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ABSTRACT

Chronic Kidney Diseases (CKD) has become a severe cause of death. A new deep learning based architecture is proposed to handle the large set of data. The architecture is designed such a way that is balance the execution time and accuracy. Kidney infection is one of the life threatening diseases and nowadays it affects all humans regardless of their age. Accurate classification of kidney tumor, cyst, calculi helps to detection of kidney failure, which decreases the kidney function rate, but it is easy to detect early. Kidney infections is classified as cyst, calculi, and tumor. This paper proposes the Deep Convolutional Neural Networks (DCNN) based classifier which classifies the kidney infection. This network consists of different Convolutional layer, pooling layer and fully connected layers. Three architectures were defined for DCNN classifier each one is trained with different patch size. DCNN is applied to the Ultrasound image for classification of cyst, calculi and tumor. The proposed architectures were evaluated on the DCNN database and compared with other classifier such as Artificial Neural Network (ANN) and Support Vector Machine (SVM). The experimental result shows that the DCNN achieved the better performance.

Keywords: *Deep Learning, Convolutional Neural Network,Cyst, Calculi, Tumor, Ultrasound images.*

1. INTRODUCTION

Chronic renal failure represents the end result of conditions that greatly reduce renal function by destroying renal nephrons and producing a marked decrease in the glomerular filtration rate (GFR). Signs of renal failure begin to appear as renal function moves from renal insufficiency (GFR 50% to 20% normal), to renal failure (20% to 5% normal), to end-stage renal disease (<5% normal). When the GFR decreases to less than 5% of normal, dialysis or kidney transplantation is necessary for survival.The manifestations of chronic renal failure represent the inability of the kidney to perform its normal functions in terms of regulating fluid and electrolyte balance, controlling blood pressure through fluid volume and the renin-angiotensin system, eliminating nitrogenous and other waste products, governing the red blood cell count through erythropoietin synthesis, and directing parathyroid and skeletal function through phosphate elimination and activation of vitamin D.

Our mission is to become aware of the presence of renal filure in patient ultra sound scans of kidney with and without early stage renal failure. We intend to use methods from computer vision and deep learning, particularly 2D and 3D convolutional neural networks, to build an accurate classifier. An deep learning classifier could speed up and reduce costs and allowing for more widespread early detection and improved survival. The goal is to construct a risk factor analysis using deep learning algorithm that take the early detection of kidney and decide whether the patient has renal failure or not [1]. Deep Learning techniques based on Neural Networks represent an important area in the Digital Pathology field. These machine learning methods, such as Convolutional Neural Networks (CNN), are becoming central in VS analysis since they give promising results in difficult tasks like region detection and classification[2].

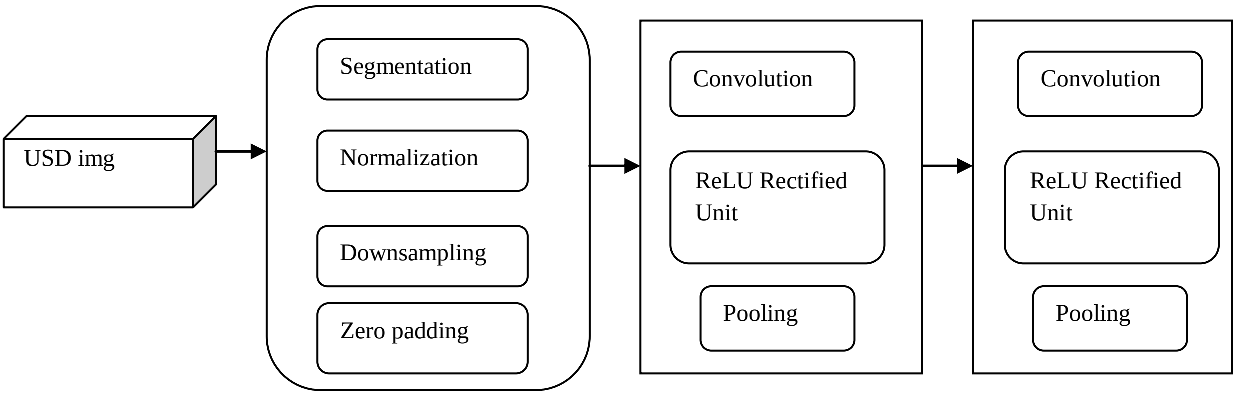


Fig 1: Convolution Neural Network

- Size and shape: In a healthy kidney before sectioning, Glomeruli present a spherical shape with fixed size (diameter ranges between 350 and 100 _m), but its aspect can change due to the presence of medical diseases. For instance: Glomeruli can present a swell aspect under hypertension or diabetes conditions. After sectioning, the presence of pathologies affect the appearance inside the VS. Moreover, the dissimilar Glomeruli sizes detected could vary dependent on where the cross-section was taken with deference to each Glomerulus sphere.

- Color: In our configuration, we use PAS (Periodic Acid Schiff) stain in tissue sections, which gives a purple-magenta color to the slides. The amount of stain present in each slide will determine the color intensity of the segments under analysis. Since this process is not perfect, each slide can present different intensities. Moreover, the presence of medical diseases can vary the amount of stain present in the Glomeruli under study.

2. LITERATURE REVIEW

Deep learning is a session of machine learning algorithms that use a torrent of numerouscovers of nonlinear considering units for piece extraction and transformation. Each successive layer uses the output from the previous layer as input. It learn in supervised (e.g., classification) and/or unsupervised (e.g., pattern analysis) manners. It also hearnumerous levels of symbols that correspond to different levels of abstraction; the levels form a hierarchy of concepts. Deep learning algorithms seek to exploit the unknown structure in the input distribution in order to discover good representations, often at multiple levels, with higher-level learned features defined in terms of lower-level features. Huge number of architecture were defined for deep learning algorithm. Three major architecture are Alex-net, Google-net, U-net architecture.

2.1 Alex-net architecture:

This architecture was one of the first deep networks to push ImageNet Classification accuracy by a significant stride in comparison to traditional methodologies. It is composed of 5 convolutional layers followed by 3 fully connected layers. ReLu is given by f(x) = max(0,x)The advantage of the ReLu over sigmoid is that it trains much faster than the latter because the derivative of sigmoid becomes very small in the saturating region and therefore the updates to the weights almost vanish. This is called vanishing gradient problem. In the network, ReLu layer is put after each and every convolutional and fully-connected layers(FC).Alex net architecture looks weird because there are two different streams. This is because the training process was so computationally expensive thus they have to split the training set onto 2 GPUs.

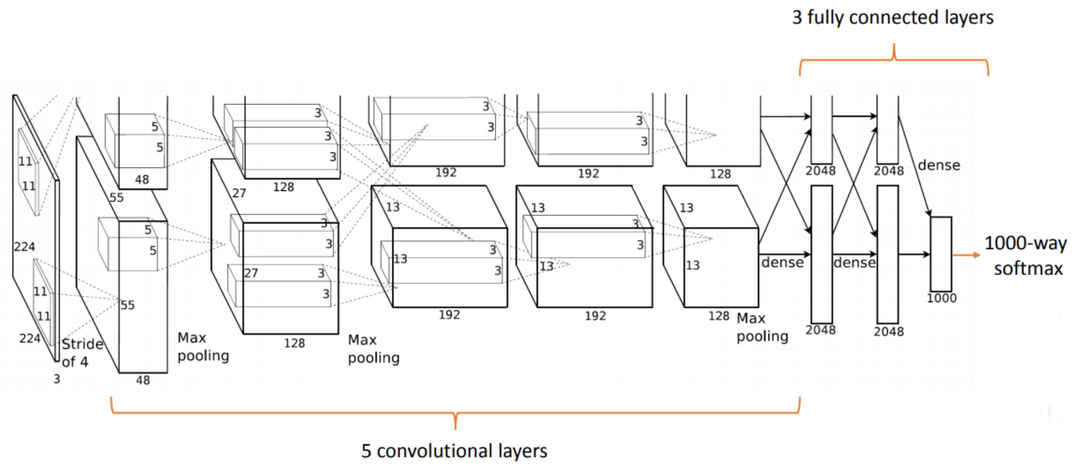


Fig 2: Alex Net Architecture

2.2 Google Net architecture:

Two different approaches have been considered. First, a technique called fine-tuning has been used. That is, taking a previously trained model that has proven reliable (with good general features) and apply that to our own dataset, modifying the weights to be adapted to this problem. The model used was a pre-trained AlexNet model from the ImageNet challenge. The architecture of this network is composed of eight layers: five convolutional and three fully-connected. Given that, it was possible to achieve good results with only a few iterations. In order to increase the variability of architectures the GoogleNet architecture was employed also with both techniques. The training process was carried out using two different sets of parameters, depending on whether the network was pre-trained or not. For the pre-trained network the learning rate is started with an initial of 0.001, decreasing it with drop factor of 0.1 with a period of eight. It takes around 9 min to perform the training process for AlexNet and 25 min for GoogleNet.

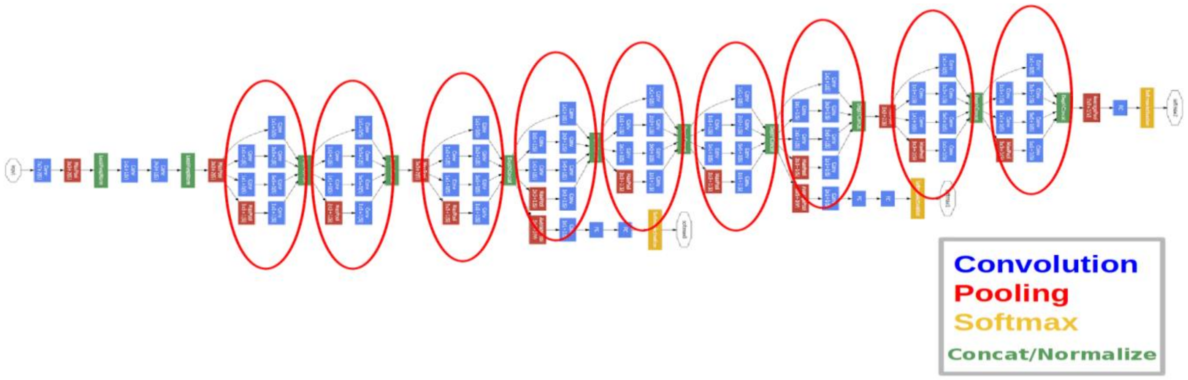


Fig 3: Google Net Architecture

2.3 U-net architecture:

We also proposea fully automated segmentation framework based on U-Net architecture which was initially developed for 2D microscopy image segmentation. UNet has the ability to capture local and global information for the image segmentation task and is able to generalize wellfrom a small set of training samples. Variations of this network have also shown successful results for volumetric medical image segmentation. We propose a 3D segmentation algorithm based on the 3D version of this architecture for automatic renal parenchyma segmentation in DCE-MR images. Thus, we propose to divide our problem into two sub-problems that can be solved more efficiently in terms of time and memory when separated out: First, we apply a modified 3D U-Net on low resolution and augmented data for localizing the right and left kidneys; and second, we will apply

U-Net on each extracted kidney region from the previous step for segmentation. Each of these sub-problems can be solved more quickly and need less memory compared to the naïve approach. Our total test time is < 5 seconds for each new patient.

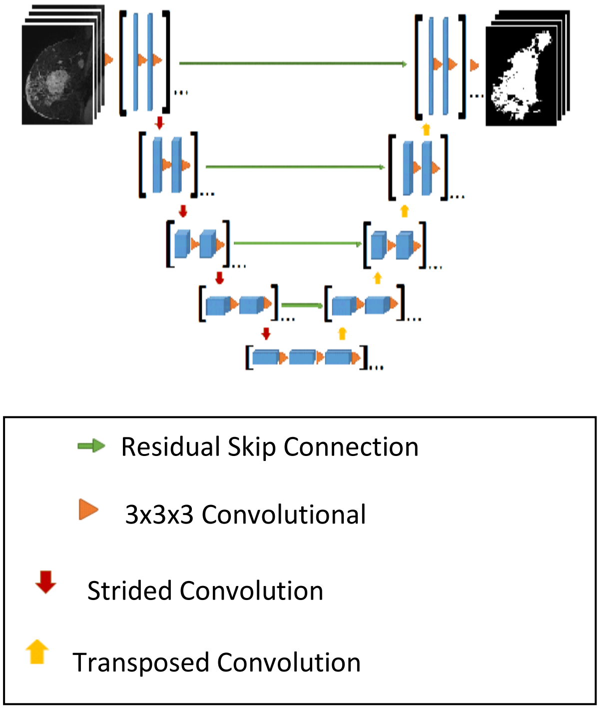


Fig 4: U-Net Architecture

In [1] the author reveals a computer-aided diagnosis (CAD) system for lung cancer classification of CT scans with untouched nodules. Thresholding was used as an early segmentation approach to segment out lung tissue from the rest of the CT scan. Thresholding formed the next best lung segmentation. The early advance was to openly provide for the segmented CT scans into 3D CNNs for classification, but this prove to be insufficient. Instead, a modified U-Net trained on LUNA16 data was used to first detect nodule candidates in the CT scans. The U-Net nodule revealing created many artificial positives, so regions of CTs with segmented lungs where the most likely nodule candidates were located as determined by the U-Net output were fed into 3D Convolution Neural Networks (CNNs) to ultimately classify the CT scan as positive or negative for lung cancer. The 3D CNNs produced a test set Accuracy of 86.6%.

In [2] the author describes Glomerulus classification and detection in kidney tissue segments are key process in nephropathology used for the correct diagnosis of the diseases. Here, we arranged with the challenge of automate Glomerulus classification and discovering from digitized kidney slide segments using a deep learning framework. The proposed method applies Convolutional Neural Networks (CNNs) between two classes: Glomerulus and Non-Glomerulus, to detect the image segments belong to Glomerulus regions. We configure the CNN with the public pre-trained AlexNet model and adapt it to our system by learning from Glomerulus and Non-Glomerulus regions extracted from training slides. Once the model is qualified, labeling is performed by applying the CNN classification to the image blocks under analysis.

In [3] the author enables Kidney function estimation using dynamic contrast-enhanced MRI (DCE-MRI) images could help in diagnosis and treatment of kidney diseases of children. Automatic segmentation of renal parenchyma is an important step in this process. We also propose a time and memory capable fully computerized segmentation technique which achieves high segmentation accuracy with running time in the order of seconds in both normal kidneys and kidneys with hydronephrosis. The proposed method is based on a cascaded application of two 3D convolutional neural networks that employs spatial and sequential information simultaneously with the aim of learning the tasks of localization and segmentation of kidneys, respectively. Segmentation performance is evaluated on both normal and abnormal kidneys with varying levels of hydronephrosis.

In [4] the author used fully automatic technique to segment the kidney into multiple components: renal cortex, renal column, renal medulla and renal pelvis, in clinical 3D CT abdominal images. The projected fast repeated segmentation technique of kidney consists of two main parts: localization of renal cortex and segmentation of kidney components. In the localization of renal cortex phase, a method which totally combine 3D Generalized Hough Transform (GHT) and 3D Active Appearance Models (AAM) is applied to localize the renal cortex. In the segmentation of kidney components phase, a modified Random Forests (RF) process is projected to slice the kidney into four components based on the result from localization phase. During the performance, a multithreading knowledge is useful to speed up the segmentation process. The proposed method was evaluated on a clinical abdomen CT data set, including 37 contrast-enhanced volume data using leave-one-out strategy.

In [5] the author introduces a computer-aided kidney shape finding method appropriate for volumetric (3D) ultrasound images. Using shape and texture priors, the projected technique automated the process of kidney detection, which is a difficulty of great consequence in computer-assisted trauma diagnosis. It introduces a new complex-valued contained shape model which represents the multi-regional arrangement of the kidney shape. The difficult values of the shape model and classification outputs are selected and incorporated in a new similarity metric such the shapeto- volume registration process only fits the shape model on the actual kidney shape in input ultrasound volumes. The algorithm's accuracy and sensitivity are evaluated using both simulated and actual 3D ultrasound images, and it is compared against the performance of the state-of-the-art.

In [6] the author introduces a network for volumetric segmentation that learns from lightly annotate volumetric images. We sketch two smart use cases of this method. First, the semi-programmed system, the user annotate some slices in the quantity to be segmented. The network learns from these spare explanation and provide a solid 3D segmentation. Secound, a fully automated setup, we suppose that a agent, sparsely annotated training set exists. Trained on this data set, the network closely segments new volumetric images. The planned network extend the previous u-net architecture by replacing all 2D operations with their 3D counterparts. The performance on elastic deformations for efficient data augmentation during training. It is trained end-to-end from scratch, no pre-trained network is necessary. We analysis the presentation of the projected technique on a complex, highly variable 3D structure, the Xenopus kidney, and achieve good results for both use cases

In [7] the author describes Deep learning (DL) based semantic segmentation methods have been provided that modern presentation in the preceding few years. Further purposely, these technique have been effectively applied to medical image classification, segmentation, and detection tasks.we suggest a Recurrent Convolutional Neural Network (RCNN) based on U-Net in addition to a Recurrent Residual Convolutional Neural Network (RRCNN) based on U-Net models, which are named RU-Net and R2U-Net correspondingly. The projected technique utilizes the power of U-Net, Residual Network, as well as RCNN. Primarly, a residual unit helps when training deep architecture. Secondarily, feature accumulation with recurrent residual convolutional layers ensures better feature representation for segmentation tasks. Thirdly, it allows us to design better U-Net architecture with same number of network parameters with better performance for medical image segmentation.

In [8] the author enables significant movement has been made in image recognition, first and foremost due to the accessibility of large-scale annotated datasets (i.e. ImageNet) and the stimulation of deep convolutional neural networks (CNN). CNNs allow learning data-driven, highly delegate, layered hierarchical image features from enough preparation data. Still, obtaining datasets as widely annotated as ImageNet in the medical imaging domain remains a challenge. We first discover and evaluate different CNN architectures. The calculated models contain 5 thousand to 160 million parameters, and vary in numbers of layers. Then calculate the power of dataset scale and spatial image context on performance. Finally, we check when and why transfer learning from pre-trained ImageNet (via fine-tuning) can be useful.

In [9] the author describes the accessibility of medical imaging data from clinical records, research literature, and clinical manuals, attached with recent advance in computer visualization offer the chance for image-based diagnosis, teaching, and biomedical research. This test is compounded by variation in the exterior of images based on the diseases depicted and a lack of enough training data for some modalities. We establish a new method for classifying medical images that uses an ensemble of different convolutional neural network (CNN) architectures. CNNs are a state-of-the-art image classification technique that learns the optimal image features for a given classification task. Here we develops a new feature extractor by fine-tuning CNNs that have been initialised on a large dataset of natural images.

In [10] the author obtained a novel kidney segmentation method for computed tomography patient data with kidney cancer is proposed. The segmentation process is based on Hybrid Level Set method with elliptical shape constraints. Using segmentation results, a fully automated technique of kidney region classification is introduced. It enables to resolve main problems connected with region classification such as class imbalance and the number of voxels to classify. The classification is based on 64- element feature vectors calculated for the kidney region that consist of 3D edge, region, orientation and spatial neighborhood information. The proposed methodology was evaluated on clinical kidney cancer CT data set. Segmentation effectiveness in Dice coefficient meaning was equal to 0.85±0.04. Overall accuracy of the proposed classification model amounts to 92.1%. Presented results confirm usefulness of the proposed solution.

3. PROBLEM STATEMENT

The kidney fault can be life time frightening, thus discovery of kidney problem in the earlier stages is critical. In order to carry out surgical operation, first have to identify kidney at earlier stage. The CT images of kidney contain speckle noise and are of low contrast which makes the detection of kidney abnormalities a challenging task. As a result the doctors may have problem to identify the small kidney stones and their type properly.The previous algorithms are not work well for kidneys whose structures are not significantly altered by diseases. If diseases such as kidney tumor, calculi,stone causes dramatic change in kidney morphology or texture, the AAM which are trained on the normal dataset may not perform well. For renal cortex and column segmentation, the renal cortex thickness model is also designed for normal cortex shape.For random forest classification, to segment kidney with significant change in morphology or texture, training on specific dataset is not well defined. Another limitation of the previous method is all images used were contrast-enhanced. The segmentation task is more difficult for non-contrast-enhanced CT images.

4. PROPOSED WORK

Significant development has been made in image recognition, mainly due to the accessibility of large-scale explained datasets and the recovery of deep convolutional neural networks (CNN). CNNs assist learning data-driven, highly representative, layered hierarchical image features from sufficient training data sets. In this study, we explore, evaluate and analyze the influence of various CNN Architectures, dataset and CNN transfer learning from non-medical to medical image domains. These three key elements of building effective deep CNN models are described

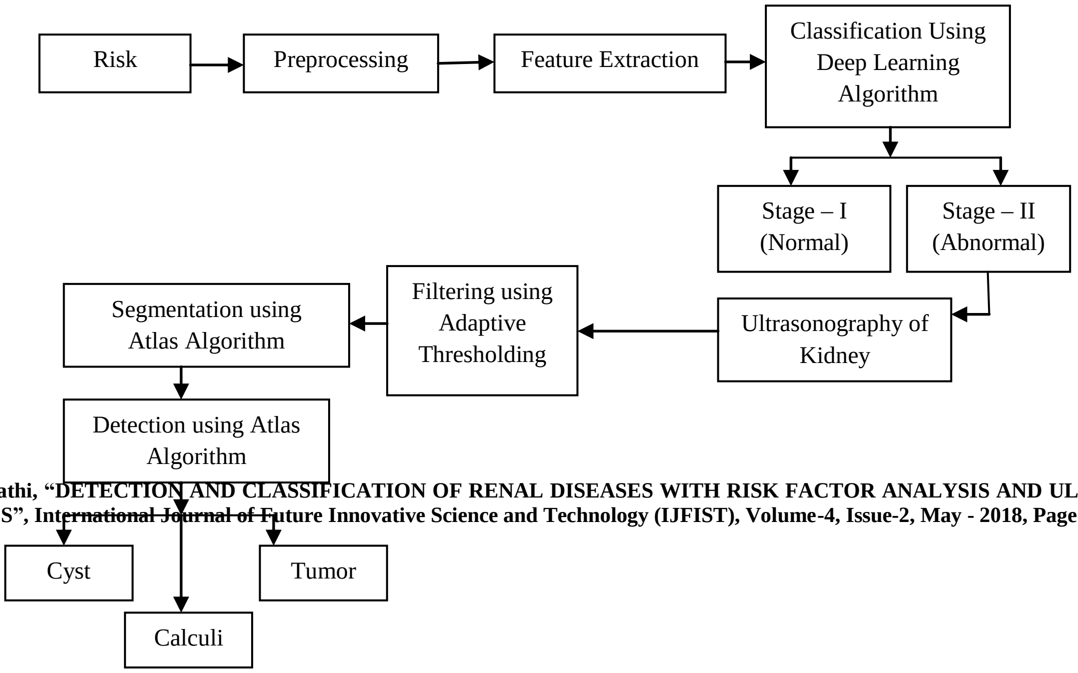


Fig 5: Overview of Proposed System

4.1 Convolutional Layer Work:

Convolution Neural Networks are very similar to ordinary Neural Networks from the previous chapter: they are made up of neurons that have learnable weights and biases. Each neuron receives some inputs, performs a dot product and optionally follows it with a non-linearity. The whole network still expresses a single differentiable score function: from the raw image pixels on one end to class scores at the other. And they still have a loss function (e.g. SVM/Softmax) on the last (fully-connected) layer and all the tips/tricks we developed for learning regular Neural Networks still apply.

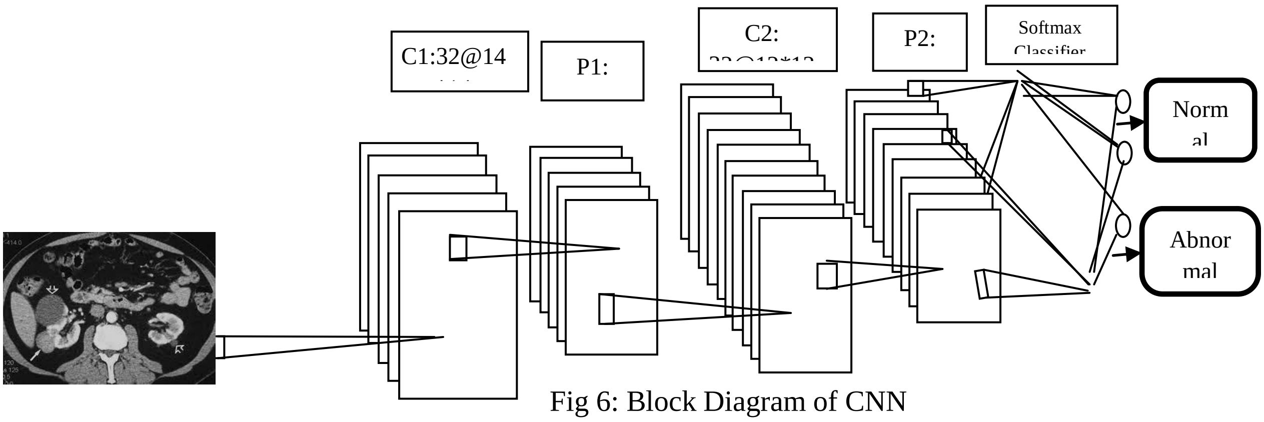
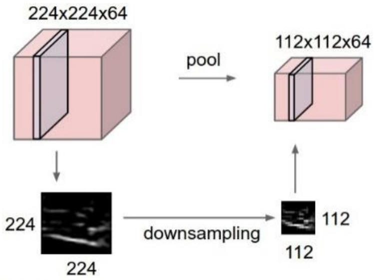
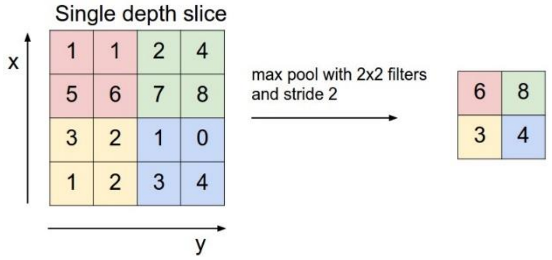


Fig 6: Block Diagram of CNN

4.2 Pooling Layer Work:

It is common to periodically insert a Pooling layer in-between successive Conv layers in ConvNet architecture. Its function is to progressively reduce the spatial size of the representation to reduce the amount of parameters and computation in the network, and hence to also control over fitting. The Pooling Layer operates independently on every depth slice of the input and resizes it spatially, using the MAX operation. The most common form is a pooling layer with filters of size 2x2 applied with a stride of 2 down samples every depth slice in the input by 2 along both width and height, discarding 75% of the activations. Every MAX operation would in this case be taking a max over 4 numbers (little 2x 2 regions in some depth slice). The depth dimension remains unchanged.





1	1	2	4
5	6	7	8
3	2	1	0
1	2	3	4

6	8
3	4

Fig 7: Down sampling. Fig 8: Matrix Formation

4.3 Fully Connected Layer:

Neurons in a fully connected layer have full connections to all activations in the previous layer, as seen in regular Neural Networks. Their activations can hence be computed with a matrix multiplication followed by a bias offset. See the Neural Network section of the notes for more information.

4.4 SoftMax Classifier:

The Softmax classifier is a generalization of the binary form of Logistic Regression. Just like in hinge loss or squared hinge loss, our mapping function f is defined such that it takes an input set of data x and maps them to the output class labels via a simple (linear) dot product of the data x and weight matrix W:

$$f(x_i, W) = Wx_i$$

However, unlike hinge loss, we interpret these scores as unnormalized log probabilities for each class label — this amounts to swapping out our hinge loss function with cross-entropy loss:

$$L_i = -log(e^{s_{y_i}} / \sum_j e^{s_j})$$

To start, our loss function should minimize the negative log likelihood of the correct class:

$$L_i = -logP(Y = y_i | X = x_i)$$

This probability statement can be interpreted as:

$$P(Y = k | X = x_i) = e^{s_{y_i}} / \sum_j e^{s_j}$$

Where we use our standard scoring function form:

$$s = f(x_i, W)$$

As a whole, this yields our final loss function for a single data point, just like above:

$$L_i = -log(e^{s_{y_i}} / \sum_j e^{s_j})$$

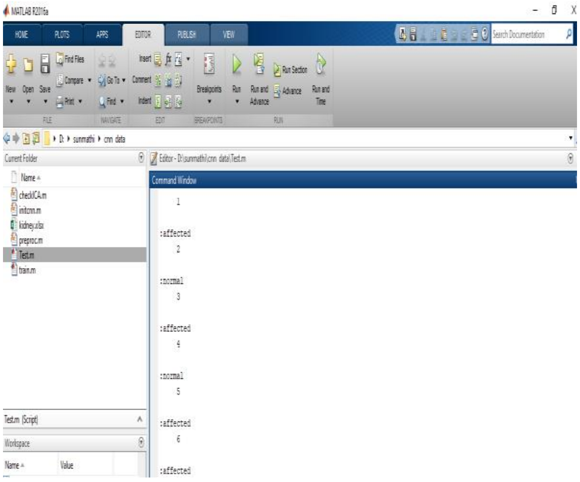
The actual exponentiation and normalization via the sum of exponents is our actual Softmax function. The negative log yields our actual cross-entropy loss.

Just as in hinge loss or squared hinge loss, computing the cross-entropy loss over an entire dataset is done by taking the average:

$$L = \frac{1}{N} \sum_{i=1}^{N} L_i$$

5. OUTPUT:

The proposed system starts with preprocessing the ultrasound scans using segmentation, normalization, downsampling, and zero-centering. The initial approach was to simply input the preprocessed ultrasound scans into 3D CNNs, but the results were not upto level. So an additional preprocessing was performed to input only regions of interests into the 3D CNNs. To identify regions of interest, a U-Net was trained for nodule candidate detection. Then input regions around nodule candidates detected by the U-Net was fed into 3D CNNs to ultimately classify the ultrasound scans as positive or negative for kidney problem detection. The overall architecture is shown in Fig. 1.



```
     1

:affected
     2

:normal
     3

:affected
     4

:normal
     5

:affected
     6

:affected
```

Fig 9: CNN classification analysis based on given datasets.

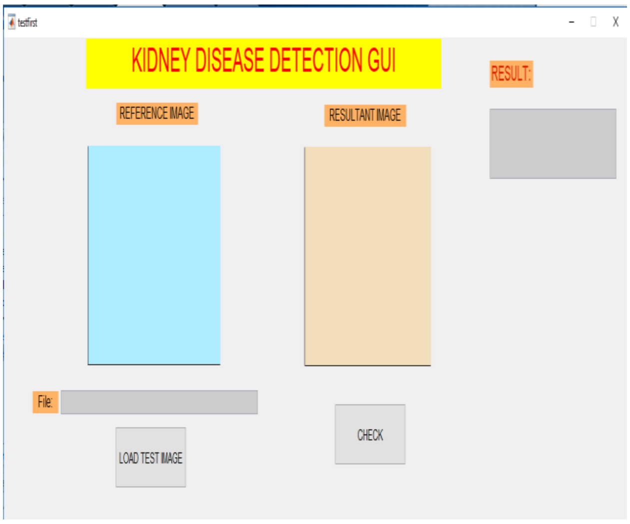


Fig 10: The initial approach of uploading the kidney image for scanning process

Preprocessing and Segmentation:

For each patient, pixel values was first converted in each image to Hounsfield units (HU), a measurement of radiodensity, and 2D slices are stacked into a single 3D image. Because cyst, calculi, tumors form on kidney tissue, segmentation is used to mask out the kidney layer and other substances that would make data noisy, and leave only kidney layer information for the classifier. A number of segmentation approaches were tried, including thresholding, clustering (Kmeans and Meanshift), and Watershed. K-means and Meanshift allow very little supervision and did not produce good qualitative results. Convolutional Neural network produced the best qualitative results. After segmentation, the 3D image is normalized by applying the linear scaling to squeezed all pixels of the original unsegmented image to values between 0 and 1. Spline interpolation downsamples each 3D image by a scale of 0.5 in each of the three dimensions. Finally, zero-centering is performed on data by subtracting the mean of all the images from the training set.

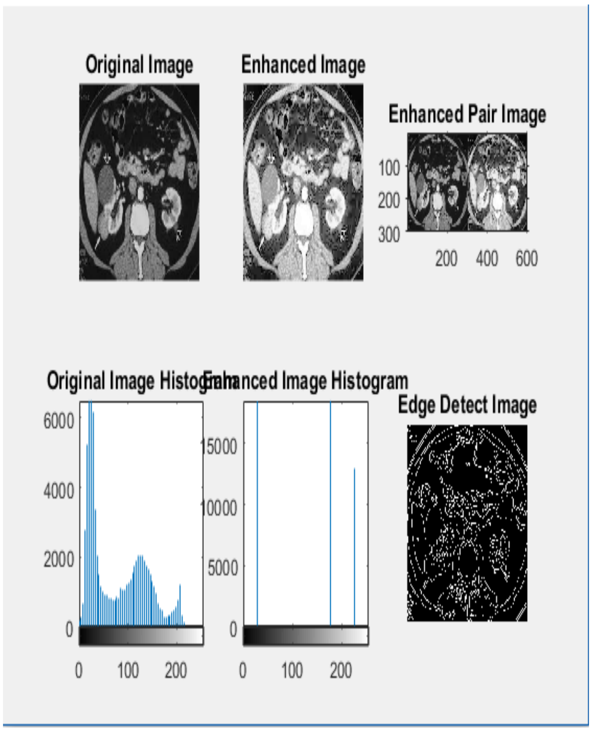
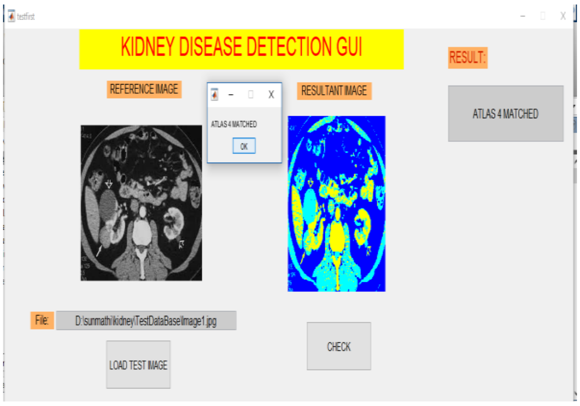


Fig 11: Histogram of corresponding axial slices of sample patient 3D ultrasound images at various axial



ATLAS 4 MATCHED

ATLAS 4 MATCHED

File: D:\sunmathi\kidney\TestDataBase\Image1.jpg

Fig 12: Original 2D slice of sample patient, kidney segmentation mask by 3D CNN of sample patien and final infected segmentation mask of sample patient.

6. PERFORMANCE ANALYSIS

The experiments are conducted using convolutional neural network dataset. In this dataset, ultrasound images from high-risk patients are given. The CNN database consists of ultrasound scans and it is differentiated in to slices. Each scan contains a series with multiple axial slices of the kidney. Each scan has a variable number of 2D slices (Fig. 5), which can vary based on the machine taking the scan and patient. The CNN files have a header that contains the necessary information about the patient id, as well as scan parameters such as the slice thickness.

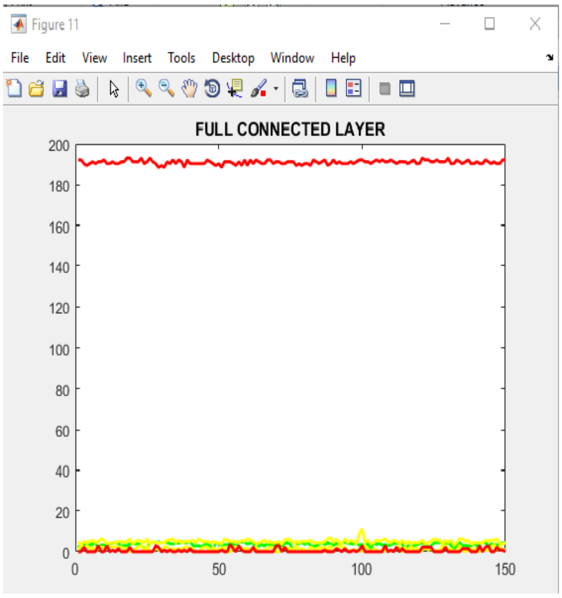


Fig 8: Fully Connected Layer

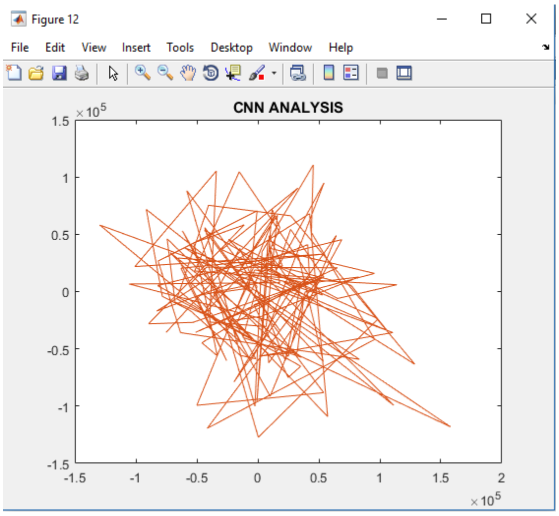


Fig 9: CNN Analysis

For simplicity in training and testing we selected the ratings of a single radiologist. All experiments were done using 50% training set, 20% validation set and 30% testing set. To evaluate the results we considered a variety of testing metrics. The accuracy metric is the used metric in our evaluations. In our first set of experiments we considered a range of CNN architectures for the binary classification task. Early experimentation suggested that the number of filters and neurons per layer were less significant than the number of layers. Thus, to simplify analysis the first convolutional layer used seven filters withsize 5×5×5, the second convolutional layer used 17 filters with 5×5×3 and all fully connected layers used 256 neurons. These were found to generally perform well and we considered the impact of one or two convolutional layers followed by one or two fully connected layers. Our results suggest that two convolutional layers followed by a single hidden layer is one of the optimal network architecture for this dataset. The average error for training is described in Fig. 9.

7. CONCLUSION

In this paper, we exploit and extensively evaluate three important, factors on deep convolutional neural networks (CNN) architecture, dataset characteristics, and transfer learning. We have introduced an end-to-end learning method that semi-automatically and fully-automatically segments a 3D volume from a sparse annotation. The deep 3D CNN model, specifically the U-Net based model, Alex based model, Googlenet-based model performed the finest on the test set. As an exciting study, the first activation layer of one of our older models (where we input the entire CT volume) for a validation example that was labeled as positive for kidney problem. The bright pixels usually corresponded with the location of calculi, stone, cyst so it could be possible to extend our current model to not only determine whether or not the patient has kidney problem, but also determine the exact location of the kidney infection. Other opportunities for improvement include making the network deeper, and more extensive overexcited factor modification. Also, we saved our model parameters at best validation, but possibly we could have saved at other metrics. Other future work includes extending our models to 3D images for other kidney problems. Deep learning has not been used in this research because it needs a huge training dataset to overcome challenges due to the nature of ultrasound imaging and kidney shape variability among patients. By inspiring from deep learning, we will continue this work by applying trained based features instead of using analytical Gabor filters. Also, as a future work, the proposed kidney detection method will beused in a processing pipeline for computer-assisted diagnosis.

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