



Kid-ML: ML For Kidney Malignant Tissues Identification

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Abstract

A considerable worldwide medical and health burden is imposed by kidney disease due to its high rates of morbidity and death as well as its high economic cost. Imaging tests can be used by doctors to detect kidney tumors or other diseases. Imaging studies include Magnetic Resonance Imaging(MRI), Computed Tomography(CT) scan, and ultrasound scan which consume a lot of time from doctors to detect kidney cancers through them. In order to help doctors to identify tumors in their early stages, they can use simple Machine Learning(ML) techniques or Deep Learning techniques through diagnostics and predictions applications. A rise in interest in deep learning algorithms, which are Artificially Intelligently (AI) based, on a worldwide scale has enabled recent improvements in medical imaging and kidney segmentation. Deep Learning techniques which are AI-based can offer and identify the kidney tumor in a more efficient method, allowing for the development of a more effective kidney tumor detection system. An input layer, one or more hidden layers, and an output layer

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are the components of Artificial Neural Networks(ANNs) which is one kind of Deep Learning(DL) algorithm that imitates biological neurons. Another kind is Convolutional Neural Networks(CNNs) which are often the most effective and well-liked in computer vision for image categorization in medical imaging. Deep learning techniques based on CNNs have shown promising results in a variety of medical image processing applications. However; all deep learning techniques consume very high computational power. In this work, we study the use of simple machine learning algorithms such as Decision Tree(DT), K Nearest Neighbor(KNN), Random Forest(RF) and Logistic Regression(LR) algorithms and compare their results. Simple machine learning algorithms consumes minimum computational power. We discuss the behavior of those machine learning algorithms while changing the resolution of the images. We found that the accuracy of simple machine learning algorithm is stable while decreasing the resolution of images to be 32pixels.

Keywords: kidney tumor, k nearest neighbour, random forest, decision tree, logistic regression.

1. Introduction

Kidney tumor continues to be a global health issue due to a large number of patients. In the human body, the kidneys remove waste and impurities from the blood [1]. Tumors (cancers) are caused by abnormal cell proliferation, which affects people differently and manifests in the form of a variety of symptoms [2]. The manual imaging tests like ultrasound, magnetic resonance imaging (MRI), and computerized tomography (CT) cannot determine the complexity and aggressiveness of kidney tumors in its early stages. Tumors are frequently discovered while the patients are receiving treatment for other illnesses. Tests might unintentionally reveal kidney tumors, which can manifest in patients as masses, kidney cysts, or abdominal pain. In this case, a computerized tomography (CT) scan of the patient's not only abdomen but also pelvis, contains properties that are analyzed carefully to determine if a kidney has a tumor or not. CT is one of the necessary tests to diagnose a tumor [3]. An important step in lowering the risk of further disease progression is the early diagnosis of kidney tumors (KT). Towards this purpose, the properties of the cell systems which model the tumor and can be applied in algorithms need to be made simpler and less complex in order to develop more effective models that can be applied across different disciplines [3]. The AI detects the tumor by enabling doctors to identify it more accurately and in a short time.

Applications for artificial intelligence (AI) in medicine are constantly growing and touch almost every facet of oncologic treatment. In general, AI is the study of how to make computers mimic human abilities [4]. AI includes a wide range of methods for teaching computers to learn from their mistakes and to adapt. Although AI is in its early stages of being used in kidney cancer research, it has already shown promise in a variety of clinical settings, including diagnosis, disease characterization, and treatment planning [5]. Machine learning and other branches of AI are currently being investigated in kidney cancer (computer algorithms that can automatically learn and improve through exposure to data), computer vision, deep learning, and natural language processing [5]. With a focus on their capacity to address some of the unmet clinical needs in the treatment of patients with kidney cancer and current difficulties for clinical implementation, we review the performance of AI solutions currently available in kidney cancer.

The detailed analysis of current kidney tumor detection research concentrates on deep learning approaches and traditional machine learning techniques for early diagnosis of kidney tumors based on CT scans [4]. It discusses a comparison of various early detection systems and strategies for kidney tumors using machine learning methodologies. As more training data became available, more advanced CNN architectures and training methods are applied, and the achievement of kidney tumor segmentation algorithms continues to improve [6].

In the field of deep learning, Convolutional neural networks (CNNs) are often employed to extract image properties and identify different objects inside human body [1] [7]. It is a neural network that functions on the concept of sharing weight. For a wide range of pattern identification tasks, people often use CNNs. One of the most typical applications of CNNs is image classification and semantic segmentation utilizing fully convolutional

networks. Convolutional layers and partial down-sampling are the two most important layers of CNN (pooling) [3]. Information Technology specialists do research in the interdisciplinary field of kidney disease diagnosis to support medical staff by simulating the biological functions of the human kidney and providing accurate diagnostic outcomes. Automatic detection methods can speed up prediction, reduce expenses, increase test accuracy, and ease the workload for radiologists compared to the tedious efforts and wasted time spent in traditional diagnostics. This is offered by the diagnostic models and tools for detecting kidney cancer in computed tomography (CT) tests. Gong & Kan suggested CNN models for the detection and classification of Kidney Tumors [2]. They have developed algorithms for kidney segmentation [8] [9]. In terms of ranking and segmentation of medical screenings, CNN has achieved exceptional results. When segmenting and categorizing renal tumors, the segmentation technique can produce superior results. Deep learning can be applied to different methods of evaluation standards for segmentation outcomes and medical images evaluation. The segmentation methods in kidney tumor use different approaches to highlight the constituent parts of the tumor [10].

In the field of Machine Learning (ML), computers are trained to learn from examples of data and analyses data processing experience instead of being explicitly programmed to perform predetermined tasks. Examples of algorithms include the extreme gradient boosting, the support vector machine, and the random forest algorithm [11]. Rules that precisely specify a series of operations are known as algorithms. The main objective of machine learning (ML) is to develop algorithms that take input data as input, analyze the data using computers to predict output values within a reasonable accuracy range, find patterns and trends within the data, and learn from past experiences. ML uses 2 types of techniques which are Supervised Learning and Unsupervised Learning [12]. With supervised learning, you use an algorithm to learn the mapping function from the input to the output ($Y = f$) given input variables (X) and an output variable ($Y(X)$). In order to support future judgments, supervised machine learning systems give learning algorithms access to known quantities. Finding patterns in data is done using a class of machine learning techniques called unsupervised learning [13]. Unsupervised learning is when there are no corresponding output variables, only input data (X). Unsupervised learning aims to learn more about the data by simulating its underlying structure or distribution.

In this paper, we discuss how to decrease the computational power required for processing images by decreasing the resolution of images while maintaining almost the same accuracy of classification success. We start by explaining the methodology used in our work in section two. In section three, we discuss our proposed solution. We start by explaining how the dataset was collected. Then, we analyze the block diagram for our algorithm and how it was applied to our dataset. We illustrate the results achieved. In section 4, we analyze those results and explain how they can help us in reducing the required computational power for processing our algorithms. In section 5, we draw conclusion and describe some future work which we think is needed to confirm the results achieved in this work.

2. Methodology

In this work, we use four simple machine learning classification techniques which are K-Nearest Neighbor (KNN), Logistic Regression (LR), Decision Tree (DT) and Random Forest (RF). They are used to classify the input CT scan images to either benign or malign classes. A summary about each of the algorithms is as shown next.

The most popular technique for creating prediction models for binary outcomes is logistic regression, which has been expanded for the classification of illness. Omitting the feature selection stage can lead to significant error estimates in down-forward prediction, so this two-stage approach requires additional statistical tools [12]. With the aid of parametric bootstrap, the prediction error of a model-building process may be quickly assessed. Interpretable decision trees, which are regarded as classification approaches in data mining, are one of the machine learning types. One of the most popular ways to use decision trees is to present the findings as a straightforward decision tree method that is basic enough for most researchers to understand. The decision trees are capable of non-parametric adjustment, control over heterogeneous data, and the best classification of consecutive data even if features are not normalized and scaled [11]. A large number of decision trees are generated and combined to form a 'forest' using a complex and flexible supervised machine learning method known as Random Forest [14]. Regression and classification problems can be solved with this decision tree. The accuracy of the expected results for a data set is increased by averaging the results of several decision trees applied to different subsets of the same data set. Instead of relying on just one decision tree, the random forest collects the data from each tree and predicts the future using the majority of predictions. The k-nearest neighbors' algorithm sometimes referred to as KNN is a supervised learning classifier that uses proximity to produce ratings or predictions about the aggregation of a single data point [15]. Although it can be applied to issues of classification or regression, it is most commonly used as a classification algorithm because it is based on the idea that similar points can be detected near each other. KNN degrades with time, impairing the performance of the entire model. Simple recommendation systems, pattern recognition, data mining, financial market forecasting, intrusion detection, and other applications are among their frequent uses.

For the evaluation of the results, we use the percentage accuracy which is the percentage of true positive results.

3. Methodology

We understand that the Deep learning algorithms have a very promising future in identifying cancer tissues. AI is a deep learning method which shows very promising results in differentiating between malignant tissues and benign tissues. However, deep learning methods are computationally very expensive. In this paper, we study the effect of reducing the resolution of CT scans on the accuracy of true detection of Kidney cancer. We use four simple machine learning algorithms to show how the dependency of the detection accuracy varies with changing resolution. In this section we describe the dataset and how we obtained it. Then we describe the image processing techniques which we applied on our images to reduce the resolution of each image. Finally we use the four machine learning techniques namely KNN, DT, RF and LR to conclude our work.

3.1. Dataset

A kidney tumor, which can be benign or malign, is the growth of abnormal tissue in one or both kidneys. According to doctors, Kidney Tumors can start when "mutations" or "changes" which take place in the DNA of some kidney cells, where in this case the DNA contains instructions for the cell that it should abnormally grow and divide quickly.

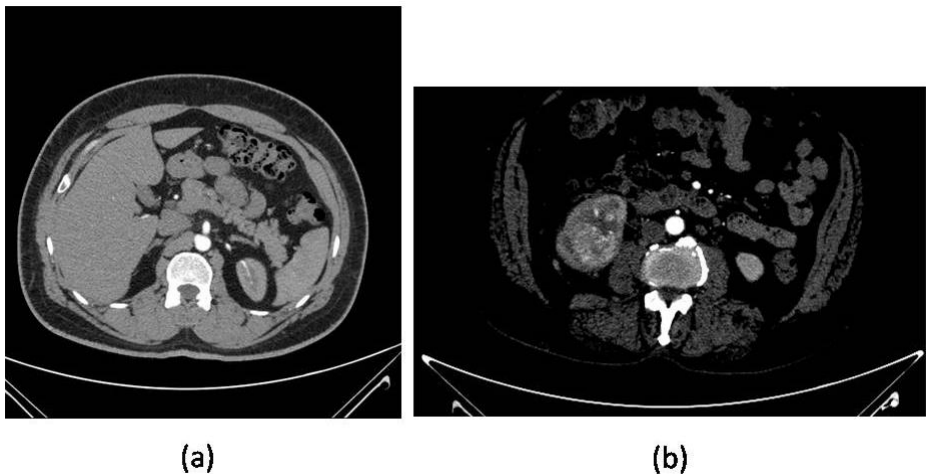


Fig. 1: (a) Normal (benign) CT image, (b) Tumor (malign) CT image [16]

Additionally, the tumor may originate from inside the kidney, and in some instances, it is a secondary tumor that has metastasized from nearby organs. Cancerous cells may divide and spread from one part to other parts of the body. The four categories of the dataset used in this work are stones, tumors, normal tissues, and cysts [16]. We select a dataset that include images of benign and malign kidney cells. The four categories contain around 10,000 files in size. In each class, images of different segments of the same kidney are included so for each patient a batch of more than 10 images is found. So in this work, we selected randomly from each batch of images for a single patient one image to represent the patient's case. Accordingly, we selected 101 images only from each of the tumor class and the normal class. The aim is to use this dataset and make use of simple machine learning algorithms to test how efficiently we can reduce resolution of images used to save computational power. The dataset is divided to 80% and 20% which are going to be used for training and testing respectively. By definition, every data file in the dataset is a CT scan of a kidney. Each file is an RGB image file. The files have different resolutions. In fig 1a and 1b, we can find an example of CT scan for benign and malign tissues of a kidney in RGB format. Next, we discuss the details of the algorithm which is going to be applied on this dataset.

3.2. Proposed Block Diagram

A block diagram showing the steps undertaken on each image is shown in fig. 2. In fig. 2 we can see that, the dataset is passed through some preprocessing techniques to standardize the data and deal with any missing data.

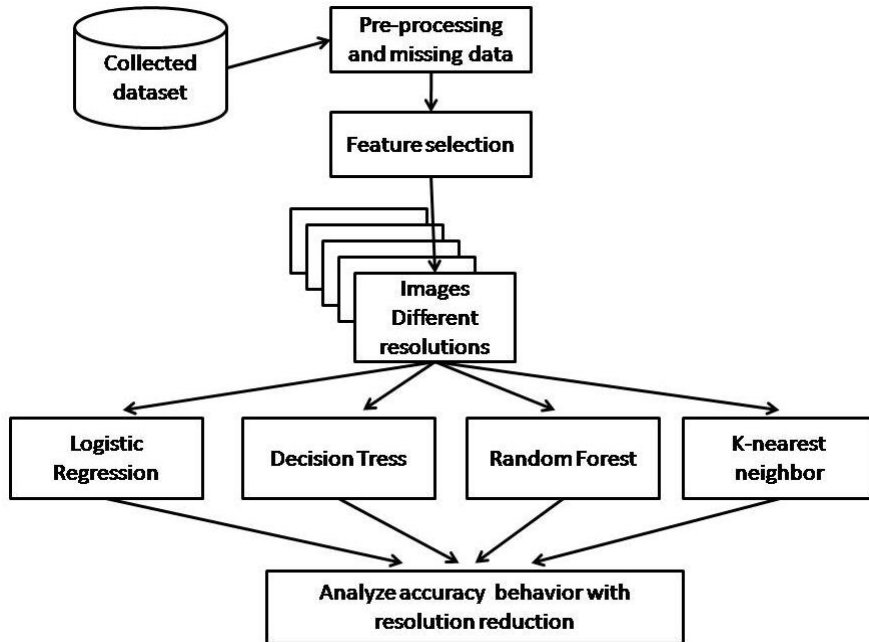


Fig. 2 classification techniques tools

Preprocessing steps include unifying the resolution of the images and changing the RGB images to be gray one. Matlab is used in calculations of both steps. The function “rgb2gray” is used to change each file image from RGB image to a gray one. Then the function “imresize” is used to change all images to be equal the same resolution of 2048 by 2048 pixels. As for the missing data, we selected randomly 101 images from the normal kidney and tumor kidney classes. We made sure that images contain full CT scans and so there was no missing data.

Then, a feature selection method was used to select the most important features in each image. Two steps were applied for feature selections which were max-pooling and image projection. Both steps were applied using Matlab on each image. In fig. 3, we can see an example of how the max pooling function was applied on each of our images. Four parameters have to be identified for the max-pooling function. The input size is the size the image. The window size is the size of pixels on which the max-pooling function is applied. The stride size is the number of pixels to move each time the max-pooling function is applied. The output size is the size of the output image. We made the window size in our calculation to be 2 by 2. We chose the stride to be 2pixels.

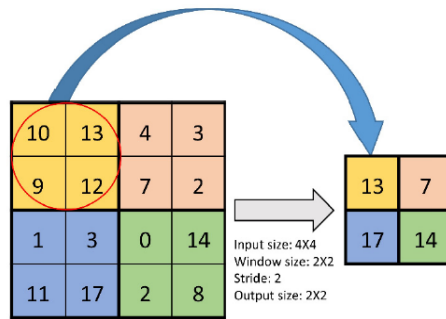
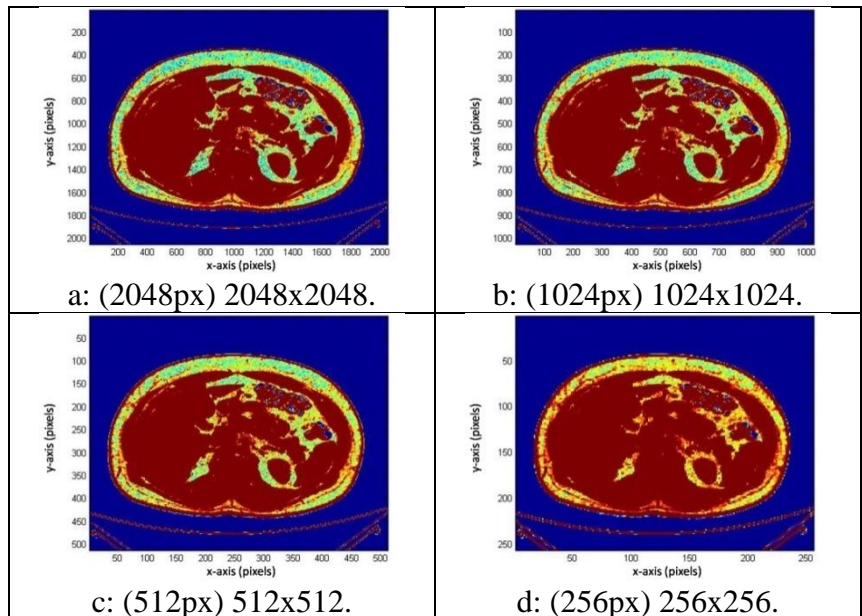


Fig 3: An example of a max-pooling function applied to an image. [17]

When applying the window size and the stride values defined above then the output image will always be equal to half the size of the input image. In fig. 4, we can find an example of a gray image to which the max-pooling function is applied. The 10 subfigures are for a single image to which the max-pooling function is applied several times. Each time the function is applied the number of pixels is divided by half. The figs. 4a to 4j contain the same square image but at different resolutions after applying the max-pooling function. The resolutions in figs. 4a to 4j are 2048, 1024, 512, 256, 128, 64, 32, 16, 8 and 4px (pixels).



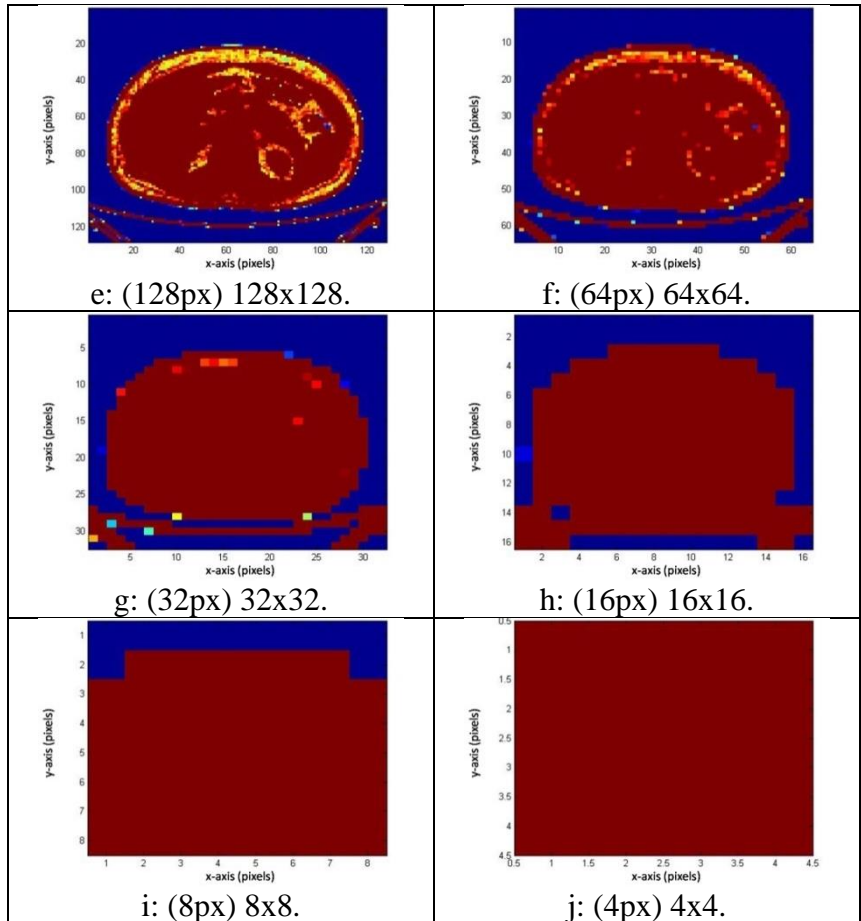


Fig. 4: A single CT image of a kidney displayed in different resolutions after applying the max-pooling function.

Then, the projection of each image is calculated once on the horizontal-axis of the image and another on the vertical-axis of the image. Fig. 5a contains the projection of the image shown in fig. 4a along the vertical-axis. The x-axis of fig. 5a shows the pixel number on the vertical-axis of the image. The y-axis of fig. 5a shows the projection of the image along the vertical-axis which is equal to sum of the values of the pixels along each row in the image. While, fig. 5b contains the projection of the image shown in fig. 4a along the horizontal-axis. The x-axis of fig. 5b shows the pixel number on the horizontal-axis of the image. The y-axis of fig. 5b shows the projection of the image along the horizontal-axis which is equal to sum of the values of the pixels along each column in the image. The number of readings along each projection is 2048 points. The points for the projection along the horizontal-axis and that along the vertical-axis form the features to be passed to the machine learning algorithm.

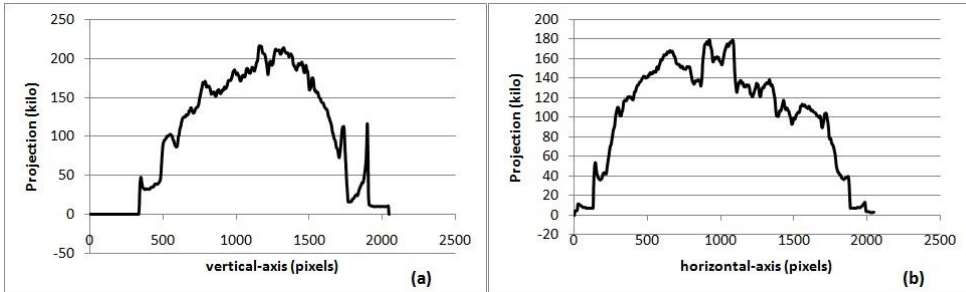


Fig. 5: (a) The projection of the image displayed in fig. 4a along the vertical-axis. (b) The projection of the image displayed in fig. 4a along the horizontal-axis.

Four machine learning algorithms for image classification were applied to the images as shown in fig. 2. The four classification methods are Logistic Regression (LR), Decision Tree (DT), Random Forest (RF) and K-Nearest Neighbors (KNN). A comparison between the results of each algorithm and identification of which can achieve higher accuracy in kidney cancer detection are discussed.

3.3. Results

In this section, we show the results of applying the four classification algorithms to our dataset. The accuracy of each algorithm is analyzed while changing the resolution of the used images. The aim is to find the optimum size of the images to be used and the best classification algorithm to be used in identifying tumors in a kidney. Next, the results of applying the RF, KNN, DT and LR are shown.

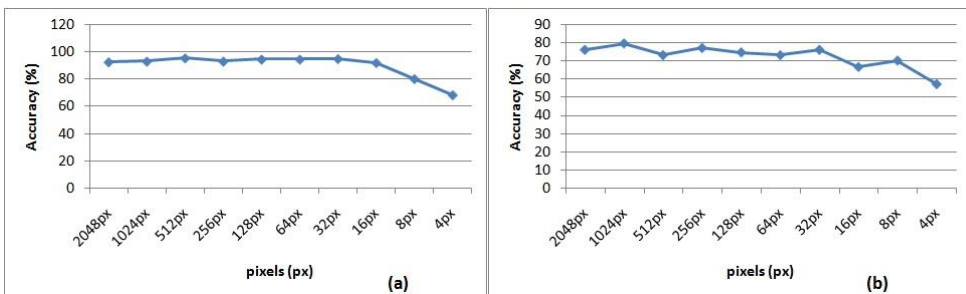


Fig. 6: (a) The accuracy of kidney cancer detection using KNN algorithm. (b) The accuracy of kidney cancer detection using DT algorithm.

In fig. 6a, the percentage of true detection is calculated for images with different resolutions using the KNN algorithm. The x-axis shows the resolution of the image used in the calculations. The y-axis shows the percentage of accuracy for true detection for the corresponding resolution. The percentage of accuracy is almost stable as the resolution of the images drops from 2048 pixels (px). The accuracy reaches a maximum of 95.5% at a resolution of 512px. The accuracy ranges from 92.6 to 95.5% with an average of 94% as the

resolution drops from 2048px to 32px. Then, the accuracy drops suddenly to reach 68.3% at resolution 4px.

In fig. 6b, the percentage of true detection is calculated with images with different resolutions using the DT algorithm. The percentage of accuracy is almost stable as the resolution of the images drops from 2048 pixels (px). The accuracy reaches a maximum of 79.7% at a resolution of 1024px. The accuracy ranges from 73.3 to 79.7% with an average of 76% as the resolution drops from 2048px to 32px. Then, the accuracy drops suddenly to reach 57.4% at resolution 4px.

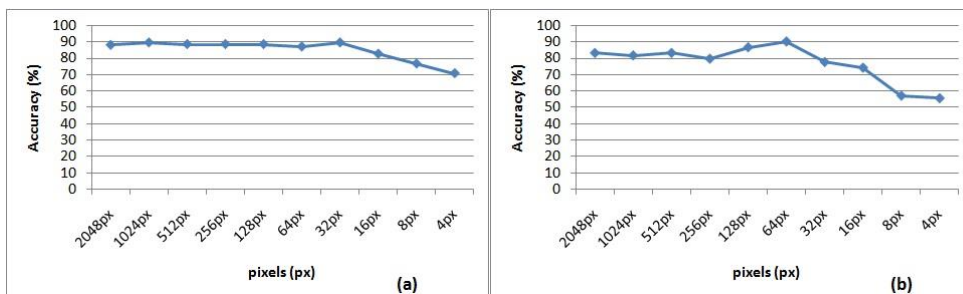


Fig. 7: (a) The accuracy of kidney cancer detection using RF algorithm. (b) The accuracy of kidney cancer detection using LR algorithm.

In fig. 7a, the percentage of true detection is calculated with images with different resolutions using the RF algorithm. The percentage of accuracy is almost stable as the resolution of the images drops from 2048 pixels (px). The accuracy reaches a maximum of 89.6% at the two resolutions of 1024px and 32px. The accuracy ranges from 87.1 to 89.6% with an average of 88% as the resolution drops from 2048px to 32px. Then, the accuracy drops to reach 70.8% at resolution 4px.

In fig. 7b, the percentage of true detection is calculated with images with different resolutions using the LR algorithm. The percentage of accuracy is almost stable as the resolution of the images drops from 2048 pixels (px). The accuracy reaches a maximum of 90.1% at the resolution of 64px. The accuracy ranges from 77.7 to 90.1% with an average of 85% as the resolution drops from 2048px to 32px. Then, the accuracy drops to reach 55.9% at resolution 4px. Next, we analyze the results and their meaning.

4. Discussion

In this work we address the problem of determining the type of kidney tumors and to analyze the patient's situation with kidney tumors injury. Using renal CT scans as a base, the features are extracted and used through training and testing to identify a class for each image (Normal/Tumor or Benign/Malignant). We started by pre-processing the images used and removing any missing data. The preprocessing process included changing the type of images to be gray scale ones and then unifying the size of the input images. Removal of missing data included selected randomly the images to be included in our dataset and

making sure they visually contain a full scan of a kidney. Then, we continued to select the best features in each image to represent the image. Two processes were applied to each image. A max-pooling function was applied to each image to reduce the resolution of the images from 2048px down to 4px. Then a projection process was applied to obtain the projection of each image horizontally and vertically. The values of both projections were taken to be the features representing each image. We applied the KNN, DT, RF and LR algorithms on our dataset. Our proposed simple machine learning algorithms were found to be effective for our randomly selected dataset. The average accuracy percentages were 94%, 88%, 85% and 76% for the KNN, RF, LR and DT algorithms respectively. The KNN algorithm proved to be the best in correctly classifying images into one of two groups either benign or malign. In general, the reduction in the number of resolution of the used images has almost no effect on the calculated accuracies down till 32px. This was true for all four used classification algorithms. The curve representing the accuracy was almost constant as the resolution dropped from 2048px to 32px. Then as the resolution decreased from 32px to 4px, the accuracy dropped to the lowest value.

5. Conclusion

AI-based tools have transformed many facets of contemporary technology and are gradually permeating virtually every area of medicine, including the treatment of patients with kidney cancer. Physician-led efforts to determine the best function to learn will be necessary to fully appreciate the power of these tools in a clinical workflow. In order to collect datasets that accurately reflect the variety of patients we see in our clinics; it will also be necessary for centers to work together. However, AI-based solutions which are deep learning methods are computationally very expensive. This made us think that using simple machine learning algorithms can pave the way into cheaper processing power AI-based solutions. We collected the dataset by taking a sample of 101 images from two groups of CT scan images which are normal and tumor images. This made us sure that no missing data or repetition problem can be faced. Then we applied a preprocessing process on the images by changing each image to gray scale one and unifying the resolution of all images. Then we applied a feature selection process through applying the max-pooling function and the projection function on each image. The horizontal and vertical projection of the image is used as feature parameters for each image. Following, we calculated the accuracy of cancer detection on all the dataset for different resolution of the images. Our aim is to find the optimal resolution at which we can get the best result at this will reduce processing power needed. Also, we wanted to find the best machine learning algorithm within the four algorithms put under investigation. We found that the minimum resolution for the images to be processed should not be lower than 32px. In addition, we arranged in descending order the percentage of accuracy in cancer detection for the four algorithms KNN, DT, LR and RF. We found that their order is KNN with highest percentage followed by RF, then LR and finally DT.

For future work, we propose running the same algorithm on a larger dataset to confirm the results achieved here. Then, we propose applying the deep learning algorithms on images with smaller resolution to study if the behavior of the algorithms imitates what

was discussed here which is that the same accuracy can still be achieved while using lower computational power.

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