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A Comprehensive Review of Artificial Intelligence Approaches in Kidney Cancer Medical Images Diagnosis, Datasets, Challenges and Issues and Future Directions

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ABSTRACT: Various diseases are prevalent in global populations and can be attributed to human lifestyles, economic conditions, social factors, genetics, and other country-specific factors. Our study provides a detailed analysis of the current methods and uses of artificial intelligence (AI) in diagnosing kidney cancer. This literature review examines the most recent advancements and uses of AI in diagnosing cancer of the kidneys, emphasizing its significant influence on medical diagnosis and patient treatment. Evaluate their efficacy, explore prospective areas for future study and development, and identify obstacles and constraints, offering a fundamental review of critical advancements in AI, machine learning, and deep learning. AI-powered diagnostic tools expedite the analysis of intricate images and enhance the early identification of diseases, ultimately leading to improved patient results. Furthermore, the utilization of AI-driven image processing enables the customization of treatment regimens, thereby enhancing the efficiency of healthcare provision. This review primarily highlights the importance of conducting additional research and improving AI to transform the detection and treatment of kidney cancer.

Keywords: Kidney cancer diagnoses, Deep learning, Machine learning, The Cancer Genome Atlas (TCGA) dataset, Classification, Segmentation.

1. INTRODUCTION

The kidneys are essential organs just below the rib cage on each side of the spine. Kidney cancer, sometimes called renal cancer, can develop in any of these places. Urine production, fluid and electrolyte balance maintenance, waste products, and excess fluid filtration are all vital functions of these essential organs. Most instances of kidney cancer are renal cell carcinomas (RCCs). Wilms tumor, which is more prevalent in youngsters; renal sarcoma; and transitional cell carcinoma are three other, less frequent types. Kidney cancer risk factors include advancing age, gender (males are more likely to get the disease), smoking, being overweight, having high blood pressure, and having certain hereditary traits. Constant aches and pains in the back or sides, lumps or masses in the abdomen, sudden and unexplained weight loss, extreme tiredness, and blood in the urine are all possible signs of kidney cancer. When kidney cancer is in its earliest phases, and no symptoms are present, detection can be quite difficult. Surgery, targeted treatments, immunotherapy, and radiation therapy are all part of the treatment options available for cancer, which might differ according to the patient's condition, the stage of the disease, and the particular form of cancer. The prognosis and results for patients identified as having kidney cancer are greatly affected by the lack of early identification, which is why periodic medical examinations are necessary[1][2] .

By providing advanced diagnostic methods and furnishing cutting-edge analytical tools, radiomics and artificial intelligence (AI) are reshaping the assessment of kidney lesions. Medical imaging specialists employ artificial intelligence techniques, namely machine learning (ML) and deep learning (DL) models, to analyze extensive datasets of kidney images obtained from CT, MRI, or ultrasound scans. By automating lesion identification, segmentation, and classification, these algorithms significantly improve radiologists' ability to understand kidney lesions and their features quickly and accurately. AI's remarkable pattern recognition capabilities in medical images allow for more accurate and efficient evaluation of kidney lesion existence, size, and probable malignancy[3] .

One common and possibly fatal disease that affects the kidneys is renal cell carcinoma (RCC), sometimes known as kidney cancer. The key to successful therapy and better patient outcomes with kidney cancer is early and precise diagnosis The application of AI in medical imaging has emerged as a transformative approach to enhance the detection and handling of kidney cancer and other malignant condition. ML and DL methods, in particular have demonstrated significant promise in automating the processing of medical images., which might lead to more accurate and efficient diagnosis of kidney lesions [4]. Magnetic resonance imaging (MRI), Computed tomography (CT), and ultrasound are often employed imaging techniques in traditional kidney cancer diagnoses. However, radiologists need experience and a lot of time to manually analyze these imaging modalities because of how complicated their interpretations can be. Automated detection, segmentation, and classification of kidney lesions are some ways that AI-based solutions are trying to tackle these difficulties. This will help speed up the diagnostic process and give vital insights into tumor features [1] .

This study explores the latest developments in using artificial intelligence in medical imaging to detect kidney cancer. Our goal is to illuminate how artificial intelligence algorithms might transform the identification and characterization of kidney lesions by reviewing the relevant literature, methods, and results. We will also review the problems, solutions, and plans for using AI in kidney cancer imaging, emphasizing how it might improve diagnostic precision, treatment efficacy, and patient care. The main contributions of this paper are:

- **Test the Effectiveness of AI Approaches for Identifying Kidney Lesions:** To show how AI algorithms can identify kidney abnormalities from different imaging modalities, including MRI, CT, and ultrasound, by doing a thorough literature review of current studies and research publications. Please find out the efficacy of several models using machine learning and deep learning in detecting and pinpointing lesions, emphasizing their strengths and weaknesses.
- **Investigate How AI Is Changing Pre-Diagnosis and Treatment Planning:** to show how AI might help with kidney cancer early detection and how it could affect treatment strategies. Investigate the use of AI algorithms in the early diagnosis of kidney lesions, which enables more efficient intervention approaches. Please find out how well these technologies may help doctors tailor their treatments to each patient's unique kidney cancer by revealing essential details about lesions, including shape, size, and enhancing patterns.
- **Analyze the Possibilities and Obstacles of AI-Powered Imaging for Kidney Cancer**: Figure out what problems arise when using AI to diagnose kidney cancer and talk about them. Discuss the need for standardized datasets, the difficulty of making algorithms understandable, and data privacy. In addition, the study will examine the present status of artificial intelligence (AI) in the field of kidney cancer imaging and explore potential advancements in the future. Such as integrating multi-modal data, improving patient outcomes through collaboration between AI and medical professionals, and the progress of automated image interpretation.

The rest of the arrangement of this study is as follows: Addresses machine learning for kidney cancer diagnoses in section 2. Deep learning for kidney cancer diagnoses in section 3. Dataset used in kidney cancer diagnoses in section 4. Challenges and issues of using AI for kidney cancer diagnoses present in section 5. Section 6 presents future direction for research and development in the field of AI for kidney cancer diagnoses. Finally, section 7 summarizes the main findings of the review.

2. Kidney Cancer Diagnoses based on Machine learning

In recent years, machine learning (ML) has become an invaluable resource for renal imaging diagnostics, providing novel approaches to improve the speed and precision of disease detection and diagnosis. The ML algorithms may be trained to automatically recognize tumors, cysts, and other abnormalities in kidney pictures, which helps with early and accurate diagnosis. Machine learning also helps with kidney structure segmentation, which helps diagnose diseases since it allows for in-depth research of various areas inside the organ. Measurements of kidney image properties such as blood flow patterns, tissue texture, and lesion size are aided by ML's quantitative analytic capabilities. In addition, ML is very good at pattern recognition, which allows us to find complicated patterns linked to many kidney illnesses. By evaluating kidney pictures and prior patient data, the technology may also be used for risk assessment and prognosis of certain diseases, which allows for early intervention and individualized treatment strategies [5][6] .

Combining ML with additional data sources like genetics, medical history, and test findings allows for a more complete image, more precise diagnoses, and tailored treatment plans. The ML automates image pre-screening, highlights areas of interest for medical professionals, and can shorten the time needed for a thorough diagnosis, greatly accelerating diagnostic processes. Not only that, but ML is a decision-aid application that provides healthcare professionals with more insights and helps them make better judgments, especially in complicated circumstances. Furthermore, ML models enhance renal imaging quality, facilitating data visualization and interpretation for healthcare providers, particularly in the case of mild or early-stage problems. In ML models, adaptation and learning are built in, so they may increase their precision periodically by learning from new data and responding to patterns or modifications to the distribution of that data. To guarantee patient safety and data security, it is essential to implement stringent testing, validation, and compliance with ethical and privacy requirements before using ML in healthcare uses such as renal image diagnostics. ML use for medical purposes will be more critical in the future for better diagnostics and patient outcomes as technology progresses [7] .

Many studies made on the kidney diagnosis such as [2]. The primary focus of the proposed strategy is on the segments and classifications. The initial stage entails acquiring the renal CT images of the kidney, applying preprocessing techniques to eliminate any unwanted disturbances, segmenting the processed image using a close morphological operation, and subsequently utilizing GLCM to extract the distinctive features. Multi-SVM surpasses prior methods by accurately classifying tumors or their constituent cells into many categories, achieving an accuracy rate of approximately 89%. Another study by [8] outline the proposed steps for automatically segmenting kidneys on abdominal CT scans using the K-means method. This stage encompasses pre-processing and post-processing operations which differ from previous techniques. Subsequently, the segmented areas undergo feature extraction to facilitate classification. Ultimately, the SVM-based algorithm is employed to identify renal cell carcinoma. The Dice coefficient yielded a segmentation measurement of 89.3%. The classification's efficacy was determined using Sensitivity, Specificity, and Accuracy, measured at 84%, 92%, and 88%, respectively. Also, [9] propose utilizing distinct datasets for feature extraction in pre-trained DNN models and employing support vector machines for classification. Multiple pre-trained deep neural networks (DNNs), including Shuffle Net, MobileNet-v2, and ResNet-101, are merged, and the ultimate predictions are determined through the vast majority voting technique. The ensemble model surpasses the individual models in classification by amalgamating the projections from many DNNs. The ensemble model has classified the kidney ultrasound scans into four unique categories regular, cyst, stone and malignancy. The experimental results indicate that the suggested strategy outperforms the present methods in successfully classifying most photos, achieving the maximum classification accuracy.

New study by [10] The proposal involves the development of a dual-channel architecture called the Example Segmentation Network (FS-Net) to enhance the process of segmenting kidneys and malignancies. This was achieved by leveraging the U-Net model. Following the tumor segmentation, the radionics analysis was conducted, and several support vector machines (SVMs) were trained to differentiate between benign and malignant tumors. This was achieved by constructing a feature space and implementing transfer learning. Based on the experimental findings, the Dice coefficients for the segmented kidney and the tumor areas were 0.9662 and 0.7685, respectively, surpassing the results obtained by the most recent methodologies. The utilization of radionics properties in a categorization strategy can efficiently categorize most malignancies. According to [11] Offer an organized structure for categorizing renal computerized tomography (CT) images either as normal or malignant. The framework employs deep features extracted from pre-trained models including VGG16, VGG19, ResNet50, ResNet101, DenseNet121, and DenseNet201. Ultimately, these characteristics are employed (KNN) for binary classification. According to the findings of this research, the utilization of pre-processed CT slices enables the (KNN) method in attaining a detection accuracy of 100%. In this work conducted by [7] Eight machine-learning algorithms were developed and assessed to predict the presence of kidney cancer metastases and the likelihood of surviving for three years. The selection of variables was based on clinical expertise and statistical relevance. The logistic regression approach got the greatest Area Under the Receiver Operating Characteristic (AUROC) score of 0.741. for forecasting 3-year survival. and 0.804 for predicting tumor metastasis out of the eight examined models. This model can assist individuals diagnosed with renal carcinoma make informed choices on early intervention. Furthermore, [6] presented The study attempts to utilize a radionics-based method to automatically detect kidney cancers from normal kidney tissues using computed tomography (CT) images. In order to build the binary logistic regression strategy, the scientists selected three radionics features from over 800 elements taken from CT image regions of interest. According to the CT radionics classification model, the accuracy (ACC) of the test sets was 0.98%, and the Youden index for both the training and test sets. exceeded 0.85. The summary on the related works on kidney diagnosis using ML techniques presented in Table1.

Table1: The summary on kidney diagnosis using ML techniques.

Author(s)/ Year	**Methods/Techniques**	**Brief Description**	**Dataset**	**Strengths**	**Weaknesses**
Rohith V et.al (2019) [2]	Multi SVM classification model	The proposed method is focused on segmentation and classification, the preprocessed image is segmented using close morphological operation followed by extracting the features using GLCM. Multi-SVM used to classify the various kinds of tumors or cells in the tumor	CT images	1- Multi SVM is used for more than two classifications 2- Increases the accuracy level Which classify to multi classes with approximately 89% of accuracy compared to other methodologies	The study does not include information regarding the sample size, or the number of the kidney's tumor images utilized.
Seda Arslan Tuncer, Ahmet Alkan (2018) [8]	K-means segmentation model ,Support Vector Machines (SVM) classification model	The study suggests automating kidney segmentation on abdominal CT images using the K-means algorithm. This process involves distinct pre-processing and post-processing steps, which differ from previous methods. Subsequently, feature extraction is conducted on the segmented regions for classification purposes. Finally, an SVM-based classification technique is employed to detect renal cell cancer	130 different CT images	1- Utilizing an innovative feature vector as the input to the classifier has the potential to enhance the system's performance in comparison to conventional approaches. 2- The Dice coefficient for measuring segmentation has been shown to be 89.3%. and the classification performance Sensitivity, Specificity, Accuracy were obtained as 84%, 92%, 88% respectively	1- The small sample size of only 100 CT images used to test the system, which limit the generalizability of the results.
S Sudharson, Priyanka Kokil (2020) [9]	ResNet-101, shuffleNet and MobileNet-v2 for feature extraction, support vector machine (SVM) classification model	The suggested methodology entails utilizing diverse datasets to extract features using pre-trained deep neural network models, followed by employing a support vector machine for classification. The procedure entails merging multiple pre-trained deep neural networks, including ResNet-101, ShuffleNet, and MobileNet-v2,	4940 CT augmented images	1- The combined approach exhibits improved performance in classification in comparison to each of the techniques by consolidating the predictions of many DNNs. 2- The provided method attained a peak	Does not provide a detailed description of the methodology, specific details regarding the network architectures, training process, hyperparameter selection, or optimization techniques are not provided.

		and subsequently generating final predictions by the majority voting technique..		classification accuracy of 96.54% when tested with high-quality images and 95.58% when tested with images containing noise.	
Xi-Liang Zhu et.al (2022) [10]	U-Net segmentation model, and multiple support vector machines (SVMs) classification model	The study suggested implementing a dual channel structure that employed a fine segmentation network (FS-Net) derived from the model of U-Net to enhance the segmentation of kidneys and tumors. The system utilized radiomics and transfer learning techniques to create a space of features and trained multiple (SVMs) to distinguish between benign and malignant tumors.	210 3D CT images	1- Research demonstrates that the dual-channel FS-Net outperforms the U-Net architecture in accurately segmenting kidneys and tumors. 2- The utilization of radiomics characteristics in the classification model yields favorable outcomes, showcasing its efficacy and resilience for the limited data set..	1-The study employs transfer learning to exploit information from an auxiliary dataset (KiTS19). However, it acknowledges that the accessibility of of annotated data and models that have been trained for particular 3D medical images remains restricted. 2- The extent to which transfer learning is useful in the context of segmenting renal cancers in 3D CT images has not been thoroughly investigated or discussed.
Venkatesan Rajinikanth et.al (2023) [11]	VGG16, VGG19, ResNet50, ResNet101, DenseNet121, DenseNet201for feature extraction Additionally, a K-Nearest Neighbor (KNN) classification model	The study's suggested structure employs deep features extracted by pre-trained methods, these models include VGG16, VGG19, ResNet50, ResNet101, DenseNet121, and DenseNet201. These features are then utilized for binary classification of kidney (CT) images into healthy or cancerous classifications, utilizing the K-Nearest Neighbors (KNN) algorithm.	2,680 CT images	1- The suggested strategy effectively utilizes fused characteristics, resulting in a significantly enhanced recognition accuracy (100%) compared to alternative methods 2- The model utilizes a well-balanced dataset comprising of 2,680 images, with an equal distribution of 1,340 images for both the healthy class and the cancer class. This balanced dataset	The study exclusively utilizes axial-plane renal CT slices from the dataset, focusing solely on healthy and cancer axial-plane images for analysis. This limited dataset not be representative of all possible cases of kidney cancer.

				significantly improves the accuracy of the classification process.	
Yuxiang Zhang et.al(2022) [7]	Support Vector Machines, Logistic Regression, Decision Trees, Random Forests, XGBoost, AdaBoost, K-Nearest Neighbors, and Multilayer Perceptron classification model	The study showcased and assessed eight machine learning models for prognosticating the 3-year survival and recurrence of kidney cancer. Logistic Regression exhibited the highest (AUROC) curve for both predicting 3-year survival and tumor metastasis.	12,394 clinical data	Logistic Regression outperforms the other seven predictive machine learning methods by the highest possible AUROC in both prediction situations.	The study selected variables based on both statistical and clinical significance. The choice of variables influences the performance and accuracy of the machine learning techniques. The exclusion or inclusion of certain variables also impact the predictive capabilities of the models.
Yunfei Li et.al (2023) [6]	A binary logistic regression classification model	The primary objective of this study is to employ radiomics techniques to accurately distinguish between malignant kidney tumors and healthy kidney tissues by analyzing CT images. The researchers acquired more than 800 radiomics characteristics from specific regions of interest in CT scans and utilized binary logistic regression to construct an initial classification model	210 CT images	The AUC values obtained from the ROC curve for the training and test sets were 0.9798 and 0.9841, respectively. These values exhibited a substantial increase compared to 0.7. Furthermore, the ACC, SENS, SPEC, and Youden indices all exceeded 0.85.	1 The present research utilized a restricted amount of samples. 2- The design and optimization of the model were impacted by the CT picture quality and the precision of human lesion segmentation.

3. Kidney Cancer Diagnoses based on Deep learning

Deep learning is a highly potent machine learning technique that can autonomously acquire and comprehend many characteristics and patterns without the need for human involvement. DL facilitated the development of prediction algorithms for the early detection of malignant illnesses, Furthermore, researchers utilized well-established methods for analyzing patterns. The algorithms used in deep learning have surpassed classic machine learning approaches in terms of their extraordinary precision in generating outcomes. A revolutionary development in kidney imaging diagnostics. Deep learning has the capacity to greatly enhance the efficiency and accuracy of disease detection and assessment [12] . One area where deep learning models, particularly CNNs, really shine is in extracting complicated patterns from medical pictures; this allows for the accurate and early identification of a wide range of kidney illnesses. Healthcare providers benefit from this automated method since it simplifies the diagnosis process and helps improve patient outcomes by allowing quicker treatments. Deep learning allows for a more complete picture of renal diseases by quantifying evaluations of kidney function and combining them with other diagnostic tools. Furthermore, these models add to customized medicine by customizing treatment programs according to unique patient traits. The benefits of deep learning extend beyond healthcare applications and into research and education. It helps analyze massive datasets to uncover disease causes and is an excellent tool for teaching medical personnel how to interpret images [13]. Deep learning's impact on renal image diagnostics goes beyond only improving diagnostic accuracy; it also influences the development of data-driven, patient-specific healthcare systems in the future. In kidney image diagnosis, deep learning might be revolutionary because it could make diagnostics more accessible, lessen reliance on human knowledge, and add to the continuous improvement of medical practices—all while revolutionizing the sector. A constant and dependable way to analyze varied renal diseases is by using deep learning models, which can adapt to complex patterns and variances in kidney pictures [5] . These models are valuable instruments for widespread and affordable diagnoses, especially in areas with limited resources, because they can work alone or with healthcare experts. When combined with other diagnostic data, deep learning provides a holistic method for evaluating renal illness. The influence of deep learning on kidney image identification goes beyond clinical settings as technology keeps improving. It helps with research, teaching, and, ultimately, the main aim of improving nephrology patient care and outcomes.

3.1 Kidney Cancer Classification studies

Classification is a crucial aspect of diagnosing a patient's condition. It involves categorizing the tumor's type and subtype to determine the most suitable treatment approach. This process aids in minimizing the disease's risk, altering its progression, and ultimately preserving the patient's life. To assess the performance criteria of the feature extraction process, it is necessary to choose a suitable classification method. Various optimization techniques have been employed to address classification difficulties. Hence, the differentiation between one categorization approach and another resides in its capacity to discern the disparities among the comparison regions. Regardless of the effectiveness of the feature extraction procedure, the accuracy and quality of the extracted feature can only be achieved if a suitable classifier is employed in the classification design. [14] . displays the findings from the relevant tumor classification studies.

The study conducted by [15] Created an extensive deep-learning model that accurately distinguishes between five primary histologic categories of kidney cancers, encompassing benign and malignant tumors. The ResNet-101 model underwent training and testing using CT data from 308 individuals who had undergone nephrectomy for renal malignancies. The AUC value obtained was 0.889. Afterwards, the model was verified using a distinct dataset of 184 cases from The Cancer Imaging Archive. The dataset's receiver operating characteristic curve was calculated to be 0.855. Also, [16] Developed the Deep Auto Encoder (DAE) approach as a lower-dimensional vector in their research. This method is utilized to derive in-depth characteristics from gene biomarkers. The neural network (NN) classifies the sample type, main diagnosis, tumor stage, and vital state. The experiments conducted indicate that the COST-HDL strategy outperforms standard machine learning and data mining methods in terms of efficiency when using gene expression data for kidney cancer prognosis. Another study by [17] suggests that using a deep learning neural network (DLNN) can enhance doctors' accuracy in assessing the stages of kidney cancer, particularly in distinguishing Stage 1 from higher settings. The DLNN was trained, validated, and tested using (TCIA) database. The classification accuracy was measured using the AUC metric. The AUC values for the training, validation, and test sets were 0.97, 0.91, and 0.90, respectively. In the study conducted by [18] , it is recommended that the preprocessing of miRNA data be carried out as the initial stage. During the second stage, the task is to pick candidate miRNAs with significant discriminatory ability. This selection process employs an appropriate feature selection technique that utilizes the AMGM measure. The suggested neuro-fuzzy system with deep rules classifies the kidney cancer subtypes (TCGA-KIRC, TCGA-KIRP, TCGA-KICH, TARGET-WT, and TARGET-RT) in the final phase using a collection of selected miRNAs. Within the identical TCGA dataset, the suggested approach effectively identified and classified miRNAs with an impressive precision of 93.2%. This stands in opposition to alternative methods.

Also, another study by [19] developed a framework for categorizing renal cell subtypes using CT images. The framework utilizes deep learning CNN (GoogLenet) and ROIs provided by radiologists. The study yielded promising results, with an accuracy of 0.85, sensitivity ranging from 0.64 to 0.98, specificity ranging from 0.83 to 0.93, and an AUC of 0.9. According to [20] proposed an ensemble-pyramidal deep learning model that accurately distinguishes between papillary and clear renal cell carcinoma. This model utilizes a hierarchical approach, employing three convolutional neural networks (CNNs) to interpret histopathological images at various sizes. The map was subjected to Gauss-Markov random field smoothing to ensure homogeneity. In comparison to existing cutting-edge methods, the framework demonstrated superior performance by precisely categorizing all four classes, the pixel accuracy for ResNet18 is 0.89, while the proposed technique achieves a pixel accuracy of 0.92. New study by [21] aim to conduct a study that involves two models: An ANN, is trained with blood sample test data to precisely forecast the occurrence of kidney cancer. Additionally, a CNN is trained to effectively identify CT scans of both malignant and normal kidneys. When contrasting the two proposed deep learning scenarios, Artificial Neural Network and Convolutional Neural Network, their training accuracy is 96% and 99%, respectively. In addition, the validation accuracy of the two algorithms has increased to 97% and 99%, respectively. Also, the proposed framework by [5] aims to categorize kidney cancer subtypes by employing machine learning techniques, CT scans, and clinical metadata. The main focus is on identifying and selecting kidney cancer for surgical intervention. Convolutional neural networks , specifically DenseAUXNet201, a technique based on deep learning are utilized for training on CT scans to accurately categorize kidney cancers into distinct subtypes, including clear cell, chromophobe, papillary, and oncocytoma. The DenseAUXNet201 architecture exhibited enhanced performance across all evaluation criteria. The XGBoost algorithm demonstrated excellent performance achieving an accuracy of 85.66%, precision of 84.18%, recall of 85.66%, and an F1-score of 84.92%. In contrast, logistic regression demonstrated superior reliability, achieving an accuracy rate of 90.63%, precision rate of 90.83%, recall rate of 90.61%, and F1-score of 90.50%.

The study by [12] Suggested employing 2D-CNN methods for the detection of KTs in computed tomographic scans. The researchers specifically analyzed three models: a 2D convolutional neural network consisting of six layers, denoted as CNN-6, a ResNet50 with a total of fifty layers, and a VGG16 with sixteen layers. These models were specifically designed to detect KT (Normal Tumor). The optimal model is a 2D (CNN-4) specifically developed for the classification of KT as either benign or malignant. The models used for detection, specifically 2D CNN-6, ResNet50, and VGG16, achieved accuracy rates of 97%, 96%, and 60% respectively. The accuracy of the 2D CNN-4 classification model reached 92% simultaneously. Another study by [3] They have proven that their approach surpasses the most recent deep-learning approaches in accurately segmenting kidney tumors using the KiTs19 dataset, achieving the highest segmentation performance. The proposed system utilizes a 3D deep learning structure termed Res-UNet to initially distinguish between the kidneys and renal mass areas. Subsequently, a dual-path classification network is employed, which is founded on convolutional neural networks (CNNs). This network efficiently utilizes global as well as local characteristics to precisely predict the subtypes of the most prevalent renal cell carcinomas (RCCs), including clear cell, chromophobe, oncocytoma, papillary, and other RCC subtypes. The Dice coefficient is 0.866, sensitivity is 0.912, specificity is 0.881, and pixel accuracy is 0.953. Also, [4] proposed using bounding box selection and seed placement segmentation techniques to extract lesion patches from various phases of MRI, consisting of T2-WI and T1-WI before contrast administration, as well as post-contrast imaging during the arterial and venous phases. Subsequently, an advanced convolution neural network system named AlexNet was optimized to differentiate between ccRCC and oncocytoma. The AI system achieved a 91% accuracy rate in this task, with an AUC of 0.9. The accuracy of classifying AI, radiologist 1, and radiologist 2 in the corresponding sub-dataset was 81%, 78%, and 70%, respectively. Furthermore, [13] proposed utilizing a modified ResNet50V2 Convolutional Neural Network (CNN) for analyzing 2D CT scans. Instead of explicitly segmenting regions showing tumors. Their approach is based on the CNN's network inherent ability to autonomously select the relevant images for categorization. The DataTest_1 test yielded a particular an AUC value of 0.973, a specificity rate of 93.5%, and an accuracy rate of 93.3%. The findings from DataTest_2 indicate that the Area Under the Curve (AUC) is 0.946, with an accuracy rate of 90.0% and a specificity rate of 98.0% when assessing images separately.

In a study conducted by [22] Convolutional neural networks, also known as CNNs were employed to train entire-slide images of renal cell carcinoma (RCC) and healthy tissues. The RCC categorization accuracy reached 93.39%, whereas for normal tissues it was 87.34%. The classification accuracy of RCC subtypes, such as clear cell, chromophobe, and papillary RCC, was 94.07%. The work utilized histopathology pictures that contained significant indicators of illness progression. The method employed a novel approach utilizing support vector machines to handle the issue of unbalanced data in multi-class classification. The approach involved dividing the multi-class issue into many binary classification challenges, necessitating the training of DAG-SVM and performing subtype classification. Another study by [23] Applied a convolutional neural network, specifically ResNet50, to distinguish between high-grade (a grade III–IV) and low-grade (a grade I–II) carcinomas of renal cells in phases I and II. The network underwent training using standard MRI data obtained from the TCGA/TCIA dataset. The deep-learning model attained a test accuracy of 0.88 sensitivity value of 0.89, and a specificity score of 0.88. Also, [24] introduced a Renal Cell Carcinoma Grading Network (RCCGNet) that can accurately detect renal cell carcinoma (RCC) at different stages of malignancy in kidney histopathology images. The RCCGNet is fully automated, resilient, and computationally feasible. The classifications range from Normal/Non-cancerous (a grade 0) to grade 4. The results of the experiment confirm that the proposed RCCGNet surpasses the performance of the eight latest classification techniques on both of the suggested and BreakHis datasets. The RCCGNet model demonstrated strong performance based on the recommended quality criteria. The KMC kidney dataset yielded an accuracy of 90.14% and an F1-score of 89.06%, whereas the BreakHis dataset produced an accuracy of 90.09% and an F1-score of 88.90%. Furthermore, [25] devised a 2D SCNet model that combines segmentation and classification using convolutional neural networks. The objective was to enhance the precision of kidney tumor segmentation and categorization., hence assisting medical practitioners in making diagnoses. By employing classification and segmentation approaches in the 2D SCNet model, they reach a remarkable accuracy rate of 99.5% for both the malignant and benign categories. The segmentation using the "2D SCNet + three-label" approach resulted in Dice coefficients of 0.946 and 0.846 for the relevant outcomes.

New study by, [26] Suggest a novel and advanced weakly supervised deep learning method for categorizing renal cell carcinoma (RCC) at many scales. Firstly, standardize the RGB histogram of each slide image to mitigate the impact of color disparities on the system's effectiveness. To maintain tissue connectivity, employ multiple learning approaches by segmenting the input data into overlapped patches. Three CNNs with multiscale architecture are trained to determine the ultimate categorization., and their anticipated output is combined via decision fusion. The RCC subtype method of classification has a total accuracy for classification of 93.0% ± 4.9%. The sensitivity of this test is 91.3% ± 10.7%, meaning it accurately identifies ccRCC and distinguishes it from ccpRCC or non-RCC tissues. Additionally, it has a high specificity of 95.6% ± 5.2%. The proposed approach has shown superior efficacy in comparison to the cutting-edge Resnet-50 approach. Also, [27] conducted a study where UNet, SegNet, and two CNN-based medical image segmentation models were trained. The task involved manually segmenting the kidneys on CT scans. The process of kidney segmentation is accomplished through the utilization of UNet and SegNet, both of which are automated techniques. Ultimately, three convolutional neural network (CNN) based deep learning models including MobileNetV2, VGG16, and InceptionV3, are employed to detect kidney cancers using a transfer learning technique. The test set yielded classification accuracies of 95.29%, 99.48%, and 97.38% for the models, with the VGG16 model exhibiting the best levels of sensitivity and specificity. According to [1]. Presented a technique for detecting renal malignancies in CT scans utilizing Transfer Learning and Deep Convolutional Neural Networks (DCNN). The number of CT images totaled 5,284 of kidneys and tumors were obtained from the KiTS21 dataset and underwent initial processing. Subsequently, a pre-trained VGG16 Deep Convolutional Neural Network (DCNN) which has been developed on the ImageNet dataset, is utilized to generate the classification layers of the DCNN. The metrics of accuracy, precision, recall, specificity, and F1 scores were calculated, resulting in values of 92.54%, 80.45%, 92.38%, 92.38%, and 0.8628, respectively. Also, [28] proposed a method called SCNet that utilizes CT scans and multitasking convolutional neural network (CNN) to detect and locate renal cell carcinomas accurately. The segmentation approach employed by SCNet is a two-stage process. Firstly, it utilizes a pyramid pooling module (PPM) to extract features from the input images at many scales. Secondly, a ternary classification phase is performed to categorize the enriched feature maps into three classes: backdrop, kidney, and tumor. The binary classification process distinguishes the kidney and tumor from the surrounding environment. Based on the experimental findings, the dice coefficient for segmenting the tumor region is 0.882, while the classification accuracy is 100%. The study conducted by [29] offer a new method for autonomously segmenting and classifying renal masses on CT scan in their paper. This strategy leverages the distinct benefits of U-Net and ResNet architectures in the context of healthcare image classification and segmentation problems. The method employs two consecutive 3D U-Net models in a cascade configuration. A methodology utilizing the 3D U-Net was used to delineate the kidneys' boundaries on the CT scans accurately. This delineation was subsequently utilized as a region of interest to detect abnormal kidney growth. A 3D U-Net ensemble learning model was utilized for the purpose of detecting and segmenting the masses. Later on, a ResNet algorithm was employed for the purpose of classification. The technique attained a Dice similarity coefficient of 0.99 while segmenting the two-sided kidney boundary in the test set. The 3D U-Net earned mean Dice Similarity Coefficients of 0.75 and 0.83 for delineating renal masses respectively. The test set yielded a classification accuracy of 91.97% for masses more significant than 5mm and 86.05% for groups smaller than 5mm. The summary on the related works on kidney diagnosis using DL classification techniques presented in Table2.

Table 2: The summary on kidney diagnosis using DL classification techniques.

Author(s)/ Year	**Methods/Techniques**	**Brief Description**	**Dataset**	**Strengths**	**Weaknesses**
Kwang et.al (2021) [15]	(3D) CNN-based classification model	This study utilizes a three-dimensional convolutional neural network (CNN) segmentation model to extract the kidney and tumor masks from the complete CT volume for each stage. In addition, a Convolutional Neural Network (CNN) classification model called ResNet-101 is used to differentiate between the five main histological categories of renal malignancies, which include both malignant and benign tumors.	1035 CT images	• Accomplished precise classification: Effectively classified kidney cancers into five primary pathological subgroups, encompassing both benign and malignant tumors. • Potential for automation: Illustrated the capacity of fully computerized systems to aid radiologist in the diagnosis of kidney cancer in patients. which can improve diagnostic accuracy	The dataset comprised solely of patients from Seoul Saint Mary's Clinic. To ensure the model's performance is reliable, it is essential to validate it using both the external TCIA dataset and a separate internal test set. Additionally, it is crucial to collect data from several centers in other countries to train and test the model on a wider spectrum of populations

				and efficiency	
HO Sun Shon et.al (2020) [16]	Cost Sensitive Hybrid Deep Learning classification model	The study presented a novel method called Deep Auto Encoder for extracting profound characteristics from gene biomarkers, leading to the creation of a vector with reduced dimensions. A neural network (NN) is employed to determine the sample's kind, initial diagnosis, tumor stage, and vital condition using imbalanced kidney cancer data.	1157 gene expression and clinical data	1-When comparing the suggested COST-HDL method to other established methods, it consistently shown superior performance in predicting the expression of genes data. 2- The complex characteristics acquired from the DAE model demonstrated greater discriminative capability in comparison to the features created from the approach known as PCA and the characteristics selected using the LASSO approach, for both the training and testing datasets.	1 The research has limitations in terms of identifying relevant biomarkers and interpreting the algorithm used for deep learning. 2- The datasets exhibit a significant imbalance, particularly the dataset pertaining to the sample type prognosis.

Nathan Hadjiyski (2020) [17]	Inception V3 Deep Learning Nural Network Classification model	The study aims to develop a design utilizing Inception V3 to predict the stage of kidney cancer, specifically distinguishing between Stage 1 and higher stages. This will be achieved by analyzing cropped CT images that contain kidney cancer. The objective is to provide physicians with a more precise assessment of the stage of kidney cancer.	More than 4200 CT images	The DLNN technique achieved an accuracy rate of 86% in distinguishing between initial stage carcinoma of the kidney and later stages. This was evaluated on a test set including 98 patients.	The DLNN model is not flawless and may occasionally misclassify the stage of kidney cancer. For instance, it mistakenly categorized a test case of Stage 1 kidney cancer and also misclassified a Stage 3 test case of kidney cancer.
Saeed Pirmoradi et.al (2021) [18]	neuro-fuzzy system classification model	The initial part of the study is preprocessing the miRNA data. In the next phase a feature selection technique is employed to choose candidate miRNAs that have a high level of discriminating ability, using the AMGM measure. The final phase involves utilizing the suggested neuro-fuzzy system, which incorporates complex rules, to categorize the subtypes of kidney cancer (TCGA-KIRC, TCGA-KIRP, TCGA-KICH, TARGET-WT, TARGET-RT)	1881 miRNA expression (RNA-sequence data)	1-The suggested deep neuro-fuzzy approach effectively addressed the issue of curse of dimensionality and achieved accurate classification of cancer of the kidney types. This was accomplished by utilizing complex rules derived from deep learning	1- unbalanced data having a low number of samples

		based on specific miRNAs that have been chosen.		techniques in the rule layer 2- Despite the presence of certain subtypes have a restricted amount of samples and the absence of techniques such as augmentation and resampling, this classifier is capable of accurately classifying unbalanced data 3-The proposed method is more dependable as it applies feature selection and classification directly to the source data.	
Seokmin Han et.al (2019) [19]	Deep CNN (GoogLenet) classification model	The study proposed the utilization of a deep learning neural network called GoogLenet to accurately categorize the different subtypes cancer of the kidney cells. This classification is achieved by using the regions of interest (ROIs) produced by radiologists as inputs and the biopsy findings as labels.	169 CT scan	Demonstrated encouraging outcomes in categorizing different types of kidney cells, achieving an accuracy of 0.85, sensitivity ranging from 0.64 to 0.98, specificity ranging from 0.83 to 0.93, and an AUC of 0.9.	1-Exhibited unsatisfactory outcomes in the classification of three subtypes, suggesting a significant degree of overlap amongst the categories. 2- Moreover, it seems that the optimization of the result nodes for the three-subtype issue necessitates a greater volume of data compared to the exit nodes for the two-subtype issue, despite both being provided a fixed number of data.

Hisham Abdeltawab et.al (2022) [20]	3 CNN automated classification model	The researchers suggested a hierarchical deep learning model consisting of three convolutional neural networks (CNNs) that handle various image sizes. The purpose of this model is to differentiate between clear cell renal cell carcinoma and papillary renal cell carcinoma.Initiated the process by partitioning the Whole Slide Image (WSI) into smaller sections to be inputted into the Convolutional Neural Networks (CNNs).	64 CT images	1- The utilization of GGMRF smoothing improved the classification of the input slide image by effectively eliminating irregularities. 2- The classification of the four classes was successfully accomplished, and the proposed technique demonstrated improved performance in comparison to established cutting-edge methodologies. The ResNet18 model achieved a pixel accuracy of 0.89, while the proposed technique achieved a pixel accuracy of 0.92.	1- The investigation was carried out utilizing a rather limited dataset of kidney whole-slide histology images. 2- The study primarily examined the categorization of clear cell papillary RCC and clear cell RCC. However, it remains uncertain how effectively the suggested approach will function when applied to other forms of kidney cancers..
K.Rajkumar et.al (2023) [21]	CNN and ANN Classification model	This study involves the utilization of (CNN) with an augmented quantity of convolution layers. to classify CT images of cancerous kidneys and healthy kidneys. Additionally, an (ANN) is employed to forecast kidney cancer by utilizing dataset values derived from blood test samples. This research will provide valuable assistance in the timely	7360 CT images for CNN AND 400 rows with 26 features for ANN	Upon examination of the two models, it was found that the training accuracy of one model is 99% and the other model is 96%. These accuracy rates demonstrate significant improvement	1-The dataset used is imbalanced, with fewer tumor images than normal kidney images 2- The proposed models have not been tested in real-world healthcare settings, and their effectiveness in clinical practice remains to be seen

		and precise detection of kidney cancer		compared to previous studies.	
Sakib Mahmud et.al (2023) [5]	(CNNs) DenseAUXNet201, logistic regression, k-nearest neighbors (kNN), support vector machine (SVM), random forest, extra trees, linear discriminant analysis (LDA), gradient boost (GradBoost), adaptive boost (AdaBoost), XGBoost, light GBM (LGBM) , ElasticNet, ridge, and multilayer perceptron (MLP) classification model	The proposed approach employs a fusion of CT scans and clinical metadata to categorize kidney cancers into primary subclasses, including clear cell, chromophobe, papillary, and oncocytoma. The framework employs DenseAUXNet201, a deep learning model, to train on the CT images for classification purposes. AdditionallyMachine learning algorithms are utilized to analyze clinical data and forecast the optimal surgical intervention for particular individuals with kidney cancer.	300 3D CT scan images and Clinical Data	1- This work is the initial investigation into the classification of kidney tumors by utilizing a combination of CT scans and their related clinical features. 2- The integrated strategy demonstrated a notable degree of performance, with an accuracy of 85.66%, precision of 84.18%, recall of 85.66%, and an F1-score of 84.92%. The selection of surgical methods for malignant tumors (RCC) was shown to be highly dependable, with an accuracy of 90.63%, precision of 90.83%, recall of 90.61%, and an F1-score of 90.50%.	The main constraint of the present research was the universality of the KiTS database 2-mention a marked data imbalance in the dataset
Dalia Alzu'bi et.al (2022) [12]	2D CNN-6, ResNet50, and a VGG16 for detection AND 2D (CNN-4) For classification	The study offered three 2D-CNN models for KT identification: a 6-layered CNN (CNN-6), a 50-layered ResNet50, and a 16-layered VGG16. The final model is a two-dimensional	8,400 CT scans images.	1- This study represents the initial investigation into the detection and classification of	The study does not mention whether the proposed models were validated on an external dataset or in a different clinical setting

		Convolutional Neural Network (CNN-4) designed for KT classification, distinguishing between benign and malignant cases		renal cancers using novel data 2- It has surpassed prior studies in terms of accuracy, with a 97% accuracy rate for tumor detection and a 92% accuracy rate for tumor categorization..	
Jingya Liu et.al (2023) [3]	(3D Res-UNet) segmentation model, CNN-based classification model	This paper introduces an innovative system for diagnosing kidney renal masses. The structure consists of a 3D segmentation network called 3D Res-UNet, which automatically segments the kidney and renal mass regions. Additionally, a subtype classification network is employed to accurately identify renal mass subtypes using a dual-path strategy	210 3D CTs for training NIH datasets (TCGA-KICH 15 cases TCGA-KIRP 20 cases TCGA-KIRC 40 cases) for testing	1- The approach exhibits superior segmentation performance in comparison to cutting-edge deep neural network methods. 2- Dual-path training technique for subtype categorization enhances both the accuracy of predictions and the prevention of false-positive predictions for renal masses.	1- Dataset is limited 2- The study primarily addressed the categorization of the predominant subtypes of RCC
Moozhan Nikpanah et.al (2021) [4]	Deep Convolutional Network(CNN) AlexNet Classification model	The study utilized seed placement segmentation and boundary box selection techniques to extract the lesion patches from T2-weighted imaging (T2-WI), T1-weighted	243 renal masses MRI	An AI system utilizing convolutional neural networks (CNNs) demonstrated a diagnosis accuracy	A limited number of lesions, specifically oncocytomas, were used in this investigation.

		imaging pre-contrast (T1-WI pre-contrast), post-contrast arterial, and venous phases in MRI. Subsequently, the AlexNet model underwent fine-tuning to accurately differentiate between ccRCC and oncocytoma.		of 91% in discriminating clear cell renal cell carcinoma from oncocytoma, as shown by an area under the curve value of 0.9.	
Mikkel Pedersen et.al (2020) [13]	ResNet50V2 classification model	They suggested an altered iteration of the ResNet50V2 model. The 2D CT scans utilized CNN. The study methodology does not involve explicit segmentation, which means it does not specifically select image regions that display tumors. Instead, it relies on the convolutional neural network's to automatically identify the significant picture features for classification.	20,000 2D CT images	CNNs and deep learning technology demonstrate exceptional precision in classifying kidney tumor masses as oncocytoma.Implementing this diagnostic approach has the potential to mitigate unnecessary medical interventions for individuals with renal masses.	The sample size is rather small, and there are variations in slice thickness and phase of scan pictures due to varied techniques used in various urology departments
SairamTabibu et.al (2019) [22]	Convolutional Neural Networks (CNNs)(ResNet-18 and ResNet-34),SVM Classification model	The study employed Convolutional Neural Networks (CNNs) that were trained using entire-slide images of Renal Cell Carcinoma (RCC) and normal tissues. The study involved the categorization of RCC subtypes using a novel method based on support vector machines. This method effectively divided the multi-class task into several binary classification tasks which allowed for enhanced performance of the models. performance and better handling of data imbalance. The	1027 KIRC 303 KIRP 254 KICH tumor histopathological images, 379, 47 and 83 normal histopathological Images	1- KIRC demonstrates higher performance when taught on images with a magnification factor of 40x, but KICH produces better outcomes when taught on images with a magnification factor of 20x. 2- The CNN model effectively differentiates these	1- lack of data,limited sample size, and the class imbalance 2- The study did not perform a comparison of the performance of deep learning algorithms and that of human pathologists.

		researchers trained the DAG-SVM and used it to perform the subtype classification		subtypes by accurately capturing their distinct properties, achieving a high AUC of 0.93. 3- Present a unique DAG-SVM classifier that partitions the classification of multiple classes task into many classification binary tasks. This approach enhances the model's performance and effectively addresses data imbalance	
Yijun Zhao et.al (2020) [23]	(ResNet50)	(ResNet50) is employed to distinguish between low-grade (a grade I-II) and high-grade (a grade III-IV) renal cell carcinoma in stage I and II, respectively, using regular MRI.	430 MR images	1- The suggested model effectively mitigates overfitting and resolves the issue of disappearing gradients in deep neural networks. 2- The training set employed the augmentation strategy, enabling a significant expansion of the cohort's size and mitigating the risk of overfitting.	Selection bias occurs since only RCC tumors with histological grades confirmed by pathology were included.
Amit Kumar Chanchal et.al (2023) [24]	RCCGNet Classification model	This study presents a reliable and computationally effective automated Renal Cell Carcinoma Grading Network for identifying the malignancy	722 slides of histopathology dataset AND BreakHis dataset	1- This study presents an innovative method for automatically assessing kidney	Does not mention whether the proposed model has been clinically validated or tested on real patient data.

		levels of renal cell carcinoma in kidney histopathology pictures. The RCCGNet categorizes the malignancy into five grades: Normal/Non-cancerous (Grade-0), Grade-1, Grade-2, Grade-3, and Grade-4.		cancer from kidney histopathology photos that are yet to be studied in detail. 2-The experimental findings demonstrate that the suggested RCCGNet outperforms the eight latest methods for classification on both the suggested dataset and the BreakHis dataset. The recommended KMC kidney dataset yielded an accuracy of 90.14% and an F1-score of 89.06%. The RCCGNet model achieved an accuracy of 90.09% and an F1-score of 88.90% on the BreakHis dataset.	
Zheng Gong and Liang Kan (2021) [25]	2D SCNet model for segmentation and classification	The research effort aims to construct a two-dimensional SCNet model that simultaneously performs segmentation and classification tasks thus enhancing the accurateness of kidney cancer segmentation and categorization.	168 data images of CTA and CTU	The utilization of segmentation and classification techniques in the 2D SCNet results in a remarkable accuracy rate of 99.5% for both benign and malignant categorization. The segmentation using the '2D SCNet + three-label' approach achieved Dice	1- The malignant results of classification exhibit a small superiority over the benign classification results. This is due to the fact that, despite the increase in data, the number of malignant tumors is greater than that of benign tumors. 2- The limited size of the training image results in a lower Dice coefficient when segmenting the tumor region

				coefficients of 0.946 and 0.846, respectively.	and renal area. using the Dice Net-SCNet, compared to the Res Net50+ PPM-2D SCNet.
Yasmine Abu Haeyeh et.al (2022) [26]	Automated CNN classification model	The paper suggests a system for classifying histologic sub-types of renal cancer using a weakly supervised multiscale learning strategy. The suggested approach entails consolidating the judgments of three Convolutional Neural Networks (CNNs) in order to attain a superior level of accuracy in histopathology categorization	52 Histopathology images	This study is the inaugural use of the suggested idea of amalgamating the decisions of three Convolutional Neural Networks (CNNs) to get a notable level of accuracy in histopathology categorization.	The study recognizes the presence of a significant data imbalance due to the clear cell subtype being the predominant category in the clinical instances.
Md Humaion Kabir Mehedi et.al (2022) [27]	UNet along with SegNet segmentation model, Mobile NetV2, VGG16 and InceptionV3 classification models	The paper suggests the utilization of UNet and SegNet for the automatic segmentation of kidneys. Additionally, it offers applying three deep learning models based on convolutional neural networks (MobileNetV2, VGG16, and InceptionV3) with a method of transfer learning to identify kidney malignancies.	5,077 are normal, 2,283 are tumor CT images	Out of the three different designs, VGG16 demonstrates the greatest degree of accuracy, achieving a remarkable 99.48%.Additionally, it demonstrates the highest levels of sensitivity and specificity	1- Dataset is limited which the performance of the model may be limited 2-used manual segmentation subjective and time-consuming, and may introduce human error or bias into the results
Sefatul Wasi et.al (2023) [1]	VGG16 as DCNN and TL(transfer learning) Classification model	The paper developed a methodology utilizing (DCNN) and (TL) for the purpose to accurately detect kidney cancers from CT scans. The classification layers of a DCNN are trained by utilizing a pre-	5284 CT images	1- The proposed approach is fully automated, which can save time and reduce the risk of human error in the identification of kidney tumors from CT scans.	1- The presence of implants in the CT scans is another factor that may impact the performance of the

		trained VGG16 DCNN from the Visual Geometry Group, which was originally trained with the ImageNet dataset.		2- The proposed approach has demonstrated encouraging outcomes, with final metrics of 92.54% accuracy, 80.45% precision, 93.02% recall, 92.38% specificity, and an F1 score of 0.8628.	suggested technique.
Tan Pan et.al(2019) [28]	(SCNet) segmentation and classification	The proposed have SCNet that includes a 2-step segmentation strategy, which involves a binary classification step to distinguish kidney and tumor from the background, followed by a ternary classification step to classify the enhanced feature maps into background, kidney, and tumor classes. Additionally, a pyramid pooling module (PPM) is employed to extract features at many scales from the input photos	30 3D CT images benign tumor 101 3D CT images malignant RCCs	The trial results demonstrate that the SCNet methodology attains a classification accuracy of 100% and a segmentation dice coefficient of 0.882, surpassing the outcomes of a single method.	1- Dataset is unbalanced 2-The paper only compares the proposed approach with a solitary classification network and segmentation network
Tongtong Zhao et.al (2023) [29]	Cascade 3D Y-Net ,ResNet segmentation and classification model	The paper introduces a new strategy using two consecutive 3D U-Net models for segmenting renal masses and ResNet for classifying them in CT images. This automated method aims to evaluate renal masses.	610 CT image , 300 CT scan	1- The automated model exhibited exceptional accuracy in segmenting renal masses,attaining a significant level of spatial agreement with the reference standard as seen by the elevated Dice Similarity Coefficient (DSC). 2- The classification model demonstrated a notable level of accuracy in differentiating between several categories of	When comparing cystic renal masses with AML, the lower DSC indicates that they are more difficult to segment than solid masses.

				renal masses, with an overall accuracy rate of 90.56% in the test set	

3.2 Kidney Cancer Segmentation Studies

Image segmentation is a widely used technique for identifying objects and defining boundaries inside images. It can be used to detect curves, lines, edges, colors, intensities, or textures. The objective is to identify regions with consistent texture and accurately label them with their respective categories, while considering texture boundaries where window samples may include various textures. Precise segmentation of kidneys and renal malignancies is crucial in clinical practice because it aids in disease diagnosis and therapy planning. Kidney segmentation by hand is laborious and might yield diverse results because each specialist is unique. The implementation of computational tools, specifically deep convolutional neural networks, has resulted in an increase in the popularity of kidney segmentation tasks. These techniques aid in the early diagnosis of kidney cancers. Precise delineation of Kidney Tumors is crucial for later diagnosis and treatment strategizing. [14]. DL offers the benefit of autonomously generating the features necessary to differentiate kidneys and tumors from the remaining parts of the scan [30] . Researchers are now developing deep learning systems that can accurately identify and outline kidney regions through semantic segmentation. These techniques allow for the automated and accurate separation of the kidney and tumor, making it easier to diagnose and treat the disease. Moreover, they have the potential to enhance both labor and time efficiency. Ultimately, these strategies yield reliable and exceedingly precise identification outcomes [31] .

Many studies made on the kidney diagnosis such as [30] . The paper proposed a novel approach that combines deep learning (DL) with two internal neural networks. The initial network employed is a 2D Faster R-CNN with ResNet50, utilized to identify kidney cancers in CT scans of the entire body. The 3D V-Net algorithm subsequently segments the tumors and kidneys separately from the extracted volumes. The technique yielded a recall rate of 96.13% and a Jacquard score of 95.4%. Another study by [31], proposed pre-processing and verification strategies for each CT scan. The ResNet model is utilized in the pre-processing stage to train processed training data to analyze performance indicators. The steps can be categorized into three groups: alternative process labeling, picture screening, and statistical HU windowing. The evaluation of pre-processing performance involves the utilization of various initial weights for the pretrained parameters utilized by the ResNet and EfficientNet segmentation methods. According to the experimental findingsThe suggested preliminary processing approaches or methods greatly increase the accuracy rate comparison to the scenario when preliminary processing of data is not performed. More precisely, the dice score for kidney segmentation rose from 0.9436 to 0.9648, while the dice score for overall tumor detection showed an improvement to 0.7294. Also, [32] proposes a two-phase approach for segmenting kidneys and renal cancers in three-dimensional CTscans. The course progresses from a rough segmentation to a more detailed one. A novel training technique involving contour assistance is suggested to enhance the network's capacity to comprehend border outlines and precisely extract the picture of the area of fascination, , encompassing the kidney and kidney cancer, at the beginning stage of segmentation. An enhanced U-net network, LC-Unet, is provided for the OK segmentation step. This network combines ConvLSTM and 3D CNN to improve performance. The cross-validation tests yielded a mean segmentation accuracy of 96.39% for kidneys and 78.91% for renal cancers. The findings surpass those achieved by other neural network techniques, such as 3D Res-Unet, which had success rates of 95.4% and 72.35%, respectively. Study conducted by [33] Presents a novel hybrid V-Net model comprising an encoder and decoder block structure. The input parameters of the encoder block were intentionally constructed to pass through the combination of the V-Net model, enabling the recording of all features throughout the segmentation phase. The ET-Net algorithm's ability to extract edges was leveraged and then transferred to the ResNet++ block. The layers were subsequently joined during the decoder phase. The proposed approach demonstrated superior performance regarding segmentation compared to the existing imaging models. The hybrid V-Net approach attained mean Dice coefficients of 97.7% and 86.5% for the segmentation of the kidney and cancer, respectively. According to [34] . An advanced 2D model, known as cascaded SE-ResNeXT U-Net (SERU), is presented for the purpose of segmenting kidney tumors. This model effectively utilizes the surrounding context and important sections that comprise the left and right kidney. This approach integrates the benefits of SE-Net, ResNeXT, and U-Net. The model is developed using a hierarchical approach, starting with a rough approximation and gradually refining it. Contrast the FCN and U-Net with the proposed SERU concept, The SERU model has the potential to attain DSC of 96.77% specifically regarding the kidney. 74.32% for the tumor, and an average DSC of 85.55%.

The study conducted by [35] proposed using a convolution-and-transformer network to segment kidney, kidney malignancies, and kidney cysts consecutively. The COTRNet encoder-decoder design incorporates skip connections to establish a relationship between the encoder and the decoder. Furthermore, employ deep supervision and pre-trained weights to optimize segmentation performance further. The experimental results demonstrate that the kidney, masses, and malignancies had dice scores of 92.28%, 55.28%, and 50.52%, respectively. Another study by [36] introduces a method for automatic kidney segmentation that utilizes deep learning and active contour techniques. The active contour is employed to extract the renal areas. Subsequently, preprocessing was conducted on each volume to augment the textures present in the images. Later, the three-dimensional U-Net (CNN) model was employed to segment the left and right kidneys individually. Ultimately, the last renal segmentation is achieved by combining the data of the third stage. The approach outlined in the literature demonstrated outstanding validation metrics, exceeding a Dice score of 97.62%, a Jaccard index of 95.74%, an average sensitivity of 98.28%, a specificity of 99.95%, and an accuracy of 99.93% across the validation dataset. Also, [37] . The recommended model for the study is a collection of U-Net models that utilize deep learning techniques. This model consistently exhibits strong efficiency on both the separate test dataset employed in the end of the contest and the local trial dataset. The algorithm successfully attained results in regional testing. The kidney segmentation achieved a Dice score of 0.949, whereas the tumor segmentation had a Dice value of 0.601. The model attained Dice coefficients of 0.9470 and 0.6099 in the final competitive evaluation. According to [38] This study suggested the utilization of a 3D Multi-Scale Residual Fully Convolutional Neural Network ,a new deep neural network has been developed to enhance the precision of segmenting voluminous cancers of the kidneys in CT scans. The network achieves this by incorporating an extra encoding pathway to obtain comprehensive contextual information. The recommended 3D-MS-RFCNN system demonstrated improved precision in comparison to the Res3D U-Net approach. It achieved a dice score of 0.9390 for the KiTS dataset and 0.8575 for the external dataset, surpassing the current best method. Furthermore, [39] . The paper proposes employing the (Attention gate DenseU-Net) 2.5D model for the purpose of segmenting kidneys, tumors, and cysts. Before this, the kidney volume data will undergo preprocessing using an automated downsampling method for 3D images. AgDenseU-Net improves the model's ability to extract features using attention gates and a unique Dense Block. The segmentation findings obtained using HECs showed dice scores of 0.971, 0.883, and 0.815 for the kidney, tumor, and mass, respectively. The segmentation outcomes, with the exception of the HECs, demonstrated that the kidney, tumor, and cyst obtained dice scores of 0.950, 0.878, and 0.746, respectively. New study by[40] suggested approach for leveraging CT data in cascaded semantic segmentation consists of two phases: During phase 1, the data is segmented using the ResUNet model to extract regions of interest (ROI). In phase 2 the (ASPP) technique is employed to extract features that include significant spatial information. This is done by utilizing different receptive fields obtained from a pre-trained DenseNet-161 core. The entirety of this process is executed with CT data. In addition ,the RBCA module was designed to incorporate reverse, boundary, and channel attention for the purpose of detecting lesions of different shapes and sizes. The proposed model demonstrates strong performance compared to multiple architectures achieving Dice Similarity Coefficients (DSCs) of 0.9408 for a kidney and 0.7149 for the tumor. Another study by [41], introduces an innovative technique for precisely segmenting kidney cancers from CT scans, using an advanced deep learning model. The initial stage involved preprocessing the CT scans, which encompassed three substeps: windowing, proportional dataset distribution, and real-time data augmentation (DART). After the preprocessing phase an approach to deep learning was implemented to achieve kidney tumor segmentation. The model utilized the DeepLabv3+ 2.5D model with the dual path network (DPN)-131 were employed as an encoder. To reduce the occurrence of incorrect positive results, the slices of both healthy kidneys and kidney tumors were also equalized. The proposed technique achieved an accuracy of 99.71%, a sensitivity of 84.24%, a specificity of 99.82%, a dice coefficient of 85.17%, a Jaccard index of 75.62%, a Hausdorff distance of 18.39 mm, and an average area distance of 3.36 mm. The findings are similar to the outcomes obtained by cutting-edge 3D neural networks. According to [42] the study included a novel boundary attention mechanism to improve the U-Net model, resulting in a more advanced version termed boundary attention U-Net (BAUNet). The statistical evaluation of the suggested method yields mean dice similarity coefficients (DSC) of 98.04% for kidney and 84.09% for kidney cancers. The system includes an additional branch that produces attention maps for the boundaries to improve the desired areas' segmentation. Also, [43] as a comprehensive learning system, the suggested network is implemented promptly on 3D dimensional images. This study introduced a novel method for precisely dividing the kidney and kidney tumor in CT angiography images. The approach involves integrating the pyramid pooling module with a three-dimensional fully convolutional network known as 3D_FCN_PPM. The mean dice coefficients achieved for renal tumor and kidney are 0.802 and 0.931, respectively. Furthermore, [44] introduced a new technique called Dueling DQN, an autonomous learning-based data augmentation method to classify kidney cancers from medical images accurately. This method utilizes (DRL) to automate the process of data augmentation and conceptualizes the augmentation problem as an iterative process of experimentation and learning. Evaluate the segmentation accuracy using the dice ratio (DSC) and mean the union's interest (mo). The obtained values are mIoU(%) 75.8 and DSC(%) 84.0. Therefore, compared to other reference points, the proposed technique can accurately determine the tumor's boundaries.

New study by [45] introduces a kidney tumor segmentation approach that utilizes deep learning. In this method, the 3*3 convolution of the original U-Net model is substituted with 3*3 residual convolution blocks. The upsampling technique integrates the NAM (Normalization Attention Module) module to improve the network's feature extraction capabilities. The recommended network outperforms other networks regarding recall, Dice coefficient, IOU, F1 score, and accuracy, obtaining values of 0.917, 0.938, 0.921, 0.960, and 0.887, respectively. The approach proposed in this paper has enhanced the detection of small targets and reduced instances of absence. According to [46] Introduced a computerized segmentation approach for the identification and separation of renal and kidney malignancies. The RAU-Net approach utilizes residual and attention mechanisms to perform end-to-end tumor segmentation. By utilizing the combined weighted dice loss function and the cross-entropy loss function, the algorithm effectively distinguishes samples that are positive and enhances cancer sensitivity. The model exhibited exceptional performance in contrast to the other three others, the mean dice values for kidney and cancer segmentation are 0.96 and 0.77, respectively. The global dice values for the corresponding segments are 0.96 and 0.92. The study conducted by [47] Presented a novel convolutional neural network called Crossbar-Net for the purpose of segmenting kidney cancers in CT images. The crossbar patches sequentially train two sub-models, namely the horizontal and vertically parts. This approach simultaneously captures kidney tumors' global and local appearance information from both horizontal as well as vertical perspectives. Contrasting the Dice similarity coefficient with the real positive percentage, Crossbar-Net outperforms other techniques with a higher coefficient of 0.913 and a fraction of 0.915. Also,[48] employed a 3D U-Net as their initial model in their study. Subsequently, they used a mindful sampling technique and (LASSO) were employed to determine the clinical variables that were most pertinent to the segmentation objective. The implementation of mindful sampling significantly enhanced the segmentation efficacy of the 3D U-Net approach. The resulting Dice scores were 0.90, 0.39, and 0.38 for the relevant segments. According to [49] the study proposes using SeResUNet, a new type of encoder-decoder network that incorporates squeeze-and-excitation mechanisms. The SeResUNet encoder integrates a SeResNet to acquire advanced semantic features and capture the extensive connections among various channels of the acquired feature maps. The U-Net, in its original configuration, employs an identical decoder. The experimental findings indicate that including deep supervision greatly enhances the segmentation outcomes of the model. Specifically, the dice scores for kidneys, masses, and cancers achieved by the SeResUNet model are 91.6%, 58.8%, and 54.16%, respectively.

The study conducted by [50] Introduce a network that operates in three stages and is capable of guiding itself explicitly designed for segmenting kidney malignancies. In addition, they propose incorporating a hybrid loss and dilated convolution block into the model to collect information on challenging scenarios and small objects effectively. Under extreme conditions, the recommended approach can provide a precise and seamless boundary between the kidney and tumor, yielding average dice values of 0.9674 and 0.8454 for each, respectively. Another study by[51] proposes an adaptive threshold technique within the Class Activation Map (CAM) algorithm to enhance the precision of kidney segmentation. Furthermore, they provide a method for semantic segmentation that is weakly supervised, meaning it uses image-level labels to segment kidney tumors. In contrast to the fully supervised method used in the KITS19 challenge, which achieved a Dice score of 0.974 for renal segmentation and 0.851 for segmentation of tumors, the method shows impressive outcomes (Dice score of 0.823 for kidney segmentation and 0.583 for tumor segmentation) using solely image-level labels. Also, [52] proposes a technology that utilizes semantic segmentation to detect kidney cancers by merging the encoder stage of EfficientNet with U-Net models. from the EfficientNet family. The method demonstrated exceptional precision in segmenting kidneys and tumors, Producing remarkable IoU_Scores regarding the segmentation of the backdrop, kidney, and tumor. The average Intersection over Union (IoU) scores varied from 0.976 for B0 to 0.980 for B4. The (IoU) metric quantifies the effectiveness of a model. B7 obtained the highest (IoU) score for kidney segmentation, while B4 gained the highest IoU score for tumor segmentation. Furthermore, [53] introduces an innovative method for segmenting kidneys in abdominal CT images via hyperparameter adjustments. EfficientNet-B5 and FPN were integrated using an encoder-decoder architecture for kidney segmentation. Multiple tests were conducted to improve the model's effectiveness in windowing approaches, loss functions, and data augmentation. Based on a comparison with various existing methods, the recommended model outperforms other 2D methods and is comparable to some 3D techniques. The summary on the related works on kidney diagnosis using DL segmentation techniques presented in Table3.

Table 3: The summary on kidney diagnosis using DL segmentation techniques.

Author(s)/ Year	**Methods/Techniques**	**Brief Description**	**Dataset**	**Strengths**	**Weaknesses**
Yuliia Kamkova et.al (2019) [30]	Faster R-CNN, V-net segmentation model	The study introduced a novel integrated deep learning (DL) approach, comprising two neural networks internally. The initial network employed is a 2D Faster R-CNN with ResNet50, which is utilized to detect the presence of kidney tumors in complete body CT scans. Subsequently, the extracted volumes are sent to 3D V-Net with the purpose of segmenting the kidneys and the tumors themselves.	300 CT images	1- Presented an innovative integrated methodology for segmenting kidneys and tumors, which combines both 2D and 3D techniques. Additionally, the strategy incorporates two advanced deep learning approaches for detecting and segmenting kidneys 2- Capable of achieving rapid and accurate recall (96.13) and a high Jacquard similarity score (95.4).	variability of organ size, shape, and texture from patient to patient pose a challenge for segmentation, particularly when a tumor is present
Chiu-Han Hsiao et.al (2022) [31]	ResNet-41, EfficientNet-B7, merged ResNet-41 and U-Net Segmentation models	The ResNet model is utilized to train the processed training data for measuring performance metricsThe training encompasses statistical HU windowing, picture screening, and different methods of tagging as its approaches. Subsequently, the ResNet and EfficientNet segmentation algorithms assess the effectiveness of the preliminary processing.	210 CT images	1- The utilisation of EfficientNet-B7 in conjunction with a fixed encoder and preliminary processing algorithms yields the optimal performance 2- When ResNet-41 and EfficientNet-B4 are employed with an unfrozen encoder and data preliminary processing, demonstrated superior performance compared to when pre-processing was not applied..	The study did not conduct a comparative analysis of the proposed methodologies and other cutting-edge strategies for kidney segmentation

Li Kang et.al (2022) [32]	3D CNN and ConvLSTM segmentation model	During the coarse segmentation phase, the suggested approach utilises a previous contour to improve the network's capacity to learn edge contours and accurately extract the area of interest, which consists of the renal and renal tumor. The fine segmentation step utilizes an improved U-net network called LC-Unet, which integrates ConvLSTM and 3D CNN.	300 CT image	The average accuracy of segmentation for renal and kidney tumors is 96.39% and 78.91% respectively, as verified through cross-validation testing. The results indicate that this approach is superior to existing neural network methods, such as 3D Res-Unet, achieving accuracies of 95.4% and 72.35% for the same tasks.	The segmentation outcomes exhibit a minor decline for samples containing tumors of smaller sizes
Fuat et.al (2020) [33]	Hybrid V-Net segmentation model	This study introduces an innovative hybrid model that incorporates the beneficial features of prior V-Net systems. The model illustrates a considerably improved system, distinguished by advancements in both the encoding and decoding stages.	210 CT image	1- The hybrid V-Net models exhibited superior performance compared to the previous V-Net versions when identifying complex information. 2- The suggested approach demonstrated superior segmentation performance compared to existing imaging models. Specifically, the hybrid V-Net approach achieved mean Dice coefficients of 97.7% and 86.5% for kidney and tumor segmentation, respectively.	Training period is long and system structures are complex
Xiuzhen Xie et.al (2020) [34]	SE-ResNeXT U-Net (SERU) segmentation model	The researchers provide a novel 2D kidney tumour segmentation system named sequential SE-ResNeXT U-Net (SERU). which integrates the strengths of	300 CT images	1- The SERU model demonstrates superior performance, the kidney+tumor Dice Similarity Coefficient	During the initial phase, the suggested technique demonstrates proficiency in

		SE-Net, ResNeXT, and U-Net. The model is used in a step-by-step way, starting with a general approach and gradually refining it to effectively utilize contextual information and important slices		(DSC) was successfully attained at 96.77%, while the tumour DSC reached 74.32%. The average DSC obtained was 85.55%. 2-The shown comparisons and quantified findings demonstrate both the advantages of the backbone SERU network in extracting characteristics from renal CT scans and the efficacy of the coarse-to-fine segmentation technique	segmenting kidneys, but exhibits worse performance in segmenting malignancies
Zhiqiang et. al (2021) [35]	A Convolutional-Transformer Network (COTRNet) segmentation model	This research presents a convolution-and-transformer network as a solution to accurately segment kidneys, kidney tumors, and kidney cysts.	300 CT scans	• Utilize the previously trained ResNet to build the encoding algorithm, thus expediting the optimization procedure and protecting the algorithm from getting trapped in local optimum. • The strategies significantly improved COTRNet's performance, resulting in dice scores of 92.28%, 55.28%, and	Requires a substantial amount of GPU memory in comparison to the convolution operation

				50.56% for kidney, masses, and tumor, respectively.	
Mohit Pandey, Abhishek Gupta (2022) [36]	3D U-Net segmentation model	This study employs an active contouring approach for obtaining renal areas. Subsequently, the process of segmenting the left and right kidneys was carried out independently utilizing the 3D U-Net Convolutional Neural Network (CNN) model. Finally, merge the results to achieve the ultimate kidney segmentation	210 CTs	• The use of the active contouring method was employed to minimize expenses related to training and equipment requirements in order to choose the pixel of interest in the CT region. • The approach exhibited quite favorable results, with a Dice score of 97.62%, Jaccard index of 95.74%, sensitivity of 98.28%, specificity of 99.95%, and accuracy of 99.93%.	1- The dataset comprises intricate and heterogeneous data. 2- only tested on a single dataset
Jason Causey et.al (2022) [37]	ensemble U-Net segmentation model	The proposed study presents a deep learning architecture comprising an ensemble of U-Net models. This model is specifically intended to automatically partition renal tumors using CT scans of patients.	300 CT scans	The approach obtained localized test Dice scores of 0.949 for renal and tumor segmentation, and 0.601 for tumor segmentation. The model acquired Dice	The model was incrementally built throughout the competition, which may have resulted in overfitting due to the influence of evaluation input

				scores of 0.9470 and 0.6099 for kidney and tumor segmentation, respectively, in the last competitive test.	
Ehwa Yang et .al (2022) [38]	(3D-MS-RFCNN) segmentation model	The 3D Multi-Scale Residual Fully Convolutional Neural Network architecture was suggested to enhance the precision of categorizing large renal lesions in CT scans. This was accomplished by integrating an extra encoding pathway to obtain comprehensive contextual data.	300 CT scan from the KiTS19 dataset 270 CT scan external dataset	When compared to the cutting-edge approach, Res3D U-Net method, the 3D-MS-RFCNN model showed higher accuracy with a dice score of 0.9390 for the KiTS dataset and 0.8575 for the external dataset.	The performance of the suggested 3D-MS-RFCNN algorithm for segmenting moderate and tiny kidney tumors was found to be inferior when compared to the Res3D U-Net framework
Peng Sun et.al (2022) [39]	AgDense U-Net (Attention gate Dense U-Net) 2.5D Segmentation model	This study suggests implementing an automated procedure of reducing the resolution of the 3D image as a preliminary step in preparing the kidney data. The AgDenseU-Net 2.5D framework is suggested for effectively segmenting the kidneys, tumors, and cysts. This strategy seeks to strike a compromise between utilization of memory and model intricacy	300 CT scan	1- The kidney obtained a dice value of 0.971, the bulk achieved a die score of 0.883, and the tumor achieved a dice score of 0.815. In addition, the model was assessed without HECs and received a dice coefficient of 0.950 for the kidney, 0.878 for the tumor, and 0.746 for the cyst. 2- AgDenseU-Net utilizes a novel Dense Block and attention gates to enhance the model's capacity to extract characteristics, while also achieving superior segmentation outcomes	The automatic down-sampling of 3D images may preserve excessive background information, impeding the model's ability to accurately capture subtle characteristics such as tumors or cysts

				with less computational resources.	
Gyeongyeon Hwang et.al (2022) [40]	RBCA-Net utilizes DenseNet-161 segmentation model	The researchers suggested employing CT data in a two-step Sequential Semantic Segmentation methodology. Initially, the ResUNet model was employed to segment the retrieved Area of Attention. During the second phase, they utilized Atrous Spatial Pyramid Pooling) to capture features that cover a substantial quantity of spatial information. This was accomplished by employing different fields of reception derived from a previously trained DenseNet-161 core. In addition, they introduce the RBCA component, which integrates Reverse, Boundary, and Channel Attention methods to accurately detect lesions of all sizes and shapes.	210 CT images	The suggested technique exhibits superior performance compared to existing architectures, with a Dice Similarity Coefficient (DSC) of 0.9408 for kidney segmentation and 0.7149 for tumor segmentation	Not all dataset available
Luana Batista da cruz et.al (2022) [41]	DeepLabv3+ 2.5D segmentation model	This research presents an innovative technique for accurately distinguishing renal tumors from CT scans using an advanced deep learning model called DeepLabv3+ 2.5D. The process includes obtaining the dataset, preparing it, segmenting the tumors, and applying post-processing techniques	210 CTs image	1- The 2.5D neural network technique yields results that are equivalent to those achieved by high-performance 3D neural networks. 2- The approach proposed achieved an accuracy of 99.71%, a sensitivity of 84.24%, a specificity of 99.82%, a Dice coefficient of 85.17%, a Jaccard index	1- The study did not include automated kidney segmentation, hence restricting the search area for kidney cancers. 2- Convolutional Neural Networks (CNNs) utilized in this research, typically possess several hyperparameters.

				of 75.62%, a Hausdorff distance of 18.39 mm, and an average surface distance of 3.36 mm	
Zhongchen zhoe et.al(2022) [42]	Boundary Attention U-Net (BAUNet) segmentation model	The study presents a refined version of the U-Net concept called boundary attention U-Net (BAUNet), which includes a new boundary attention mechanism. BAUNet comprises a primary branch that divides the areas of interest into segments and a secondary branch that creates boundary interest maps to improve the procedure for segmenting.	400 3D CT images	1- The BAU-Net approach surpasses all other competing teams in the KiTS2021 competition. 2- The procedure is assessed quantitatively using the metric of Differential Scanning Calorimetry (DSC), yielding accuracy rates of 98.04% for the kidney and 84.09% for the kidney tumor.	1- There is no discussion of clinical validation or integration into clinical workflows.
Guanyu Yang et.al (2018) [43]	3D (FCN) segmentation model	The paper presented a new framework, namely 3D_FCN_PPM, that employs a 3D fully convolutional network with a pyramid pooling module to accurately segment kidneys and renal malignancies in CT angiography scans .	140 CT angiography images	1-A novel technique is suggested for accurately dividing kidneys and kidney tumors in CT angiography pictures. 2-achieves high accuracy in segmenting kidneys and renal tumors with averaged dice coefficients of 0.931 and 0.802, respectively.	Does not evaluate the efficacy of the suggested approach against manual segmentation, which is commonly considered the benchmark for measuring segmentation accuracy.
Tiexin Qin et.al (2020) [44]	DQN and substitute segmentation network.	The study presented a (Duelling DQN) technique for the segmentation of medical pictures. This methodology considers the augmentation issue as an iterative process and use deep reinforcement learning	3,753 CT slices	This study represents the initial endeavor to integrate data augmentation and segmentation in a holistic approach to optimize performance enhancement.	The proposed method require significant computational resources and time for training due to the use of deep

		to accomplish precise kidney tumor segmentation.			reinforcement learning.
Xiaojuan Chen et.al (2022) [45]	U-Net segmentation model	The approach employs the U-Net neural network architecture, wherein a 3*3 residual convolution block is substituted for the typical 3*3 convolution block in the U-Net network. Additionally, an attention mechanism NAM module was added at each stage of the network model after the jump connection to increasing the ability to extract features	300 CT scans	1 The suggested approach employs a U-Net neural network architecture, where a 3*3 residual convolution block is substituted for the typical 3*3 convolution in the U-Net network. This substitution enhances the accuracy of kidney and tumor segmentation. 2- An attention mechanism NAM module was added at each stage of the network model after the jump connection to increase the ability to extract features and obtain better segmentation results 3- The proposed network achieves 0.917, 0.938, 0.921, 0.960 and 0.887 in terms of recall, Dice coefficient, 1OU, F1 score and accuracy compared with other networks.	The efficacy of the suggested technique was assessed exclusively on the KITS19 dataset and it is unclear how well it would perform on other datasets or in clinical settings
Jingna Guo et.al (2021) [46]	RAU-Net Segmentation model	The study introduced a novel model of RAU-Net.The suggested model employs the U-Net architecture as its core framework, integrating remaining connections inside every convolutional layer and including skip connections using attention. This allows the	300 CT scans	The suggested approach demonstrates superior performance in comparison to prior models, attaining an average dice coefficient of 0.96 and 0.77, as well as an overall dice coefficient of 0.96 and	The research only evaluates the proposed model on a single dataset

		decoder to concentrate on the segmentation goal. The from beginning to end technique allows for complete automation in segmenting the kidney and renal malignancies.		0.92 for kidney and tumor segmentation, respectively.	
QianYu et.al (2019) [47]	Crossbar-Net novel CNN segmentation model	The study introduced a novel convolutional neural network called Crossbar-Net. The approach relies on a cascaded trainable segmentation model that combines two innovative schemes for recording both the overall and localized visual characteristics of kidney tumors.	3500 CT slices	1-presents a novel convolutional neural network named Crossbar-Net, specifically developed for the segmentation of kidney tumors in CT scans. 2- The findings demonstrate that the method outperforms cutting-edge segmentation algorithms in various metrics, including the Dice similarity coefficient, true positive fraction, centroid distance, and Hausdorff distance. 3- Utilize the generalization to apply Crossbar-Net to other segmentation problems such as segmenting the heart in MR images and segmenting breast masses in X-ray images. Demonstrate the positive outcomes achieved in these two tasks.	Does not provide clinical validation of proposed method
Christina B. Lund and Bas H.M. van der Veden (2021)	3D U-Net segmentation model	In order to enhance the automated segmentation of kidney tumors, the researchers	300 CT scans	1-This study proposed a novel approach to to enhance the automatic	Only compared their approach to nnU-Net and did not

[48]		utilized clinical characteristics alongside imaging data. They employed a 3D U-Net as their initial model and subsequently implemented a cognizant sampling strategy and a Least Absolute Shrinkage and Selection Operator to determine the most significant clinical characteristics for the segmentation task.		segmentation of kidney tumors on CT scans by leveraging clinical characteristics in addition to imaging. This technique has a chance to enhance the accuracy and efficacy of kidney tumor detection and treatment. 2-Their approach significantly improved the segmentation performance and got remarkable Dice scores.	compare it to other cutting-edge techniques.
Jianhui Wen et.al (2021) [49]	SeResUnet Segmentation model	The paper presents SeResUNet, a squeeze-and-excitation encoder-decoder network. The encoder of SeResUNet utilizes a SeResNet to capture semantic characteristics at the high level and model the dependencies that are long-range. The decoder is identical to the standard U-Net architecture.	300 CT scans	1- The ability to handle data imbalance by utilizing the weight cross-entropy loss function 2- The segmentation outcomes for tumors and cysts have significantly enhanced, suggesting that the model has superior performance in capturing fine details.	The study does not provide information on the computational requirements or training time of the proposed architecture
Xiaoshuai Hou et.al (2020) [50]	3D U-Net Segmentation model	The study introduced a triple-stage self-guided network to accurately separate kidney tumors from 3D CT images. The author proposed the utilization of a dilation convolution block and hybrid loss to enhance the model's ability to capture data from tiny items and difficult examples.	300 CT image	1- The suggested method effectively produces precise and seamless boundaries of the kidney and tumor even in challenging scenarios, For instance, photos with minimal contrast and tumors that are anatomically linked to other organs. 2- The 3D U-Net with DCB module has been optimized to	1-The limited size of the dataset 2-Does not mention whether the proposed method has been validated or tested in a clinical setting with human patients.

				effectively focus on tiny items and difficult examples by employing an integrated loss function. 3- Assess the proposed methodology and achieve an average dice score of 0.9674 for the kidney and 0.8454 for the tumor.	
Mohammad Hossein Sadeghi et.al (2021) [51]	Weakly supervised segmentation model	The paper suggests a methodology that involves obtaining a kidney filter and subsequently identifying tumor cells. It then introduces an adjustable threshold CAM to improve the localization of the kidneys on the maps. After obtaining a kidney filter for each piece, an unsupervised technique is utilized to delineate the tumor location.	210 CT images	1- The article introduces a novel technique for precisely dividing kidney tumors in CT scans by employing weakly-supervised segmentation based on semantics. By utilizing image-level labels rather than pixel-level annotations 2-The study introduces an adaptive threshold approach within the Class Activation Map (CAM) algorithm, resulting in improved kidney segmentation accuracy. 3-The study combines multiple techniques, including weakly-supervised semantic segmentation, the CAM technique, adaptive thresholding, and knowledge-based techniques. This multi-faceted approach	The study evaluates the proposed approach on a specific dataset, but it does not mention whether the model has been validated on real-world clinical data or in a clinical setting

				enhances the overall segmentation accuracy	
Abubaker Abdelrahman, and Serestina Viriri (2023) [52]	EfficientNet with U-Net Segmentation model	The paper presents an approach that utilizes semantic segmentation to analyze renal tumors. This is achieved by combining the encoder stage of the EfficientNet model with the U-Net model from the EfficientNet family. This model exemplifies a highly effective system with enhanced encoder and decoder functionalities.	7,899 CT scans	1- The suggested method demonstrated exceptional accuracy in delineating tumors and kidneys on CT slices, surpassing previous established methods for kidney tumor segmentation. 2- EfficientNet B7 achieved the highest Intersection over Union (IoU) score for kidney segmentation, whereas B4 achieved the highest score for tumor segmentation. 3- The study employs cutting-edge deep learning architecture called EfficientNet family U-Net models for the purpose of semantically segmenting tasks..	Lacks an elaborate exposition of the pre-processing methodologies employed in the research..
Chiu-Han Hsiao et.al (2022) [53]	EfficientNet-B5 and FPN segmentation model	This research presents an encoder-decoder framework designed specifically for the purpose of kidney segmentation. An optimization approach for hyperparameters is constructed, which involves developing a model architecture, selecting a windowing method and a loss function, and applying data augmentation. The architecture comprises of EfficientNet-B5	210 CT Scan and 7 cases from 3D-IRCADb-01	1- Optimal performance achieved with a Dice score of 0.969 2- Comparing the suggested model with various current approaches reveals the model that is suggested surpasses other 2-dimensional techniques and achieves comparable	The suggested model exhibits suboptimal performance in extraordinary scenarios, like horseshoe kidney or low-contrast CT scans, due to the inherent imbalance of data in these situations..

		serving as the encoder and a feature pyramid network functioning as the decoder.		performance to some 3D methods.	

Based on the table above, Researchers are pouring resources into developing computational approaches to aid professionals in analyzing medical images using image processing and machine learning technologies., primarily because of the clinical relevance of this field. Combining these methods has led to the development of CAD and CADx systems, which have been used to analyze different kinds of medical pictures and aid in diagnosing various diseases. With appreciation for these systems, the analysis becomes more efficient, and professionals have less work to do. Consequently, they can facilitate the prompt detection and diagnosis of issues by pre-analyzing the information given by the photographs.

Including the areas of the kidney domain overlaid by aberrant structures is one of the primary obstacles to CT kidney segmentation. Due to the maintenance of contrast between the kidney areas and their boundaries, CAD approaches often produce dependable segmentation when patients are healthy or, for instance, have tiny nodules. However, individuals may experience kidney anomalies due to illnesses in more complicated situations. As a result, the kidney segmentation work is much trickier in such instances. So, to aid professionals in detecting kidney diseases, this work aims to propose a method for autonomously partitioning kidneys in CT images.

These results show that kidney segmentation is not a new problem; instead, it is an old problem that has been solved using many strategies that have yielded more and more impressive outcomes over the years. Methods that rely on active contours are time-consuming to run on big pictures, need precise beginning contour points and parameters, and fail to track topological changes in objects. The convergence strategy determines their accuracy and is also sensitive to local minimum states. Deformable approaches, on the other hand, rely heavily on atlases and expertise. One drawback of this strategy is that it uses a fixed size for solving the problem in a group of photographs. When testing fresh images with varying atlas sizes, there needs to be assurance that the method will work.

4. Dataset used in kidney cancer diagnoses

Early and accurate diagnosis is crucial in the fight against kidney cancer, which is one of the most widespread and complex malignancies. This is where powerful data comes into play, providing the fuel for AI algorithms to revolutionize diagnostic approaches. Introducing a unique and valuable resource unlocking the secrets of kidney cancer through the lens of artificial intelligence. The use of datasets in kidney cancer diagnostics is crucial since they provide the groundwork for medical studies that help us understand the intricacies of the illness. Researchers can find kidney cancer risk factors, trends, and possible biomarkers by analyzing large amounts of clinical and genetic data. With these datasets, physicians may create more targeted treatments that take into account each patient's unique traits to maximize their treatments' efficacy[5]. In addition, healthcare providers can make better judgments about diagnosis and treatment using clinical decision-support tools and predictive models based on extensive datasets. Insights derived from databases fuel improvements in research, science and technology, and healthcare quality generally; they are also essential in medication improvement, research, and epidemiological research. In kidney cancer, careful evaluation of datasets leads to better patient outcomes, more accurate diagnoses, and the possibility of individualized medication. By revealing problem areas and assisting public health programs, databases contribute to the never-ending quest to improve healthcare service quality. These databases provide information that helps researchers study kidney cancer, including its occurrence, distribution, and risk factors. This information is invaluable for epidemiological studies. In kidney cancer, databases serve many purposes: they enhance medical knowledge, improve diagnostic and therapeutic procedures, and boost the overall efficacy of healthcare practices. There are many datasets used for kidney cancer diagnosis based on AI approaches summarized in Table 4.

- (TCIA): The collection is sourced from The Cancer Imaging Archive, an extensive publicly accessible repository of medical cancer images. DICOM serves as the main file format for storing images in TCIA. The system incorporates widely utilized imaging modalities including PET, CT, MR, etc., and employs exclusively authentic data sets obtained from a medical laboratory comprising CT scans of patients with kidney cancer. CT scans are an invaluable tool for analyzing the kidneys to identify disorders that include tumors, ulcers, kidney stones, congenital defects, polycystic nephropathy, a buildup of liquid around the kidneys, and abscesses. [2] . TCIA supported by the National Cancer Institute, Bethesda, Maryland, USA [17] .
- TCGA: TCGA has a diverse range of gene information, including single-nucleotide polymorphism (SNP) and gene expression (mRNA expression) data, derived from a substantial number of individuals with cancer. This data is housed within a database. RNA analysis was used to quantify gene expression, and the expression data (transcriptome profiling) were combined and converted into

digital format after assigning unique transaction IDs [16]. Within the TCGA database, there are five distinct projects designated for kidney cancer. Each project is specifically associated with a certain subtype and consists of three TCGA studies and two TARGET projects. Examined many forms of kidney cancer, including Kidney Renal Clear Cell Carcinoma, Kidney Renal Papillary Cell Carcinoma, and Kidney Chromophobe, in TCGA projects. Also investigated High-Risk Wilms Tumor and Rhabdoid Tumor in TARGET programs. [18] .

- KIT19: The Kidney and Kidney Tumor Segmentation Challenge 2019 dataset comprises arterial phase CT scans of patients who had nephrectomy for kidney tumors at the University of Minnesota Medical Center from 2010 to 2018. This dataset is intended for the development of a segmentation model. For the 2019 MICCAI Kidney Tumor Segmentation Challenge, a group of 210 patients' cases were chosen as the training set and made available to the public. An additional 90 cases were kept privately online for separate testing purposes. [10]. Medical students performed hand segmentation annotations for each CT scan under the guidance of radiologists, incorporating surgical pathology. This process assists in accurately localizing tumors and avoiding cysts. The NIFTI format is used for storing CTs. The dimensions of each volume's slices were 512×512 pixels, with a range of 29 to 1059 slices per volume. Initially, the KiTS19 data sets consisted of masks that included three distinct classes: 0, 1, and 2. These classes corresponded to the backdrop, kidney, and tumor, respectively [36]. This dataset exhibits notable disparities in image quality, geographic resolution, and field-of-view. The voxel spacing in the plane resolution varies between 0.44 × 0.44 and 1.04 × 1.04 mm. The image slices have a thickness that varies between 0.5 mm and 5 mm [38]. The objective of this challenge is to expedite the research and creation of innovative nephrometric resources. Developing semantic segmentation methods for kidneys and renal tumors can provide valuable structural information regarding irregularities and measurements of kidney size and tumor size. This, in turn, can greatly assist in the prognosis and treatment planning for kidney cancers. Radiotherapists utilize this information in the course of treatment [41] .
- KIT21: The competition involves teams competing to create the most effective method for automatically segmenting renal tumors and the surrounding anatomy based on semantic analysis. Utilized the openly accessible "Kidney and Kidney Tumor Segmentation Challenge 2021" (KITS21) dataset. The KiTS21 dataset comprises individuals from M Health Fairview and Cleveland Clinic medical institutions who undergone either partial or radical nephrectomy procedures between 2010 and 2020. Each of the 544 initial instances was retrospectively examined to select only those patients who had additionally had a contrast-enhanced CT scan of the entire kidney(s) and the related renal tumors. The ultimate assembled dataset comprised 3D-CT slices from a total of 300 individuals, with each subject having ground truth masks annotated by a consortium of professionals and trainees. KITS21 is an expanded iteration of the previous KiTS19 project, which offered accurate annotations or masks for benign cysts in addition to masks for kidneys and tumors. KiTS21 incorporates accurate masks for 90 test individuals derived from the original KiTS19 challenge [5] . The collection includes kidney CT images including tumors as well as images without tumors. The KiTS21 dataset is the most recent version of the KiTS dataset and contains abdomen CT scans from 300 individuals. The data of each patient is saved in a folder that has been anonymised, and they are referred to as cases. Each instance has the CT data stored as a 'image' file, along with three separate segmentation files for the kidney, tumor, and cyst. The two classifications are specifically referred to as 'kidney' and 'tumor'. The 'Kidney' class consists of photographs depicting kidneys without tumors, while the 'Tumor' class includes images of kidneys with tumors. The imaging file contains abdominal CT scan data organized in a three-dimensional format, with dimensions specified as slice number × height × width. Each slice has a height and width of 512 pixels [1] .

Table 4: kidney cancer Dataset sources

Dataset Name	**No. of samples**	**Data set Type**	**The dataset source link**
TCIA	Over 350,000 images across multiple cancer types	imaging (CT, MRI and PET)	https://www.cancerimagingarchive.net/access-data/
TCGA	Over 20,000 tumor samples across 33 cancer types	Multi-omics (genomic, transcriptomic, epigenomic, proteomic)OR(gene expression profiles, DNA methylation patterns, and clinical	The Cancer Genome Atlas Program (TCGA) - NCI

		outcomes)OR(mRNA, DNA methylation, CNV datat)	
KIT19	210	CT Scan only	Data - Grand Challenge (grand-challenge.org)
KIT21	300	CT, MRI and PET	KiTS21 | The 2021 Kidney Tumor Segmentation Challenge (kits-challenge.org)

5. Challenges and Issues

Diagnosing kidney cancer can be a complex and challenging task. While advancements in medical technology have yielded improved tools, several obstacles still hinder early and accurate detection, impacting patient outcomes:

- **Data availability and quality**: To build and verify AI techniques for kidney cancer diagnosis, obtaining enough high-quality data is a major problem. CT scan, MRI, PET and miRNA are examples of such diverse datasets. Given that accurate and dependable forecasts depend heavily on the quality and amount of data used in training and verifying models. data availability and quality are the major obstacles and constraints when AI techniques are used in kidney cancer diagnosis. Underfitting, in which the model does not transfer to new data, and overfitting, in which the model closely matches the training data and performs badly on new data, are the consequences of a lack of appropriate high-quality data.
- **Limited access:** Sensitive medical data is often protected by privacy regulations and ethical considerations, restricting access for researchers and developers. This hinders the development and training of robust AI models.
- **Data quality**: Inconsistent data formats, missing values, and errors can significantly impact the accuracy and reliability of ML models.
- **Class imbalance**: Kidney cancer is relatively rare compared to benign kidney conditions. Imbalanced datasets can lead ML models to prioritize the majority class (benign lesions) and miss subtle patterns in the minority class (cancerous lesions), impacting accurate diagnosis
- **Bias and fairness:** Data collection and pre-processing can introduce bias based on factors like demographics, socioeconomic status, or healthcare access, leading to unfair and discriminatory outcomes in diagnosis and treatment recommendations.
- **Subtype bias**: Within kidney cancer, various subtypes exist with distinct characteristics and treatment needs. If training data disproportionately favors specific subtypes, the model might perform poorly on others, compromising diagnosis accuracy for underrepresented subtypes.
- Using AI techniques in diagnosing kidney cancer are difficult and are limited by many factors. Kidney cancer data comes in various formats (images, genetic data, clinical records) with inherent noise and missing values. Algorithms need to handle this complexity and extract meaningful patterns for accurate diagnosis. Different kidney cancer subtypes have unique characteristics. Algorithms need to be able to differentiate between these subtypes for optimal treatment planning, which can be difficult due to subtle variations in imaging and genomics data. Understanding how algorithms arrive at their diagnostic decisions is crucial for building trust and confidence among healthcare professionals. Some algorithms, particularly deep learning models, lack transparency, making it difficult to interpret their decision-making process. Algorithms trained on specific datasets might not perform well on different datasets with varying distributions or characteristics. Ensuring good generalizability and reproducibility across different clinical settings is crucial for real-world implementation, and thus algorithms for correctly recognizing and diagnosing kidney cancer are challenging. Also, limitations of imaging techniques. Early-stage tumors can be small and subtle, potentially escaping detection during routine imaging like ultrasounds or CT scans.
- While AI shines a promising light on improving kidney cancer diagnosis, its path is shadowed by the lurking dangers of privacy and security. Sensitive medical data, including scans, genetics, and medical history, forms the bedrock of AI training and application. Yet, accessing and utilizing this data raises alarms about potential breaches, leaks, and unauthorized access, exposing patients' most intimate medical details. The threat of cyberattacks poses a serious threat to large databases, and de-identification techniques struggle to maintain true anonymity. The consequences of a privacy or security breach are dire, eroding trust, fueling discrimination, and potentially weaponizing data for nefarious purposes. To unlock the full potential of AI in kidney cancer diagnosis, we must prioritize robust cybersecurity, data governance transparency, patient empowerment, and continuous evolution of de-identification methods. Only by actively addressing these challenges can we navigate the

minefield of privacy and security, ensuring AI empowers accurate diagnoses while safeguarding the fundamental right to privacy in healthcare.

6. Future Directions

Kidney cancer, medically referred to as renal cell carcinoma, is a prevalent and highly lethal malignancy. With advances in technology and understanding of the disease, future directions in kidney cancer diagnosis will focus on improving early detection methods, identifying biomarkers for precise diagnosis and prognosis, and developing targeted therapies for personalized treatment. These innovations play a vital role in enhancing patient outcomes and decreasing the morbidity and mortality rates linked to kidney cancer. Recently, there have been notable improvements in the field of kidney cancer diagnostics.

1. While some studies had to deal with the problem of data inconsistency, others used insufficient data. The reason for both issues is that not all pertinent studies have completely addressed the subject of data imbalance. Because of this, we suggested using augmented data and conducting data augmentation for small groups. This method makes sure that different classifications are balanced.
2. Multimodal data integration: Combining imaging modalities like MRI, CT scans, and ultrasound with clinical data and genomics using DL models could create a more comprehensive picture of the tumor and improve diagnostic accuracy, especially for early-stage and complex cases.
3. Computer-aided diagnosis (CAD) systems: Develop highly specialized DL-based CAD systems that not only detect tumors but also analyze their characteristics like size, shape, and texture, aiding in differentiating benign from malignant lesions and guiding biopsies.
4. Personalized risk assessment: Develop models that predict the risk of developing kidney cancer based on individual factors like genetics, family history, and lifestyle, enabling early intervention and prevention strategies
5. Predicting treatment response: Train DL models on genomic and transcriptomic data to predict a patient's response to specific treatments, leading to personalized therapy plans and maximizing efficacy while minimizing side effects
6. Non-invasive liquid biopsy: Develop DL models to analyze circulating tumor DNA (ctDNA) in blood samples for early detection and monitoring of kidney cancer progression, avoiding the need for invasive biopsies
7. Real-time analysis: Integrate DL models directly into diagnostic tools used by radiologists and urologists, allowing for real-time analysis of scans and immediate feedback during examinations
8. Explainable AI: Develop transparent and interpretable DL models that healthcare professionals can trust and understand, facilitating informed decision-making and building trust with patients
9. Decision support systems: Build AI-powered decision support systems that assist clinicians in choosing the most appropriate diagnostic and treatment options for individual patients based on their unique profile
10. Hybrid learning techniques, combining predictions from multiple different models such as deep learning and conventional machine learning. and optimization approaches can lead to more robust and reliable diagnoses kidney cancer and analyze large amounts of patient data involving test results and medical histories.
11. Quantum image processing**:** Quantum algorithms could outperform classical algorithms in analyzing medical images like CT scans and MRIs, potentially detecting subtle patterns and characteristics of kidney tumors with greater accuracy and sensitivity. Combining quantum computing with machine learning models could significantly accelerate training times and enhance the accuracy of models for kidney cancer diagnosis, especially when dealing with complex datasets.

7. Conclusion

Contemporary literature focuses on artificial intelligence (AI), which has achieved great strides in the past decade. The expansion of complicated data sets and advancements in processing power are driving this trend toward new methods of analysis and interpretation. Due to improved imaging techniques, the majority of cancers are now detected at an earlier stage, the number of cases of renal cell carcinoma (RCC) is on the rise. The fact that some co-morbid groups, such as the obese and the elderly, have a greater risk of complications before and after an intervention complicates matters significantly, primarily when histological evaluations classify 10%-17% of kidney tumors as benign. AI can improve diagnostic and therapeutic decision-making by providing more precise information and direction as an alternate option. The narrative review laid the groundwork for RCC AI by outlining the fundamentals and giving a synopsis of all the available methods. Diagnostics, care following surgery, pathologists, and follow-up are only a few areas of RCC management that now use AI. Commonly employed models include neural networks, random forests, support vector machines, and regression. Healthcare practitioners must build fundamental knowledge and form interdisciplinary cooperation to standardize datasets, identify significant outcomes, and unify interpretation. Only then can this be implemented in everyday practice. This study concludes with a thorough evaluation of where AI stands in its ability to diagnose kidney cancer. The attempts that have been made thus far, the field's advancement, the remaining challenges, the most recent advancements, the effectiveness of AI-based techniques, and the directions for future research and development are all covered in the conversation. The use of AI in kidney cancer diagnosis can significantly improve diagnostic accuracy, speed, and efficiency. The current level of advancement in AI, ML and DL as it relates to a decreased risk of kidney cancer diseases and how that might impact clinical practice is briefly discussed in this research. This study's primary goals are to enhance patient outcomes by utilizing AI-based methods for kidney cancer detection and to pinpoint areas in which additional research on the application of AI to kidney cancer diagnosis and treatment is required.

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