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Diagnosis of Kidney Renal Cell Tumor through Clinical data mining and CT scan image processing: A Survey

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ABSTRACT

This study deals with the systematic study of the mining of data and medical image-based CAD to classify or predict Kidney Renal (KRCC) tumors. Kidney tumors are of different types having different characteristics and have different methodologies to classify or predict tumor and its stages. KRCC is the most common type of cancer of the kidney, but there are others. Several factors may increase the risk of a person developing KRCC disease like smoking, obesity, High blood pressure, and many more. In almost all cases, only a single kidney is affected, but in rare cases, both can be affected by KRCC. As cancer grows, it may invade structures near the kidney, such as surrounding fatty tissue, veins, renal gland, or the liver. It might also spread to other parts of the body, such as the lungs or bones. It becomes essential to detect the KRCC tumor and classify it at the early stage to assist the pathologist in identifying the cause and severity of the tumor and in monitoring treatment. The pathologist examines the kidney diseases by using two different modes of data (Medical images and clinical databases). In this study, we reviewed different CAD tools to classify or predict KRCC tumor and its stages. For this study, two groups of methods that are data mining and medical image processing methods are selected. These methods allow the accurate quantification and classification of KRCC tumors from the clinical tools. Computer-assisted medical image and clinical database analysis show excellent potential for tumor diagnosis and monitoring.

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INTRODUCTION

Kidney Renal Cell Carcinoma (KRCC) is the most common kidney tumor, accounting for 2 to 3% of all new cases in India (Abraham *et al.*, 2016). From country to country, the KRCC case varies, but the extreme western parts of the world affected are more. Recent Surveillance, Epidemiology, and End Results (SEER) data show that 1 in 5 adults with different ages is a Kidney Cancer survivor (Abraham *et al.*, 2016). To assist the pathologist in KRCC tumor diagnosis, proper classification with stage identification is necessary. The patient's condition depends on cancer's stage, which describes how far it has spread in the patient's body. The kidney cancer (KRCC) stage can be classified based on the physical exam, imaging tests, and clinical database. Predicting the right stage of KRCC helps doctors diagnose disease (Abraham *et al.*, 2016). With medical advances, Kidney Renal Cell Carcinoma (KRCC) tumor can be detected at an early stage and can be diagnosed. Recent multidimensional data and clinical images of kidney tumors patients provide opportunities for better investigation of the medical model to assist radiographers, pathologist, and so on. The demand for advanced CAD tools with image analysis and clinical database analysis has opened enormous opportunities for revealing new knowledge of Kidney tumors. The TCGA (Bhalla *et al.*, 2017) has opened numerous opportunities for revealing new insights on the genomic data basis of RCC tumor, it is imperative to address the issue of integration with the available multidimensional data to understand cancer phenotypes (NCIA, 2014) better and thereby providing an enhanced global view of the interaction between various data and knowledge levels.

Recently many researches are going on to explore the intelligent techniques of patient's diagnosis for classification and prediction in the biomedical field (Choi *et al.*, 2012). However, very few researchers are going on multiple types like genomic data, clinical database, and kidney organ biological data. Many researchers have investigated the classification of KRCC cancer using one modality, i.e., either clinical database or imaging modalities (Abraham *et al.*, 2016; Bhalla *et al.*, 2017; Choi *et al.*, 2012). In this study, we are investigating the learning models on two types of data: clinical database and imaging technique to classify the KRCC patient. This paper is organized as follows. In section II, background works are discussed. Section III deals with the methodological categorization of KRCC tumor-related research works. Section IV addresses the challenges and future scope of research in intelligent CAD of KRCC tumors.

Motivation For Research

Overall, 10% of the global population has kidney functioning problems. According to the National Institute of Diabetes and Digestive Kidney Diseases (NIDDK) (Abraham *et al.*, 2016), as shown in Figure 1 in India, 7% of peoples are suffering from various kidney diseases. Figure 1 shows the different percentage of kidney diseases suffering people country-wise (Bhalla *et al.*, 2017).

Background

The kidney organs, as shown in Figure 2 (Bhalla *et al.*, 2017), are bean-formed human organs in the stomach pit of the human body on two sides of the spinal section. The Kidney Renal tubule regulates the fluid in the human body. These Renal tubules help in the excretion of waste, blood filtering, and for the generation of urine. The kidney organ performs filtration of 180-liter (Bhalla *et al.*, 2017) liquid volume each day for a steady health condition. Kidney failure refers to temporary or permanent damage to the kidneys that hampers normal kidney function.


Figure 1: Worldwide Kidney Tumor Status

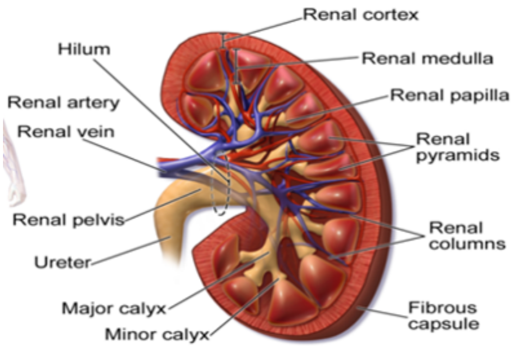

Figure 2: Kidney Anatomy

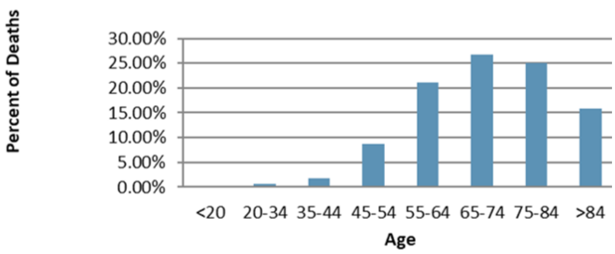

Figure 3: Kidney RCC tumor analysis

Some harmful factors for kidney failures are Hypertension, Obesity, Smoking, Family History, and particular medications like Phenacitin (Abraham *et al.*, 2016; Ray *et al.*, 2016), workplace exposures, and so on. There are two types of kidney failures — acute and chronic. Acute Kidney (Bhalla *et al.*, 2017) failure has an abrupt onset and is potentially reversible. Chronic kidney (Bhalla *et al.*, 2017) failure progresses slowly over at least three months and can lead to permanent kidney failure. Chronic kidney diseases are kidney tumors, kidney stones, and kidney infections. A kidney tumor is a disease in which kidney cells become cancerous, forming a tumor. Generally, the kidney tumor is categorized into indolent (Choi *et al.*, 2012), malignant (Choi *et al.*, 2012), or benign (Choi *et al.*, 2012). Malignant tumor (Choi *et al.*, 2012) is harmful and can develop and spread all over the human body parts. Indolent tumor (Choi *et al.*, 2012) is dangerous but has a minimum probability of spreading all over the body. Benign tumor (Choi *et al.*, 2012) can increase its size but cannot spread to other organs of the

Table 1: Summaryof CT scan dataset for Kidney RCC Cancer

S.NO	Image Statistics	Dataset
1	Modalities	CT, MR
2	Number of male Patients	346
3	Number of Female Patients	191
4	Vital Status (alive)	360
5	Vital Status (Dead)	177
6	Age	26 Yrs. To 90 Yrs.

human body. Based on the size of the tumors and its type J. R. Egner (Egner, 2010; Ng *et al.*, 2008) categorized cancer stages into different levels. Most of the radiologist follows cancer stages (Egner, 2010) to classify kidney tumor size and its type.

In 2018 in the western world, the estimated new cases are 65,340, and estimated deaths are 14970. It is 3.8% of all recent cases of cancer. Figure 3 shows the kidney RCC tumor analysis for different age group people. It also shows the age-wise percent of deaths by Kidney tumor (Bhalla *et al.*, 2017; CC, 2004). According to NIH, in 2017, the RCC Cancer rate may increase in the 35-44 age groups of people (NCIA, 2014). The large-scale cancer communities like International Cancer Genomic Consortium (ICGC) and The Cancer Genomic Atlas (TCGA) are doing systematic studies on genomic, clinical, and relative multidimensional data on different cancer data modalities (Varma, 2008). These communities are making data available to researchers in KRCC cancer (Bhalla *et al.*, 2017).TCGA provides multiple types of data like a clinical database, and Table 1 gives a summary of imaging modalities related to KRCC diagnosis. Similar to the TCGA American Joint Committee and International Union against Cancer (UICC) (Deng *et al.*, 2017) have designed a staging system to reflect the mode of spreads in KRCC.

To KRCC diagnosis. Similar to the TCGA American Joint Committee and International Union against Cancer (UICC) (Deng *et al.*, 2017) have designed a staging system to reflect the mode of spreads in KRCC.

In developing a prediction and classification models for KRCC, the stage of the cancer is the main factor in determining the expected outcome of a disease. The main tests for diagnosing kidney cancer are urine, blood tests, imaging scans, and tissue sampling (biopsy). From these medical tests, prediction models use gene expression data of RNA seq (Dalgin *et al.*, 2007) experiments from the TCGA project by implementing different techniques. Besides classifying KRCC stages, different medical imaging modalities like CT, MRI & Ultrasound images are used with CAD tools to assist the doctor. Many researchers developed CAD tools by using machine learning techniques to diagnose KRCC disease by using gene expression data of RNA seq (Dalgin *et al.*, 2007), medical images, clinical database. In classifying and predicting KRCC disease, all the CAD tools include data pre-processing, feature selection, and many more steps with different algorithms/techniques.

MATERIALS AND METHODS

Systematic and Meta-analysis have become essential in Computer-Aided Diagnosis in medical informatics. Computer-aided diagnosis is essential in kidney tumor classification and stage prediction. The KRCC tumor can be diagnosed by using different data like kidney volume (Bhalla *et al.*, 2017; Choi *et al.*, 2012; Dalgin *et al.*, 2007; Deng *et al.*, 2017), Glomerular Filtration Rate (GFR) (Choi *et al.*, 2012), Gene expression, RNA seq (Deng *et al.*, 2017), etc.; In this review, literature methods are grouped into image processing and data mining based on the clinic tools used for diagnosis.

Methods on CT scan image analysis

The use of a CT scan image is a capability of detection of tumor and its size, which may assist radiologists. Essential components in a CAD (Kim and Park, 2004) system that assist the radiologist is described below.

Pre Processing

CT scan image pre-processing phase reduces the noise to increase the accuracy of the CAD systems next level components such as kidney tumor segmentation and feature extraction. Variations in the CT scan image are caused by many factors such as radiologist experience, selection of seed point to quantify the kidney tumor size, resizing of the image, contrast enhancement of CT scan kidney organ image is the significant challenge to provide accurate assistance to the radiologist.

The pre-processing phase consists of noise filtering, contrast enhancement, and without contrast enhancement. Noise can reduce the accuracy of the

Table 2: CT — Summary of diagnostic accuracy

Study	Intervention	Sensitivity	Specificity
(Choi *et al.*, 2012)	Quadriphasic multidetector helical CT	94%	41%
(Divgi *et al.*, 2013)	Multiphasic contrast-enhanced CT	76%	47%
(Kim *et al.*, 2016)	Three-phase MDCT	82%	85%
Kutman 2013	Dynamic Contrast-enhanced CT	88%	87%
(Gerst *et al.*, 2011)	Contrast-enhanced CT	81%	64%
(Shebel *et al.*, 2011)	Quadriphasic multidetector CT	95%	90%
(Young *et al.*, 2013)	Quadriphasic multidetector CT	86%	43%
Yuan 2011	Contrast-enhanced CT	78%	50%

segmentation of kidney tumors. Common noises in CT images are Salt and Pepper, Speckle noise Gaussian noise (Gonzalez *et al.*, 2009; Patil, 2012; McAndrew, 2015; Bin-Habtoor and Al-Amri, 2016). Noise can be removed from images using various techniques like Mean filter (Gonzalez *et al.*, 2009), Median filter, Gaussian filter (Bin-Habtoor and Al-Amri, 2016), and Weiner filter (Bin-Habtoor and Al-Amri, 2016), etc. Many researchers recommended a combination of filters as the best technique to remove the noise from the CT scan image in the pre-processing phase.

Segmentation

In this phase, the desired boundaries of kidney organ or kidney tumor and objects are identified in the CT image. There exist various segmentation methods in the literature that have applied to diagnose kidney tumors.

The most commonly used segmentation techniques are Thresholding, Clustering, and Watershed algorithms, Neural Network, SVM, and CNN. W. Thong et al. Presented techniques to detect kidney organ by employing deep learning Convolutional Neural Network technique (Thong *et al.*, 2018). Fast and accurate results are provided with few computing resources. A summary of various techniques on CT scan image to identify kidney organ and kidney tumor by authors are illustrated in Table 2. The accuracy of segmentation is calculated based on simplicity and specificity by the authors, and kidney organ segmentation accuracy reached by different authors listed in Table 3.

Feature Extraction

The feature selection is the process of removing irrelevant features. A feature selection criterion is required, which can measure the relevance of each feature with the output class/labels. Different researchers extracted kidney features by using Fuzzy techniques (Gomalavalli, 2017), texture analysis (Kim *et al.*, 2005), and contrast enhancement techniques (Linguraru *et al.*, 2009; Moretto *et al.*, 2014; Ruppert-Kohlmayr *et al.*, 2004). (Bektas *et al.*, 2019) proposed a machine learning-based CT scan texture analysis for the prediction of KRCC stages. He proposed a cross-validation method for feature selection along with optimization. The feature selection was performed using the Waikato Environment for Knowledge Analysis (WEKA) toolkit. (Park, 2019) described a useful imaging feature for differentiating renal angiomyolipoma (AML) (Song *et al.*, 2016) subtypes from renal cell carcinoma subtypes (Song *et al.*, 2009).

Classification

To quantify KRCC tumor disease and its stages, as discussed in the section, TCGA provides an online data source for different medical image formatted data sets. Researchers implemented their methods to classify stages of KRCC tumor disease using different methods to assist the pathologist. Many researchers proposed methods based on contrast-enhanced computed tomography image modality to quantify the KRCC tumor stage. Contrast-enhanced CT is the traditional gold standard for diagnosing renal cell carcinoma, which is used in many research articles. Table 2 gives a summary of the paper studied, and Table 3 gives an accuracy of the contrast-enhanced method on CT scan images.

Table 3: Studies assessing KRCC diagnosis with learning models on CT scan image modality

SNO	Author (Year)	Tool	Technique	Modality	Image Processing
1	Mostafa Atriet.al (2008)	Comparison	Quadriphasic multidetector	CT	RCC
2	(Abraham *et al.*, 2016)	Review	Multiphase CT	CT	KRCC
3	(Quaia *et al.*, 2008)	Comparative study	Contrast enhancement	CT	KRCC
4	(Ignee *et al.*, 2010)	Comparative Study	Contrast enhancement	Ultrasound and CT	KRCC
5	(Linguraru *et al.*, 2010)	MATLAB	Contrast Enhancement	CT	Cancer Quantification
6	(Li *et al.*, 2011)	Comparative Study	Kidney tumor segmentation	Ultrasound and CT	KRCC
7	(Shebel *et al.*, 2011)		Multi detective	CT	KRCC
8	(Gerst *et al.*, 2011)	Evaluation	Contrast enhancement	Ultrasound	KRCC
9	(Li *et al.*, 2011)	Comparative Study	Edge, Region growing, Texture segmentation	Ultrasound	Tumor Segmentation
10	(Linguraru *et al.*, 2011)	MATLAB	Contrast-Enhanced	CT	Renal Cancer Classification
11	(Choi *et al.*, 2012)	Simulation	Quadriphasic multidetector helical	CT	RCC
12	Raphaël Prevost et.al (2012)	MATLAB	Contrast Enhancement	Ultrasound	Renal Lesions Detection
13	(Young *et al.*, 2013)		Multidetector contrast enhancement	CT	KRCC
14	(Karlo *et al.*, 2013)	Assessment	Contrast enhancement	CT	KRCC
15	(Ghalib *et al.*, 2014)	Comparative Study	K means	CT Scan	Tumor Segmentation

Continued on next page

Table 3 continued

SNO	Author (Year)	Tool	Technique	Modality	Image Processing
16	(Kim *et al.*, 2016)		Three-phase contrast enhancement	CT	KRCC
17	(Muglia and Prando, 2015)	Comparative Study		CT, MR	Tumor Classification
18	(Hodgdon *et al.*, 2015)	MATLAB	SVM	CT	Fat - Poor RCC
19	(Mredhula, 2015)	MATLAB	Gabor Filtering	CT	Detection & Classification T
20	(Skalski *et al.*, 2016)	MATLAB	Decision Tree	CT	Tumor Segmentation and Detection
21	(Lan *et al.*, 2016)		Contrast enhancement	CT	KRCC
22	(Ertekin *et al.*, 2017)		Contrast enhancement	CT	KRCC
23	(Thong *et al.*, 2018)	MATLAB	Convolutional networks	CT	Kidney Segmentation
24	(Shah *et al.*, 2017)	Comparative Study	SVM	CT	Tumor Segmentation & Classification
25	(Lee *et al.*, 2017)	MATLAB	Contrast Enhancement using Texture	CT	Detection & Segmentation of Small Renal Mass
26	(Shah *et al.*, 2017)	MATLAB	Fuzzy C Means	CT	Tumor Classification
27	(Sun *et al.*, 2018)	MATLAB	Deep Learning (Bi-ConvRNN)	CT, MR	Tumor Segmentation
28	(Yu *et al.*, 2019)	MATLAB	Crossbar-Net	CT	Tumor Segmentation

Data mining methods

There are many different methods of data mining tasks. The most commonly used Data mining techniques are sequence patterns, prediction, clustering, and classification. There are two types of techniques for those parameters and nonparametric techniques. Parameter model description by using algebraic equations, there is no relationship between the input and output of some of the parameters specified. Nonparametric methods are more suitable for data mining applications. Nonparametric techniques include neural networks, decision trees, and genetic algorithms (Mitchell, 1999).

In the medical informatics field, data mining techniques play a vital role in classifying and predict abnormal situations. Progress in data mining applications and its implications is manifested in the areas of clinical database, image analysis, and patient care in the monitoring system and automatic identification of unknown classes. To classify or predict KRCC tumor disease from clinical, pathological features, genomic alterations, DNA methylation profile, many researchers have used RNAseq (Yoo *et al.*, 2012; Mitchell, 1999) and proteomic signatures with different data mining techniques. As reviewed in Table 4, data mining techniques are applied to gene expression to classify or predict stages of KRCC. Enormous research and development of recent years mining techniques are used on images to extract implicit knowledge of medical image modalities. Dr. R. Anbu Selvi et al. focused on comparing three different feature extraction methods using image mining techniques for abnormal brain tumor patterns.

RESULTS AND DISCUSSION

In this study, various techniques employed in different stages to diagnose kidney tumor using CT scan images and clinical databases have been discussed. There are several ways to prognosis KRCC tumor and its stages (ACS, 2018) as described below

Image prognosis for a Kidney Tumor

In the CAD system to diagnose renal kidney tumor, uses different imaging modalities in different stages. The imaging modalities like Computed tomography (CT), magnetic resonance imaging (MRI), and ultrasound are used for kidney tumor diagnosing, characterizing, and staging the renal tumors. Table 5 provides a summary of medical imaging for renal masses and its comparison to know why pathologists prefer CT scan image modality to diagnose kidney tumors.

In image prognosis preprocessing is the basic step in digital image analysis, which is performed after the image acquisition. The current research shows that most of the researchers use a combination of filter techniques to reduce the noise and to enhance the image quality.

Segmentation is one of the primary stages to identify the tumor tissues in the CT scan image. As per the literature reported, the maximum accuracy of 88 % has been achieved for 100 images using K-means and decision support system techniques (Krempel *et al.*, 2018). Technique also resolved the issue of overlapping and obstructed without any loss of kidney organ geometrical features during segmentation.

To classify kidney tumors, the extraction of features is the major and essential step in image prognosis. As per the study, Han Sang Lee et al. used textural features (Lee *et al.*, 2017) technique in detecting the kidney tumor. The textural features can further help in the grading of the tumor cells, as presented by (Lee *et al.*, 2017)

In image prognosis, different aspects impact the analysis of input images. The input image analysis accuracy depends on many factors, which include the environmental conditions, background, image magnification size, contrast, and position of medical devices. Thus, to achieve accuracy and consistent results, a standard repository with categorical information is required for validation and evaluation.

The Lab tests prognosis for Kidney Tumor

Kidney tumors might be found because of imaging tests or lab tests. Lab tests include predicting different kidney diseases. In the study, researchers made the prediction of four types of kidney diseases, namely Acute Disease, Chronic Kidney diseases, nephritic syndrome, and Glomerulonephritis's (Yoo *et al.*, 2012). In recent papers, authors used machine learning techniques for prediction and diagnosed chronic kidney diseases using the following biological, clinical lab database

Gene expression

Kidney tumors can be determined by using histological data types with different clinical behavior. The human genes are categorized into 7230 DNA microarrays containing 22648 unique cDNAs representing 17083 different UniGene clusters (Yu *et al.*, 2019).

Data Methylation

DNA methylation (Ramakrishnan and Bose, 2017) is an epigenetic mark that has suspected regulatory roles in a broad range of biological processes and diseases. The technology is now available for studying DNA methylation genome-wide (Ramakrishnan

Table 4: The summary of medical imaging for renal masses

Description	Ultrasound	CT	MRI
Usage	Medium	High	Medium
Resolutions	Axial	Spatial	Contrast
Cost	Medium	Less	High
Type of Energy	Sound Waves	X-Ray	Magnetic Field
Time to Scan	20 Min	10 Sec	40 Min
Feature Extraction	Fluid Tumors	Size / Shape and Location of tumor	Blood Vessels

Table 5: Studies assessing Kidney tumor using data mining learning models

S.NO	Author (Year)	Method	Data Set
1	(Deng *et al.*, 2017)	Similarity Network Fusion on gene expression	66 Tumor Patient Data
2	(Liu *et al.*, 2015)	Microarray gene expression	59 genes associated with RCC
3	(Tang *et al.*, 2018)	SVM gene expression	537 RCC Data
5	(Jagga and Gupta, 2014)	Machine Learning algorithms on RNAseq expression data	475 RNA Seq dataset
6	(Park *et al.*, 2016)	SVM	25 Clinical attribute
7	(Ramakrishnan and Bose, 2017)	DNA methylation	219 tumor samples
8	(Soh *et al.*, 2017)	DNA methylation	6640 tumor samples
9	(Bhalla *et al.*, 2017)	Threshold-based model	533 genes
10	(Tang *et al.*, 2018)	Tumor origin detection	256 Testing sets
11	(Krempel *et al.*, 2018)	Tumor analysis	Comparative study

and Bose, 2017), at a high resolution, and in a large number of samples.

In summary, medical image processing with data mining techniques is a growing field of research, and more and more applications are becoming part of the clinical practice. (Wang *et al.*, 2006) The medical field requires: (i) A standard publicly available repository along with a patient's clinical details are required to test and validate the tumor classification and stage prediction, which in turn helps in effective diagnosis. (ii) An efficient with the less fault system must be used to provide an opinion to the radiologist. This will help in better diagnosis by reducing the false report and workload of the radiologist. (iii) Integration of image prognosis and clinical database prognosis with multi-dimensions also helps to give implicit knowledge on kidney tumor classification and stage prediction.

CONCLUSIONS

In this study, authors have highlighted the recent trends of essential components of image analysis, and Data mining techniques for clinical database analysis have been utilized to diagnose kidney tumors. CT scan image helps how and at what stage the cancer is being diagnosed. Recent trends for kidney tumor detection and early-stage prediction techniques have been analyzed, which shows the requirement of the huge amount of data for training.

Many research publications in the health informatics of Kidney tumor diagnosis have contributed to the researchers. However, this review paper has attempted to provide feedback to the radiologist and scientific community. The authors have mentioned the best techniques in CT scan image analysis and clinical database analysis in the literature to diagnose kidney tumors. Since the existing techniques have been developed and tested on different datasets with different dimensional data, but it is difficult to suggest which technique is outperformed. TCGA and SEER have been provided a stable repository on kidney tumors to identify the best technique among the existing state of art techniques.

Although the efficient techniques exist in the literature, still there is a scope to explore the following future work, which may help in the diagnosis of kidney tumors. In the medical field, the lack of data is two-fold and more acute: there is a lack of access to publicly available data, and quality labeled data is even scarcer. Data or class imbalance in the training set is a significant issue in medical image analysis. Aside from data-level strategies, algorithmic modification strategies, and cost-sensitive learning techniques currently embedded knowledge discovery in medical image archives about diseases' progression and responses to treatments and precious experience of diagnosis are the current research challenges in the medical field. The traditional applications for KRCC are discussed in the above sections. New areas of research include visual pattern mining, image mining, computer vision in the medical field, involving surgical robots.

In summary, the CT scan image analysis, Data mining methods for KRCC tumor classification, and predictions are reviewed. A reported result in different areas of the KRCC tumor segmentation, classification, and predictions using methods are studied. In many reported results, a combination of CT scan image and clinical database are used in the treatment of unclear kidney renal tumors. Despite the poor diagnostic accuracy of an unenhanced image, many renal tumor masses are discovered incidentally on CT images by the radiologist. Lastly, there are unlimited research scopes to improve Computer-Aided Diagnosis for kidney tumors of health informatics.

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Conflicts of Interest

The authors declare that they have no conflicts of interest in this work.

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