Score	$2 \cdot \frac{Precision * Recall}{Precision + Recall}$

Table 3 explains the convolutional parameters for the proposed model.

Table 3: Convolutional parameters for the proposed architecture

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 62, 62, 32)	896
max_pooling2d (MaxPooling2D)	(None, 31, 31, 32)	0
conv2d_1 (Conv2D)	(None, 29, 29, 64)	18,496
max_pooling2d_1 (MaxPooling2D)	(None, 14, 14, 64)	0
flatten (Flatten)	(None, 12544)	0
dense (Dense)	(None, 128)	1,605,760
dense_1 (Dense)	(None, 4)	516

Total params: 1,625,668 (6.20 MB)

Trainable params: 1,625,668 (6.20 MB)

Non-trainable params: 0 (0.00 B)

In the proposed classification algorithm, 2D images as mentioned are processed as inputs. Experiments conducted to prove the classification performance of the developed model and the performance is compared with the other existing model. The validation method is experimented to analyse the performance of the different models in detecting the different category of kidney tumors. Figure 3 depicts the confusion matrix of the developed model in finding the KTs.

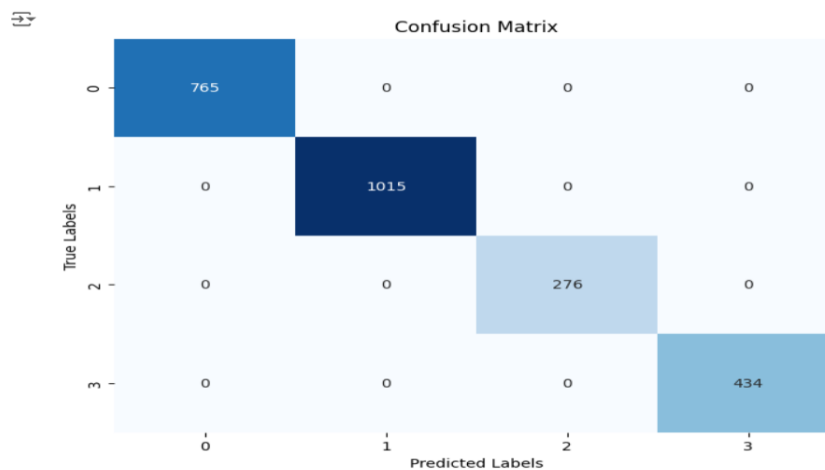


Figure 3: Confusion matrix of the proposed system in detecting KTs

Figure 4 indicates the ROC of false positive rate versus true positive rate.

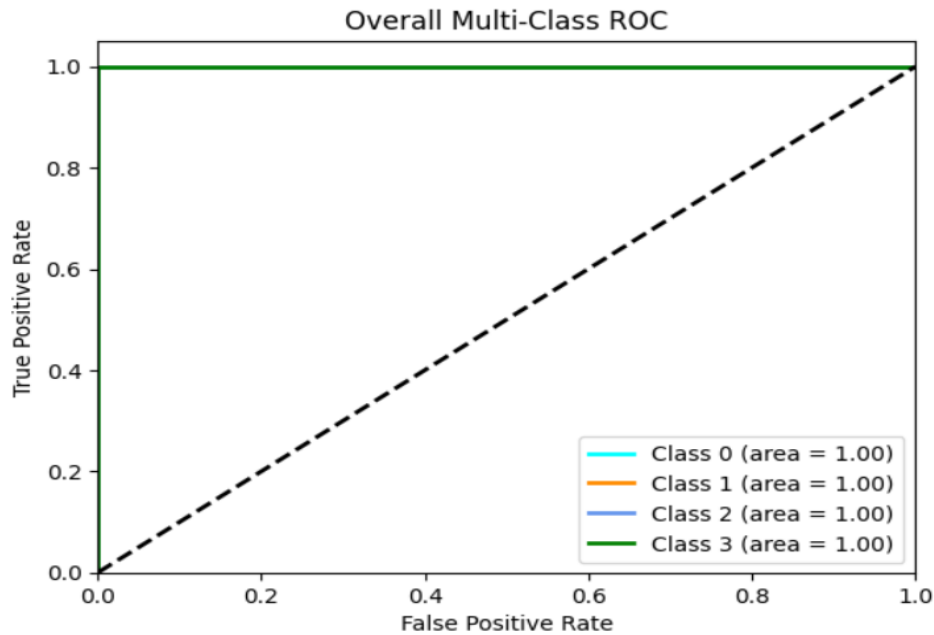


Figure 4: A graph of false positive rate versus true positive rate

COMPARISON WITH OTHER RESEARCH STUDIES

Table 4 shows the average evaluation metrics of the previous methods at the detection of tumors when K=1. The MWHO system is compared with CNN, CNN+PSO and CNN+GA through accuracy, precision, recall and F1 score. The proposed system proves to be better as in all performance metrics, it shows hundred percent. The previous methods indicate lesser values than the proposed model.

Table 4: Average performance metrics when K=1

Algorithms	Evaluation Metrics			
	Accuracy	Precision	Recall	F1-Score
CNN	0.864	0.86	0.81	0.86
CNN+PSO	0.863	0.85	0.846	0.855
CNN+GA	0.88	0.872	0.87	0.873
Proposed MWHO Model	1.00	1.00	1.00	1.00

Table 5 depicts the average performance metrics of the previous methods at the detection of tumors when K=2. The MWHO system is compared with CNN, CNN+PSO and CNN+GA through accuracy, precision, recall and F1 score. The proposed system proves to be better as in all performance metrics, it shows hundred percent. The previous methods indicate lesser values than the proposed model.

Table 5: Average performance metrics when K=2

Algorithms	Evaluation Metrics			
	Accuracy	Precision	Recall	F1-Score
CNN	0.864	0.86	0.851	0.86
CNN+PSO	0.863	0.862	0.850	0.851
CNN+GA	0.88	0.872	0.87	0.873
Proposed MWHO Model	1.00	1.00	1.00	1.00

Table 6 shows the average performance metrics of the previous methods at the detection of tumors when K=3. The MWHO system is compared with CNN, CNN+PSO and CNN+GA through accuracy, precision, recall and F1 score. The proposed system proves to be better as in all performance metrics, it shows hundred percent. The previous methods indicate lesser values than the proposed model.

Table 6: Average performance metrics when K=3

Algorithms	Evaluation Metrics			
	Accuracy	Precision	Recall	F1-Score
CNN	0.86	0.78	0.89	0.83
CNN+PSO	0.83	0.79	0.752	0.782
CNN+GA	0.872	0.87	0.863	0.87
Proposed MWHO Model	1.00	1.00	1.00	1.00

Table 7 depicts the average performance metrics of the previous methods at the detection of tumors when K=4. The MWHO system is compared with CNN, CNN+PSO and CNN+GA through accuracy, precision, recall and F1 score. The proposed system proves to be better as in all performance metrics, it shows hundred percent. The previous methods indicate lesser values than the proposed model.

Table 7: Average performance metrics when K=4

Algorithms	Evaluation Metrics			
	Accuracy	Precision	Recall	F1-Score
CNN	0.858	0.851	0.850	0.851
CNN+PSO	0.862	0.852	0.850	0.850
CNN+GA	0.870	0.87	0.863	0.87
Proposed MWHO Model	1.00	1.00	1.00	1.00

Table 8 depicts the average performance metrics of the previous methods at the detection of tumors when K=5. The MWHO system is compared with CNN, CNN+PSO and CNN+GA through accuracy, precision, recall and F1 score. The proposed system proves to be better as in all performance metrics, it shows hundred percent. The previous methods indicate lesser values than the proposed model.

Table 8: Average performance metrics when K=5

Algorithms	Evaluation Metrics			
	Accuracy	Precision	Recall	F1-Score
CNN	0.866	0.862	0.86	0.863
CNN+PSO	0.868	0.854	0.855	0.86
CNN+GA	0.90	0.882	0.87	0.87
Proposed MWHO Model	1.00	1.00	1.00	1.00

Ablation Analysis of the Proposed Algorithm (Classification)

In this part, ablation experimentation is carried out to prove the effectiveness of the each component in the proposed model. The ablation process proves the betterment of the proposed system in classifying the kidney tumors and also it is evident that it outperforms the other existing algorithms. Table 9 presents the evaluating metrics of the proposed system when comparing the previous algorithms after conducting ablation experiments.

Table 9: Performance of the proposed system after the ablation experimentation

Algorithms	Performance Metrics			
	Accuracy	Precision	Recall	F1-Score
CNN	0.86	0.78	0.89	0.83
CNN+PSO	0.83	0.79	0.752	0.782
CNN+GA	0.872	0.87	0.863	0.87
Proposed MWHO Model	1.00	1.00	1.00	1.00

CONCLUSION AND FUTURE SCOPE

CNN integrated with MWHO is developed to test and train the network in this research work. The images from the kaggle dataset are taken for the experiment. The accuracy values of CNN, CNN combined with PSO and CNN combined with GA methods are 86.6%, 86.8%, and 96%, respectively. The accuracy value for the proposed KT detection system 100%. The proposed model achieved promising results when K is equal to 5. The future work includes the detection of the tumor subtypes. The model is to be tested valid for all datasets.

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