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Adaptive Graph Cut Tweedie Regressive Deep Convolutional Learning For Kidney Cancer Classification With CT Images

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ABSTRACT:

Medical image processing is the medical image analysis for improving quality through extracting the features for efficient classification. Image classification is an important one for premature recognition as well as treatment of kidney disease. Many researchers carried out their research on automated detection and classification of kidney cancer. However, the conventional classification methods has limited multi-modal incorporation, lack of generalization and reduced analyzability. In addition, the morphological characteristics are not identified and resulted in higher risk of misdiagnosis. In order to address these issues, Adaptive Graph Cut Tweedie Regressive deep Convolutional Learning (AGCTrdCL) Model is introduced. Major aim of AGCTrdCL is to perform automated recognition and classification of kidney cancer. AGCTrdCL Model performed four process for kidney cancer diagnosis. Initially, number of CT kidney images is considered as an input at input layer. After that, Adaptive Gaussian Image Preprocessing task is carried out in hidden layer 1 for noise filtering, contrast enhancement and normalization to enhance quality of kidney CT images. Then, Graph Cut Segmentation is carried out in hidden layer 2 for segmenting the pre-processed images into number of segments. Segmented regions of CT images are sent to the hidden layer 3. In that layer, Tweedie Regressive Feature Extraction (TRFE) process and classification is carried out in AGCTrdCL Model. Tweedie Regressive Feature Extraction is used to extract the shape, color and texture of segmented regions. With the extracted features, softplus activation function is used for performing efficient classification of kidney cancer. Finally, the output layer displays the classification results. The fine tuning process of the deep convolutional learning is carried out through gradient descent concepts. This in turn, efficient kidney cancer classification is carried out with higher accuracy and minimum time complexity. The performance parameters are kidney disease classification accuracy, kidney disease classification time, peak signal-to-noise ratio, FE accuracy, Pre, Rec, f1-score.

Keywords: Medical Image Processing, Kidney Cancer, Classification, Graph Cut Segmentation, Noise Filtering, Contrast Enhancement, Normalization.

Introduction

1. Preface

Kidney illness considered as the worldwide wellbeing concern. Early kidney disease detection is an essential one to minimize the mortality and to improve the treatment results. Conventional diagnostic techniques are time-utilizing one and susceptible to human fault. But, accuracy level was not improved and time complexity was not reduced. GVITKT was introduced in [1] for kidney tumor classification. But, the time consumption was not reduced by GVITKT model. A deep learning approach was introduced in [2] for recognition of kidney illness. New DL method was introduced with the Darknet53 for kidney disease classification. The designed

approach improved the accuracy and reduced the time complexity. Though the time complexity was reduced, the precision level was not improved by designed technique.

Intellectual kidney tumor segmentation as well as categorization method was introduced in [3] for identifying the tumor at initial stage. The segmentation and classification of kidney tumors was employed to attain improved treatments. But, the segmentation time was not reduced by designed model. A computationally efficient deep-learning architecture was designed in [4] with convolutional neural networks (CNNs) for kidney cancer tissue classification. Squeeze and Extract (SE) blocks eliminated the unnecessary contributions for increasing classification accuracy. But, the recall was not improved by designed architecture.

An innovative and customizable platform was introduced in [5]. Designed model improved the kidney disease diagnosis accuracy. It failed to reduce the time complexity. MSKd_Net architecture was introduced in [6] to gather local as well as global aspects. But, computational complexity was not reduced by designed architecture.

The machine learning technique was introduced in [7] depending on feature vector for automated classification with texture feature extraction. The feature vector was employed for improving computer aided diagnosis (CAD) accuracy. But, the error rate was not reduced by machine learning technique. A hybrid deep learning approach termed SpinalZFNet was introduced in [8] with feature extraction capabilities to categorize the kidney disease with CT images. SpinalZFNet approach boosts the accuracy level. But, the time complexity was not reduced by SpinalZFNet.

A fully automated system was introduced in [9] for renal tumor classes detection by means of automated segmentation and classification. The designed system improved the accuracy, sensitivity, and specificity. But, the time complexity was not reduced by it. A deep neural network architecture termed EFF-Net was introduced in [10] for RCC grading. It increased the accuracy and precision during classification task.

An explainable artificial intelligence (XAI) framework was introduced in [11] to construct the VGG16 convolutional neural network. XAI framework attained high classification performance with transparent decision support. However, the computational overhead was not reduced by XAI framework. Spinal Convolutional Neural Network (SpinalCNN) was introduced in [12] for kidney cancer detection through separating kidney image into normal or abnormal. However, the accuracy was not improved at the required level. An automated segmentation tool was introduced in [13] to support the clinical decision-making in reliable, accurate, and reproducible manner. A fully automated pipeline was carried out for segmentation of kidneys and renal tumors. But, the error rate was not reduced by designed tool.

1.1 Key contributions of the paper

The important contributions of the AGCTrdCL Model are given as:

- To improve kidney cancer disease recognition, AGCTrdCL Model has been introduced by integrating four process with deep convolutional learning architecture
- To increase the PSNR, AGCTrdCL Model performs image pre-processing by using adaptive gaussian image processing task to enhance the image quality
- To reduce the kidney cancer detection time, the AGCTrdCL Model utilizes graph cut segmentation. Through performing the segmentation task, the different geometric features are extracted as of pre-processed CT images using tweedie regression analysis.
- To enhance accuracy of kidney disease recognition and to reduce classification error, the softplus activation function is employed to analyze features and classify the kidney diseases. In addition, the gradient descent function is used for hyperparameter fine-tuning to reduce the classification error with high precision and recall.
- Finally, the experimental evaluation is carried out with several result parameters to show better effectiveness of AGCTrdCL when compared to existing methods.

1.2 Structure of manuscript

Remainder of this manuscript is structured as. Section 2 gives evaluation of literature review. Section 3 develops AGCTrdCL Model with neat architecture diagram. Section 4 explains experimental analysis for evaluating performance. Section 5 presents result study of the AGCTrdCL Model against existing approaches using various performance metrics. Lastly, Section 6 summarize the paper.

2. LITERATURE REVIEW

An efficient deep learning model was introduced in [16] to diagnosis kidney tumor with help physicians.. The workload of radiologists was reduced because of complex structure of kidney. The convolutional neural network (CNNs) was designed in [17] classifying tumors from CT dataset.

Masked autoencoder (MAE) was introduced in [14] for kidney tumor detection to attain effective results. Self-supervised learning method extract the kidney tumor features with restricted data. A hybrid deep learning system was introduced in [15] to identify the kidney illness depending on CT scans. An optimized federated learning framework termed FedMilNet was introduced in [18] to improve the data quality. The designed framework improved the generalization and accuracy. A DL approach was presented in [19] for automated recognition of RCC at CT images. NemoNet combined 3D encoder-decoder structural design through feature study for improving tumour segmentation.

An automated deep learning diagnostic system was introduced in [20] for efficient kidney disease recognition as well as categorization. Hybrid feature extraction approach and lightweight convolutional neural network was introduced in [21] for automated kidney cancer detection. The designed approach helped the radiologists in clinical diagnosis and increased reliability.

Machine learning (ML) was designed [22] for accurate kidney tumor classification through CT images. The designed model improved the diagnostic precision and addressed the overfitting issues. A machine learning (ML) framework was designed in [23]. E2E AI-driven routine kidney as well as renal mass analysis approach was designed in [24] to identify abnormal areas in kidney.

A new framework was designed in [25] to categorize renal CT images to vigorous/tumor. Hybrid neural fuzzy inference scheme was designed in [26] thorough joining CNN as well as ML for detection and segmentation of tumor in kidneys. A computationally efficient deep-learning architecture was designed in [27] with CNNs to perform the for kidney tumor tissue categorization.

Intellectual kidney tumour segmentation as well as categorization method was designed in [28] for classifying the benign and malignant tumour at an early stage. A DL method was introduced in [29] for identifying kidney illnesses for addressing the global scarcity of urologists. The designed model categorized the images into kidney stones, cysts, and tumors. A computational framework termed Kidney Ensemble-Net was introduced in [30] to improve renal carcinoma classification accuracy.

3. METHODOLOGY

Kidney disease remained major public health concern. More than 10% of patients are enduring as of CKD. Kidney tumors are the abnormal development in kidneys that are cancerous or non-cancerous one. The early prediction of kidney tumor reduces the mortality rates with the preventive measure to help the patients. Automated kidney disease diagnosis using deep learning algorithms improved the diagnosis speed. But, the existing kidney diagnosis techniques are time utilizing and minimum precise one. To address these issues, a new model termed AGCTRdCL Model is introduced in this article. The main objective of AGCTRdCL Model is to perform efficient and automated classification of kidney tumor through minimum time difficulty using deep learning concepts.

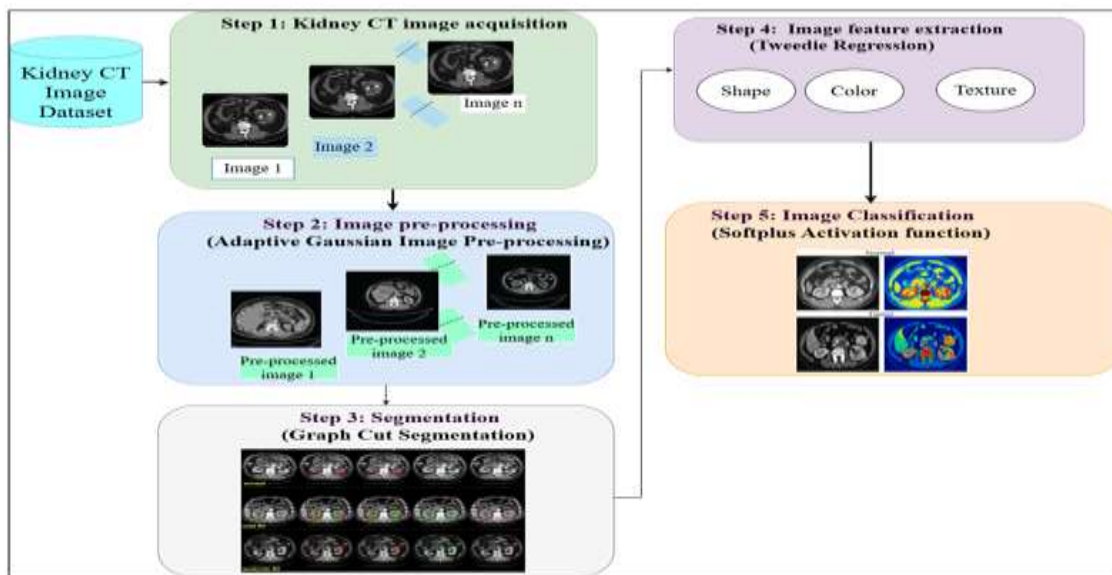


Figure 1 Architecture Diagram of Proposed AGCTRdCL Model

Figure 1 depicts overall structure of AGCTrdCL Model for accurate kidney disease diagnosis effectively. AGCTrdCL Model includes the four process. Initially, number of CT images is considered as an input. After that, the image pre-processing process is used to denoise the input CT image from input database. Then, the segmentation process is carried out to partition the input CT images into number of segments. In the segmented region, the image features are extracted for image classification. With the extracted features, the CT image classification is performed into different classes, namely grade 0, 1, 2, 3, 4 and 5.

3.1 VGG16 deep Convolutional Learning based Kidney Cancer Diagnosis

The proposed AGCTrdCL Model uses VGG16 deep Convolutional Learning has one input, convolutional, pooling, fully connected , one output layers. Deep convolutional learning NN is DL method for kidney CT image classification. VGG-16 model is CNN structural design through convolutional as well as fully connected layers. VGG-16 improved the simplicity and effectiveness to achieve improved kidney CT image classification.

Figure 2 illustrates the structural design of deep convolution learning model for precise kidney disease diagnosis. Every layer contains the artificial neurons that serve as processing units. The input layer comprised the number of kidney CT images. The neuron transmits the input kidney CT images into the hidden layers for efficient image classification with four different tasks namely preprocessing, segmentation, feature

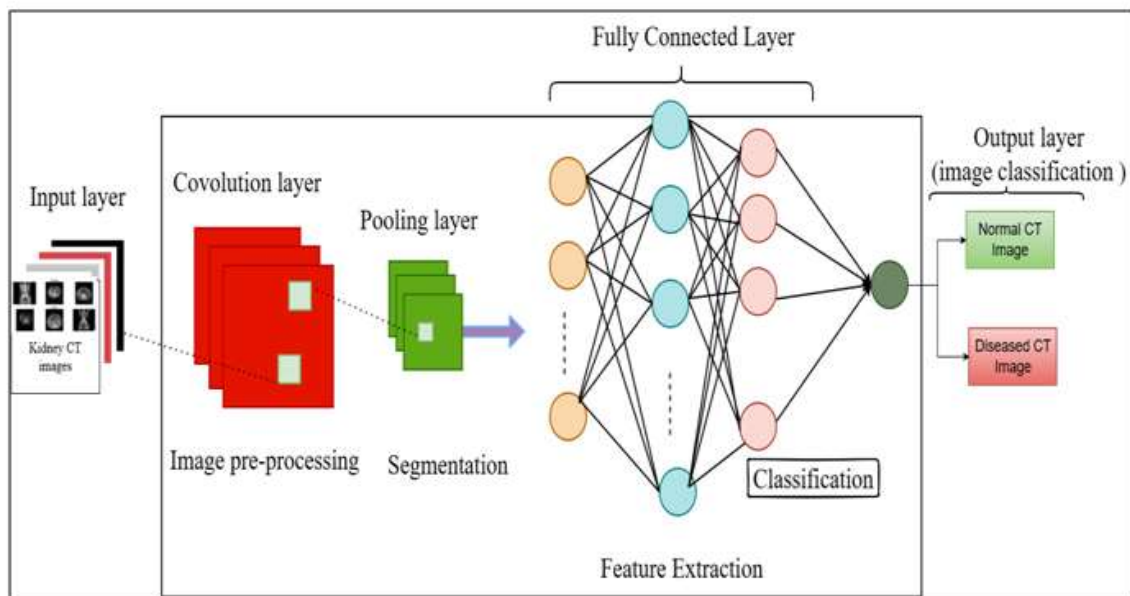


Figure 2 Structure Design of Deep Convolutional Learning Model

extraction and classification. Finally, the output layer attains different classes of kidney diseases.

- **Image Acquisition**

The first process of proposed AGCTrdCL Model is the collection of number of CT images from input database for efficient analysis and processing. In order to perform the stroke disease detection, CT kidney images are gathered from the Kidney Cancer Image Dataset considered as of <https://www.kaggle.com/datasets/jayaprakashpondy/kidney-cancer-image>. The image dataset includes a total of 5887 training images differentiated into two classes, namely tumor and normal images. The image details of training folder and validation folder are provided in the table 1 and table 2.

Table 1 Training folder CT image details

S. No	CT Image classes	Number of images
1	Normal	4061
2	Tumor	1826
Total images		5887

Table 2 Validation folder CT image details

S. No	CT Image classes	Number of images
1	Normal	1016
2	Tumor	457
Total images		1473

From the above table, the dataset description is explained. Let us consider that the number of CT kidney images ' $KI_1, KI_2, KI_3, \dots, KI_n$ ' are given to input layer. Each neuron receives input kidney CT images are collected from the input dataset. The neurons then compute a weighted sum of these inputs, which is expressed mathematically as follows,

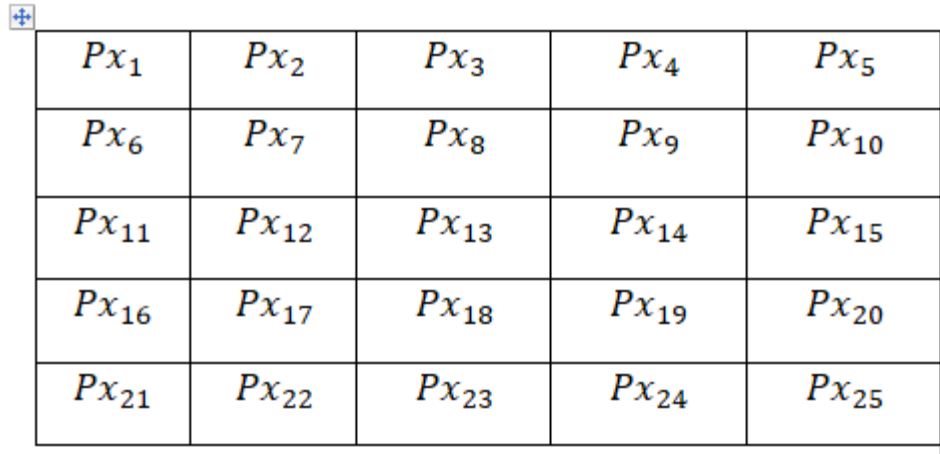
$$In = \sum_{i=1}^n (KI_i * W_{ih}) + b \quad (1)$$

From (1), ' In ' represent the weighted sum output. ' W_{ih} ' symbolize the weight between input and hidden layer. The number of kidney image samples ' KI_i '. ' b ' represents the bias denoted as '1'. The input CT is transferred into the next hidden layer for preprocessing.

- Image Pre-processing**

In the first hidden layer (i.e., convolutional layer) of proposed AGCTrdCL Model, the image preprocessing eliminates the noisy pixels for performing efficient kidney disease diagnosis. The image pre-processing task increases the image quality through eliminating the noise from images for efficient processing. The proposed AGCTrdCL Model uses the adaptive Gaussian kernel function for efficient image denoising. Adaptive Gaussian denoising is carried out to adjust the resolution based on their future process. The denoising process is carried out for noise removal and for preserving image quality.

Let us consider that the input dataset ' DS ' with number of CT kidney images as ' $KI_1, KI_2, \dots, KI_n$ '. Number of pixels in each CT image is denoted by ' $Px_1, Px_2, Px_3 \dots Px_m$ ' with size $p * p$.



Px_1	Px_2	Px_3	Px_4	Px_5
Px_6	Px_7	Px_8	Px_9	Px_{10}
Px_{11}	Px_{12}	Px_{13}	Px_{14}	Px_{15}
Px_{16}	Px_{17}	Px_{18}	Px_{19}	Px_{20}
Px_{21}	Px_{22}	Px_{23}	Px_{24}	Px_{25}

Figure 3 $p * p$ Filtering window

Figure 3 shows the $p * p$ filtering windows. After that, the pixels are arranged in the filtering window. After arranging the pixels, the scale space representation process is carried out and given by,

$$St(a, b, t; \sigma_{a,b}) = AG(a, b, t) * Px(a, b) \quad (2)$$

$$AG(a, b, t; \sigma_{a,b}) = \frac{1}{2\pi t \sigma_{a,b}^2} \exp \left[-\frac{a^2 + b^2}{2t \sigma_{a,b}^2} \right] \quad (3)$$

From (2) and (3), ' $St(a, b, t; \sigma_{a,b})$ ' represent the scale space representation of input kidney CT image with the adaptive Gaussian kernel ' $AG(a, b, t)$ ' in two-dimensional space. '*' denotes the convolution operator. ' a, b ' are the pixel distance from the center in the filtering window. The scale parameter denotes the variance ($\sigma_{a,b}^2$) of the adaptive gaussian filter with smoothing. After smoothening process, pixel variation is computed between the original kidney ' $KI(a, b)$ ' and Gaussian smoothed images ' $AG(a, b, t)$ ' to identify the noisy or normal pixels. It is formulated as,

$$PV(a, b) = |Px(a, b) - AG(a, b, t)| \quad (4)$$

From (4), residual magnitude ' $RM(i, j)$ ' between the pixels, $P(x, y)$ denotes an original value of the pixel at coordinates (x, y) , $G(x, y, t)$ denotes the adaptive gaussian smoothed pixel at the coordinates (a, b) . It is given as,

$$PO = \begin{cases} PV(a, b) \leq T ; & \text{normal pixels} \\ PV(a, b) > T ; & \text{noisy pixels} \end{cases} \quad (5)$$

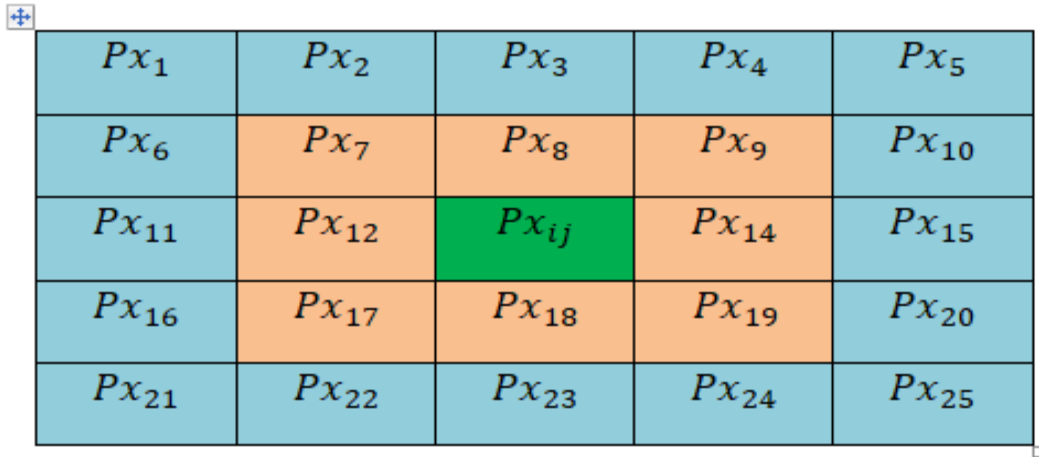
From (5), ' PO ' denotes the pre-processing outputs. When the pixel variation is lesser than threshold, the pixel is considered as normal one. Otherwise, the pixel is considered as the noisy one. After that, the noisy pixels are eliminated and image quality gets enhanced. The below algorithmic steps describes the image pre-processing task.

// Algorithm 1: Adaptive Gaussian Image pre-processing	
Input:	CT Kidney Image Dataset 'DS'
Output:	Preprocessed kidney CT images
Begin	
Step 1: Collect the kidney CT images:	
Step 2: For each kidney CT image $\in DS'$ do	
Step 3:	Extract pixels from input CT image
Step 4:	Organize pixels in filtering window
Step 5:	Measure Gaussian Scale Space representation using (2)
Step 6:	Compute pixel variation ' $PV(a, b)$ ' using (4)
Step 7:	If $(PV(a, b) > T)$ then
Step 8:	Pixels is identified as noisy and removed
Step 9:	else
Step 10:	Pixels is identified as normal
Step 11:	End if
Step 12: Remove noisy pixels	
Step 13: Return (quality enhanced kidney CT image)	
Step 14: End for	
End	

Algorithm 1 illustrates the step by step process for enhancing image quality by removing noisy pixels from the input image. The data acquisition process gathers the number of kidney CT images from input dataset. The pixel values are arranged into filtering window. Adaptive Gaussian kernel function is used for computing the pixel variation. Pixels with high variation are treated as noisy pixel. Pixels with less variation are treated as the normal pixel. The denoising step improves the kidney CT image excellence through elevated PSNR. By this way, kidney image pre-processing is carried out with high PSNR. The preprocessed kidney image is sent to the second hidden layer.

• Segmentation

In the second hidden layer (i.e., pooling layer) of proposed AGCTRdCL Model, the image segmentation process is the second step for performing kidney cancer diagnosis. Image segmentation is the process used to partition the kidney CT image into meaningful segments by grouping pixels with similar characteristics. Image segmentation process is used to examine the parts of image at a pixel level for medical diagnosis. For performing efficient image segmentation process, Graph cut algorithm is used in proposed AGCTRdCL Model. Graph cut segmentation is carried out in proposed AGCTRdCL Model with pre-processed kidney CT images. The kidney CT images are considered as the weighted graph to identify the optimal cut. The graph cut segmentation separates the affected region from the kidney CT images. Graph cut segmentation identifies the pixel discontinuities between the neighboring one.



Px_1	Px_2	Px_3	Px_4	Px_5
Px_6	Px_7	Px_8	Px_9	Px_{10}
Px_{11}	Px_{12}	Px_{ij}	Px_{14}	Px_{15}
Px_{16}	Px_{17}	Px_{18}	Px_{19}	Px_{20}
Px_{21}	Px_{22}	Px_{23}	Px_{24}	Px_{25}

Figure 4 Smoothened Pixel Alignments

Figure 4 illustrates the smoothened pixel alignment in matrix format with rows and columns. First, the central pixel positioned in the two dimensional space (P_{ij}) and the smoothened pixel connectivity. It is formulated as,

$$GCS = ST(a, b) \quad (6)$$

$$ST(a, b) = \begin{cases} 0 \\ w_{i,j} \end{cases} \quad \begin{matrix} L_a = L_b \\ L_a \neq L_b \end{matrix} \quad (7)$$

$$w_{i,j} = \exp\left(-\frac{KI_i - KI_j}{2\theta^2}\right) \quad (8)$$

From (6), (7) and (8), 'GCS' denotes the graph cut segmentation results. 'ST(a, b)' symbolizes the smoothness term. ' KI_i ' and ' KI_j ' represents the kidney CT images. ' $w_{i,j}$ ' represent the weight value. ' L_a ' and ' L_b ' represents label output (affected region or normal region). Finally, the similar pixels results merged to form the infected regions. This in turn, graph segmentation is carried out to find the kidney disease affected region. The algorithmic steps of graph cut segmentation is given as,

// Algorithm 2: Graph Cut Segmentation
Input: Number of preprocessed CT images
Output: Segment the infected region
Begin Step 1: Collect the pre-processed CT images Step 2: For each pre-processed image Step 3: Measure the smoothness term between pixels from pre-processed image Step 4: If $(ST(a, b) = 0)$ then Step 5: Pixels are said to be similar Step 6: else Step 7: Pixels are said to be not similar Step 8: End if Step 9: Merge the similar pixels Step 10: End for End

Algorithm 2 explains the step-by-step process of graph cut segmentation in proposed AGCTrdCL Model. The pixel smoothness between center and neighboring pixels are computed in graph cut segmentation. Finally, the similar pixels are extracted by eliminating the irrelevant regions from pre-processed CT image to reduce the time consumption. After that, the segmentation result is sent to the third hidden layer for efficient feature extraction.

• Feature Extraction

The third step is termed as the feature extraction in fully connected layer. In the feature extraction task, the visual image characteristics like textures, color and shape are identified to compute the content of entire image. The feature extraction process also helps in minimizing the time complexity for image classification process. For efficient feature extraction, tweedie regression analysis is carried out in proposed AGCTrdCL Model. Tweedie regression analysis is a generalized linear model used for extracting the shape, contrast, color and texture. Color feature extraction is the method of finding the identifying the color characteristics in kidney CT image. The color features are extracted through computing the mean, variance and skewness. The mean represents the average color intensity of a channel. It is formulated as,

$$Mean = \frac{1}{q} \sum_{j=1}^q Px_j \quad (9)$$

From (9), ' Px_j ' denotes the pixel intensity. ' q ' symbolizes the total number of pixels. Based on computed mean value, the variance ' V ' is calculated. It is given as,

$$V^2 = \frac{1}{q} \sum (Px_j - Mean)^2 \quad (10)$$

From (10), ' V^2 ' represent the variance. ' Px_j ' symbolizes the pixel. Then, the skewness is calculated as,

$$S = \frac{\frac{1}{q} \sum (Px_u - \text{Mean})^3}{\left(\frac{1}{q} \sum (Px_u - \text{Mean})^2\right)^{3/2}} \quad (11)$$

From (11), 'S' denotes the skewness. The shape feature is extracted by their boundary value. Euclidean distance between consecutive points of pixels with their boundary is computed as,

$$\text{Dist} = \sum_{u,j=1}^m \sqrt{(x_{u+1} - x_v)^2 + (y_{u+1} - y_v)^2} \quad (12)$$

From (12), 'Dist' symbolizes the distance. Texture computes the pixel intensities across segmented CT image. In texture analysis, contrast and correlation are used to compute the relationship between neighboring pixel intensities. Contrast helps to compute the pixel variation between neighboring ones. The high contrast denotes the stronger local intensity variations. The stronger intensity variations attained greater level of texture variation within CT kidney image. It is formulated as,

$$\text{Con} = \sum_{u,v} (u - v)^2 Px_{uv} \quad (13)$$

From (13), 'Con' represent the contrast. '(u,v)' represent the pixel pairs with intensities at spatial relationship in CT image. Correlation is used to compute the relationship between gray levels of neighboring pixels. Correlation computes the intensity value variation regarding another one across CT image. Correlation denotes the degree where pixel intensities are dependent. It is computed as,

$$\text{Cor} = \sum \frac{Px_{uv} (u - \text{Mean}_u)(v - \text{Mean}_v)}{d^2} \quad (14)$$

From (14), 'CC' represents the correlation of CT image, 'd' represents the deviation of pixels. The tweedie regression analysis in proposed AGCTRDCL Model extracts color, shape and texture features and it is given by,

$$\text{FEO} = \text{Tweedie}(\text{shape}, \text{color}, \text{texture}) \quad (15)$$

$$\text{Var}(\text{FEO}) = \phi \mu^P \quad (16)$$

From (15) and (16), 'FEO' denotes the feature extracted output results. 'φ' denotes the dispersion parameter. 'μ' denotes the mean response parameter. 'P' represent the tweedie power parameter. Finally, the extracted color, shape and texture features are considered for kidney disease classification.

• Classification

Image classification is the method of allocating the predefined label to CT kidney image based on its visual content. The softplus activation function provides the multiclass results of kidney CT images. It is formulated as,

$$af_{sp} = \frac{e^{[KI_k]}}{\sum_{k=1}^C e^{KI_k}} \quad (17)$$

$$\text{CO} = af_{sp} [Hd_o * W_{ho}] \quad (18)$$

From (17) and (18), 'af_{sp}' represents the softplus activation function. 'Hd_o' denotes the hidden layer results. 'W_{ho}' represent the weight between hidden layer and output layer. 'KI' indicates the output of kidney CT images. The softplus activation function provides the probability distribution outcome over the two different classification results. The output of classifier is analyzed with the outcomes such as normal CT image and diseased CT image. Then, fine tuning process increases accuracy of kidney cancer classification with

minimum error rate. Stochastic gradient descent is used in proposed AGCTRdCL Model for tuning the weights between layers to minimize the error in kidney cancer classification. The input weight is updated as,

$$W_{new} = W_{cur} - \eta \left[\frac{\partial E}{\partial W_{cur}} \right] \quad (19)$$

From (19), ' W_{new} ' represent the newly updated weight. ' W_{cur} ' symbolizes the current weight. ' η ' represent the learning rate. ' $\left[\frac{\partial E}{\partial W_{cur}} \right]$ ' symbolizes the partial derivative of error rate ' E ' through ' W_{cur} '. The above procedure is repeated till reached the objective function which is given below.

$$OF = \arg \min E \quad (20)$$

From (20), ' OF ' represent the objective function. ' $\arg \min$ ' denotes the argument of minimum function. E is estimated depend on squared difference among actual output as well as classification output. It formulated as,

$$E = [CO - AO]^2 \quad (21)$$

From (21), ' E ' represent the error rate. ' AO ' represent the actual output. ' CO ' represent the classification output. Finally, the fine tuned classification outcomes are sent to output layer. By this way, an efficient kidney cancer classification is carried out with higher accuracy and minimum time complexity. The algorithmic steps of feature extraction and classification is given as,

Algorithm 3: Tweedie Regressive Feature Extraction
Input: Preprocessed input image CT images
Output: Categorizes the kidney CT images
Begin
Step 1: Collect all pre-processed CT images
Step 2: For each pre-processed CT image ----- Fully connected layer
Step 3: Compute color features based on mean, variation and <u>skewness</u>
Step 4: Compute texture features
Step 5: Compute shape features
Step 6: Apply <u>tweedie</u> regression for feature extraction
Step 7: End for
Step 8: Collect the extracted features
Step 9: For each extracted features and pre-trained feature
Step 10: Measure the <u>softplus</u> activation function
Step 11: if ($af_{sp} = 1$) then
Step 12: Image is categorized into diseased class
Step 13: else
Step 14: Image is categorized into normal class
Step 15: End if
Step 16: End for
Step 17: For each classification result
Step 18: Compute classification error
Step 19: Update the weights
Step 20: Verify objective function
Step 21: End for
Step 22: Obtain kidney disease classification results at the output layer
End

In Algorithm 3, In third hidden layer, image features, namely color, shape and texture are extracted for image classification task. Feature extraction is performed by tweedie regression study to produce final kidney disease classification outcomes. Then, softplus activation function is used for performing kidney disease classification. After that, the error value is computed for every classification result. Depend on E value, weights are assigned as well as revised with help of stochastic gradient descent function. The process gets

iterated until objective function is met. Finally, the kidney cancer classification results are attained at the output layer. The AGCTrdCL Model significantly improves kidney cancer classification performance with higher accuracy and minimal error rate.

4. EXPERIMENTAL SETUP

An experimentation of proposed AGCTrdCL Model with existing methods including GVITKT [1] and deep learning approach [2] for accurate kidney cancer detection and diagnosis. The implementation is carried out using Python programming language for image preprocessing, segmentation, feature extraction, classification and fine-tuning.

4.1 Dataset Description

For conducting the experiments, the proposed AGCTrdCL Model used Kidney Cancer Image database as <https://www.kaggle.com/datasets/jayaprakashpondy/kidney-cancer-image>. The dataset comprises the diverse set of kidney CT scan images with normal and tumor cases. It includes sum of 5887 training CT images categorized to two groups. Each image is labeled for classification and model training. Homogeneous similarity transformation is a geometric transformation to generate the many kidney CT images by changing the size and shape. The image augmentation process increases the dataset size in deep learning. In image resizing process, the input image is rotated horizontally or vertically. In addition, the image resizing process involves zooming or reducing the dimensions to attain particular target size. Finally, the resized pixel images are considered as synthetic CT images for accurate kidney cancer detection. For conducting experiments, the number of kidney CT images is varied from 1000 to 10000.

Table 3 Experimental setup

Name	Description
Dataset name	Kidney Cancer Image Dataset
Number of kidney CT images	1000-10000 images
Operating system	WINDOWS 10 and above
Software	Python high-level programming language 3.10.11
RAM	8GB
Hard drive capacity	1TB
Processor	Intel® Core™ i3 Processor

4.2 Quantitative analysis of AGCTrdCL Model using Kidney CT Images

Quantitative analysis of proposed AGCTrdCL Model is compared to analyze their efficiency in kidney cancer disease detection. The evaluation includes different steps as below

Step 1: Image acquisition

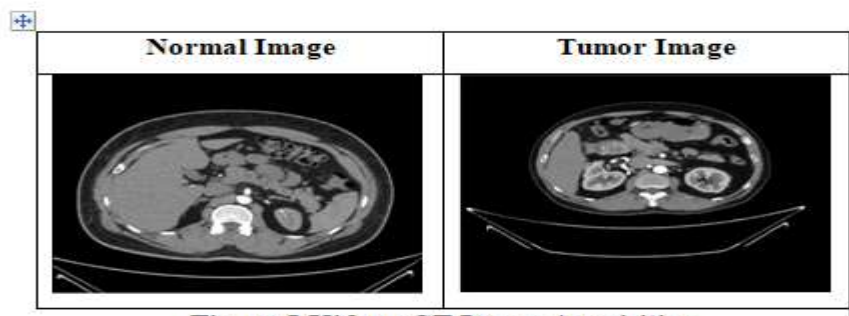


Figure 5 Kidney CT Image Acquisition

Figure 5 illustrates acquisition of kidney CT images categorized into two different class namely normal image and tumor image. The images are gathered from Kaggle repository to guarantee the kidney disease diagnosis.

Step 2: Image preprocessing

After performing the CT images collection from the dataset, an adaptive gaussian image preprocessing is carried out to improve the image quality and contrast. This preprocessing task eliminates the noise and retains the structural characteristics. The diagrammatic representation of adaptive gaussian image preprocessing is shown in Figure6.

Normal Class:



Tumor Class:

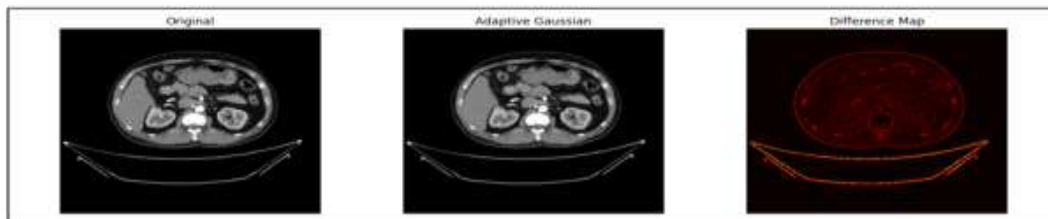
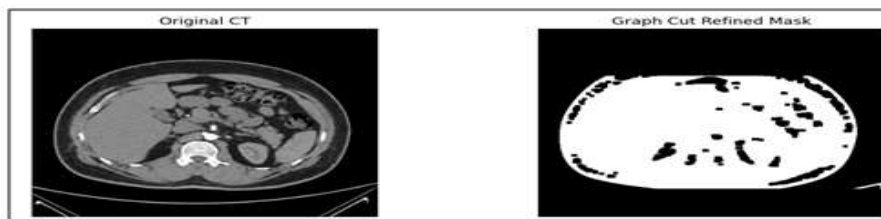


Figure 6 Kidney CT image preprocessing

Step 3: Image Segmentation

After preprocessing task, graph cut segmentation is employed for partitioning the kidney CT images into meaningful regions for accurate identification of disease-affected areas. Figure 7 illustrated the image segmentation results.

Normal Class:



Tumor Class:

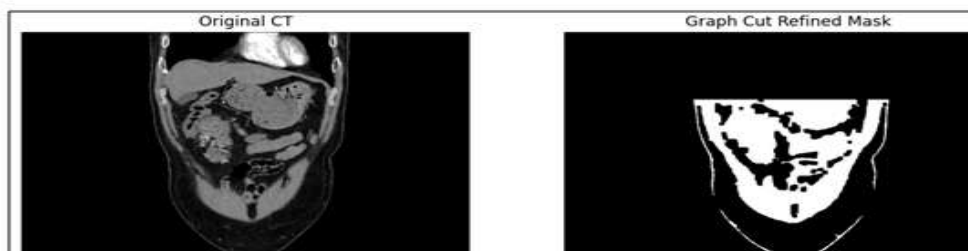


Figure 7 Kidney CT segmented image

Step 4: Feature Extraction

After performing the image segmentation process, the proposed AGCTrdCL Model performed the feature extraction. The meaningful information is obtained from the enhanced CT images. In this phase, discriminative features related to color, shape, and texture are effectively extracted for accurate kidney disease classification. Figure 8 shows the feature extraction results for normal and tumor classes.

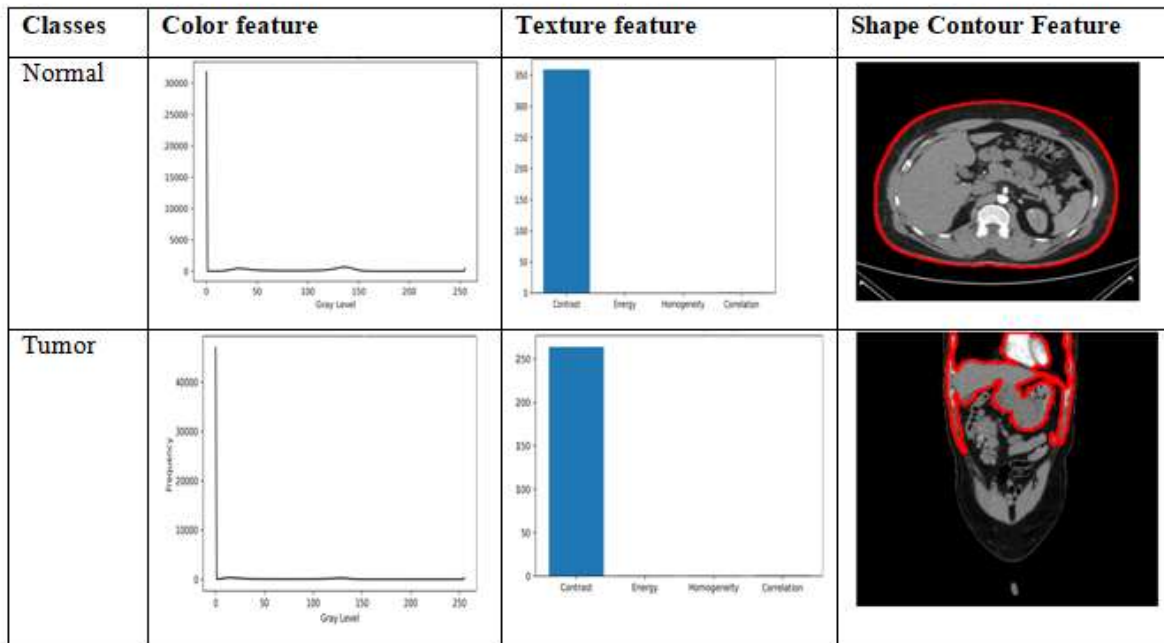


Figure 8 Feature Extraction

Step 5: Kidney Disease Classification

Finally, it is performed with extracted features to categorize images to normal class as well as tumor class. Figure 9 illustrates the kidney disease classification results.

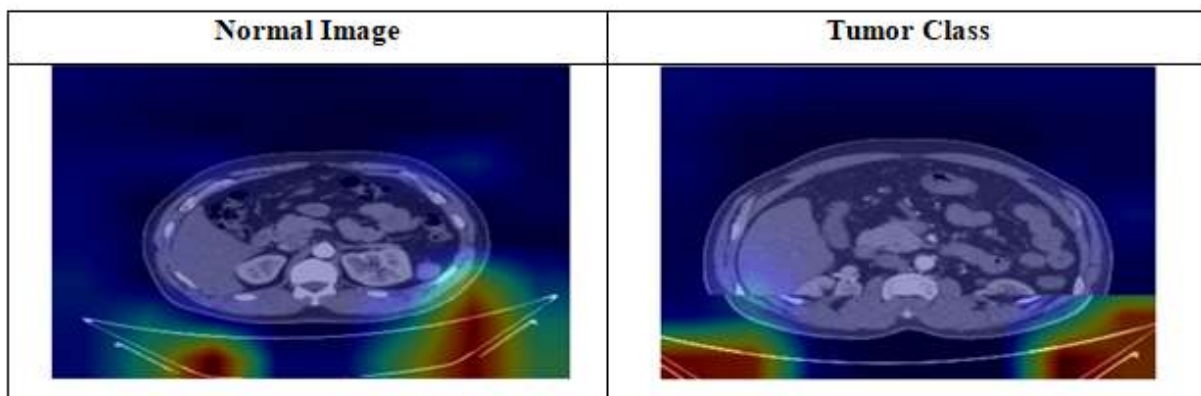


Figure 9 Kidney Disease Classification

5. RESULT

It provides quantitative result comparison among AGCTrdCL and two existing namely GVITKT [1] and deep learning approach [2]. The performance evaluation is carried out with PSNR, kidney cancer classification accuracy, precision, recall and segmentation time. The result parameters are used to evaluate efficiency of proposed AGCTrdCL Model.

5.1 Impact on PSNR:

PSNR employed to evaluate quality of preprocessed CT image through evaluating through original CT image. It is calculated based on MSE. It is formulated as,

$$MSE = [KI_p - KI_o]^2 \quad (22)$$

$$PSNR = 10 * \log_{10} \left[\frac{Px_{max}^2}{MSE} \right] \quad (23)$$

From (22) and (23), 'PSNR' represents the peak signal-to-noise ratio, ' Px_{max} ' represents the maximum possible pixel value (255). 'MSE' represent the mean square error. ' KI_p ' indicates preprocessed kidney CT image size. ' KI_o ' denotes original kidney CT image size. It is computed in terms of decibels (dB).

Table 4 Tabulation of PSNR

Image Size (KB)	PSNR (dB)		
	Proposed AGCTrdCL Model	GVITKT [1]	Deep learning approach [2]
124.29	62.87	56.81	53.37
118.36	61.48	58.23	55.58
194.23	62.04	59.42	57.72
193.39	65.35	61.97	58.67
193.28	59.41	54.74	51.37
83.32	62.87	58.42	56.18
79.78	60.94	58.89	54.98
81.94	63.68	59.66	57.47
81.66	59.76	55.74	52.35
81.73	65.15	61.25	58.78

Table 4 and Figure 10 illustrates the PSNR results for different kidney CT images. Let us consider that CT image size of 124.29 KB, the proposed AGCTrdCL Model achieved a PSNR of 62.87 dB while existing [1] and [2] attained PSNR value of 56.81dB and 53.37dB. For every kidney CT image, different PSNR results are attained. Finally, ten results denote that the AGCTrdCL Model improved PSNR by 6% when compared to [1] and 12% when compared to [2]. This is due to the application of adaptive gaussian kernel smoothing to improve the image contrast through eliminating the noise pixels. Lastly the high contrast images are attained by reducing the mean square error (MSE) and increased the image quality of kidney CT images.

5.2 Impact on Kidney Cancer Classification Accuracy:

It is defined as ratio of numeral of CT images that are properly classified to whole number of input CT images collected from dataset. The kidney cancer classification accuracy is calculated as,

$$KCCA = \frac{TP+TN}{TP+TN+FP+FN} * 100 \quad (24)$$

From (24), 'KCCA' denotes the kidney cancer classification accuracy. The true positive rate (TP) refers to the images accurately recognized as diseased one. TN images correctly categorized as healthy or non-diseased. FP) denotes the image categorized as diseased. FN represents diseased images wrongly categorized as normal. It is measured in terms of percentage (%).

Table 5 Tabulation of Kidney Cancer Classification Accuracy

Number of CT images	Kidney Cancer Classification Accuracy (%)		
	Proposed <u>AGCTrdCL Model</u>	GVITKT [1]	Deep learning approach [2]
1000	96.5	93.5	91.5
2000	96.68	93.69	91.32
3000	96.29	93.42	91.89
4000	96.85	93.57	91.23
5000	96.41	93.36	91.58
6000	96.92	93.42	91.27
7000	96.19	93.37	91.22
8000	96.84	93.56	91.56
9000	96.96	93.12	91.77
10000	96.23	93.93	91.68

Table 5 and Figure 11 illustrate the kidney cancer classification accuracy with respect to number of CT image samples ranging from 1000 to 10000. The proposed AGCTrdCL Model attained better accuracy results than GVITKT [1] and deep learning approach [2]. Let us consider that 1000 CT image samples, AGCTrdCL Model achieved an accuracy of 96.5%, compared to 93.5% and 91.5% for the [1] [2] methods correspondingly, Among the three methods, The result shows that the AGCTrdCL Model achieved kidney cancer classification accuracy enhancement of 3% over [1] and 6% over [2]. This is because of using adaptive gaussian image preprocessing task to perform contrast enhancement and kidney CT image quality enhancement. Graph Cut Segmentation performed pre-processed image partition into number of segments. Tweedie Regressive Feature Extraction and softplus activation function are used to extract the shape, color and texture of segmented regions and to perform efficient classification of kidney cancer. By this way, an efficient CT kidney image classification is carried out with high accuracy.

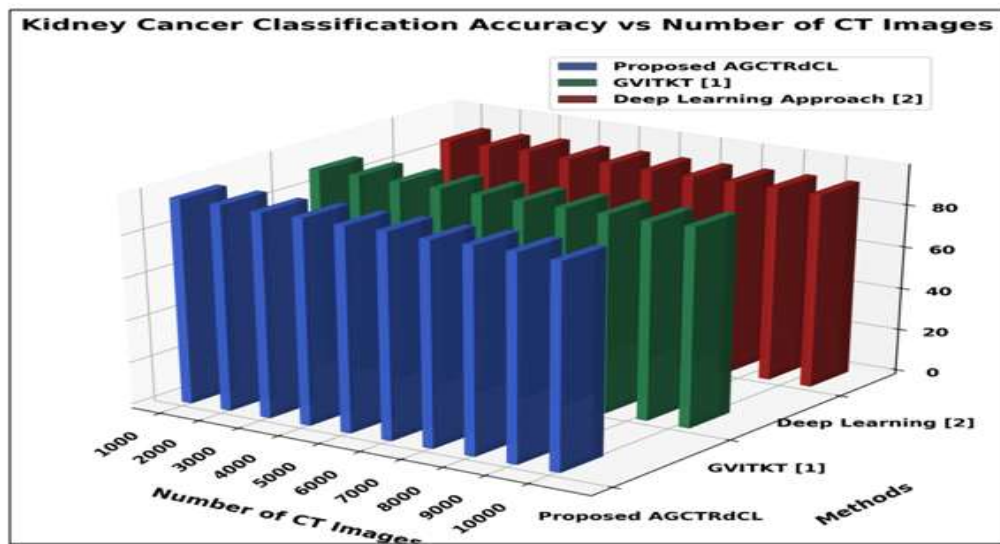


Figure 11 Measurement Analysis of Kidney Cancer Classification Accuracy

5.3 Impact on Precision:

Precision has model capability to properly recognize particular class of kidney cancer from the input CT images. The precision is calculated separately for each class using the following formula:

$$PRE = \frac{TP}{TP+FP} * 100 \quad (25)$$

From (25), *PRE* denote a precision, '*TP*' denotes the true positive, '*FP*' represents the false positive.

Table 6 Tabulation of Precision

Number of CT images	Precision (%)		
	Proposed AGCTRdCL Model	GVITKT [1]	Deep learning approach [2]
1000	96.21	95.92	95.33
2000	96.17	95.88	95.71
3000	96.83	95.71	94.86
4000	96.68	95.66	94.18
5000	96.96	95.42	94.37
6000	96.28	95.67	94.46
7000	96.17	95.53	94.63
8000	96.35	95.49	94.52
9000	96.42	95.35	94.24
10000	96.39	95.41	94.83

Table 6 and Figure 12 illustrate the precision analysis with respect to number of CT image samples ranging from 1000 to 10000. Assume, 1000 CT image samples, AGCTRdCL Model achieved the precision of 96.21%.

The existing method attained precision of 95.92% and 95.33% when compared [1] and [2] methods correspondingly. Among the three methods, AGCTRDCL Model attained best precision performance when compared to other methods. The result shows that the AGCTRDCL Model achieved precision improvement of 1% than [1] and 2% than [2]. This is because of using Tweedie Regressive Feature Extraction and softplus activation function to extract the shape, color and texture of segmented regions and to perform efficient classification of kidney cancer. This in turn, efficient CT kidney image classification is carried out with high precision.

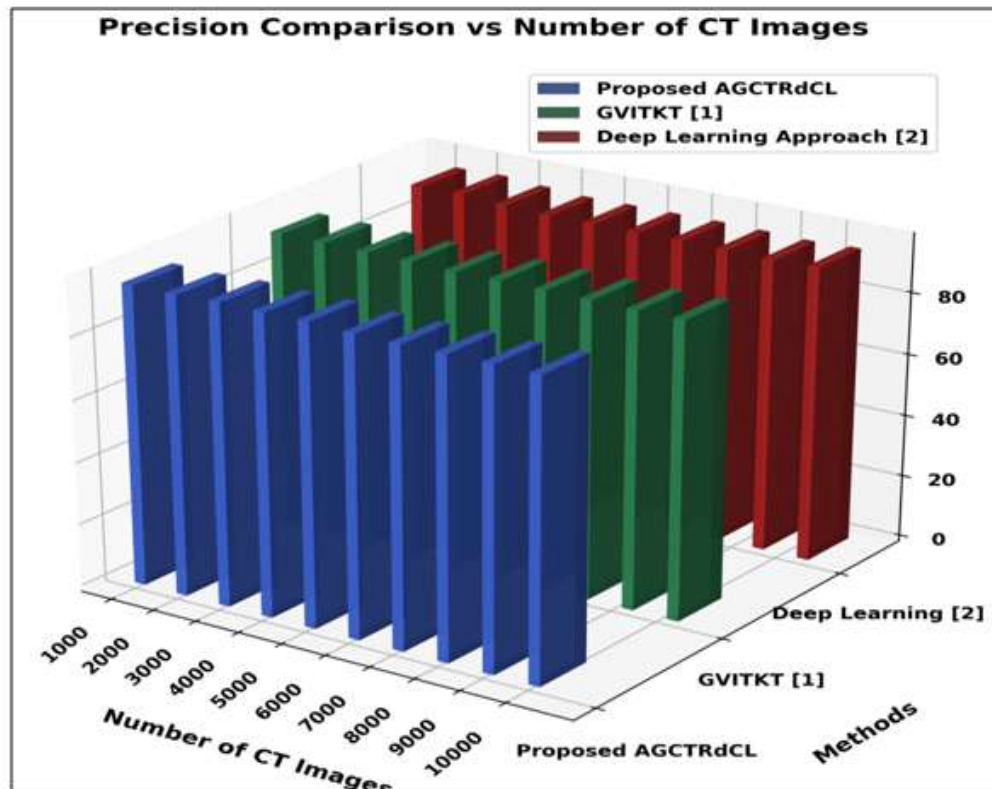


Figure 12 Measurement Analysis of Precision

5.4 Impact on Recall:

Recall is otherwise termed as sensitivity. Recall is a measure of model ability to correctly identify the kidney cancer disease presence or absence. It is formulated as,

$$REC = \frac{TP}{TP+FN} * 100 \quad (26)$$

From (26), 'REC' represent the recall. 'TP' denotes the true positive. 'FN' represent the false negative.

Table 7 Tabulation of Recall

Number of CT images	Recall (%)		
	Proposed <u>AGCTRdCL</u> Model	GVITKT [1]	Deep learning approach [2]
1000	97.28	94.84	93.48
2000	97.96	94.33	93.65
3000	97.59	94.92	93.13
4000	97.44	94.19	93.62
5000	97.15	94.82	93.33
6000	97.36	94.23	93.24
7000	97.28	94.95	93.13
8000	97.97	94.66	93.85
9000	97.56	94.53	93.67
10000	97.68	94.12	93.28

7
13

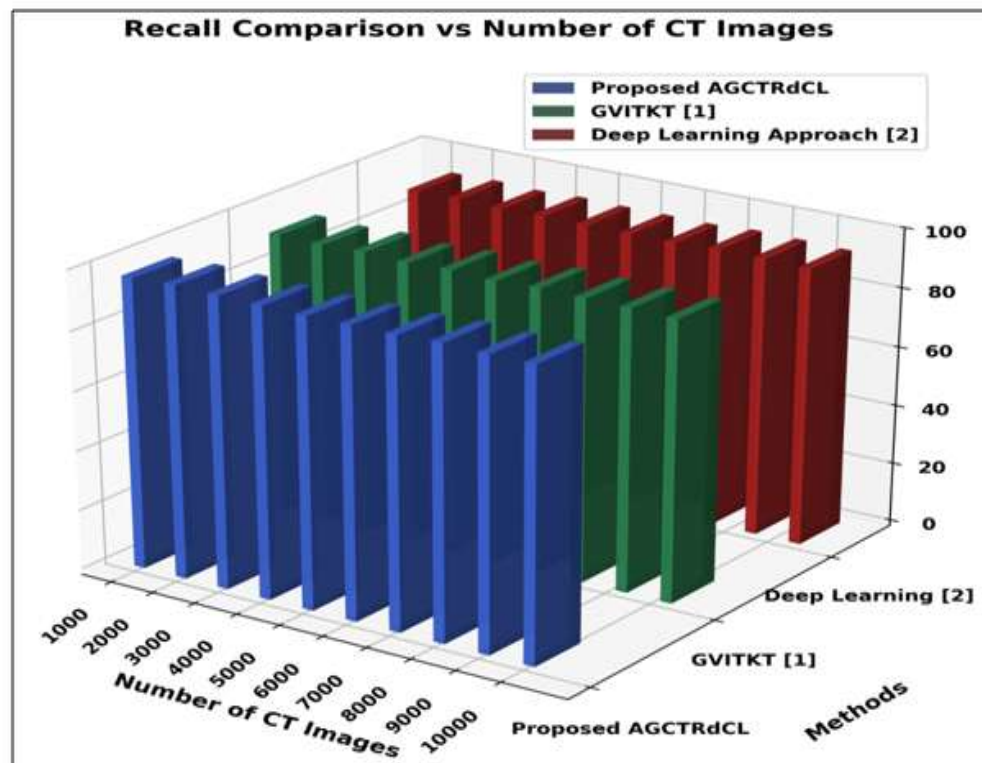


Table
and
Figure

Figure 13 Measurement Analysis of Recall

illustrate the recall results. Proposed AGCTrdCL attains higher *REC* than the [1] , [2]. Assume, number of kidney CT image as 1000, the proposed AGCTrdCL Model achieved the recall of 97.28% while existing methods [1] and [2] attained 94.84% and 93.48% respectively. From the ten iterations, the average recall of AGCTrdCL Model improved by 3% than [1] and 4% than [2]. The better recall performance of AGCTrdCL Model is achieved due to application of gradient descent function for fine-tuning process in deep convolutional learning architecture. By using fine-tuning process, the AGCTrdCL Model minimizes the classification error between classified output results and actual outcomes. The weights of error value are assigned and adjusted to minimize the false negatives for kidney cancer classification within CT images.

$$ST = \sum_{i=1}^n KI_i * Time [(Segmentation)] \quad (27)$$

5.5 Impact on Segmentation time:

It is amount of time consumed required through method to perform image segmentation. Segmentation time is expressed as,

From (27), 'ST' represent the segmentation time. 'n' Symbolizes the number of CT samples 'CTI'. 'Time(Segmentation)' denotes time for segmentation. It is calculated in milliseconds (ms).

Table 8 Tabulation of Segmentation Time

Number of CT images	Segmentation Time (ms)		
	Proposed AGCTrdCL Model	GVITKT [1]	Deep learning approach [2]
1000	34	40	44
2000	37.8	45.4	48.5
3000	40.1	49.1	52.6
4000	45.8	53.2	55.3
5000	49.2	56.3	61.1
6000	54.7	59.7	66.7
7000	60.9	63.8	69.1
8000	66.7	69.4	75.2
9000	69.4	72.9	79.8
10000	67.9	72.9	78.6

Table 8 , Figure 14 illustrates the graphical result analysis of segmentation time using the proposed AGCTrdCL Model outperforms better than existing methods, namely GVITKT [1] and deep learning approach [2]. The graphical chart shows the segmentation time against the number of input CT image samples varying from 1000 to 10000. When the number of input CT images increases, the segmentation time for all three methods also increases correspondingly. The horizontal axis denotes the number of input CT images from input dataset. The vertical axis denotes the corresponding segmentation time. Let us consider that 1000 image samples, the AGCTrdCL Model attained segmentation time of 34ms whereas existing methods [1] and [2] attained segmentation time as 40ms and 44ms correspondingly. Among three methods, the AGCTrdCL Model reduces the segmentation time by 11% and 17% when compared to the conventional models respectively.

This is due to application of graphcut algorithm for segmentation in deep convolution learning model. The graph cut segmentation helps in segmenting the affected region from pre-processed kidney CT images through finding the pixel discontinuities between the neighboring one. This in turn, reduced the segmentation time gets reduced during kidney cancer classification.

6. CONCLUSION

Kidney tumors are the abnormal growths in renal tissue of one or both kidneys. In order to minimize the kidney disease severity, a novel AGCTRdCL Model is introduced using CT images. The pre-processing task of proposed AGCTRdCL Model enhances the image quality through eliminating the noisy pixels with high PSNR performance. Then, segmentation and feature extraction processes of AGCTRdCL Model minimize the time consumption of kidney cancer disease detection. The proposed deep convolutional learning architecture analyzes the extracted features using tweedie regression analysis to obtain accurate kidney cancer classification results. Finally, fine-tuning is performed by gradient descent function. An extensive experimental evaluation is performed with CT image dataset for various metrics. The results of proposed AGCTRdCL Model enhance kidney cancer classification accuracy while considerably reducing the time when compared with existing approaches.

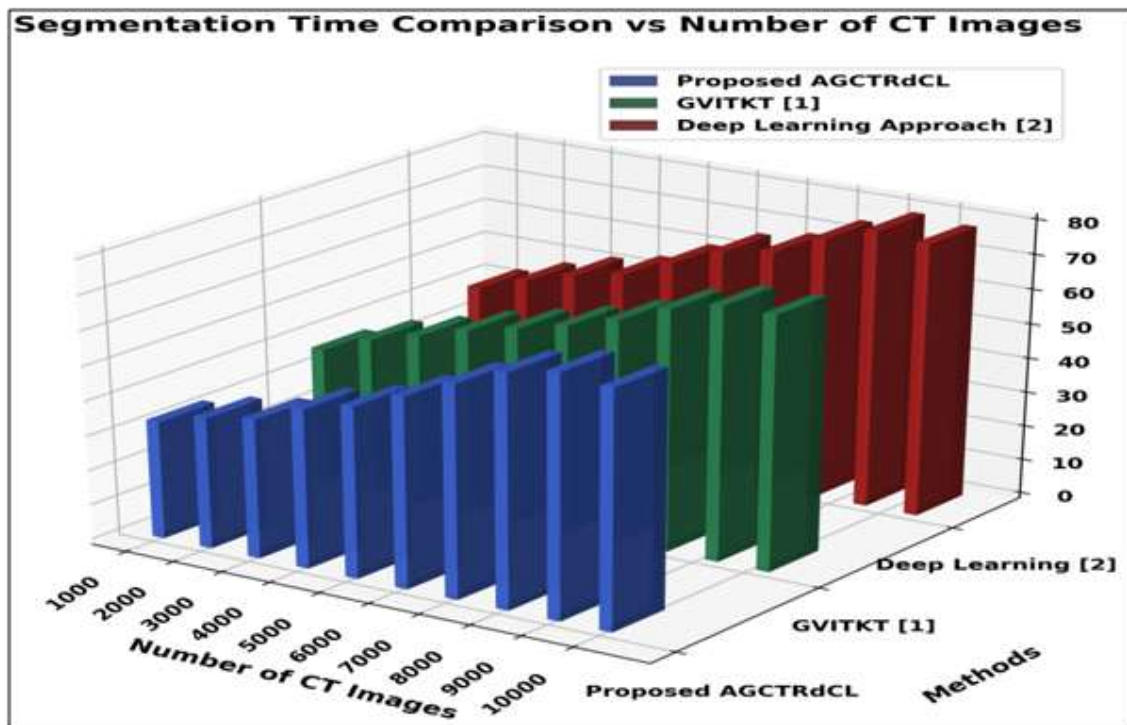


Figure 14 Measurement Analysis of Segmentation Time

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