IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

Received April 19, 2020, accepted May 5, 2020, date of publication May 18, 2020, date of current version June 9, 2020.

Digital Object Identifier 10.1109/ACCESS.2020.2995310

Prediction of Chronic Kidney Disease Using Adaptive Hybridized Deep Convolutional Neural Network on the Internet of Medical Things Platform

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ABSTRACT Chronic Kidney disease is a severe lifelong condition caused either by renal disease or by impaired functions of the kidneys. In the present area of research, Kidney cancer is one of the deadliest and crucial importance for the survival of the patients ' diagnosis and classification. Early diagnosis and proper therapy can stop or delay the development of this chronic disease into the final stage where dialysis or renal transplantation is the only way of saving the life of the patient. The development of automated tools to accurately identify subtypes of kidney cancer is, therefore, an urgent challenge in the recent past. In this paper, to examine the ability of various deep learning methods an Adaptive hybridized Deep Convolutional Neural Network (AHDCNN) has been proposed for the early detection of Kidney disease efficiently and effectively. Classification technology efficiency depends on the role of the data set. To enhance the accuracy of the classification system by reducing the feature dimension an algorithm model has been developed using CNN. These high-level properties help to build a supervised tissue classifier that discriminates between the two types of tissue. The experimental process on the Internet of medical things platform (IoMT)concludes, with the aid of predictive analytics, that advances in machine learning which provides a promising framework for the recognition of intelligent solutions to prove their predictive capability beyond the field of kidney disease.

INDEX TERMS Chronic kidney disease, deep learning, convolutional neural network, IoMT.

I. INTRODUCTION

Kidney cancer is among the deadliest, and unfortunately, it is difficult to detect early on by normal clinical means [1]. Despite being one of the top ten killer cancers, research into renal cancer is lacking [2] in the present area of research. Many types of cancer in the medical community have dominated it, which has delayed modern diagnosis and treatment methods. Patients with renal cancer have restricted treatment options for decades, and life expectancy is analyzed in most cases below one year. Automatic diagnostic tools will, therefore, help a doctor to easily and quickly identify the disease and help patients survive [3]. In many automatic medical diagnostic tools, classification methods are often used and It's a difficult task to identify early kidney disease [4]. The testing pressure can be reduced by utilizing the tool [5] and Chronic renal disease (CKD) impacts kidney structure and function. A longer disease can cause complications, including weak bones, high PB, anemia, nerve damage, blood or heart vessel issues, etc [6]. The disease occurs at several levels depending on the stage of the glomerular filtration rate (GFR) [7]. Chronic renal disease (CKD) has grown rapidly and is linked with the extreme risk of cardiovascular and final-stage renal disease that may be avoided by early discovery and therapy of humans at risk. Recently, Machine learning algorithms can be utilized to efficiently evaluate the disease in the previous step [8]. Machine predicted analysis is nowadays the most common for kidney disease detection. It is known as one of the health hazards of establishing and emerging countries in the early stages; therefore, it is a couple of side effects that the

The associate editor coordinating the review of this manuscript and approving it for publication was Wei Wei.

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CKD may not become apparent until vital kidney function is impeded. CKD therapy concentrates on minimizing the movement of kidney risk by regulating the basic reason for the disease at the initial stages [9]–[11].

The development of the CKD with many other clinical features is related to epidemiology. In general, nephraphrologists use two tests to check for the use of CKD, blood testing and urine tests [12]. Factors that can affect CKD are genetics, diabetes, obesity, and aging. The blood test tests to check, how well the kidneys filter the blood to eliminate creatinine, a normal muscle breakdown waste [13]. In comparison, the urine test will indicate that protein remains in the urine and In particular, protein (albumin) is a blood component that is usually not transmitted into the urine by the kidney filter [14]. When the urine test indicates that albumin occurs, it means that the kidney filters are damaged and can represent chronic kidney disease. This article describes the prototyping of a wireless embedded health monitoring framework which is used as the IoMT portal. This paper presents multiple models of early prediction kidney disease analytics which could be incorporated into a proposed architectural monitoring system for addressing a lack of health analytics within the existing monitoring system [15]. In general, a patient's health condition could be tracked or assessed by taking other physiological signs into account. Hence, Relying on the physiological parameter of the disease which is inadequate to detect or to predict its occurrence for difficult chronic diseases such as kidney diseases and diabetes [16].

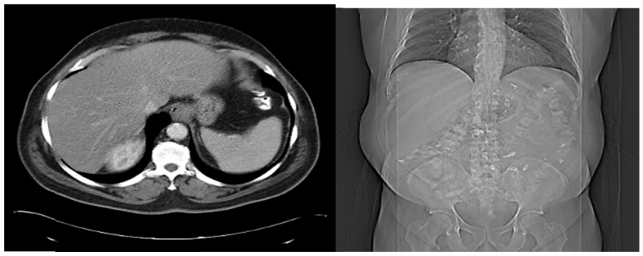


FIGURE 1. (a) Abdominal CT scan of revealed metastatic kidney disease (b) Coronal computed tomography image of Polycystic kidneys [17].

In this research paper, the Adaptive Hybridized Deep Convolutional Neural Network (AHDCNN) has been proposed for the detection and diagnosis of Chronic Kidney Disease. The proposed model extracted the CNN features that has been fed to support vector machine with its development and observed kidney mitosis. A pre-trained CNN trained on a large scale to detect renal cancer by removing features from CT images. An automatic CNN-based magnetic resonant image segmentation system has been discussed and the corresponding dataset images have been shown in Figure.1.(a & b). Further, it has been examined the local and global contextual features of the CNN model, the system increased speed and successfully detected the kidney cancer by utilizing a fully connected layer within the final layer of CNN. A fully convolutional network(FCN) and conditional random fields (CRFs) have been used for the segmentation of kidney cancer. First, the image patches has been used for the training on the FCN model and the training of conditional random fields has been performed. Finally, the system has calibrated directly with the image slices. Adjacent image patches in a single pass are paired with a complex CNN model training scheme. After the 3D segmentation of images using CNN modality, the false positives has been eliminated by utilizing the fully-connected 3D random field [18]–[20].

A. The main outcomes of the paper are,

- To propose the Adaptive Hybridized Deep Convolutional Neural Network (AHDCNN) for the prediction and diagnosis of Chronic Kidney Disease.
- To examine the ability to use either blood or urine tests to predict CKD and then assess its precision and applicability. Use the most important and representative parameters for the early prediction of CKD by machine learning methods.
- The experimental results has been performed on the Internet of Medical Things platform and the sample datasets has been taken from https://nihcc.app.box.com/v/DeepLesion

The remainder of the paper represented as follows: Section 1 and section 2 discussed the background and existing methods for chronic kidney disease prediction. In section 3 the adaptive hybridized deep convolutional neural network has been proposed for the early detection and diagnosis of chronic kidney disease. In section 4 experimental outcomes has been illustrated. Finally, section 5 concludes the proposed article.

II. RELATED WORK

Muhamed Ali *et al.* [21] proposed the Neighbourhood Component Analysis (NCA) for the classification of kidney cancer subtypes utilizing miRNA genome data. The classification of a given miRNA sample in kidney cancer subtypes is intended to extract discriminative properties out of miRNAs and Long Short Term Memory (LSTM), the form of recurrent neural network. Dataset 35 of the most biased miRNAs were selected by the NCA process. This sub-set of miRNAs allows LSTM to group kidney cancer miRNAs into five sub-types with an average accuracy of about 95% and Matthews's correlation coefficient values of about 0.92 under 10 random clustered 5 times, which are very close to the average output of all miRNAs for rating purposes.

Sheehan *et al.* [22] introduced the Deep Neural Network (DNN) for the detection and classification of novel renal histologic phenotypes. They demonstrate that machine learning with DNN has strong widespread performance in several processing tasks of histologic images. The neural network extracted and used quantitative image features as classifications to classify variations between mice of different genotypes. The segmentation of non-glomerular and the genotype of the animal-based on its quantitative image features was shown to achieve excellent performance.

In a systemic pathologic analysis on the Internet of medical things platform (IoMT), these features were not found.

Ren *et al.* [23] suggested the Hybrid Neural Network (HNN) for detecting kidney disease. They modeled the prediction problem in particular as a binary classification function to capture the information fully in Electronic Health Records(EHR), They suggested a hybrid neural network that integrating a bidirectional long short term memory (BiLSTM) and autoencoding networks. Based on many of the raw EHR data, the authors reported building a data set. The collection contains 35,332 reports from patients with hypertension. Test results show that 89.7 percent of the accuracy of the proposed neural model for the task is achieved. The model was presented with a synthetic neural network with the findings of the analysis of various models that have shown to the efficacy of the suggested neural model depends on the built data set.

Kallenberger and Schmidt [24] initialized the Recurrent Neural Network (RNN) to forecast the development of acute kidney injury. The RNN will determine the input sequence so that responses to previous sections of the sequence are considered at a certain point in the sequence. The probability of Acute Kidney Injury (AKI) in clinical parameter sequences was predicted by RNN. For each of AKI's defined severity levels, the model correctly predicted around 56% of all AKI episodes would advance clinical diagnosis in a time interval of up to 48 hours at the chosen point of operation with 33% accuracy. That means AKI was present in one patient out of three predicted cases, while the prediction in the other two was reported wrong. Further testing has shown that in patients with chronic kidney disease with 57 percent of false-positive estimates have occurred.

Santini *et al.* [25] introduced the Ensembling Multi-stage deep learning approach (EMS-DLA) for kidney tumor segmentation. To integrate prediction results from previous phases, a combining procedure will be applied to the variance between individual models. The average Dice score for kidney and children's tumors is 0.96 and 0.74, respectively on 90 unidentified test cases. The findings are positive and might be improved by taking advance knowledge of benign cysts into account, which frequently decreases tumor segmentation on the Internet of medical things platform (IoMT). The outcomes are significantly reduced and have been reported in this paper. The relatively large batch size was utilized, batch normalization properties were better exploited in contrast to the previously attempted smaller batches (8-16). The results obtained by 32 samples were improved among the assessments.

To overcome these issues, in this paper, the Adaptive hybridized Deep Convolutional Neural Network has been proposed for the prediction of chronic kidney disease. In several computer vision tasks like object detection, image recognition, and semantic segmentation, Convolution neural networks (CNN's) demonstrated superior performance. The main advantage of CNNs is that they require no handcrafted features compared with many other machine-learning-based approaches (e.g. random forests). CNN's for the location and segmentation of kidneys with mild morphological changes with patch-sensitive approaches to CT has been previously suggested with medical imaging.

III. ADAPTIVE HYBRIDIZED DEEP CONVOLUTIONAL NEURAL NETWORK (AHDCNN)

In this paper, the Adaptive Hybridized Deep Convolutional Neural Network (AHDCNN) has been proposed for the prediction diagnosis of chronic kidney disease. In this paper, the datasets has been taken from http://www.mediafire.com/datasets. AHDCNN has been trained to achieve the best object recognition performance in the large scale image of kidney disease. Each convolutional layer comprises 3 stages: spatial max pooling, group normalization ReLU gating, and linear convolution. The output of every layer has been extracted for each image input of CNN to form the image hierarchy features. Compared to an FCN, smoothing and prior knowledge can be used to achieve an accurate segmentation of the integrated system through AHDCNN. Besides, it is integrated the model in the training phase to adjust the CNN differently than the use of the model as a post-processing tool. It provides the utilization of unlabeled data in a semi-monitored environment during preparation. Unlike the MRI signals, the understanding of kidney cell activity has been transformed into a CNN understanding of functionality representation by training a mapping of MRI signals to hybridized functionality derived from Convolutional Neural Networks. Figure 2 shows the proposed AHDNN method architecture.

This research aims to explore whether a deep learning model for consistent renal cell rating forecasts from CT (CECT) improvement can analyze the tumors. The affected tumors has been annotated manually with radiology based on radiology records, which is based on qualified radiology residents of the CECT corticomedullary process. Rectangular ROIs has been chosen and used as inputs to the Deep CNN pre-trained in ImageNet and transfer learning through the adjustment of two coefficients in the last two convolutional layers. Figure 3 shows the ROI extraction of the Kidney disease image.

Preposition 1: As inferred from figure.3.CNN is a neural feed-forward network that processes the signal directly without loops and cycles. That can be depicted as follows,

$$H\,(y) = h_M\,(h_{M-1}\,(\ldots(h_1\,(Y)))) \tag{1}$$

As shown in the equation (1) where M indicates the number of hidden layers, Y is the input signal and h_M indicates the respective function to the layer M. A fundamental CNN model has a convolutional layer which contains a function h with multiple convolutional kernels $(g_1, \ldots g_{l-1}, g_l)$. Each g_l indicates a linear function in l^{th} Kernal expressed as the following equation.

$$g_l\,(y, x) = \sum_{w=-n}^{n} \sum_{r=-u}^{m} \sum_{u=-t}^{s} U_l\,(w, r, u)\,Y\,(y - w, x - r, z - u) \tag{2}$$

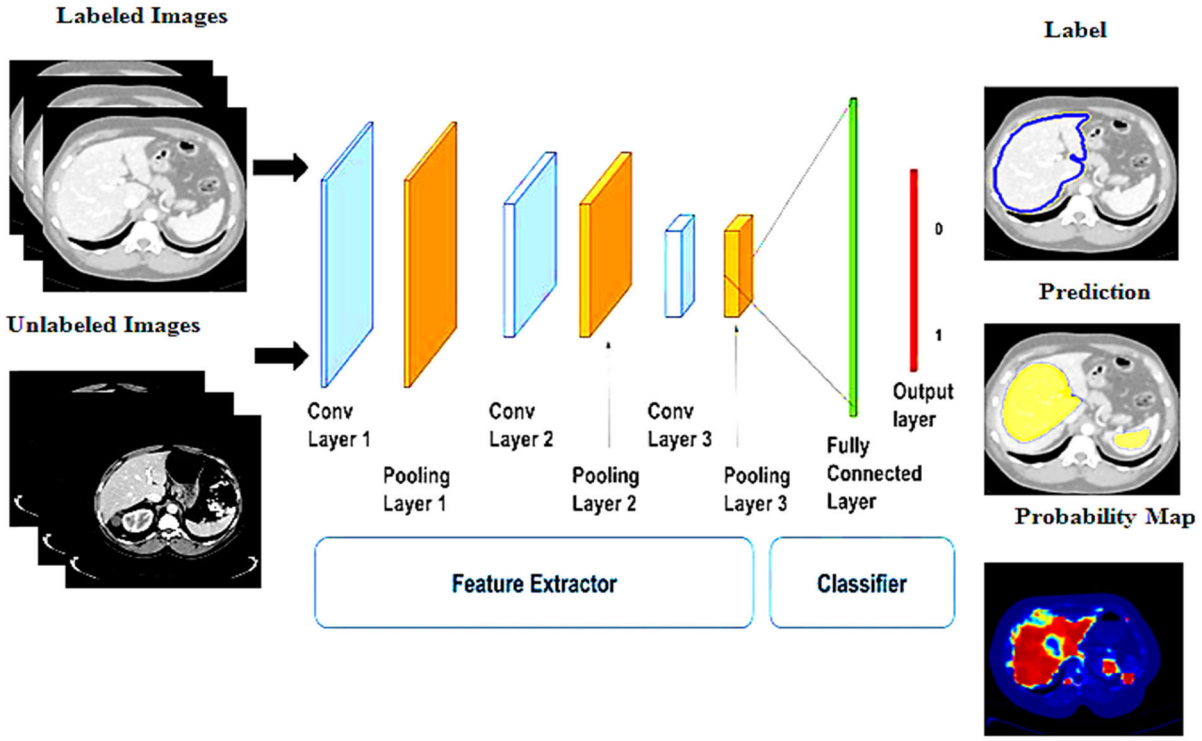


FIGURE 2. The proposed AHDCNN method.

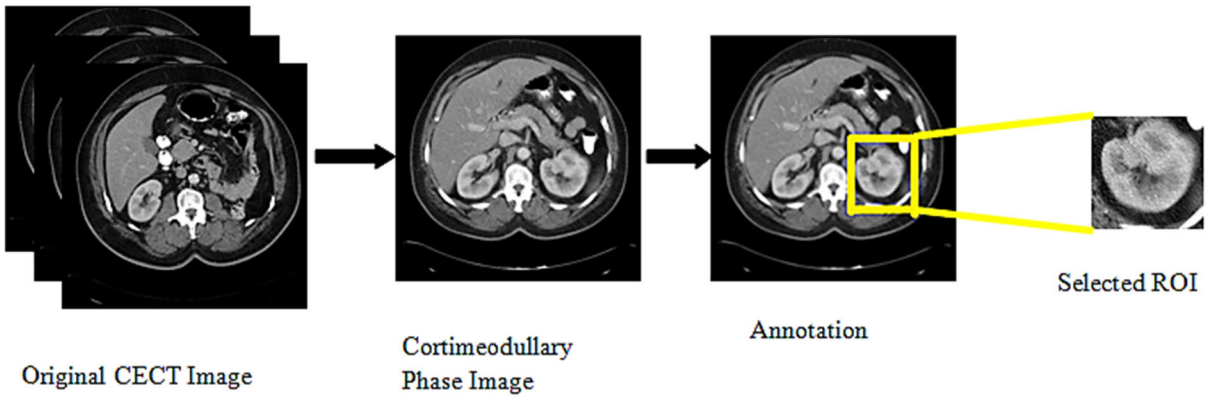


FIGURE 3. Kidney tumor ROI extraction.

As shown in equation (2) where (y,x,z) denotes pixel position of input Y, n denotes height, m indicates the width, s is the depth of the filter, and U_l denotes the weight of l^{th} kernel.

In CNN, the main purpose of pooling is to subsample the nearby pixels, i.e. they are summarized and replaced by summarized characteristics in the results at a place. This Pooling reduces dimensionality and invariance of rotary transformations and translation. Many pooling functions are available; hence it is one of the most common is max pooling, where the output is the maximum value of the rectangle pixel field. The output is the average of the rectangular neighborhood in the average pooling function. The weighted average is another form based on the distance from the center pixel. Pooling helps to make the image invariant to small modifications of the input translation.

The following equation refers to Atrous Convolution:

$$x[j] = \sum_{l=1}^{L} y[j + t \cdot l]s[l] \tag{3}$$

As shown in the equation (3) where y[j] is the 1D input signal, s[l] is the filter of the length of l, and t is the stride rate with that the input signal is sampled. x[j] is the output of the atrous convolution. Atrous convolution is applied over the input y

for each location j on the output x and a filter s with atrous rate t, which respect to the stride rate.

Deep residual learning is used to address the degradation problems that arise as deep networks converge, i.e. the increasing complexity of the depletion of precision and degradation. The residual network makes the layers stacked directly to fit into the map instead of into a predetermined context frame. The experimental results improve residual network optimization and achieve precision with a substantial increase in depth. The Skip connections help deep neural networks with transverse information, Because many layers move through, gradient information may be lost, known as the problem of the disappearance gradients. With the Skip Connection function information is passed to lower levels so that the minute details are easier to distinguish. Any spatial information is lost as a result of full pooling while skipping connections allow more information about the final layer to increase the accuracy of classification.

Various activation functions which can be used in the activation layer:

(i) A sigmoid activation function is given by equation (4):

$$\rho\,(y) = \frac{1}{1 + e^{-y}} \tag{4}$$

The composition is non-linear and allows us the ability to merge the layers. The range of the y is fairly steep, concerning small variations in the values of x, from ± 2 on the x-axis. The Y values are suddenly altered in the y values. Their output remains within the range of (0,1) one of the advantages of this activation function.

(ii) Tanh function is stated as follows,

$$f\,(y) = \tanh\,(y) = \frac{2}{1 + e^{-2y}} - 1 \tag{5}$$

The scaled sigmoid function is defined as:

$$\tanh\,(y) = 2sigmoid\,(2y) - 1 \tag{6}$$

It is between -1 and 1. The gradient for the tanh is stronger than the sigmoid function.

(iii) The most commonly employed activation function is a Rectified linear unit (ReLU), where the g represents a non-linear pixel-wise function. That is, the output x is given, where x is positive, otherwise, it is 0.

$$h\,(y) = \max(0, y) \tag{7}$$

ReLU is non-linear in its combination, which means that various layers can be stacked. The range is between zero and infinity, so that activation will blow up as well. For the pooling layer, h decreases the functional size when acting as a nonlinear layer-sampling function. The 1×1 convolutional kernel is a fully connected layer and the prediction layer is a softmax that predicts the likelihood of Y_i belonging to different classes.

The hidden vector sequence $f = (f_1, \ldots f_R)$ is estimated by CNN from the input sequence $u = (u_1, \ldots u_R)$ by iteration of r = 1 to R and an output sequence $o = (o_1, \ldots .o_R)$ is calculated.

$$f_r = F\left(S_{uf}u_r + S_{ff}f_{r-1} + a_f\right) \tag{8}$$

$$o_r = S_{fo}f_r + a_o \tag{9}$$

As shown in the above equations where S indicates the weight matrix and it denotes the bias vectors. F is the hidden layer function, which is a sigmoid function.

The segmentation pipeline begins with a preprocessing phase that mixed histogram equalization with a non-parametric bias correction, which partially reduces inconsistencies and noise due to low-frequency non-uniformity intensity inhomogeneity. Accurate segmentation of the renal is a demanding task because of kidney movement because of breathing and heart beatings; changes in kidney form due to anatomical differences between the patient; low contrast between the renal and other abdominal images and, in particular, higher gradient strengths and length. Low SNR and artifacts complicated by long acquisition time image alignment and geometric distortions. Our segmentation uses several image features to precisely delineate the kidney to meet these challenges and thus facilitate an analysis of the transplant status. Figure 4 shows the MRI samples of typical coronal cross-section of (a) low contrast between surrounding and kidney abdominal tissues (b) inter-patient anatomical variances (c) image artifacts (d) geometric distortion boundaries.

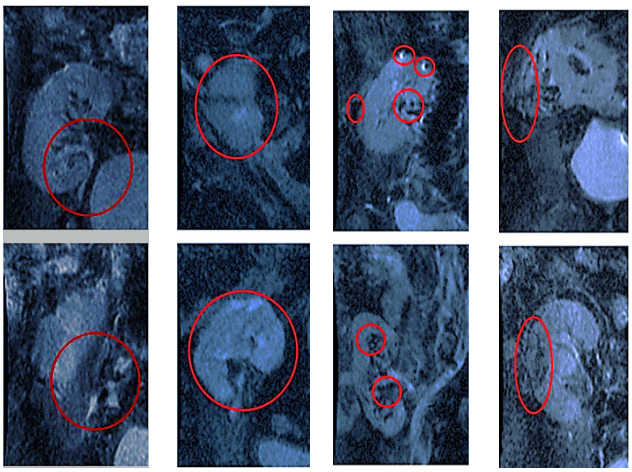


FIGURE 4. Coronal cross-section MRI sample images (a) low contrast between surrounding and kidney abdominal tissues (b) inter-patient anatomical distinctions (c) image artifacts (d) geomet5. classification of kidney cancer.

Preposition 2 (Autoencoders Mathematical Modeling): Autoencoders are part of the neural network's unsupervised learning class. They learn a lower dimension representation from the input data. Further, The input layer followed by a hidden layer and the output layer has a simple AE structure. Two phases of training: coding and decoding have been completed. In the initial step, input J is encoded by depictions of

I by a weight matrix $\Upsilon_{J,I}$ and bias $A_{J,I}$.

$$I = \rho\left(\Upsilon_{J,I}J + A_{J,I}\right) \tag{10}$$

As shown in the equation (10) where ρ is an activation function.

In the next stage, the representation I is decoded utilizing new weight matrix $\Upsilon_{I,\hat{J}}$ and bias $A_{I,\hat{J}}$ to rebuild $\hat{J}$,

$$\hat{J} = \rho'\left(\Upsilon_{I,\hat{J}} + A_{I,\hat{J}}\right) \tag{11}$$

As shown in the equation (11) where ρ' is the new activation function. $\Upsilon_{I,\hat{J}}$ can be reviewed as the transpose of $\Upsilon_{J,I}$. These Autoencoders are trained to reduce the error stated as,

$$\arg\max_{\Upsilon,A} \left\| J - \hat{J} \right\|^2 \tag{12}$$

Patients' survival time with deep convolutional neural networks directly from the pathological images for renal cancer has been successfully predicted. A pre-trained, large-scale CNN for kidney cancer detection by eliminating features from the CT images. They used 2D CT images to identify kidney nodes, 3D CT images to be used for end-to-end testing on CNN multi-view pictures. The 2D patches has been extracted from the 3D images and used on CNN to extract features. After fusion, the features has been fed to the classifier.

This model is intended to solve the variable nodule size problem. This provides the multi-scale functionality by replacing the max-pooling layers in the CNN system with the multi-crop pooling layer. A randomized rectified linear unit (RReLU) has been used for non-linear transformation. Convolutional operation is as follows defined,

$$x^k = RReLU\left(\sum\nolimits_l b^{lk} \times g^l + a^k\right) \tag{13}$$

As shown in the equation (13) where g^l is the l^{th} input map and x^l is the l-th output map. b^{lk} are the convolutional kernel between the l-th input map and the kth output map. a^k is the bias of the kth output map. RReLU is stated as (10)

$$RReLU = \begin{cases} y \; if \; y \geq 0 \\ \dfrac{y}{c} \; if \; y < 0, \quad c \sim V\left(a_k, a_v\right) \end{cases} \tag{14}$$

As shown in the equation (14) where $V\left(a_k, a_v\right)$ is the uniform distribution and b is a random factor sampled from this distribution. a_k is the lower bound of the distribution and a_v is the upper bound of the distribution. The utilized max-pooling is stated as,

$$x^j_{(i,l)} = \max_{0 \leq n,m<w} g^j_{(i-w+n,l-w+n)} \tag{15}$$

As shown in the equation (15) where $x^j_{(i,l)}$ and $g^j_{(i-w+n,l-w+n)}$ are neurons position at (i,l) and (i-w+n, l-w+n) in the jth output correspondingly, and n and m are position offsets, whereas w is the pool size. The technique of multi-crop pooling captures nodule central features while the standard max pool is used for the collection of subsets of features and the reduction of map size. It can, therefore, be said that essentially, the pooling process decreases the features by one point. Repetitive pooling strategies are used to allow the system to achieve multi-level features in multi-crop pooling. Let's consider the three mixed up nodule centric features $f = [f_0, f_1, f_2]$ created from T_0, T_1 and T_2 correspondingly. The size T_0 is $k \times k \times m$, T_1 has the size $k/2 \times k/2 \times m$ and T_2 has the size $k/4 \times k/4 \times m$. m is the number of features.

$$f_j = max - pool^{(2-j)}T_j, j = 0, 1, 2 \tag{16}$$

As shown in the equation (16) where $max - pool$ is the frequency of the max pooling on regions T_j. T_1 is the center region cropped from the T_0 is one time for the max pool to generate the feature f_0. T_0 is the max -pooled twice and generates the feature f_1. T_2 is the center region cropped from T_1; it is not max-pooled it serves as a feature f_2. The result of a multi-crop is the concatenation of these features. For the learning of this Network, entropy is minimized and defined as:

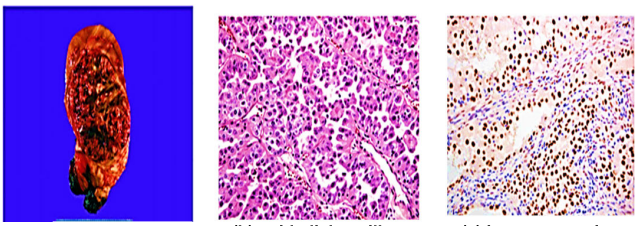
$$LOSS = -\left(plogQ_1 + (1-p)\log q_0\right) \tag{17}$$

As shown in the equation (17) where p has the suspiciousness value of 1 for high suspiciousness and 0 for low suspiciousness. For the training of the network, gradient descent is followed. The dataset used consists of 100 patients with a diameter of a nodule of between 3 and 30 mm. They achieved an accuracy of 97.14%, 0.77% sensitivity, and 0.93% specificity.

Kernel trick is a mathematical function that converts non-linear, non-separable data into linearly separable data by transforming the data into their higher dimensional space,

$$L\left(n, m\right) = \langle f(n), f(m) \rangle \tag{18}$$

The deep model of implementation on the classification of kidney cancer can capture information of interest in respect of only considering the kidney nodules with renal masses with the hemorrhagic area as shown in Figure.5(a).



(a) Kidney Renal mass surface (b) epithelial papillary cells (c) immunoreactive tumor cells

FIGURE 5. Classification of kidney cancer.

They have calculated 26 hand-crafted features to avoid this additional information and fused them with the detection of CNN-extracted lung nodular epithelial papillary cell features as shown in Figure.5.(b). Instead of using a pre-trained CNN, picked the candidate region for ground-glass opacity (GGO) using the CNN model, determined the GGO candidate

regions by the equation:

$$h(y,x,z) = \sqrt{\left(\frac{\Delta\sigma y}{\Delta y}\right)^2 + \left(\frac{\Delta\sigma x}{\Delta x}\right)^2 + \left(\frac{\Delta\sigma z}{\Delta z}\right)^2} \quad (19)$$

As shown in the equation (19) where y,x and z directions of the immunoreactive tumor cells of figure.5.(c) been calculated by the following equations,

$$\Delta\sigma y = |\sigma(y+1,x,z) - \sigma(y,x,z)| + |\sigma(y,x,z) - \sigma(y-1,x,z)| \quad (20)$$

$$\Delta\sigma y = |\sigma(y,x,x+1,z) - \sigma(y,x,z)| + |\sigma(y,x,z) - \sigma(y,x-1,z)| \quad (21)$$

$$\Delta\sigma y = |\sigma(y,x,z+1) - \sigma(y,x,z)| + |\sigma(y,x,z) - \sigma(y,x,z-1| \quad (22)$$

The morphology has been followed by the techniques of labeling and the noise has been reduced using thresholding methods for each sphericity of the volume. The GGO candidates has been done with this operation and the data has been analyzed using the Internet of medical things platform (IoMT). They used the support vector classification and achieved true positives of 93% and false positives of 52% based on the simulated result which has been shown as follows,

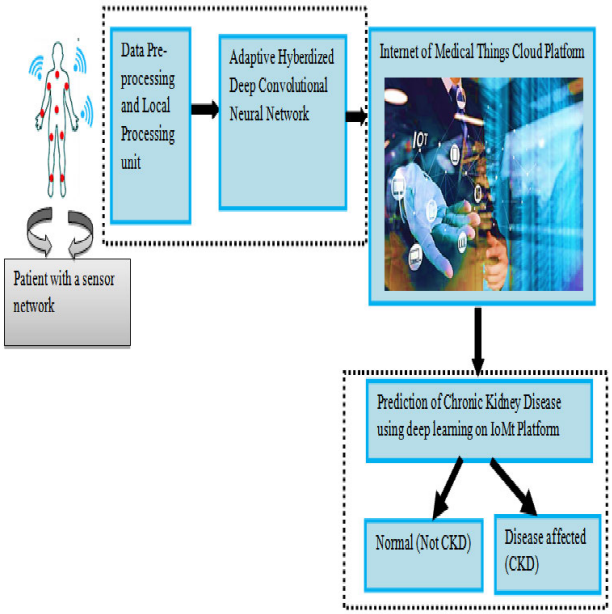


FIGURE 6. Internet of medical things for chronic kidney disease prediction.

IV. EXPERIMENTAL RESULTS

This paper describes the prototyping of an integrated health care model depends on the IoMT model. Figure 6 shows the Internet of Medical Things for chronic kidney disease prediction block diagram. IoMT's implementation has enabled the advancement in medical supervision from face-to-face consultation to telemedicine or e-health systems. Using IoMT, the physical body state can be remotely tracked and doctors can detect abnormalities. This paper presents the analysis framework for kidney disease and diabetes in health care. The forecast results show the potential for integrating a classification model into the suggested system to determine possible risks in the early treatment stages of certain diseases. The monitoring of vital signals by remote sensors and the delivery of permanent and real-time information to the respective expert using cloud services are an example of the Internet of Things solutions for health care. Internet of Things relies on cloud computing and serves as a network for the collection of data from sensors instead of the hardwired machine-to-machine (M2M) system with its many wired connections, which take up precious space. Internet of Things links individual devices to the Internet, stores cloud data and displays the information gathered on a mobile, tablet or network-based computer. Figure 7 shows the example of kidney image segmentation as shown in figure 7(a) which shows the input kidney image with different complexities. Figure 7(b) shows the adjust intensity values to a specified range.

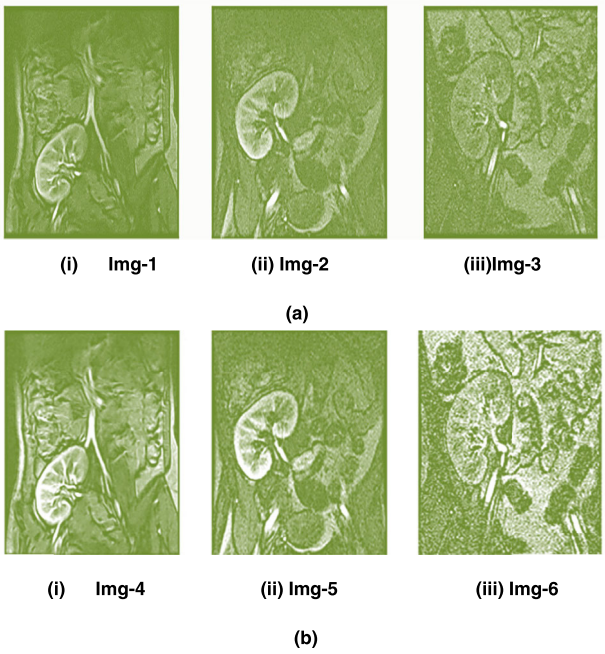
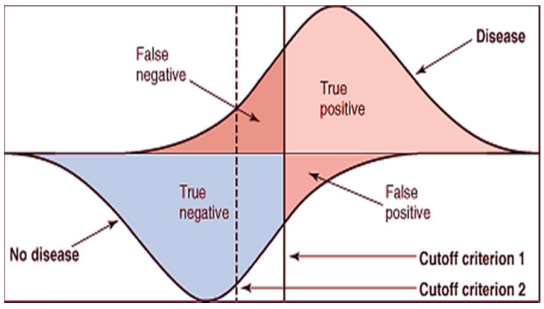


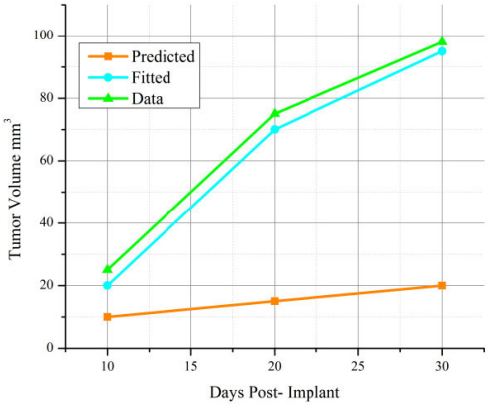
FIGURE 7. (a) Example of kidney image segmentation (a) input kidney images with various complexities (img-1 to img-3) (b) Adjust Intensity values to specified Range(img-4 to img-6).

A. ACCURACY ANALYSIS FOR NUMERICAL CONSISTENCY

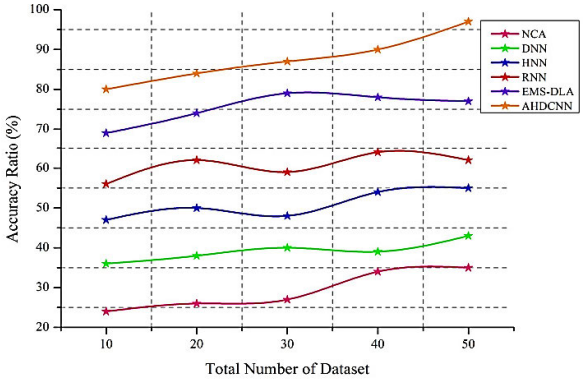
The combined deep features and processing features. Two SVM classifiers has been included in the proposed system, one on local binary patterns and robust speed-up features; the other on raw images using the deep features derived from the CNN model and probability scores has been generated as shown in Figure.8(a). In the final decision, the higher scores has been taken.



(a)



(b)



(c)

FIGURE 8. (a) Specific probability analysis. (b) Growth curve prediction (c) Accuracy ratio analysis.

Deep residual learning is used to address the problems of degradation which occur when the deep network converges, i.e., with the saturation of accuracy and degradation as the depth increases. The residual network requires the stacked layers directly to fit into the residual maps instead of the desired frame. The experimental results make it easier to model residual networks and achieve precision with a significant increase in size. Figure 8(b) shows the growth curve prediction using proposed AHDCNN and 8(c) shows the accuracy ratio of the proposed AHDCNN method. Accuracy establishes the right classification of the number of true positive TP, true negative TN, false-positive FP, and false-negative FN, (23) as shown at the bottom of this page. ReLU is nonlinear in its combination, which means that various layers can be stacked. The range is between zero and infinity, so that activation will blow up as well. For the pooling layer, h decreases the functional size when acting as a nonlinear layer-sampling function. The 1×1 convolutional kernel is a fully connected layer and the prediction layer is a softmax that predicts the likelihood of Y_i belonging to different classes with an accuracy ratio as shown in table.1.

TABLE 1. Accuracy analysis with numerical consistency.

Total Number of datasets	NCA	DNN	HNN	RNN	EMS-DLA	AHDCNN
10	24.5	36.7	47.7	56.7	69.8	80.2
20	26.7	38.9	50.1	62.3	74.5	84.5
30	27.9	40.1	48.2	59.8	79.2	87.2
40	34.5	39.8	54.4	64.5	78.6	90.4
50	35.7	43.2	55.9	62.9	77.2	97.3

1) F1 SCORE

Precision: This monitors the accuracy of the model by testing the true positive effects of the predicted ones. The proportion of positive items correctly predicted to the total predicted items is:

$$Precision = \frac{True\ positive}{true\ positive + False\ positive} \tag{24}$$

Recall: The number of true positive values recorded and labeled as positive by the model is determined.

$$Recall = \frac{True\ positive}{True\ positive + False\ Negative} \tag{25}$$

F1-score is the precision and recall function. The balance is determined if a precise-recall balance is required.

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{26}$$

Figure 9 shows the f1-score of the proposed AHDCNN method. The proposed AHDCNN method achieves a high precision-recall ratio when compared to NCA, DNN, HNN, RNN and EMS-DLA existing methods.

Table 2 shows the F1-score of the proposed AHDCNN method. Renal Disease Diet Changes and Walser formulae

$$Accuracy = \frac{True\ Positive + True\ negative}{True\ positive + True\ negative + false\ positive + false\ negative} \tag{23}$$

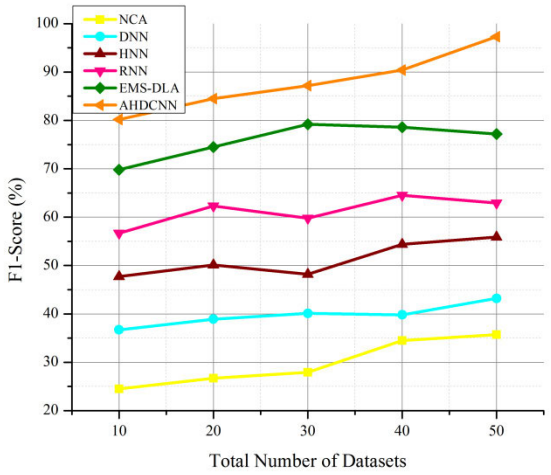


FIGURE 9. F1-Score analysis with numerical results.

TABLE 2. F1-score evaluation.

Total Number of datasets	NCA	DNN	HNN	RNN	EMS-DLA	AHDCNN
10	24.5	36.7	47.7	56.7	69.8	80.2
20	26.7	38.9	50.1	62.3	74.5	84.5
30	27.9	40.1	48.2	59.8	79.2	87.2
40	34.5	39.8	54.4	64.5	78.6	90.4
50	35.7	43.2	55.9	62.9	77.2	97.3

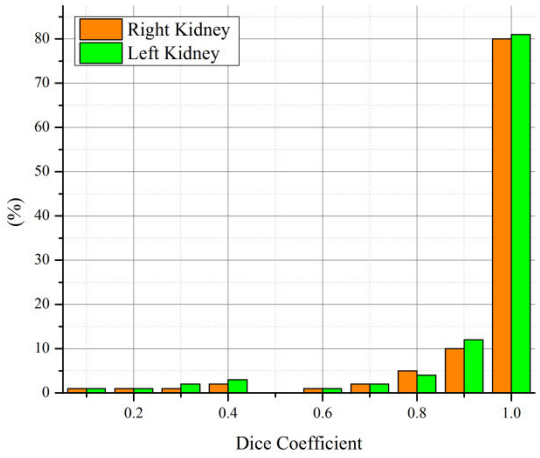


FIGURE 10. Dice COEFFICIENT ratio.

showed the best results with the lowest biases and highest precision. The proposed AHDCNN method has high precision and recalls ratio when compared to other existing methods.

2) DICE COEFFICIENT RATIO

The results, including the detection stage, for the automatic segmentation, has been compared by the Dice Index with the ground truth. The histograms of the two kidney ratings are shown in Figure 10. The right identification and segmentation has been performed in 80% of the kidneys (Dice > 0.90). In only 6% of the instances, the algorithm failed (Dice < 0.65). The total time of implementation is approximately 10 sec. It is a statistical analysis of the similarity between two samples:

$$Dice_{cof} = \frac{2 \times TruePositive}{2 \times True\ positive + false\ positive + falseNegative} \tag{27}$$

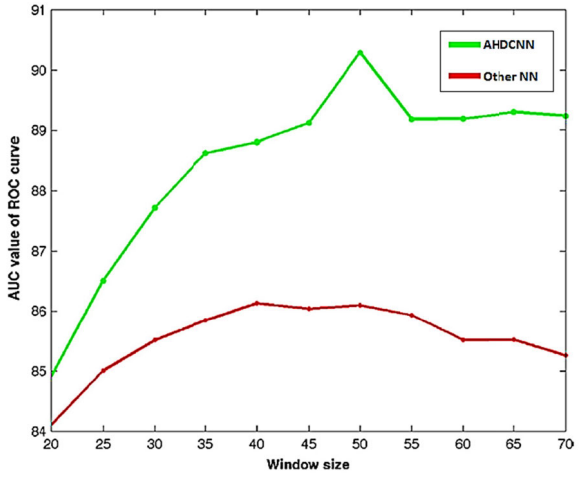


FIGURE 11. Receiver operating curve with AUC values.

3) RECEIVER OPERATING CURVE (ROC)

The ROC curve (ROC-curve) represents the efficiency of the proposed model at all classification thresholds. This is the representation of True positive vs. false positive ratio (TPR vs. FPR). The area under the integrated ROC curve of (0, 0) to (1, 1) is given by AUC. It gives the total measurement of all possible thresholds for classification. AUC is between 0 and 1. AUC The AUC value will be 1.0 for a graded 100% correct version, and 0.0 if there is a 100% incorrect classification. For two reasons, it is attractive: first, it has an invariant scale which means it tests how well the model is expected and not the absolute values. Second, it has an invariable classification threshold as it checks the accuracy of the model regardless of the threshold. Figure 11 shows the AUC values of the ROC curve of the proposed AHDCNN method. The following equations represent the TPR and FPR ratio.

$$TPR = \frac{True\ positive}{True\ positive + False\ Negative} \tag{28}$$

$$FPR = \frac{False\ positive}{False\ positive + True\ Negative} \tag{29}$$

4) THE LOSS FUNCTION OF AHDCNN

The loss function is useful for assessing the efficacy of AHDCNN in the dataset of kidney disease. The low loss function value indicates that according to assessment based on the sensitivity and specificity scale, the AHDCNN method

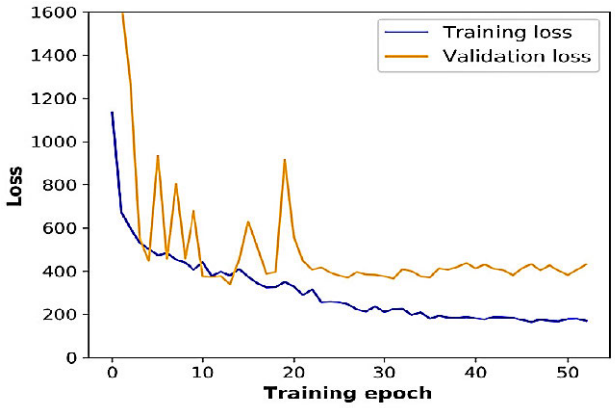


FIGURE 12. Loss function of AHDCNN.

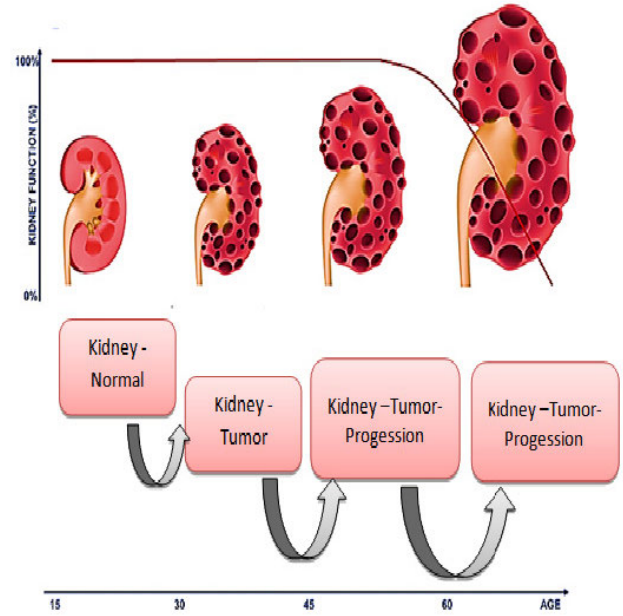


FIGURE 13. Kidney progression analysis.

classifies normal and abnormal kidney disease with greater precision. One of the methods used to determine the exactness of the AHDCNN process is its sensitivity. The estimate is as follows:

$$sensitivity = \frac{True\ positive}{True\ positive + fals\ positive} \tag{30}$$

Figure 12 shows the loss function, cross-entropy values of the proposed AHDCNN method.

Hence the loss function has been analyzed based on the Accurate segmentation of the renal which is a demanding task because of kidney movement because of breathing and heart beatings; changes in kidney form due to anatomical differences between the patient; low contrast between the renal and other abdominal images and, in particular, higher gradient strengths and length.

Deep residual learning is used to address the degradation problems that arise as deep networks converge, i.e. the increasing complexity of the depletion of precision and degradation. The residual network makes the layers stacked directly to fit into the map instead of into a predetermined context frame. The experimental results improve residual network optimization and achieve precision with a substantial increase in depth (Figure 13).

V. CONCLUSION

This paper presents the Adaptive Hybridized Deep Convolutional Neural Network (AHDCNN) for the early prediction and diagnosis of Chronic Kidney Disease (CKD). A deep learning system is used for identifying the distinctive subtypes of lesions from CT images in renal cancer. The collected data will initially be analyzed and the missing value will be replaced by the median value estimate. Different features associated with kidney disease are determined from the noise-free data and fed in the classifier implemented to identify variations in kidney patterns. By measuring the weight and bias value, the system trains feature in each hidden layer. The trained features are further taught by the multiple layers of the deep-belief network to recognize the irregular patterns. The efficient use of the learning and activation mechanism is a method of doubles-training to avoid kidney disease effectively. The study of regression and distribution of the data are then determined. The proposed approach is based on the method for deeper learning and ROIs given by radiologists has shown promising results in the classification of renal cell subtypes.

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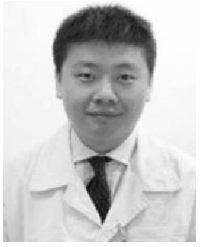

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