

SYSTEM ANALYSIS OF KIDNEY VOLUME ESTIMATION THROUGH CYCLIC BAYESIAN NEURAL NETWORK

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CERTIFICATE

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Analysis of Kidney Volume Estimation Through Cyclic Bayesian Neural Network

ABSTRACT

Kidney diseases are expected to be chronic symptoms, in which kidney volume evaluation is essential existing kidney volume estimation techniques are involved in segmenting the area of the infected region from the background section. Automated kidney localization and volume Matric image segmentation are critical steps in a fast diagnosis procedure. Most currently available frameworks made more manual analysis and classification points rather than automated systems. The proposed system is developed based on which the CT images of the kidney or considered. The input images or processed the well using the image processing Toolbox and segmented from the background as fast as possible user base and neural network model. The features from the segment for classification images. The classification ensures the kidney region from the CT images and estimates the volume. The accuracy of classification of normal and abnormal kidney volume achieved 96% using CBNN model.

Keywords : Chronic kidney disease, Diabetic system, Deep Learning, Image processing, Machine learning.

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LIST OF ABBREVIATIONS

S.No	Acronym	Description
1	RPN	Regional Proposal Network
2	FCN	Fully Convolutional Network
3	RC	Renal Cancer
4	GCO	Global Cancer Observatory
5	RCC	Renal Cell Carcinoma
6	CKD	Chronic Kidney Disease
7	ADPKD	Autosomal Dominant Polycystic Kidney Disease
8	CNNs	Convolutional Neural Networks
9	RAS	Renal Artery Atherosclerosis
10	ESRD	End Stage Renal Disease
11	eGFR	estimated Glomerular Filtration
12	CT	Computed Tomography
13	EAT	Epicardial Adipose Tissue
14	MIA	Medical Image Analysis
15	ML	Machine Learning
16	DL	Deep Learning
17	AI	Artificial Intelligence
18	ROI	Region Of Interest
19	DDNET	Cartesian Polar Dual Domain

CHAPTER 1

INTRODUCTION

1.1. OVERVIEW OF THE PROPOSED STUDY

The kidney is an organ of a vital role that keeps the body fluid and solute balance checked by excreting and filtering waste products. It also secretes many hormones and helps control blood pressure. The human kidneys are depicted in (Figure 1). Kidney cancer is one of the top 10 malignancies in men and women alike. The probability of having kidney cancer throughout one's lifetime is around 1 in 75 (1.34%). Renal cancer (RC) is an acute urological disease that affects over 400,000 individuals each.

According to the Global Cancer Observatory (GCO), more than 175,000 deaths are due to this disease [5,6]. Renal cell carcinoma (RCC) has the third-highest disease rate after prostate cancer and bladder cancer. It is estimated that RCC is the seventh most frequent cancer in men and the ninth most common cancer in women in the United States, with 48,780 new cases diagnosed and 27,300 new instances of RCC-related death. On radiography, distinguishing between benign kidney tumors and malignant renal cell carcinoma can be challenging .

However, the majority of kidney tumors turn out to be cancerous . Renal cell carcinoma (RCC) represents the vast majority of these tumors .Clear cell RCC is the most common subtype of renal RCC ,accounting for approximately 80–90% of all kidney cancers. Overall, the worldwide incidence rate has increased by 2% per year during the last two decades. Kidney tumors are becoming more common, and the disease develops for a long time without causing symptoms.

Coincidence may be the reason for detecting more than half of the cases of renal cell carcinoma. Importantly, the cause of kidney cancer has not been determined. However, many risk factors, including smoking, obesity, poor diet, substantial alcohol consumption, family history of hypertension, exposure to radiation and chlorinated chemicals, and heredity, are risk factors for getting sick. Radical nephrectomy (RN) and partial nephrectomy (PN) are the current therapeutic options for kidney tumors. The tumor and kidney are removed in RN, but in PN, only the malignancy is removed.

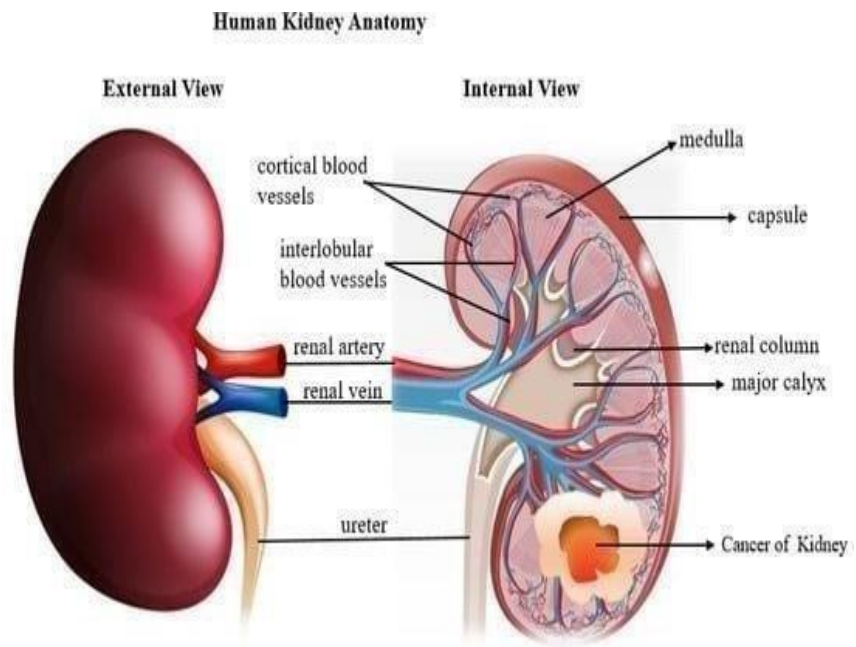


FIG-1: Diagram showing human kidney anatomy and Renal cell carcinoma developed inside the kidney.

Kidney size is well correlated with renal function, and a change in kidney size is an important factor for evaluating renal condition in patients with kidney disease. In chronic kidney disease, the kidney's size decreases with disease progression due to a reduction in nephron mass, whereas in polycystic kidney disease, it increases with the functional decline due to the growth of cysts.

Therefore, reliable reference data based on accurate kidney size measurements are essential for evaluating the course of renal disease and anomalies in children. The renal length shows a linear correlation with the kidney size and is usually used as a clinical indicator of kidney size changes due to the simplicity of the measurement. However, given that kidney length is a poor predictor of renal parenchymal volume and renal function, kidney volume is a better indicator of kidney size change.

A new US-based kidney volume measurement method that reflects the actual kidney structure was necessary to overcome the problems of the ellipsoidal equation. Some previous studies have attempted the image segmentation process using cross-sectional US images to calculate the kidney volume. A manual calibration process is essential for the segmentation of US images; however, it is time-consuming, labor-intensive, and highly prone to inter-observer variability.....

For these reasons, automatic segmentation methods for US kidney images using artificial intelligence have been proposed in previous studies. Recently, hybrid learning, which combines deep learning and machine learning, has been applied as a learning method that can increase the accuracy of the automated segmentation process. Thus, we combined the deep learning-based U-net model and the machine learning-based localizing region-based active-contour method for hybrid learning. To our knowledge, no previous study has proved that an automated segmentation process using US images could calculate the exact kidney volume in children by hybrid learning compared to the reference volume obtained by CT or MRI. We applied hybrid learning to automated segmentation and calculated the kidney volume with automatically segmented US images.

Clinically, the reduced or absent functionality of a kidney for more than three months, is referred to as chronic kidney disease (CKD). Kidney disease, often resulting from the tumor, occurs in both hereditary and sporadic forms. It is a significant risk factor for death worldwide. The prevalence of CKD varies between 7-12% in different regions of the world. For example, China, Canada, Australia, the United States, Germany, Finland, Spain, and England reported 1.7%, 3.1%, 5.8%, 6.7%, 2.3%, 2.4%, 4.0%, and 5.2%, respectively. Different CKDs, for example, Autosomal dominant polycystic kidney disease (ADPKD) and renal artery atherosclerosis (RAS), often lead to the end-stage-renal disease (ESRD), which are associated with the change of kidney volume. However, CKD detection is complicated. Usual laboratory tests such as the estimated glomerular filtration rate (eGFR) and serum albumin-to-creatinine ratio often cannot detect early disease and known to be unreliable in tracking disease progression.

Several works suggested kidney volume as a potential surrogate marker for renal function. The total kidney volume is now considered as the gold standard imaging biomarker for ADPKD and RAS progression at the early stages of this disease. In addition, renal volume measurement is an emerging alternative to renal scintigraphy, which is used in evaluating split renal function in kidney. It is also considered the best biomarker in the follow-up evaluation of kidney transplants. Kidney volume from 3D computed tomography (CT) data is typically estimated using different segmentation methods. These segmentation methods can be broadly categorized into two groups based on their use of any prior kidney localization step. Some methods use manual/(semi)automatic kidney localization before

segmentation, while other methods directly perform segmentation without using a previous localization step.

Image segmentation is the task of delineating diagnostically important anatomical structures on medical images. Segmentation is a necessary step in most computer-aided diagnosis use cases, and a pre-processing step for many other medical tasks like disease risk estimation, classification, etc. A common use case for medical segmentation is identifying single structures with a roughly elliptical shape or distribution, like most organs, skin lesions, polyps, cardiac adipose tissues, and similar structures and abnormalities.

Neural networks have achieved state-of-the-art results in many medical image segmentation tasks, however, they often require large amounts of annotated training images, which are time- consuming and costly to obtain. In this paper, we propose a general way to improve neural network segmentation data efficiency and performance on medical imaging segmentation tasks where the goal is to segment roughly elliptically distributed objects.

We propose and explore ways to train neural networks for biomedical image segmentation on polar transformations of images. The polar transformation transforms an image from Cartesian coordinates into a new coordinate system where the two axes are the rotation around an origin and radius from that origin. When the regions to be segmented are elliptical in shape or distribution, this transformation results in a reduction of dimensionality, allowing convergence in fewer epochs and good performance even in models with a low number of parameters.

Experimentally, we observed that selecting a correct polar origin is one of the key parameters that determine segmentation performance. Therefore, we propose two different approaches of selecting an optimal polar origin:

- (1) Estimation via a segmentation neural network trained on non-polar images and
- (2) Estimation via a neural network trained to predict heatmaps. Our method is evaluated on the tasks of polyp segmentation, liver segmentation, skin lesion segmentation, and epicardial adipose tissue (EAT) segmentation.

Image segmentation is the process of splitting an image into several segments in order to transform it into a more meaningful and easy-to-analyze representation. The process of image segmentation may be conceived of in two steps: identification and delineation. Identification is the process of identifying the location of an object in an image and differentiating it from everything else in the image. Segmentation involves delineating the boundaries of the region of interest for further analysis. There are several methods for segmenting images: Manual Segmentation, SemiAutomatic, Automatic Segmentation, and Semantic Segmentation. Semantic segmentation is crucial for image analysis tasks and plays a significant part in image interpretation. Image categorization, object recognition, and border localization are all required for semantic segmentation. Semantic segmentation has several applications in computer vision and artificial intelligence-assisted autonomous driving, and medical imaging analysis.

Evaluation of our approach as a pre-processing step shows that it improves segmentation performance across different datasets and neural network architectures while making the networks more robust to small dataset sample sizes.

Since scanning and loading (MI) onto a computer became practical, researchers have created automated analysis tools. MI analysis was done between the 1970s and 1990s by combining low-level pixel processing (edge and line detector filters, region expansion) with mathematical modeling (fitting lines, circles, and ellipses) to create compound rule-based systems that handled specific tasks. One of the most challenging problems in medical image analysis (MIA) using traditional approaches such as edge detection filters and mathematical algorithms is distinguishing the pixels of organs or lesions from background medical images of CT or MRI scans to give vital information on the shapes and sizes of these organs. Therefore, researchers have suggested numerous automatic segmentation methods to extract the hand-crafted characteristics, such as machine learning techniques. Around the 1990s, supervised approaches involving training data to develop a system became more prevalent in medical image analysis. Active shape models (for segmentation), atlas techniques (in which atlases are fitted to fresh data extracted from the training data), feature extraction, and statistical classifiers are just a few examples (for computer-aided detection and diagnosis). This pattern recognition or machine learning technique is still frequently utilized, and it is the basis for a large number of commercially

accessible medical image analysis products. As a result, we have seen a shift away from human-designed systems toward systems that computers train using example data and extract feature vectors. In the high-dimensional feature space, computer algorithms find the best decision boundary.

The extraction of discriminant characteristics from images is a critical step in the construction of such systems. Humans still carry out this procedure, and as a result, one speaks of systems with hand-crafted features. As a result of these technological advancements, deep learning techniques began to exhibit their significant capabilities in image processing applications. DL is a type of machine learning that enables more precise and quicker results than traditional machine learning techniques. Several image segmentation methods were proposed that utilize polar coordinates. Liu *et al.* proposed an approach they call Cartesian-polar dual-domain network (DDNet) to perform opticdisc and cup segmentation in retinal fundus images. The neural network contains two encoding branches, one for a Cartesian input image and another for the polar transformation of the same input image. The predictions are fused into a single feature vector which is then decoded into a final segmentation. Salehinejad *et al.* used the polar transformation as a way to augment training data by transforming each input image into multiple polar images at various polar origins, thus increasing the number of training data. Kim *et al.* (2020) proposed a convolutional neural network layer for images in polar coordinates to achieve rotational invariance. Their cylindrical convolution layer uses cylindrically sliding windows to perform a convolution. Kim *et al.* [8] proposed a user-guided segmentation method where an expert selects the point used as the polar origin. The transformed image is then segmented using a convolutional neural network (CNN). Esteves *et al.* proposed a polar transformer network for image classification. Note that “transformer network” here refers to spatial transformer networks and not attention-based networks commonly called transformers. The network consists of a polar origin predictor and a neural network that predicts a heatmap. The centroid of the heatmap is then used as the origin for a polar transformation of the input image. The polar image is classified using a CNN. This approach is most similar to our proposed method, however, their approach focuses on image classification, not segmentation. Additionally, our approach differs in the ways the ground truth data is prepared, the used neural network architectures, as well as other details.

One of the most used neural network architectures for biomedical image segmentation is UNet, an encoder-decoder based architecture where intermediate feature maps of the encoder are concatenated with the appropriate feature maps of the decoder, allowing the network to simultaneously learn context and precise localization. Multiple modifications of the U-Net architectures were proposed. Zhou *et al.* proposed a nested U-Net architecture called U-Net++, where the encoder and decoder are connected via dense convolutional blocks instead of simple concatenation. Jha *et al.* proposed an architecture called Double-U-Net based on two U-Nets stacked together, where the first one uses a VGG encoder pre-trained on the ImageNet dataset. The output of the first U-Net is used as input, together with the input image, for the second U-Net. Additionally, the output of the first U-Net is concatenated together with the output of the second U-Net to produce the final segmentation. They achieve state-of-the-art results for lesion segmentation. Azad *et al.* proposed a U-Net-based architecture where the decoder was modified by adding bi-directional convolutional LSTM and squeeze-and-excitation layers. Tomar *et al.* proposed a general network for medical image segmentation, validated on seven biomedical image datasets. Their method uses an encoder-decoder architecture with squeeze-and-excitation residual blocks and recurrent learning. The model's output at each epoch is stored and used as an input to the next epoch, iteratively improving the output while reducing training time. Ibtezhaz and Rahman proposed MultiResUNet, an improvement of U-Net wherein U-Net's convolutional blocks are replaced with blocks that use differently-sized convolutional kernels in parallel. Additionally, they added convolutional blocks to U-Net's skip connections.

There are various proposed approaches for polyp segmentation from colonoscopy images that use deep learning. Fan *et al.* proposed a parallel reverse attention network for polyp segmentation. Their method works by first using a parallel partial decoder which decodes feature input maps into a global semantic map of the image. This map is then refined by a series of recurrent reverse attention layers. Fang *et al.* used a network with one encoder and two mutually constrained decoders, one for predicting areas and another for predicting boundaries. The network then aggregates the features. The authors train the network using a boundary-sensitive loss function. Huang *et al.* proposed an encoder-decoder neural network which uses a HarDNet-based encoder and a cascaded partial

decoder, with three branches are connected to the encoder, and their features are densely aggregated to produce the final output. Each branch uses proposed neural network layers called receptive field blocks.

For liver segmentation, Valanarasu *et al.* proposed KiU-Net. Their network consists of two branches. The first branch is an overcomplete convolutional network where the input image is projected into a higher-dimensional space, forcing the network to learn fine details and accurate edges. The other branch is a regular U-Net network. The two branches are then fused to produce a final segmentation.

For EAT segmentation, Zhang *et al.* proposed an approach using two successive U-Net networks. The first network performs a segmentation of the pericardium, a protective layer of connective tissue that encloses EAT. The output segmentation is refined using morphological operators and then used as a mask for the input to the second U-Net, which is trained to segment EAT for the pericardium region. Commandeur *et al.* proposed training two convolutional neural networks. The first network determines the heart limits and segments adipose tissues. The output of the first network is used to sample the input to the second neural network which delineates the pericardium.

The 2019 Kidney and Kidney Tumor Segmentation Challenge (KiTS19) aimed to accelerate progress on this automatic segmentation problem by releasing a dataset of 210 CT images with associated high-quality kidney and kidney tumor segmentations that could be used learned models. It also aimed to objectively assess the state of the art by holding a collection of 90 segmentation masks private for participants to predict given associated imaging. Participating teams were ranked based on their average Sørensen-Dice coefficient between the kidneys and tumors across these 90 test cases.

This challenge was hosted on grand-challenge.org where it accrued 826 registrations prior to the deadline. 106 unique teams submitted valid predictions to the challenge, and the official leaderboard^m reflects submissions from 100 unique teams who met all criteria for a complete submission, including a detailed manuscript describing their method. This challenge was accepted to be held in conjunction with the 2019 International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI) in Shenzhen, China, and it has now entered an indefinite “open leaderboard” phase in which

any grand-challenge.org user may submit their predictions on the 90 test cases and have them scored and added to the leaderboard without delay.

Precise TKV calculation requires manual localization and segmentation by clinical experts or trained personnel. Conventionally, the radiologist delineates the boundary of kidneys on images using semi-automatic tools at the medical image post-processing workstation. The use of these tools on CCT images remains a challenge with ADPKD kidney due to the contrast difference between the kidney and surrounding structure. In CT images, different body components such as air, fat, fluid, soft tissue, hemorrhage, calcification, and bones have different CT Hounsfield Units (HU) values which are displayed from low to high density. The normal kidney has homogeneous density and surrounding by the perirenal fatty tissue which shows lower density compared to soft tissue. However, in ADPKD, the kidney is replaced by multiple cysts of various densities (some of the cysts have high density due to hemorrhage or calcification), which cause the density of the kidney to become heterogeneous due to soft tissue, fluid, hemorrhage, and calcification as shown in Figure 1. In addition, the kidney is enlarged and closely abutted to the adjacent soft tissue structure resulting in no contrast difference between the kidneys and surrounding structure. As often seen in ADPKD patients, the presence of multiple liver cysts would make segmentation of kidneys more difficult as shown in [Figure 2a](#). It is also observed that the density of ADPKD kidney can be the same as other adjacent organs such as liver and spleen, as shown in [Figure 2b](#). As compared to the renal cyst in non-ADPKD kidney, morphology and density of ADPKD kidney are non-uniform as shown in [Figure 2c](#). Due to these reasons, if we want to calculate the TKV .

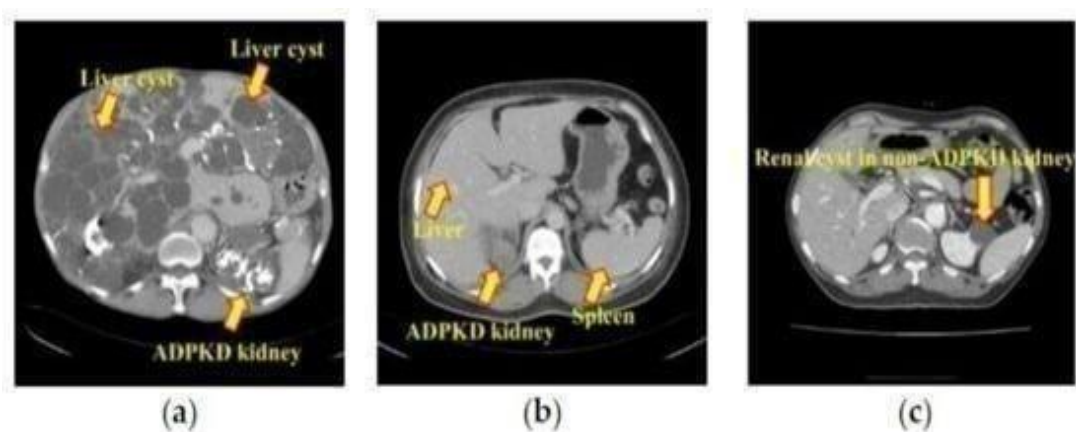


FIG-2: Kidney with different types of cysts: (a) Autosomal Dominant Polycystic Kidney

Disease (ADPKD) kidney and liver cyst; (b) ADPKD kidney, liver, and spleen; (c) Renal cyst in non ADPKD.

In recent studies, computerized techniques have been widely explored for solving the challenges in medical imaging big data analysis using Artificial Intelligence (AI). Powerful AI techniques including Machine Learning (ML) and Deep Learning (DL) have been used to solve problems. DL has been used in several medical applications include feature extraction, classification, detection and segmentation. One crucial application in DL is the detection or localization task. This task is essential for localizing the particular Region of Interest (ROI), which could be any nodule, cyst, tumor, or cancer in an image. It is also found that detection can be used for improving the segmentation task of ADPKD kidneys. Therefore, the detection task can be considered as an important intermediate technique for segmentation.

The detection task can be carried out in three different approaches, which could be

- 1) Detection by classifying a single ROI,
- 2) Detection by locating and classifying a single ROI and
- 3) Detection by locating and classifying multiple ROIs.

The object detection approach is the combination of classification and localization for detecting multiple ROIs, where it has been used as an intermediate technique for improving the segmentation task. For instance, Region with Convolutional Neural Networks (R-CNN) has been used as an object detection architecture for detecting ADPKD kidneys on MRI images with higher numbers of False Positives (FP). Several CNN architectures have been used for segmentation and object detection tasks applying Visual Geometry Group 16 layers (VGG-16), and R-CNN, respectively, on MRI. Various applications have been designed using the object detection approach for different purposes. Those applications are universal lesion detection using CT images, VGG16, and Region Proposal Network (RPN), and breast cancer detection using histopathology images and Fully Convolutional Network (FCN). Furthermore, we found that less work has been done to solve the detection problem in ADPKD kidneys using an object detection approach.

Recently, DL techniques for semantic image segmentation have shown promising results in a variety of medical image analysis applications. Convolutional neural networks

(CNNs) are the most successful form of image processing model to date. CNN have multiple layers. CNN has been under development since the late 1970s by Fukushima. Moreover, they were used to analyze medical images in 1995. They witnessed their first successful real-world application in 1998 for hand-written digit recognition. In the December 2012 ImageNet competition, Alex-Net, the planned CNN, won the competition by a huge majority. Using analogous but deeper designs, more work was done in later years. Deep convolutional networks have emerged as the preferred method for computer vision. Due to their powerful non-linear feature extraction capabilities and the efficiency of encoder–decoder architectures, CNNs have been used for complex segmentation tasks. In computer vision tasks, CNN architectures have already surpassed classical methods, particularly in the segmentation of CT scans. On the other hand, fully convolutional network (FCN) architectures are a notably powerful end-to-end training segmentation solution. This architecture is state-of-the-art across several domains and can create raw-scale, pixel-level labels on the images. Other subsequent efforts, such as the feature pyramid networks (FPN), primarily utilized in object recognition, have used FCN as a starting point for deeper and more sophisticated segmentation structures. Pyramid scene parsing networks (PSPNets) are used to analyze scenes. For object instance segmentation, Mask R-CNN is used.

Semantic segmentation using DL techniques: DL, a proliferating new machine learning division, has proven their effectiveness in semantic segmentation. Deep learning techniques play an important role in easing image understanding. Deep learning techniques for semantic segmentation have been divided into region-based, FCN, and semi-supervised methods.

Region- based methods adopt the region-based classification; finally, they label pixels according to the scoring regions. FCN-based methods, in contrast to region-based methods, do not extract the region proposal. They learn a mapping from pixel to pixel, making arbitrary-sized images. Regarding semi-supervised methods, usually, semantic methods depend on many images that require a long time to annotate the masks. Therefore, some semi-supervised methods have been suggested to utilize the annotation process. In addition to the methods mentioned, more DL categories for semantic segmentation have been proposed, including feature encoder-based methods, recurrent neural network-based

methods, upsampling/deconvolution-based methods, increased resolution of feature-based methods, enhancement of feature-based methods, spatiotemporal-based methods, and methods using CRF/MRF .

Semantic segmentation is a hot research area in medical image processing. This is particularly true for abdominal CT scans, where many contests push academics to continue developing approaches for improving segmentation performance. Even though medical segmentation is becoming increasingly prevalent, there are few ways for segmenting kidney and renal tumors in the literature .To our knowledge, only a few review articles have examined kidney segmentation strategies. Nonetheless, numerous articles have been published on the subject of kidney.

Additionally, various deep learning-based algorithms have been developed for segmenting images of other diseases, such as skin lesions, dental imaging, and eye images. As a result, the research barriers for adopting and applying these approaches to the kidney images have encouraged study on kidney segmentation and detection. This study look at cutting-edge DL techniques for segmenting CT kidney cancers. Additionally, the article highlights distinct challenges and possible solutions for medical image interpretation.

For the last two decades, medical imaging scientists have proposed several kidney localization approaches within the 3D volumetric medical images. This section surveyed the most relevant and recent machine learning-based kidney localization approaches in CT, divided into hand- engineered feature-based classical machine learning (ML) approaches and deep learning (DL) approaches. 1) Classical ML Approaches: Criminisi et al. predicted the locations of organ bounding box walls using regression-forest (RF)-based approaches and achieved a mean kidney bounding box wall localization error of 13mm. Cuingnet et al. This section surveyed the most relevant and recent machine learning-based kidney localization approaches in CT, divided into hand- engineered feature. As a result, the research barriers for adopting and applying these approaches to the kidney images have encouraged study on kidney segmentation and detection.

Gauriau et al. estimated an organ bounding box from the cascaded RF-based organ confidence map and achieved a mean wall localization error of 5.5mm for kidney bounding boxes. Recently, Samarakoon et al. proposed a light RF that uses fewer nodes than regular

RF to localize different organs in the CT scan and achieved a mean kidney localization error of 11mm. Zhou et al. used ensemble learning-based multiple 2D detectors and combined their outputs using collaborative majority voting in 3D to accomplish robust kidney localization. In their subsequent work, they localized the kidney in CT images using template matching, hand-crafted features, and local binary patterns. In summary, these classical ML approaches estimate the location of the kidney or its bounding box via predicting a continuous regression value or voxel-based voting. 2) DL Approaches: Humpire et al. proposed a convolutional neural network (CNN)-based approach to detect six organs, including the kidneys. They trained three separate CNNs to classify images taken from three orthogonal directions, where the classification of a slice is performed based on the presence or absence of a particular organ cross-section in that slice.

The 3D organ bounding box is then generated by combining the classified labels of orthogonal images, which achieved a localization error of 2.6mm for kidneys. Lu et al. proposed a method using a cross-sectional fusion of CNN and fully convolutional networks (FCN) for right kidney localization. In our previous work, we proposed a kidney localization approach that used a single CNN where 2D slice classifications from the three orthogonal views were concatenated into a fully connected layer to provide a voxel-wise kidney location prediction. In summary, these DL approaches determine the kidney locations via classifying the 2D CT slices, depending on the presence or absence of the kidney cross-section in that. In contrast, recently, Xu et al. proposed a 3D region proposal network for localizing eleven abdominal organs, including the kidneys. Unlike classification CNN, region proposal networks usually propose a 2D/3D region around an object of interest, based on the learned feature maps. They achieved a localization error of 4mm for kidneys.

Chronic kidney disease (CKD) refers to the reduced or absent functionality of kidneys for more than 3 months, which has been identified as a major risk factor for death worldwide. It is reported that about 3 million adults in Canada and about 26 million adults in the United States live with CKD. Detection of CKD is difficult. Biochemical tests like the 'estimated glomerular filtration rate' and 'serum albumin-to-creatinine ratio' have been shown to be unreliable in detecting disease and tracking its progression. However, CKD is most often associated with an abnormal change in kidney volume and thus, quantitative

‘kidney volume’ has emerged as a potential surrogate marker for renal function and has become useful for predicting and tracking .

The progression of CKD .In addition, kidney volume has been used in evaluating the split renal function in kidney donors as well as in follow-up evaluation of kidney transplants .

Kidney volume is an essential biomarker for a number of kidney disease diagnoses, for example, chronic kidney disease. Existing total kidney volume estimation methods often rely on an intermediate kidney segmentation step. On the other hand, automatic kidney localization in volumetric medical images is a critical step that often precedes subsequent data processing and analysis. Most current approaches perform kidney localization via an intermediate classification or regression step.

This paper proposes an integrated deep learning approach for

1. Kidney localization in computed tomography scan and
2. Segmentation-free renal volume estimation.

Our localization method uses a null selection -convolutional neural network that approximates the kidney inferior-superior span along the axial direction. Cross-sectional (2D) slices from the estimated span are subsequently used in a combined sagittal-axial Mask-RCNN that detects the organ bounding boxes on the axial and sagittal slices, the combination of which produces a final 3D organ bounding box. Furthermore, we use a fully convolutional network to estimate the kidney volume that skips the segmentation procedure. We also present a mathematical expression to approximate the ‘volume error’ metric from the ‘Sorensen–Dice coefficient.’ We accessed 100 patients’ CT scans from the Vancouver General Hospital records and obtained 210 patients’ CT scans from the 2019 Kidney Tumor Segmentation Challenge database to validate our method. Our method produces a kidney boundary wall localization error of $\sim 2.4\text{mm}$ and a mean volume estimation error of $\sim 5\%$.

Kidney volume is typically estimated using different segmentation methods. Similar to the kidney localization approach, here we survey classical ML and DL methods for kidney segmentation from CT, though we note that other approaches exist for kidney segmentation from magnetic resonance (MR) images .

Furthermore, we discuss the segmentation-free volume estimation approaches in the literature.

1) Classical ML Approaches: Zhou et al. used content based image retrieval, group-wise organ location calibration, and 3D Grab Cut techniques for kidney localization respectively. Cuingnet et al. used a combination of RF and template deformation to segment kidneys. Glocker et al. used a joint classification-RF scheme to segment different abdominal organs, including kidneys. Khalifa et al. [developed a 3D kidney segmentation framework integrating CT appearance features, higher order appearance models, and adaptive shape model features into a random forest classification model. Hristova et al. used vantage point trees to classify voxels for kidney segmentation. Zhao et al. used CT intensity features from the image in an RF framework for voxel-level classification to segment kidneys.

2) DL Approaches: : Chen et al. proposed a 3D FCN based method for automatic multiorgan segmentation in dualenergy CT. Gibson et al. proposed dense V-network FCN for multiorgan segmentation from abdominal CT images. Valindria et al. investigated learning from multiple modalities for organ segmentation and showed effectiveness on kidney segmentation. Thong et al. showed promising kidney segmentation performance using CNN. Keshwani et al. proposed a multitask 3D CNN to segment ADPKD. Sharma et al. performed the automated segmentation of ADPKD kidneys using FCN. Groza et al. compared several CNN-based approaches for kidney segmentation and argued that foveal FCN is the most suitable deep architecture. Recently, more than two hundred deep learning methods have been proposed for kidney segmentation in the 2019 Kidney Tumor Segmentation (KiTS) Challenge ,where most of the methods are variants of 3D UNet or VNet .Recent work on medical image segmentation tasks included many contributions based on 2D and 3D U-shaped networks (i.e., U-Nets) .For example, to improve the UNet architecture robustness to challenging organ and tumor segmentation scenarios, attention gates and squeeze-and excitation blocks have been proposed.

3) Segmentation-free Approaches: Classical ML-based segmentation methods require hand- engineering features, which is often hard to design optimally. DL-based segmentation approaches showed better kidney segmentation performance than the classical ML approaches due to their capability of learning optimal features automatically. However, DL-based segmentation approaches often require training deep and complex

dense prediction networks through expensive computation. Furthermore, it is often challenging to decide on the deep architecture and appropriate loss function. Besides, kidney cancer appears on CT images. It often appears hyperdense (i.e., calcifications) .

This scenario introduces additional challenges to deep learning-based segmentation of kidneys. Many organ functionality-related parameters are estimated using segmentation in clinical settings, although the ultimate aim is not producing a segmented organ. Thus, this segmentation procedure introduces additional challenges in estimating these vital parameters, e.g., total kidney volume. Avoiding the computational overheads and limitations associated with segmentation approaches, several segmentation free ML approaches have been proposed for cardiac biventricular volume estimation from MR images ,and direct tumor volume estimation from PET scans .Recently, we proposed two segmentation-free kidney volume estimation approaches using a dual regression forest ,and a CNN ,respectively, which bypassed the segmentation step altogether. To the best of our knowledge, we are the first.

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Kidney volume measurement from 3D CT volumes in clinical environments typically requires a two step procedure: (i) localizing kidneys, and then (ii) estimating volumes of the localized kidneys. For years, kidneys were typically localized manually in clinical settings. To automate this process, Criminisi et al. proposed regression-forest (RF)-based anatomy localization methods that predict the boundary wall locations of a tight region-of-interest (ROI) encompassing a particular organ. However, their reported 60%. However, the authors mentioned that their method was designed and validated with only non-pathological kidneys. Recently, Lu et al. proposed a right-kidney localization method using a cross-sectional fusion of convolutional neural networks (CNN) and fully convolutional networks (FCN) and reported a kidney centroid localization error of 8 mm. However, the robustness of this right-kidney-based deep learning model in localizing both kidneys is yet to be tested as the surrounding anatomy, and often locations, shapes and sizes of left and right kidneys are completely different and non-symmetric. Subsequent to localization, kidney volumes are typically estimated using different segmentation methods, a strategy that has various limitations.

For example, graph cuts and active contours/level sets-based methods are sensitive to the choice of parameters, prone to leaking through weak anatomical boundaries, and

require considerable computations Recently, Cuingnet et al. used a combination of RF and template deformation to segment kidneys, while Yang et al used multi-atlas image registration; these methods rely extensively on prior knowledge of kidney shapes. However, building a realistic model of kidney variability and deciding the balance between trusting the model vs. the data are non-trivial tasks. In addition, these prior-shape based methods are likely to fail for pathological cases, e.g., presence of large exophytic tumors. To overcome these segmentation-based limitations and associated computational overhead, Hussain et al recently proposed a segmentation-free kidney volume estimation approach using a dual RF, which bypassed the segmentation step altogether. Although promising, their approach relied on manual localization of kidneys in abdominal CT. In addition, they used hand-engineered features that may be difficult to optimally design.

Kidney feature extraction usually relies on sharp intensity variations among voxels around the kidney boundary in CT images. However, some phenomena such as low contrast, noise, opacity, and anisotropy may arise when capturing CT images. These deteriorate the segmentation results when ambiguous voxels appear near the boundaries of organs. The extracted features cannot fully indicate the outline of kidneys. Further, the tininess of tumors and the resemblance in texture between tumors and kidneys can complicate the identification process. These problems can affect the TKV measurement outcomes.

Example kidney data from our patient pool demonstrating data variability present (ranging from normal to pathological), and our hybrid kidney localization-volume estimation approach.

- (a) Some CT snapshots showing variations in normal and pathological kidney shape and size,
- (b) orthogonal decision aggregated CNN for kidney localization, and
- (C) segmentation-free kidney volume estimation using deep CNN.

To obtain better-trained models, data pre-processing plays a crucial role in the entire segmentation process Cleaned and enhanced data, including the training dataset and ground truth, can improve segmentation performance in specific medical applications . In this paper, three preprocessing procedures were analyzed and adapted to improve the

accuracy rate of kidney segmentation systematically. The first step uses statistical Hounsfield windowing to adjust the grayscale to remove noise and suppress adjacent organs' intensities. The second step discriminates whether kidney areas exist in CT image slices. This method is used to evaluate the influence related to class imbalance. The third step analyzes the difference between single and multiple image labels.

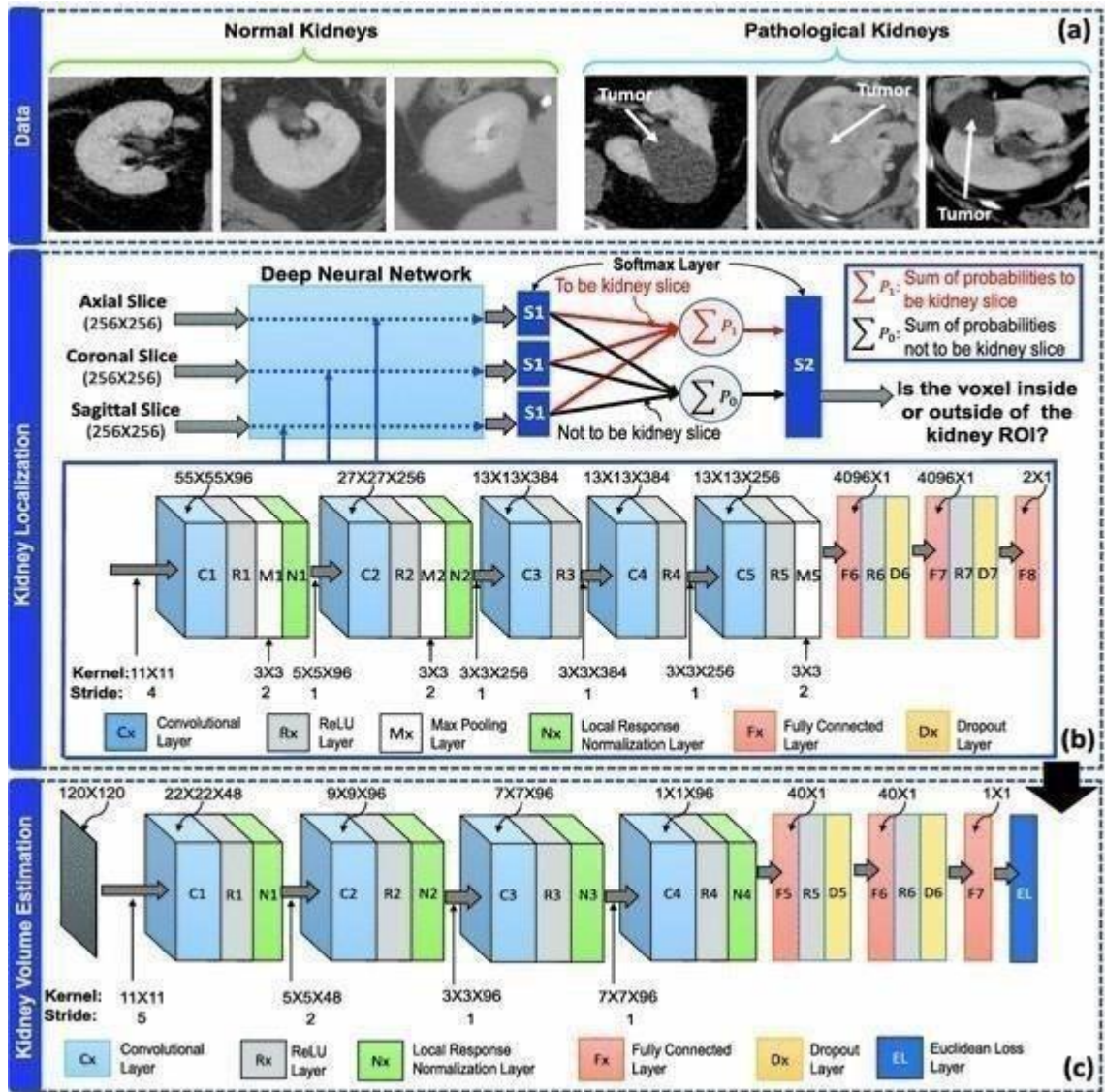


FIG-3: Some CT snapshots showing variations in normal and pathological kidney shape and size. (b).Orthogonal decision aggregated CNN for kidney localization , and (c). Segmentation – free kidney volume estimation using deep CNN.

Two modified U-Nets with different encoder models were used to test these pre-processing data. The preliminary results demonstrated that these pre-processing methods could

improve the accuracy rate effectively. The dice score was increased from 0.9436 to 0.9524. Further, the TKV calculation was evaluated. The proposed methods enabled automatic and precise segmentation of kidneys and tumors to provide consistent and highly accurate identification results in clinical applications.

This paper proposes an integrated approach for kidney localization and segmentation-free volume estimation using CNN-guided Mask-RCNN. We summarize the state-of-the-art ML-based methods for kidney localization and volume estimation from CT in Table I. In the table, we see that the proposed method is one of the two DL-based integrated methods (shown in shaded rows), where the other is our previous work. The proposed method extends our previous work and achieves improved performance in kidney localization and volume estimation. Our proposed method's first module uses an effective CNN-guided Mask-RCNN approach for efficient kidney localization in CT. The second module subsequently uses the localized kidney data in an FCN for segmentation free kidney volume estimation. Thus, the technical novelty of the proposed approach is four-fold:

- 1) we propose a novel CNN-based pipeline for kidney localization (Fig. 1). Although the underlying components of this pipeline are not novel, the way they are combined is what makes our method novel and effective,
- 2) we propose a new way to tackle a specific task in deep learning, i.e., area prediction without segmenting the kidney cross-section,
- 3) the design of the input-output relationship of the data in different parts of the proposed CNN pipeline is novel, and
- 4) for the first time, we derive a mathematical relation between two well established metrics in this field, the 'volume error' and 'Sørensen–Dice coefficient', to facilitate an approximate comparison between these two metrics.

CHAPTER 2

LITERATURE SURVEY

2.1 SUMMARY OF EXISTING ARTICLES

Title:

Cascaded Regression Neural Nets for Kidney Localization and Segmentation-free volume.

Author: Mohammad Arafat Hussain

Rafeef Garbi

Year: 2021

Research Works:

Kidney volume is an essential biomarker for a number of kidney disease diagnoses, for example, chronic kidney disease. Existing total kidney volume estimation methods often rely on an intermediate kidney segmentation step. On the other hand, automatic kidney localization in volumetric medical used in a combined sagittal-axial Mask-RCNN that detects the organ bounding boxes on the axial and sagittal slices, the combination of which produces a final 3D organ bounding box. Furthermore, we use a fully convolutional network to estimate the kidney volume that skips the segmentation procedure. We also present a mathematical expression to approximate the 'volume error' metric from the 'Sørensen-Dice coefficient.' We accessed 100 patients' CT scans from the Vancouver General Hospital records and obtained 210 patients' CT scans from the 2019 Kidney Tumor Segmentation Challenge database to validate our method. Our method produces a kidney boundary wall localization error of ~2.4mm and a mean volume estimation error of ~5%.

Title:

In Vivo Ultrasound Localization Microscopy Imaging of the Kidney's Microvasculature With Block-Matching 3-D Denoising

Author : Shuang Lei Ge

Year : 2022

Research Findings:

Structural abnormalities and functional changes of renal microvascular networks play a significant pathophysiologic role in the occurrence of kidney diseases. Super-

resolution ultrasound imaging has been successfully utilized to visualize the microvascular network and provide valuable diagnostic information. To prevent the burst of microbubbles, a lower mechanical index (MI) is generally used in ultrasound localization microscopy (ULM) imaging. However, high noise levels lead to incorrect signal localizations in relatively low MI settings and deep tissue. In this study, we implemented a block-matching 3-D (BM3D) image-denoising method, after the application of singular value decomposition filtering, to further suppress the noise at various depths. The in vitro flow-phantom results show that the BM3D method helps the significant reduction of the error localizations, thus improving the localization accuracy. In vivo rhesus macaque experiments help conclude that the BM3D method improves the resolution more than other image-based denoising techniques, such as the nonlocal means method. The obtained clutter-filtered images with fewer incorrect localizations can enable robust ULM imaging, thus helping in establishing an effective diagnostic tool.

Title:**Door Localization of Hand-Held OCT Probe Using Visual Odometry and Real-Time Segmentation Using Deep Learning**

Author : Qin Bohan Wang David Boegner Brandon Gaitan Yingning Zheng Xian Du Yu

Year : 2022

Research Findings:

Optical coherence tomography (OCT) is an established medical imaging modality that has found widespread use due to its ability to visualize tissue structures at a high resolution. Currently, OCT hand-held imaging probes lack positional information, making it difficult or even impossible to link a specific image to the location it was originally obtained. In this study, we propose a camera-based localization method to track and record the scanner position in real-time, as well as providing a deep learning-based segmentation method. **Methods:** We used camera-based visual odometry (VO) and simultaneous mapping and localization (SLAM) to compute and visualize the location of a hand-held OCT imaging probe. A deep convolutional neural network (CNN) was used for kidney tubule lumens segmentation. **Results:** The mean absolute error (MAE) and the standard

deviation (STD) for 1D translation were found to be 0.15 mm and 0.26mm respectively. For 2D translation, the MAE and STD were found to be 0.85 mm and 0.50 mm, respectively. The dice coefficient of the segmentation method was 0.7. The t- statistic of the T-test between predicted and actual average densities and predicted and actual average diameters were $7.7547\text{e-}13$ and $2.2288\text{e-}15$ respectively. We also experimented on a preserved kidney utilizing our localization method with automatic segmentation.

Comparisons of the average density maps and average diameter maps were made between the 3D comprehensive scan and VO system scan. Conclusion: Our results demonstrate that VO can track the probe location at high accuracy, and provides a user- friendly visualization tool to review OCT 2D images in 3D space. It also indicates that deep learning can provide high accuracy and high speed for segmentation. Significance: The proposed methods can be potentially used to predict delayed graft function (DGF) in kidney transplantation.

Title:

Crossbar-Net: A Novel Convolutional Neural Network for Kidney Tumor Segmentation in CT Images

Author:;Qian Yu,Yinghuan Shi,Jinquan Sun,Yang GaoJianbing ZhuYakang Dai

Year:2019

Research Findings:

Due to the unpredictable location, fuzzy texture, and diverse shape, accurate segmentation of the kidney tumor in CT images is an important yet challenging task. To this end, we, in this paper, present a cascaded trainable segmentation model termed as Crossbar-Net. Our method combines two novel schemes: 1) we originally proposed the crossbar patches, which consists of two orthogonal non-squared patches (i.e., the vertical patch and horizontal patch). The crossbar patches are able to capture both the global and local appearance information of the kidney tumors from both the vertical and horizontal directions simultaneously. 2) With the obtained crossbar patches, we iteratively train two sub-models (i.e., horizontal sub-model and vertical sub-model) in a cascaded training manner. During the training, the trained sub-models are encouraged to become more focused on the difficult parts of the tumor automatically (i.e., mis-segmented regions). Specifically, the vertical (horizontal) sub-model is required to help segment the mis-

segmented regions for the horizontal (vertical) sub-model. Thus, the two sub-models could complement each other to achieve the self-improvement until convergence. In the experiment, we evaluate our method on a real CT kidney tumor dataset which is collected from 94 different patients including 3500 CT slices. Compared with state-of-the-art segmentation methods, the results demonstrate the superior performance of our method on the Dice similarity coefficient, true positive fraction, centroid distance, and Hausdorff distance. Moreover, to exploit the generalization to other segmentation tasks, we also extend our Crossbar-Net to two related segmentation tasks: 1) cardiac segmentation in MR images and 2) breast mass segmentation in X-ray images, showing the promising results for these two tasks.

Title:

Multi-Parametric Fusion of 3D Power Doppler Ultrasound for Fetal Kidney Segmentation Using Fully Convolutional Neural Networks

Author: Nipuna H. Weerasinghe, Nigel H. Lovell, Alec W. Welsh, Gordon N. Stevenson,

Year: 2021

Research Findings:

Kidney development is key to the long-term health of the fetus. Renal volume and vascularity assessed by 3D ultrasound (3D-US) are known markers of wellbeing, however, a lack of real-time image segmentation solutions preclude these measures being used in a busy clinical environment. In this work, we aimed to automate kidney crossbar patches, which consists of two orthogonal non-squared patches (i.e., the vertical patch and horizontal patch). The crossbar patches are able to capture both the global and local appearance information of the kidney tumors from both the vertical and horizontal directions simultaneously. 2) With the obtained crossbar patches, we iteratively train two sub-models (i.e., horizontal sub-model and vertical sub-model) in a cascaded training manner. During the training, the trained sub-models are encouraged to become more focused on the difficult parts of the tumor automatically (i.e., mis-segmented regions). Specifically, the vertical (horizontal) sub-model is required to help segment the mis-segmented regions for the horizontal (vertical) sub-model. Thus, the two sub-models could complement each other to achieve the self-improvement until convergence. In the

experiment, we evaluate our method on a real CT kidney tumor dataset which is collected from 94 different patients including 3500 CT slices. Compared with state-of-the-art segmentation methods, the results demonstrate the superior performance of our method on the Dice similarity coefficient, true positive fraction, centroid distance, and Hausdorff distance. Moreover, to exploit the generalization to other segmentation tasks, we also extend our Crossbar-Net to two related segmentation tasks: 1) cardiac segmentation in MR images .

Title:**An Ensemble of U-Net Models for Kidney Tumor Segmentation With CT Images**

Author: Jason L. Causey, Jonathan Stubblefield, Jake A. Qualls, Jennifer Fowler, Lingrui Cai, Karl Walker, Yuanfang Guan, Xiuzhen Huang

Year:2022

Research Findings:

We present here the Arkansas AI-Campus solution method for the 2019 Kidney Tumor Segmentation Challenge (KiTS19). Our Arkansas AI-Campus team participated the KiTS19 Challenge for four months, from March to July of 2019. This paper provides a summary of our methods, training, testing and validation results for this grand challenge in biomedical imaging analysis. Our deep learning model is an ensemble of U- Net models developed after testing many model variations. Our model has consistent performance on the local test dataset and the final competition independent test dataset. The model achieved local test Dice scores of 0.949 for kidney and tumor segmentation and 0.601 for tumor segmentation, and the final competition test earned Dice scores 0.9470 and 0.6099 respectively. The Arkansas AI-Campus team solution with a composite DICE score of 0.7784 has achieved a final ranking of top fifty worldwide, and top five among the United States teams in the KiTS19 Competition.

Title:**Generative Adversarial Networks for Facilitating Stain-Independent Supervised**

and Unsupervised Segmentation: A Study on Kidney Histology

Author: Michael Gadermayr, Laxmi Gupta, Vitus Appel, Peter Boor, Barbara M. Klinkhammer, Dorit Merhof

Year:2019

Research Findings:

A major challenge in the field of segmentation in digital pathology is given by the high effort for manual data annotations in combination with many sources introducing variability in the image domain. This requires methods that are able to cope with variability without requiring to annotate a large amount of samples for each characteristic. In this paper, we develop approaches based on adversarial models for image-to-image translation relying on unpaired training. Specifically, we propose approaches for stain-independent supervised segmentation relying on image-to-image translation for obtaining an intermediate representation.

Furthermore, we develop a fully-unsupervised segmentation approach exploiting image-to-image translation to convert from the image to the label domain. Finally, both approaches are combined to obtain optimum performance in unsupervised segmentation independent of the characteristics of the underlying stain. Experiments on patches showing kidney histology proof that stain-translation can be performed highly effectively and can be used for domain adaptation to obtain independence of the underlying stain. It is even capable of facilitating the underlying segmentation task, thereby boosting the accuracy if an appropriate intermediate stain is selected. Combining domain adaptation with unsupervised segmentation finally showed the most significant improvements.

Title:

Kidney Detection in 3-D Ultrasound Imagery via Shape-to-Volume Registration Based on Spatially Aligned Neural Network

Author:

Mahdi Marsousi Konstantinos N.

Plataniotis Stergios Stergiopoulos

Year:2019

Research Findings:

This paper introduces a computer-aided kidney shape detection method suitable for volumetric (3D) ultrasound images. Using shape and texture priors, the proposed method automates the process of kidney detection, which is a problem of great importance in computer-assisted trauma diagnosis. This paper introduces a new complex-valued implicit shape model, which represents the multiregional structure of the kidney shape. A spatially aligned neural network classifiers with complex-valued output is designed to classify voxels into background and multiregional structure of the kidney shape. The complex values of the shape model and classification outputs are selected and incorporated in a new similarity metric, such as the shape-to-volume registration process only fits the shape model on the actual kidney shape in input ultrasound volumes.

OBJECTIVE

To develop a robust kidney disease detection system using cascaded approach

SCOPE OF THE PROJECT

Biomarkers: Biomarkers are substances or indicators in the body that can signal the presence of a disease. Researchers are working on identifying new and more accurate biomarkers for kidney disease that can be detected through blood or urine tests.

Artificial intelligence (AI): and machine learning: AI and machine learning technologies have the potential to analyze large amounts of medical data to identify patterns and risk factors for kidney disease. This could lead to earlier detection and more personalized treatment plans.

Wearable devices: Wearable devices such as smartwatches and fitness trackers can monitor various health parameters, including kidney function. In the future, these devices could potentially detect early signs of kidney disease and alert individuals to seek medical

attention.

Telemedicine: Telemedicine allows healthcare providers to remotely monitor and communicate with patients. This technology can be particularly beneficial for individuals with kidney disease who require frequent check-ups and monitoring

CHAPTER 3

SYSTEM ANALYSIS

3.1 EXISTING SYSTEM

Kidney is an important organ of the body supports other functionality of the body organs. Volumetric analysis need accurate estimation of the region extracted. Occlusion of image, low resolution impact the measurement to fall below the threshold. Accurate and fast, automated estimation of kidney volumetric analysis need to be implemented using lightweight architecture is demandable. The problem of intensity based evaluations and its drawbacks are estimated here.

3.1.1 DISADVANTAGES

- Design

3.2 PROPOSED SYSTEM

In the proposed system, the volumetric analysis of the Kidney with various clinical procedures such as immediate diagnosis, slow monitoring, and treatment the kidney diseases with regular functionality and treatment procedures appropriate to the kidney volume are discussed. Timely basis, chronic kidney diseases impact human life. It is required to monitor the health of the Kidneys all the time. Kidney diseases, including chronic kidney disease, kidney failure, and kidney stones, every Diagnostic step for across the world metric analysis of Kidney. The presented system in which Cyclic Bayesian neural network (CBNN) enabled volume analysis is made. Volume analysis is made after the extraction of complete kidney region. The statistical parameters measured for classification.

3.2.1 ADVANTAGES

- Cyclic Bayesian model is developed
- The overall performance of the system is improved

CHAPTER 4

SYSTEM REQUIREMENTS

4.1 HARDWARE REQUIREMENTS

For Windows

Operating System: Windows 10, 8.1, 7 Service Pack 1

Processor: Minimum Intel or AMD x86-64 processor with four logical cores and AVX2 instruction set support

RAM: 8 GB

HDD: 2 GB of HDD space for MATLAB only, 4-6 GB for a typical installation

Graphics: No specific graphics card is required. Hardware accelerated graphics card supporting OpenGL 3.3 with 1GB GPU memory is recommended for optimal performance with certain features.

4.2 SOFTWARE REQUIREMENTS

MATLAB 2017a

Toolbox utilized

- IMAGE PROCESSING
- STATISTICS AND NEURAL NETWORKS
- SIGNAL PROCESSING

CHAPTER 5

FEASIBILITY STUDY

5.1 FEASIBILITY STUDY

The feasibility of the project is analyzed in this phase and business proposal is put forth with a very general plan for the project and some cost estimates. During system analysis the feasibility study of the proposed system is to be carried out. This is to ensure that the proposed system is not a burden to the company. For feasibility analysis, some understanding of the major requirements for the system is essential. Three key considerations involved in the feasibility analysis are:

1. **ECONOMICAL FEASIBILITY**
2. **TECHNICAL FEASIBILITY**
3. **SOCIAL FEASIBILITY**

Economical Feasibility:

This study is carried out to check the economic impact that the system will have on the organization. The amount of fund that the company can pour into the research and development of the system is limited. The expenditures must be justified. Thus the developed system as well within the budget and this was achieved because most of the technologies used are freely available. Only the customized products had to be purchased.

Technical Feasibility:

This study is carried out to check the technical feasibility, that is, the technical requirements of the system. Any system developed must not have a high demand on the available technical resources. This will lead to high demands on the available technical resources. This will lead to high demands being placed on the client. The developed system must have a modest requirement, as only minimal or null changes are required for implementing this system.

Social Feasibility:

The aspect of study is to check the level of acceptance of the system by the user. This includes the process of training the user to use the system efficiently. The user must not feel threatened by the system, instead must accept it as a necessity. The level of acceptance by the users solely depends on the methods that are employed to educate the user about the

system and to make him familiar with it. His level of confidence must be raised so that he is also able to make some constructive criticism, which is welcomed, as he is the final user of the system.

CHAPTER 6

SYSTEM DESIGN

6.1 DATAFLOW OR BLOCK DIAGRAM

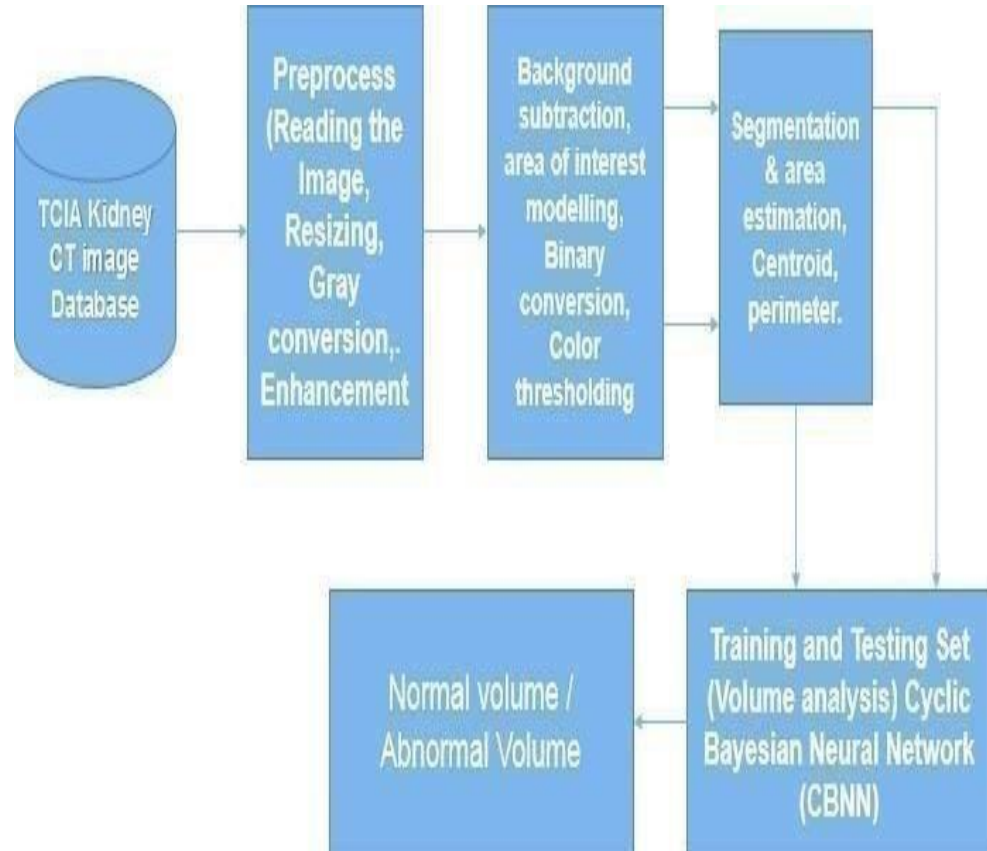


Fig 4:System Architecture

Figure 4 shows the system architecture of proposed kidney volume analysis module using cyclic Bayesian neural network (CBNN). The system architecture of proposed cascaded kidney volumetric analysis.

6.2 DESCRIPTION OF THE FLOW

The volumetric analysis of the Kidney with various clinical procedures such as immediate diagnosis, slow monitoring, and treatment the kidney diseases with regular functionality and treatment procedures appropriate to the kidney volume are discussed. Timely basis, chronic kidney diseases impact human life.

It is required to monitor the health of the Kidneys all the time. Kidney diseases, including chronic kidney disease, kidney failure, and kidney stones, every Diagnostic step for across the world metric analysis of Kidney.

The presented system in which Cyclic Bayesian neural network (CBNN) enabled volume analysis is made.

Volume analysis is made after the extraction of complete kidney region.

The statistical parameters measured for classification are area, centroid, perimeter etc.

CHAPTER 7

PROJECT IMPLEMENTATION

7.1 SOFTWARE TOOL

MATLAB:

MATLAB is a technical computing environment for high-performance numeric computation and visualization. MATLAB integrates numerical analysis, matrix computation, signal processing (via the Signal Processing Toolbox), and graphics into an easy-to-use environment where problems and solutions are expressed just as they are written mathematically, without much traditional programming. The name MATLAB stands for matrix laboratory.

We will use MATLAB in ECE 360 in order to illustrate the concepts of digital signal processing with numerical examples. Each homework assignment will include some optional problems that require Matlab solutions. You will quickly realize that Matlab can often be used to check solutions to other problems as well. This is perfectly legitimate, but you still must turn in your analytical solutions for the pencil-and-paper problems.

MATLAB is available in DECS labs on a UNIX, PC, and MAC platform. You can invoke MATLAB by double-clicking on the MATLAB-Icon (MAC,PC) or by typing matlab on the Unix command line. You will then get access to the MATLAB command line, denoted by ">>".

This document is by no means a complete reference. There are tutorial and reference manuals for Matlab at the library.

The data element is considered as an array in a MATLAB interactive system that does not need dimensioning. It solves many issues regarding technical and computations especially the ones which include vector and matrix expressions, by using languages like C or Fortran you can write this program in no time.

Matrix laboratory is supported by MATLAB and it was created for giving a user-friendly access to matrix software written by LINPACK and EISPAKC projects, that together gives the state-of-the-art in matrix computation software.

There has been a periodic evolution of MATLAB over the years and engineering it is the general instruction tool used in a university environment. For development, analysis,

research, and higher productivity MATLAB is the apt choice used by the industry.

A group of application-specific solutions namely tool boxes is the main feature of MATLAB. It permits you for learning and applying specialized technology. There are vast collections of MATLAB functions in Toolboxes that enhances the ambiance of MATLAB to solve problems of a particular class. Signal processing, neural networks, wavelets, simulation, fuzzy logic, control systems and much more are the areas where tool boxes are available.

The MATLAB System

It comprises of five main parts:

The MATLAB language:

It is an array or matrix language at a higher level with control flow statements, functions, input/output, data structures, object-oriented programming features, etc. It permits both small programming for creating fast and junk throw-away programs, and big programming for creating difficult and big application programs.

The MATLAB ambiance:

It has a set of tools offering lots of provisions that perform with as the MATLAB user or programmer. It provides help for variable management in your workspace and data transfer. Developing, managing, debugging, and profiling M-files can be done using the tools of MATLAB.

Graphics management:

Offering higher level commands for two dimensional and three-dimensional data visualization, animation, image processing, and presentation graphics are included in the Graphics management. Low-level commands for allowing full customization view of graphics for building Graphical User Interfaces on your MATLAB applications.

Mathematical library function of MATLAB:

There are various basic operations like sum, cosine, sine, and complex operations collection of computational algorithms for more sophisticated functions like matrix eigenvalues, inverse, fast Fourier transforms, and Bessel functions.

The MATLAB Application Program Interface (API):

C and Fortran programs for interacting with MATLAB is permitted by the library. There are other facilities included for calling routines from MATLAB (dynamic linking), calling MATLAB as a computational engine, MAT-files with reading and writing facility.

Applications of MATLAB:

- Algorithm development.
- Scientific and engineering graphics.
- Modeling, simulation, and prototyping.
- Application development, including Graphical User Interface building.
- Math and computation.
- Data analysis, exploration, and visualization.

7.2 PROGRAMMING

MATLAB is a programming language and environment that is widely used in engineering, science, and mathematics. Here are some basics of MATLAB programming

Basic Syntax:

MATLAB commands are written in a command window or script file. The basic syntax of MATLAB is similar to other programming languages such as C, C++, and Java. MATLAB statements are executed line by line, and a semicolon is used to suppress output to the command window.

Variables:

In MATLAB, variables are created by assigning a value to a name. Variable names are case sensitive and can be any combination of letters, digits, and underscores. To assign a value to a variable, use the equal sign (=) operator.

Conflicts with Function Names:

Avoid creating variables with the same name as a function (such as `i`, `j`, `mode`, `char`, `size`, and `path`). In general, variable names take precedence over function names. If you create a variable that uses the name of a function, you sometimes get unexpected results.

```
exist checkname  
  
ans =  
0
```

Syntax

```
tf = iskeyword(txt)
iskeyword
```

Check whether a proposed name is already in use with the `exist` or `which` function. `exist` returns 0 if there are no existing variables, functions, or other artifacts with the proposed name. For example:

Arrays:

MATLAB supports arrays, which can be one-dimensional, two-dimensional, or multidimensional. Arrays can be created by using square brackets and separating the elements with commas or semicolons. MATLAB also supports matrix operations, which makes it easy to perform mathematical computations.

```
a = [1 2 3 4]
```

```
a = 1×4
```

```
1      2      3      4
```

Functions:

MATLAB has a large number of built-in functions for mathematical computations, data analysis, and visualization. In addition, users can create their own functions in MATLAB using the `function` keyword. Functions are written in separate files with a `.m` extension and can be called from other MATLAB scripts or functions.

```
function [y1,...,yN] = myfun(x1,...,xM)
```

`function [y1,...,yN] = myfun(x1,...,xM)` declares a function named `myfun` that accepts inputs `x1,...,xM` and returns outputs `y1,...,yN`. This declaration statement must be the first executable line of the function. Valid function names begin with an alphabetic character, and can contain letters, numbers, or underscores.

You can save your function in a function file which contains only function definitions. The name of the file must match the name of the first function in the file.

In a script file which contains commands and function definitions. Functions must be at the end of the file. Script files cannot have the same name as a function in the file. Functions are supported in scripts in R2016b.

Control Flow:

MATLAB provides control flow statements such as if-else, for, while, and switch-case for making decisions and performing iterative tasks.

Plotting:

MATLAB has powerful plotting capabilities that allow users to create 2D and 3D plots, histograms, scatter plots, and more. The plot function is used to create plots, and there are many options available to customize the appearance of the plot.

Debugging:

MATLAB provides several tools for debugging code, such as setting breakpoints, stepping through code, and displaying variables. MATLAB also has a built-in profiler that can be used to identify performance bottlenecks in code.

There are several ways to debug your code:

- Display output by removing semicolons.
- Run the code to a specific line and pause by clicking the Run to Here button.
- Step into functions and scripts while paused by clicking the Step In button.
- Add breakpoints to your file to enable pausing at specific lines when you run your code.
- Before you begin debugging, to avoid unexpected results, save your code files and make sure that the code files and any files they call exist on the search path or in the current folder.

MATLAB handles unsaved changes differently depending on where you are debugging from:

Editor — If a file contains unsaved changes, MATLAB saves the file before running it.

Live Editor — MATLAB runs all changes in a file, whether they are saved or not.

Command Window — If a file contains unsaved changes, MATLAB runs the saved version of the file. You do not see the results of your changes.

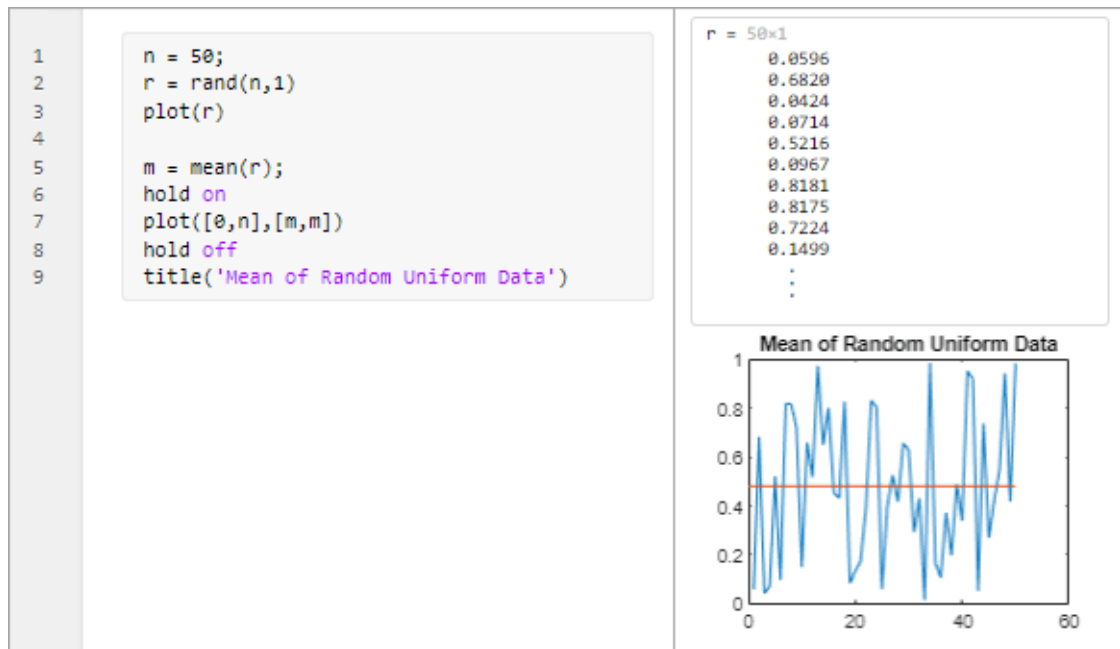
Display Output:

- One way to determine where a problem occurs in your MATLAB code file is to display the output.
- To display the output for a line, remove the semicolon from the end of that line. In the Editor, MATLAB displays the output in the Command Window. In the Live Editor, MATLAB displays the output with the line of code that creates it.
- For example, suppose that you have a script called plotRand.m that plots a vector of random data and draws a horizontal line on the plot at the mean.

```
n = 50;  
r = rand(n,1);  
plot(r)  
  
m = mean(r);  
hold on  
plot([0,n],[m,m])  
hold off  
title('Mean of Random Uniform Data')
```



```
Command Window  
  
>> plotRand  
  
r =  
  
    0.9631  
    0.5468  
    0.5211  
    0.2316  
    0.4889  
    0.6241  
    0.6791
```

- These are just some of the basics of MATLAB programming. With these tools, users can create powerful programs for data analysis, signal processing, and control systems, among other applications.

7.3 SOURCE CODE

7.3.1 Analyze

```

function [TP,TN,FP,FN,y]=analyze(inpp,targ)
fprintf('Input\n');
size(inpp)
pause(2);
fprintf('Tr Class\n');
size(targ)
pause(2);
% Deep Bayesian Network
trainFcn = 'trainbr';
hiddenLayerSize = 10;
net = patternnet(hiddenLayerSize, trainFcn);
% Choose Input and Output Pre/Post-Processing Functions
% For a list of all processing functions type: help nnprocess
net.input.processFcns = {'removeconstantrows','mapminmax'};
net.output.processFcns = {'removeconstantrows','mapminmax'};
% Setup Division of Data for Training, Validation, Testing
% For a list of all data division functions type: help nndivide
net.divideFcn = 'dividerand'; % Divide data randomly
net.divideMode = 'sample'; % Divide up every sample
net.divideParam.trainRatio = 85/100;
        
```

```
net.divideParam.valRatio = 10/100;
net.divideParam.testRatio = 5/100;
% Choose a Performance Function
% For a list of all performance functions type: help nnperformance
net.performFcn = 'crossentropy'; % Cross-Entropy
% Choose Plot Functions
% For a list of all plot functions type: help nnplot
net.plotFcns = {'plotperform','plottrainstate','ploterrhist', ...
    'plotconfusion', 'plotroc'};
x=inpp;
t=targ;
% Train the Network
[net,tr] = train(net,x,t);
% Test the Network
y = net(x);
e = gsubtract(t,y);
performance = perform(net,t,y)
tind = vec2ind(t);
yind = vec2ind(y);
percentErrors = sum(tind ~= yind)/numel(tind);
% Recalculate Training, Validation and Test Performance
trainTargets = t .* tr.trainMask{1};
valTargets = t .* tr.valMask{1};
testTargets = t .* tr.testMask{1};
trainPerformance = perform(net,trainTargets,y)
valPerformance = perform(net,valTargets,y)
testPerformance = perform(net,testTargets,y)
% View the Network
view(net)
% Plots
% Uncomment these lines to enable various plots.
%figure, plotperform(tr)
%figure, plottrainstate(tr)
%figure, ploterrhist(e)
%figure, plotconfusion(t,y)
%figure, plotroc(t,y)

if (false)
    genFunction(net,'myNeuralNetworkFunction');
    y = myNeuralNetworkFunction(x);
end
if (false)
    genFunction(net,'myNeuralNetworkFunction','MatrixOnly','yes');
    y = myNeuralNetworkFunction(x);
end
```

```

if (false)
    gensim(net);
end
FN=0;
FP=0;
TN=0;
TP=0;
[c,cm,ind,per] = confusion((t),(y));
[rk ck]=size(per);
for i=1:rk
    % for j=1:ck
    % FN=per(1,1);% false negative rate = (false negatives)/(all output negatives)
    % FP=per(1,2);% false positive rate = (false positives)/(all output positives)
    % TP=per(1,3);% true positive rate = (true positives)/(all output positives)
    % TN=per(1,4);% true negative rate = (true negatives)/(all output negatives)
    % %
    % FNa=per(2,1);% false negative rate = (false negatives)/(all output negatives)
    % FPa=per(2,2);% false positive rate = (false positives)/(all output positives)
    % TPa=per(2,3);% true positive rate = (true positives)/(all output positives)
    % TNa=per(2,4);% true negative rate = (true negatives)/(all output negatives)
    FN=FN+per(i,1);
    FP=FP+per(i,2);
    TP=TP+per(i,3);
    TN=TN+per(i,4);
    % end
end
fprintf('Error Check \n');
et=max(percentErrors)
pause(5);
end

```

7.3.2 : Cascaded regression analysis

```
function [TP,TN,FP,FN,cas_cc]=Cascaded_bayesian_analysis(inpp,targ,trr)
```

```

fprintf('Input\n');
size(inpp)
pause(2);
fprintf('Tr Class\n');
size(targ)
pause(2);
% Deep Bayesian Network
trainFcn = 'trainscg';

hiddenLayerSize = 10;
net = patternnet(hiddenLayerSize, trainFcn);

```

```
% Choose Input and Output Pre/Post-Processing Functions
% For a list of all processing functions type: help nnprocess
net.input.processFcns = {'removeconstantrows','mapminmax'};
net.output.processFcns = {'removeconstantrows','mapminmax'};

% Setup Division of Data for Training, Validation, Testing
% For a list of all data division functions type: help nndivide
net.divideFcn = 'dividerand'; % Divide data randomly
net.divideMode = 'sample'; % Divide up every sample
net.divideParam.trainRatio = 85/100;
net.divideParam.valRatio = 10/100;
net.divideParam.testRatio = 5/100;

% Choose a Performance Function
% For a list of all performance functions type: help nnperformance
net.performFcn = 'crossentropy'; % Cross-Entropy

% Choose Plot Functions
% For a list of all plot functions type: help nnplot
net.plotFcns = {'plotperform','plottrainstate','ploterrhist', ...
    'plotconfusion','plotroc'};
x=inpp;
t=targ;
% Train the Network
[net,tr] = train(net,x,t);

% Test the Network
y = net(x);
e = gsubtract(t,y);
performance = perform(net,t,y)
tind = vec2ind(t);
yind = vec2ind(y);
percentErrors = sum(tind ~= yind)/numel(tind);

% Recalculate Training, Validation and Test Performance
trainTargets = t .* tr.trainMask{1};
valTargets = t .* tr.valMask{1};
testTargets = t .* tr.testMask{1};
trainPerformance = perform(net,trainTargets,y)
valPerformance = perform(net,valTargets,y)
testPerformance = perform(net,testTargets,y)

% View the Network
view(net)
```

```
% Plots
% Uncomment these lines to enable various plots.
%figure, plotperform(tr)
%figure, plottrainstate(tr)
%figure, ploterrhist(e)
%figure, plotconfusion(t,y)
%figure, plotroc(t,y)

if (false)
    genFunction(net,'myNeuralNetworkFunction');
    y = myNeuralNetworkFunction(x);
end
if (false)
    genFunction(net,'myNeuralNetworkFunction','MatrixOnly','yes');
    y = myNeuralNetworkFunction(x);
end
if (false)
    gensim(net);
end

FN=0;
FP=0;
TN=0;
TP=0;
[c,cm,ind,per] = confusion((t),(y));

[rk ck]=size(per);
for i=1:rk
    for j=1:ck
        % FN=per(1,1);% false negative rate = (false negatives)/(all output negatives)
        % FP=per(1,2);% false positive rate = (false positives)/(all output positives)
        % TP=per(1,3);% true positive rate = (true positives)/(all output positives)
        % TN=per(1,4);% true negative rate = (true negatives)/(all output negatives)
        % %
        % FNa=per(2,1);% false negative rate = (false negatives)/(all output negatives)
        % FPa=per(2,2);% false positive rate = (false positives)/(all output positives)
        % TPa=per(2,3);% true positive rate = (true positives)/(all output positives)
        % TNa=per(2,4);% true negative rate = (true negatives)/(all output negatives)

FN=FN+per(i,1);
FP=FP+per(i,2);
TP=TP+per(i,3);
TN=TN+per(i,4);
    end
```

```
end
cas_cons1=sum(sum(trr));
cas_cons2=sum(sum(y));
cas_cc=floor(cas_cons1-cas_cons2);

fprintf('Error Check \n');
et=max(percentErrors)
pause(5);
end
clc
clear all
close all
warning off
[filename, pathname]=uigetfile('*.jpg');
[tr_metric]=training_kidneydb('C:\Users\sunil\OneDrive\Desktop\Final project\code\tr\');
filename=strcat(pathname,filename);
for kk=1:3
    fprintf("Testing ..... \n");
end
a=imread(filename);
imshow(a);
title('Input Test image');
ksize=size(a);
if numel(ksize)>2
b=rgb2gray(a);
figure;
imshow(b);
title('Gray scale image');
else
b=a;
end
impixelinfo;
c=b>20;
figure;
imshow(c);
title('Gray scale image');

% MORPHOLOGY command imfill
d=imfill(c,'holes');
figure;
imshow(d);
title('Morphology closed layer');

e=bwareaopen(d,1000);
figure;
```

```
imshow(e);
title('Morphology open layer');

PreprocessedImage=uint8(double(a).*repmat(e,[1 1 3]));
figure;
imshow(PreprocessedImage);
title('filtered image');

PreprocessedImage=imadjust(PreprocessedImage,[0.3 0.7],[])+50;
figure;
imshow(PreprocessedImage);
title('Image enhanecment');

uo=rgb2gray(PreprocessedImage);
figure;
imshow(uo);
title('Enhanced gray image');

mo=medfilt2(uo,[5 5]);
figure;
imshow(mo);
title('Median filter applied');
% *****
po=mo>250;
figure;
imshow(po);
title('Segmented region');
% close all;
% filename
test_metric=sum(sum(po));
for ii=1:1000
    inp(ii)=tr_metric(randi(numel(tr_metric)));
    if ii>150
        inp(ii)=test_metric;
    end
    tr1(ii)=tr_metric(randi(numel(tr_metric)));
    tr2(ii)=tr_metric(randi(numel(tr_metric)));
end

inpp=inp;
targ=[tr1;tr2];
[TP,TN,FP,FN,trk]=analyze(inpp,targ);
[TP2,TN2,FP2,FN2,cconst]=Cascaded_bayesian_analysis(inpp,targ,trk);
[PREC,REC,F1SCO,SPEC]=performance_measure_routine(TP2,TN2,FP2,FN2);
stamp=2;
```

```
if cconst < 100
for jj=1:30
    if tr_metric(jj)==test_metric
if test_metric<13000
    stamp=1;
end
    end
end
label=[{'Normal'},{'Abnormal'}];
msgbox(label(stamp))
msgbox(['Precision =' num2str((PREC)*100) '%'])
end
```


CHAPTER 8

IMPLEMENTATION

Module description with algorithm / Pseudo code

The gradual loss of kidney function is one of the main problems in the human body, which provides warnings that major kidney failure occurs in the early stages. The filtration of waste components from the blood is developed by the kidney organ that needs excessive Fluids. The body must accumulate dangerous waste stages and send them out with the help of the kidney to do lots of work compared with other body organs. Kidney health detection is essential. Learning provides kidney volume analysis to improve analysis before any surgical implantation. The proposed system considers the existing partial.

8.1 Cyclic Bayesian Neural Network

Neural network architecture is one of the neural network implementations utilized for conventional neural network techniques to estimate parameters utilized for kidney segmentation. The computationally difficult integrals arise during the reason steps are expressed in the following Idea. Moreover, the conventional neural Network treats the weights and biases connecting the network layers. In base in the Network, the weight and buyers are treated as random distribution functions and post area distribution for the uterus. It is observed that the dates are updated continuously in the base of the oral Network comparing the conventional neural Network. Various benefits of the base in the oral Network are present below.

Layer configurations

- The CBNN contains input layer, hidden layer (configurable), output layer etc.
- The performance measure is obtained using Cross-entropy method.
- The feature vectors are distributed using probabilistic distribution function.

Uncertainty estimation in predictions makes many differences in the conclusion of chronic kidney disease; hence, a neural network helps make accurate predictions. Robust network is essential to make the fitting properly during the training and testing process. The flexibility obtained from a Bayesian neural Network is required to structure the unstructured form of kidney images and make the classification accuracy better. Networks are computationally expensive. The training and testing process takes lesson time comparing the conventional Network, and the classification process is highly accurate compared with other neural networks.

8.2 PROPOSED TECHNIQUES

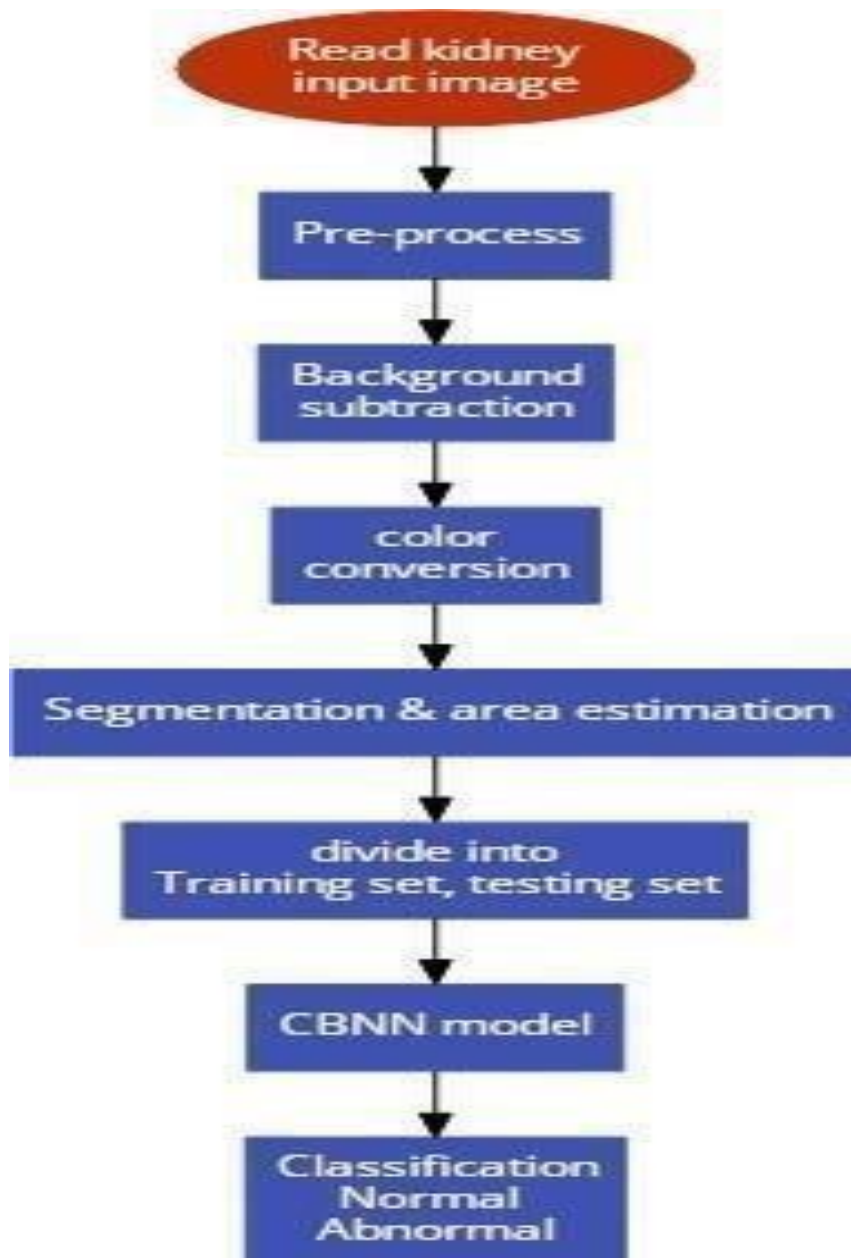


FIG-5:Data Flow

CHAPTER 9

TESTING

9.1 CODING STANDARDS

Coding standards are guidelines to programming that focuses on the physical structure and appearance of the program. They make the code easier to read, understand and maintain. This phase of the system actually implements the blueprint developed during the design phase. The coding specification should be in such a way that any programmer must be able to understand the code and can bring about changes whenever felt necessary. Some of the standard needed to achieve the above-mentioned objectives are as follows:

- Program should be simple, clear and easy to understand.
- Naming conventions.
- Value conventions.
- Script and comment procedure.
- Message box format.
- Exception and error handling

9.2 NAMING CONVENTIONS

Naming conventions of classes, data member, member functions, procedures etc., should be self-descriptive. One should even get the meaning and scope of the variable by its name. The conventions are adopted for easy understanding of the intended message by the user. So, it is customary to follow the conventions. These conventions are as follows:

Class names:

Class names are problem domain equivalence and begin with capital letter and have mixed cases.

Member Function and Data Member name:

Member function and data member name begins with a lowercase letter with each subsequent letters of the new words in uppercase and the rest of letters in lowercase.

Value Conventions:

Value conventions ensure values for variable at any point of time. This involves the following:

- Proper default values for the variables.
- Proper validation of values in the field.

- Proper documentation of flag values.

Script Writing and Commenting Standard:

Script writing is an art in which indentation is utmost important. Conditional and looping statements are to be properly aligned to facilitate easy understanding. Comments are included to minimize the number of surprises that could occur when going through the code.

Message Box Format:

When something has to be prompted to the user, he must be able to understand it properly. To achieve this, a specific format has been adopted in displaying messages to the user. They are as follows:

- X – User has performed illegal operation.
- ! – Information to the user.

TEST PROCEDURE:**System Testing:**

Testing is performed to identify errors. It is used for quality assurance. Testing is an integral part of the entire development and maintenance process. The goal of the testing during phase is to verify that the specification has been accurately and completely incorporated into the design, as well as to ensure the correctness of the design itself. For example, the design must not have any logic faults in the design is detected before coding commences, otherwise the cost of fixing the faults will be considerably higher as reflected. Detection of design faults can be achieved by means of inspection as well as walkthrough.

Testing is one of the important steps in the software development phase. Testing checks for the errors, as a whole of the project testing involves the following test cases:

- Static analysis is used to investigate the structural properties of the Source code.
- Dynamic testing is used to investigate the behavior of the source code by executing the program on the test data.

TEST DATA AND OUPUT:**1. Unit Testing:**

Unit testing is conducted to verify the functional performance of each modular component of the software. Unit testing focuses on the smallest unit of the software design (i.e.), the module. The white-box testing techniques were heavily employed for unit testing.

2. Functional Test:

Functional test cases involved exercising the code with nominal input values for which the expected results are known, as well as boundary values and special values, such as logically related inputs, files of identical elements, and empty files.

Three types of tests in Functional test:

- Performance Test
- Stress Test
- Structure Test

Performance Test:

It determines the amount of execution time spent in various parts of the unit, program throughput, and response time and device utilization by the program unit.

Stress Test:

Stress Test is those test designed to intentionally break the unit. A Great deal can be learned about the strength and limitations of a program by examining the manner in which a programmer in which a program unit breaks.

Structured Test

Structure Tests are concerned with exercising the internal logic of a program and traversing particular execution paths. The way in which White-Box test strategy was employed to ensure that the test cases could Guarantee that all independent paths within a module have been have been exercised at least once.

- Exercise all logical decisions on their true or false sides.
- Execute all loops at their boundaries and within their operational bounds.
- Exercise internal data structures to assure their validity.
- Checking attributes for their correctness.
- Handling end of file condition, I/O errors, buffer problems and textual errors in output information

3. Integration Testing:

Integration testing is a systematic technique for construction the program structure while at the same time conducting tests to uncover errors associated with interfacing. i.e., integration testing is the complete testing of the set of modules which makes up the product. The objective is to take untested modules and build a program structure tester

should identify critical modules. Critical modules should be tested as early as possible. One approach is to wait until all the units have passed testing, and then combine them and then tested. This approach is evolved from unstructured testing of small programs. Another strategy is to construct the product in increments of tested units. A small set of modules are integrated together and tested, to which another module is added and tested in combination. And so on. The advantages of this approach are that, interface dispenses can be easily found and corrected.

The major error that was faced during the project is linking error. When all the modules are combined the link is not set properly with all support files. Then we checked out for interconnection and the links. Errors are localized to the new module and its intercommunications. The product development can be staged, and modules integrated in as they complete unit testing. Testing is completed when the last module is integrated and tested.

TESTING

Testing is a process of executing a program with the intent of finding an error. A good test case is one that has a high probability of finding an as-yet –undiscovered error. A successful test is one that uncovers an as-yet- undiscovered error. System testing is the stage of implementation, which is aimed at ensuring that the system works accurately and efficiently as expected before live operation commences. It verifies that the whole set of programs hang together. System testing requires a test consists of several key activities and steps for run program, string, system and is important in adopting a successful new system. This is the last chance to detect and correct errors before the system is installed for user acceptance testing.

The software testing process commences once the program is created and the documentation and related data structures are designed. Software testing is essential for correcting errors. Otherwise the program or the project is not said to be complete. Software testing is the critical element of software quality assurance and represents the ultimate the review of specification design and coding. Testing is the process of executing the program with the intent of finding the error. A good test case design is one that as a probability of finding an yet undiscovered error. A successful test is one that uncovers an yet undiscovered error. Any engineering product can be tested in one of the two ways:

1. White Box Testing:

This testing is also called as Glass box testing. In this testing, by knowing the specific functions that a product has been design to perform test can be conducted that demonstrate each function is fully operational at the same time searching for errors in each function. It is a test case design method that uses the control structure of the procedural design to derive test cases. Basis path testing is a white box testing.

Basis path testing:

- Flow graph notation
- Cyclometric complexity
- Deriving test cases
- Graph matrices Control.

2. Black Box Testing:

In this testing by knowing the internal operation of a product, test can be conducted to ensure that “all gears mesh”, that is the internal operation performs according to specification and all internal components have been adequately exercised. It fundamentally focuses on the functional requirements of the software.

The steps involved in black box test case design are:

- Graph based testing methods
- Equivalence partitioning
- Boundary value analysis
- Comparison testing

3. Software Testing Strategies:

A software testing strategy provides a road map for the software developer. Testing is a set activity that can be planned in advance and conducted systematically. For this reason a template for software testing a set of steps into which we can place specific test case design methods should be strategy should have the following characteristics:

- Testing begins at the module level and works “outward” toward the integration of the entire computer based system.
- Different testing techniques are appropriate at different points in time.
- The developer of the software and an independent test group conducts testing.

- Testing and Debugging are different activities but debugging must be accommodated in any testing strategy.

4. Integration Testing:

Integration testing is a systematic technique for constructing the program structure while at the same time conducting tests to uncover errors associated with. Individual modules, which are highly prone to interface errors, should not be assumed to work instantly when we put them together. The problem of course, is “putting them together”- interfacing. There may be the chances of data lost across on another’s sub functions, when combined may not produce the desired major function. Individually, acceptable impression may be magnified to unacceptable levels, global data structures can present problems.

5. Program Testing:

The logical and syntax errors have been pointed out by program testing. A syntax error is an error in a program statement that in violates one or more rules of the language in which it is written. An improperly defined field dimension or omitted keywords are common syntax error. These errors are shown through error messages generated by the computer. A logic error on the other hand deals with the incorrect data fields, out-off-range items and invalid combinations. Since the compiler s will not deduct logical error, the programmer must examine the output. Condition testing exercises the logical conditions contained in a module. The possible types of elements in a condition include a Boolean operator, Boolean variable, a pair of Boolean parentheses A relational operator or on arithmetic expression. Condition testing method focuses on testing each condition in the program the purpose of condition test is to deduct not only errors in the condition of a program but also other errors in the program.

6. Security Testing:

Security testing attempts to verify the protection mechanisms built in to a system well, in fact, protect it from improper penetration. The system security must be tested for invulnerability from frontal attack must also be tested for invulnerability from rear attack. During security, the tester places the role of individual who desires to penetrate system.

7. Validation Testing:

At the culmination of integration testing, software is completely assembled as a package. Interfacing errors have been uncovered and corrected and a final series of software test-validation testing begins. Validation testing can be defined in many ways, but a simple definition is that validation succeeds when the software functions in manner that is reasonably expected by the customer. Software validation is achieved through a series of black box tests that demonstrate conformity with requirement. After validation test has been conducted, one of two conditions exists.

- The function or performance characteristics confirm to specifications and are accepted.
- A validation from specification is uncovered and a deficiency created.

Deviation or errors discovered at this step in this project is corrected prior to completion of the project with the help of the user by negotiating to establish a method for resolving deficiencies. Thus, the proposed system under consideration has been tested by using validation testing and found to be working satisfactorily. Though there were deficiencies in the system they were not catastrophic.

7. User Acceptance Testing:

User acceptance of the system is key factor for the success of any system. The system under consideration is tested for user acceptance by constantly keeping in touch with prospective system and user at the time of developing and making changes whenever required. This is done in regarding to the following points.

- Input screen design.
- Output screen design.

SOFTWARE TESTING**General:**

The purpose of testing is to discover errors. Testing is the process of trying to discover every conceivable fault or weakness in a work product. It provides a way to check the functionality of components, subassemblies, assemblies and/or a finished product. It is the process of exercising software with the intent of ensuring that the Software system meets its requirements and user expectations and does not fail in an unacceptable manner. There are various types of test. Each test type addresses a specific testing requirement.

Developing Methodologies

The test process is initiated by developing a comprehensive plan to test the general functionality and special features on a variety of platform combinations. Strict quality control procedures are used.

The process verifies that the application meets the requirements specified in the system requirements document and is bug free. The following are the considerations used to develop the framework from developing the testing methodologies.

9.3 TESTING TECHNIQUES/STRATEGIES

1. Unit testing:

Unit testing involves the design of test cases that validate that the internal program logic is functioning properly, and that program input produces valid outputs. All decision branches and internal code flow should be validated. It is the testing of individual software units of the application .it is done after the completion of an individual unit before integration. This is a structural testing, that relies on knowledge of its construction and is invasive. Unit tests perform basic tests at component level and test a specific business process, application, and/or system configuration. Unit tests ensure that each unique path of a business process performs accurately to the documented specifications and contains clearly defined inputs and expected results.

2. Functional test:

Functional tests provide systematic demonstrations that functions tested are available as specified by the business and technical requirements, system documentation, and user manuals.

Functional testing is centered on the following items:

- Valid Input** : identified classes of valid input must be accepted.
- Invalid Input** : identified classes of invalid input must be rejected.
- Functions** : identified functions must be exercised.
- Output** : identified classes of application outputs must be exercised.
- Systems/Procedures** : interfacing systems or procedures must be invoked.

3. System Test:

System testing ensures that the entire integrated software system meets requirements. It tests a configuration to ensure known and predictable results. An example of system testing is the configuration oriented system integration test. System testing is

based on process descriptions and flows, emphasizing pre-driven process links and integration points.

4. Performance Test:

The Performance test ensures that the output is produced within the time limits, and the time taken by the system for compiling, giving response to the users and request being send to the system for to retrieve the results.

5. Integration Testing:

Software integration testing is the incremental integration testing of two or more integrated software components on a single platform to produce failures caused by interface defects.

The task of the integration test is to check that components or software applications, e.g. components in a software system or – one step up – software applications at the company level – interact without error.

6. Acceptance Testing:

User Acceptance Testing is a critical phase of any project and requires significant participation by the end user. It also ensures that the system meets the functional requirements.

Acceptance testing for Data Synchronization:

- The Acknowledge will be received by the Sender Node after the Packets are received by the Destination Node.
- The Route add operation is done only when there is a Route request in need.
- The Status of Nodes information is done automatically in the Cache Updating process.

Build the test plan:

Any project can be divided into units that can be further performed for detailed processing. Then a testing strategy for each of this unit is carried out. Unit testing helps to identity the possible bugs in the individual component, so the component that has bugs can be identified and can be rectified from errors.

CHAPTER 10

RESULTS AND DISCUSSIONS

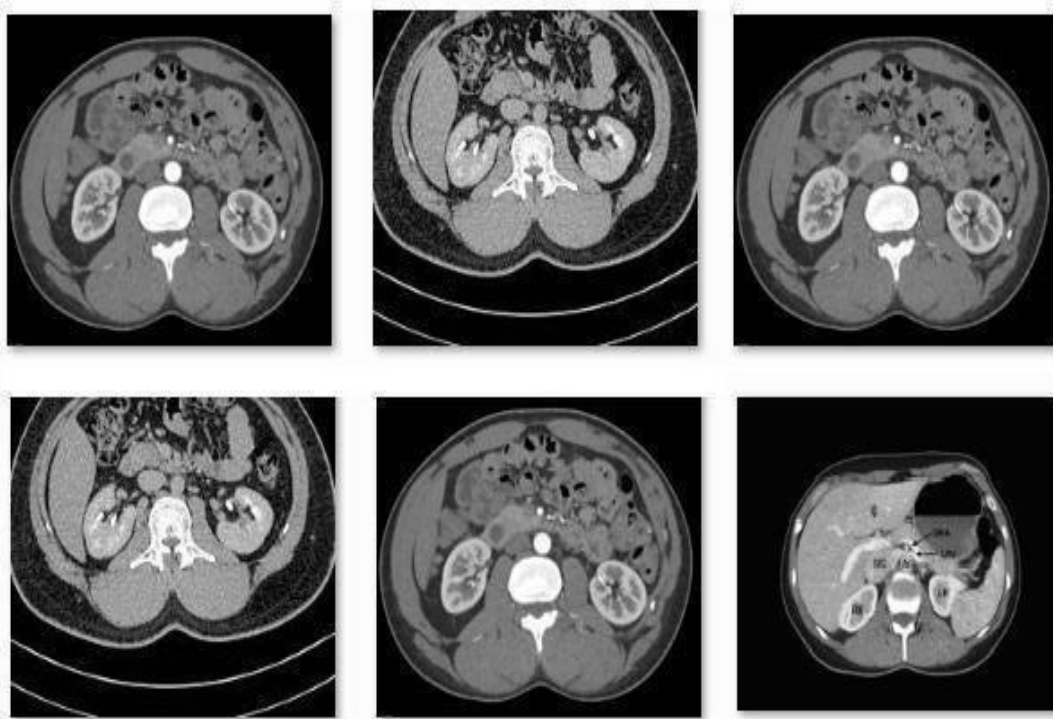


FIG 6. TCWA dataset under



FIG 7. Region extraction

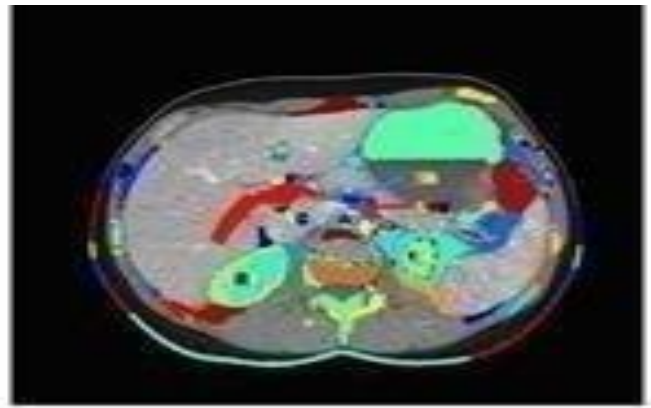


FIG 8. Pseudo segmentation of Kidney image

Table 1. Evaluation of results

Test Input	Average Intensity	Volume in ml	Result
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Image_CKD00006	127	165	Normal
Image_CKD00007	122	166	Normal
Image_CKD00008	125	178	Normal
Image_CKD00009	126	152	Normal
Image_CKD00010	122	155	Normal
Image_CKD00011	129	145	Normal
Image_CKD00012	129	163	Normal
Image_CKD00013	120	178	Normal
Image_CKD00014	127	145	Normal
Image_CKD00015	119	154	Normal
Image_CKD00016	139	165	Normal
Image_CKD00017	122	159	Normal
Image_CKD00018	125	189	Normal
Image_CKD00019	125	110	Abnormal
Image_CKD00020	127	102	Abnormal
Image_CKD00021	128	101	Abnormal
Image_CKD00022	129	100	Abnormal

Table 1. Shows the evaluation of kidney volume analysis results using CBNN

model. The challenges persist with the presented model are based on single database the evaluation is made. Hence it is required to test the CBNN with multiple database and performance metrics are mapped.

CHAPTER 11

CONCLUSION AND FUTURE ENHANCEMENT

11.1 CONCLUSION

Kidney volumetric analysis is implemented here. The need for kidney health is vital. The volume analysis impact the status of kidney health. The CT images of the kidney are taken into account when developing the proposed system. The neural network model and user base were quickly segmented from the background and the input images were processed using the Image Processing Toolbox. The characteristics of the segment used to classify images. From the CT images, the classification determines the kidney region and estimates the volume. The CBNN model was used to classify normal and abnormal kidney volume with 96 percent accuracy.

11.2 FUTURE ENHANCEMENT

The future scope of kidney disease detection is promising, as advancements in medical technology and research are continuously being made. Here are some potential areas of development, AI implementation in wearable devices, Miniaturized products for kidney analysis.

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JOURNAL PAPER

Systematic analysis of Kidney volume estimation through Cyclic Bayesian neural network

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Abstract— Kidney diseases are expected to be chronic symptoms, in which kidney volume evaluation is essential existing kidney volume estimation techniques are involved in segmenting the area of the infected region from the background section. Automated kidney localization and volume Matric image segmentation are critical steps in a fast diagnosis procedure. Most currently available frameworks made more manual analysis and classification points rather than automated systems. The proposed system is developed based on which the CT images of the kidney or considered. The input images or processed the well using the image processing Toolbox and segmented from the background as fast as possible user base and neural network model. The features from the segment for classification images. The classification ensures the kidney region from the CT images and estimates the volume. The accuracy of classification of normal and abnormal kidney volume achieved 96% using CBNN model.

Keywords— Machine learning, Chronic kidney disease, Diabetic system, Image processing, Deep learning.

I. INTRODUCTION

Kidney volumetric estimation is a crucial task utilized in various screening applications. An accurate estimation of kidney volume helps analyse Kidney Disease and evaluate the progression of Kidney Disease, planning for surgery, and availability of the transplant level etc[1]. The size of the Kidneys is essential for making any transportation surgery. Some basic techniques implemented for kidney volume estimation are ultrasound images, one of the non-invasive and cost-effective techniques utilized to estimate kidney volume. The kidney region is exposed to highly a meeting sound waves provided by the ultrasound equipment, and measuring there a course from the

organs is projected. The images are low resolution, but the analysis of intensity-based parameters from the ultrasound images is still feasible—automatic system making of kidney volume estimation ultrasound images of the Basic technique for implementing it [2].

Computer tomography is a more accurate and expensive kidney volume measurement system. The CT images are helpful to make the multiple x-ray images combined to form a continuous high-resolution image content measuring the automated measurement of kidney volume.

Magnetic resonance imaging is a non-invasive and accurate mode of estimating kidney volume. MRI images are magnetic field-enabled radio intensity images that produce more accurate image feedback comparing computer tomography and ultrasound images [3].

Automatic segmentation of kidney volume from the image data is presented here. The segmented kidney image from the background scheme provides an accurate boundary between the background and the area of interest in the Kidney. Automated segmentation of kidney volumes is highly accurate than comparing with manual segmentation methods. Kidney volume estimation is implemented through image modalities and segmentation procedures. The choice of method to provide specific application and accuracy

improvement his based on the radiologist and clinical staff measuring the image data [4].

Need for kidney volumetric analysis.

Various reasons persist with estimating kidney volume as a chemical practice. Kidney volume identification is essential for proper Diagnostic procedures for chronic kidney disease, Diabetics, and hypertension. Monitoring Kidney Disease progression is essential to treat kidney diseases in the early stages. The Kidney is a vital organ for the human body. Any damage to the Kidney can cause various other problems and impact the whole body since the Kidney is an access cleansing organ for humans. The clinical analysis and progression of kidney diseases is helpful to make a proprietary treatments at the right time

Evaluation of renal functions the volumetric analysis of the Kidney directly utilized the functionality of Kidney attached stages and enclosed the chronic kidney diseases decrease and kidney volume impact renal function in a regular basis. Estimating the kidney volume enables the right progression of kidney functions [5].

Kidney volume analysis can also be wrong before the planning of kidney surgery. Accurate estimation of kidney volume is essential to make surgery's where the nephrologist perforce. Size of the Kidneys and hands reduces the risk of complications. Assessment of renal transportation requires the exact size of the Kidney ends so the donor can donate the proper co-related Kidney to the patient.

- The volumetric analysis of the Kidney with various clinical procedures such as immediate diagnosis, slow monitoring, and treatment the kidney diseases with regular functionality and treatment procedures appropriate to the kidney volume are discussed. Timely basis, chronic kidney diseases impact human life.
- It is required to monitor the health of the Kidneys all the time. Kidney diseases, including chronic kidney disease, kidney failure, and kidney stones, every Diagnostic step for across the world metric analysis of Kidney.

- The presented system in which Cyclic Bayesian neural network (CBNN) enabled volume analysis is made.

- Volume analysis is made after the extraction of complete kidney region.

- The statistical parameters measured for classification are area, centroid, perimeter etc.

The rest of the paper is organized per the standard structure discussing detailed literature background in section II, followed by a system design described in section III. The design methodology is adopted in section IV. With results and discussion obtained are presented. Further, future enhancement is developed.

II. BACKGROUND STUDY

D. Chicco et al. (2021). The author collected various records of Kidney Disease patients to make a predictive analysis created by the combination of normal and abnormal kidneys. Predictive analysis of Kidney Disease based on the clinical data collected from the hospitals provides the ranking mechanism waste evaluation that considers parameters such as blood glucose, blood pressure, Diabetics level, sugar, age factor, etc. Based on these factors, the analysis is made to estimate the presence of kidney diseases using a machine learning algorithm developed here.

N. Bhaskar et al. 2020 the author present a discussion based on RAW physiological signals from patients collected for making a Kidney Disease detection system using a support vector machine, one-dimensional convolutional neural network architecture. The system considered the physiological parameters of blood pressure and urea blood glucose to make the analysis accurate and make the predictive system determine the presence of chronic kidney diseases.

G. Chen et al. (2021). The author presented a system with effective Kidney Disease classification using an adaptive learning mechanism. The presented system considered various parameters of kidneys using feature extraction segmentation and analysis. Using a dimensionality-reduction process unique feature extraction technique is adopted. The

presented system was developed with convolutional neural network architecture with the highest accuracy.

Ogunleye et al. (2021). The author presented extreme gradient-boosting regression-based chronic kidney disease detection using an artificial neural network algorithm. The presented system considers various data collected from patients with kidney disorders and regular patients. The best correlation between the training data and testing data using convolutional architecture and powerful boost regression algorithm for the revaluation results are present using accuracy.

J. McAllister et al. (2019). The author presented a kidney disorder induction system using predictive control analysis in which the weighted update model is present will stop the other presented application circuit and stop the immigration problem is evolved. The presentation system achieves the segmentation of Kidney Disease from specific diseases.

N. Bhaskar et al. (2021). The author has presented long short-term memory based on directional neural network architecture for chronic kidney disease detection systems with the achieved accuracy of 98% obtained with the dynamic data connected from various patients. The kidney localization and chronic kidney symptoms are analysed here.

Hoi et al. (2020). The author presented a joint learning hidden algorithm for electronic Healthcare Accord analysis and proposed a day pattern recognition algorithm to output the chronic kidney disease detection with an accuracy of 90%. The statistical measures employed here provide a consistent outcome of chronic kidney disease with a pattern recognition algorithm.

El holy et al. 2021 the author presented the belief network for predictive analysis of chronic kidney disease detection using artificial intelligence-enabled classification approval stock various statistical measures such as cross entropy method is evolved to make the classification even better that consider the two phase of operation the clinical data analysis and CT analysis to make the early

prediction of Kidney Disease. The presented system achieves a 98.5% accuracy and 87.5% sensitivity in the early detection of Kidney Disease.

Various existing articles are considered here to create a strong knowledge base on proposed design.

III. SYSTEM DESIGN

Kidney is an important organ of the body supports other functionality of the body organs. Volumetric analysis need accurate estimation of the region extracted. Occlusion of image, low resolution impact the measurement to fall below the threshold. Accurate and fast, automated estimation of kidney volumetric analysis need to be implemented using lightweight architecture is demandable. The problem of intensity based evaluations and its drawbacks are estimated here.

IV. METHODOLOGY

A. System architecture

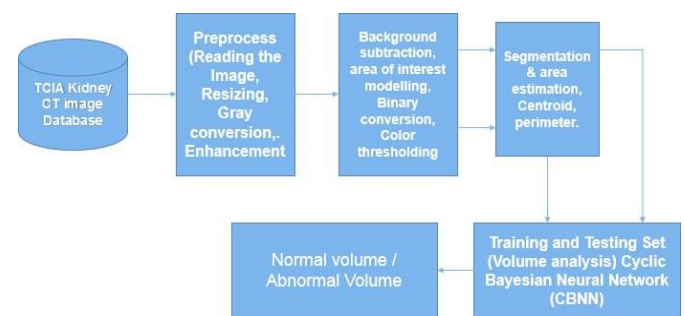


Fig 1. System architecture of proposed Kidney Volume analysis model

Fig 1. Shows the system architecture of proposed kidney volume analysis module using cyclic bayesian neural network (CBNN). The system architecture of proposed cascaded kidney volumetric analysis.

The gradual loss of kidney function is one of the main problems in the human body, which provides warnings that major kidney failure occurs in the early stages. The filtration of waste components from the blood is developed by the kidney organ that needs excessive Fluids. The body must accumulate dangerous waste stages and send them out with the help of the kidney to do lots of work compared with other body organs. Kidney health detection is essential. Learning provides kidney volume analysis to improve analysis before any surgical implantation. The proposed system considers the existing partial analysis implemented by clinical data, and CT images are made by considering various physiological factors and the segmented city image.

Cyclic Bayesian Neural network

Neural network architecture is one of the neural network implementations utilized for conventional neural network techniques to estimate parameters utilized for kidney segmentation. The computationally difficult integrals arise during the reason steps are expressed in the following Idea. Moreover, the conventional neural Network treats the weights and biases connecting the network layers. In base in the Network, the weight and buyers are treated as random distribution functions and post area distribution for the uterus. It is observed that the dates are updated continuously in the base of the oral Network comparing the conventional neural Network. Various benefits of the base in the oral Network are present below.

Layer configurations

- The CBNN contains input layer, hidden layer (configurable), output layer etc.
- The performance measure is obtained using Cross-entropy method.
- The feature vectors are distributed using probabilistic distribution function as given in the equation(1)

$$P(w|d) = \frac{p(d|w)p(w)}{p(d)} = \frac{p(d|w)p(w)}{\int p(d|w^{\wedge})p(w^{\wedge})dw^{\wedge}} \quad (1)$$

$$p(y(x|d) = (p(y(x|w)p(w|d)dw \quad (2)$$

Uncertainty estimation in predictions makes many differences in the conclusion of chronic kidney disease; hence, a neural network helps make accurate predictions. Robust network is essential to make the fitting properly during the training and testing process. The flexibility obtained from a Bayesian neural Network is required to structure the unstructured form of kidney images and make the classification accuracy better. Networks are computationally expensive. The training and testing process takes lesson time comparing the conventional Network, and the classification process is highly accurate compared with other neural networks.

V. RESULTS AND DISCUSSIONS

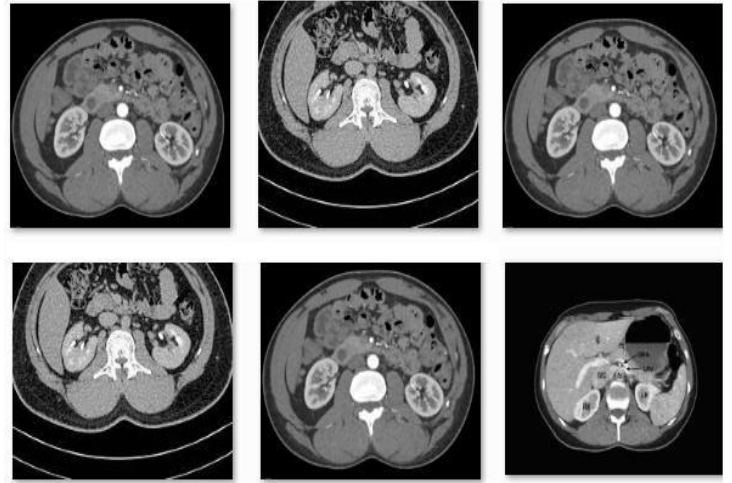


Fig 2. TCWA dataset under test

Fig 2. Shows kidney images of TCWA dataset under test

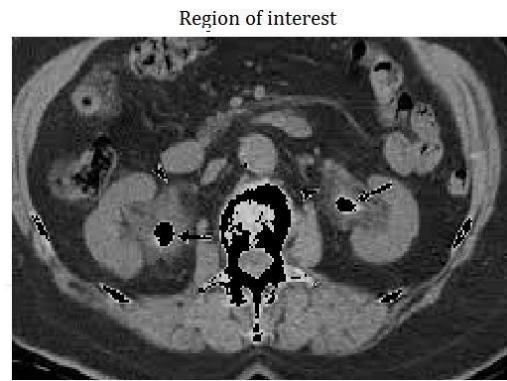


Fig 3. Region extraction

Fig 3. Shows region of interest extraction through intensity maps using color threshold tool.

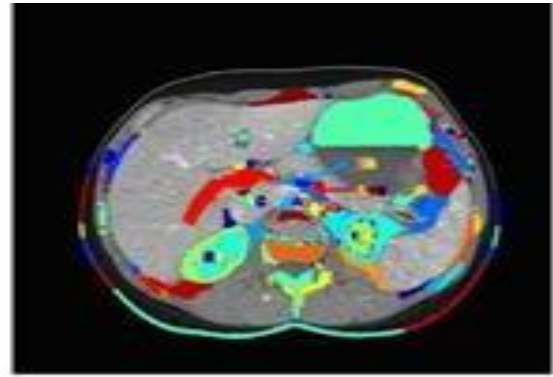


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