

X-Ray Scanner Supplementary Module: Evaluation Of Disease Progression By Pulse Coupled Neural Network

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Abstract: This paper presents a supplementary module of x-ray scanner to analyze the evolution of disease for a patient. The previous image medical examination which is stored on database will be compared with the current image scanner output. The new function is inserted between image reconstruction and visualization module. The algorithm is based on image segmentation which is handled by a particular neural network called PCNN or Pulse Coupled Neural Network. We compare the PCNN output of both images by calculating the percentage of cured/deterioration of the target and differentiate the concerned region with color marking. It will help the doctor to take an immediate decision for his patient instead of spending time for manual comparison.

Index Terms: Disease evaluation, image segmentation, Pulse Coupled Neural Network, x-ray scanner supplementary module.

1 INTRODUCTION

BY the early sixties, different radiological imaging devices had an objective to visualize the human anatomy with more precision. It is in this environment that the computed tomography (CT) x-ray was born. The principals of CT by transmission were presented for the first time in 1972 by Godfrey Hounsfield. The invention of computed tomography x-ray has been the one of the first revolutions in medical imaging and based on this, there was a great improvement included the actual scanner. The algorithm that we proposed here is applicable for x-ray scanner new generation working on mode radio, tomographic mode slice by slice and helical fashion. To proceed on the details, we'll see in the next paragraph how CT scanner works? Then the pulse coupled neural network purpose followed by the proposal method and testing.

2 X-RAY SCANNER

Tomographic imaging consists of directing x-rays at on object from multiple orientations and measuring the decrease in intensity along a series of linear paths. This decrease is characterized by Beer's law, which describes intensity reduction as a function of x-ray energy, path length, and material linear attenuation coefficient.

A specialized algorithm is then used to reconstruct the distribution of x-ray attenuation in the volume being imaged [1]. The simplest form of Beer's law for a monochromatic x-ray beam through a homogeneous material is:

$$I = I_0 \exp [-\mu x] \quad (1)$$

Where I_0 and I are the initial and final x-ray intensity, μ is the material's linear attenuation coefficient and x is the length of the x-ray path. If there are multiple materials, the equation becomes:

$$I = I_0 \exp \left[\sum_i (-\mu_i x_i) \right] \quad (2)$$

CT scanning is used commonly in medicine today. It is similar to conventional radiology as it uses x-rays. In order to obtain a CT scan patients lie in a CT scanner – similar to a bed inside a 'Polo® mint'. The x-ray tube and detectors are opposite to each other. Both of these rotate around the patient and information is obtained, usually in slices. The data are constructed by a computer and provide, most commonly, cross-sectional images in a single plan, which can be interpreted [1][2]. The above description is part of system measurement and image reconstruction (linear interpolation method, etc.).

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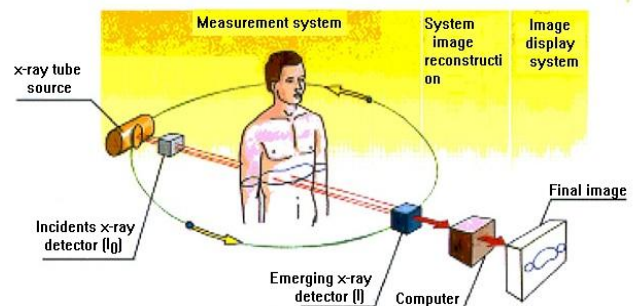


Fig. 1. Fundamental principles of x-ray scanner

There are essentially two types of CT scans:

1. Conventional CT scan: the scan is taken slice by slice and after each slice, the scan stops and moves down to the next slice, example from the top the abdomen down to the pelvis. This requires patients to hold their breath to avoid movement artifact.
2. Spiral/helical CT scan: this is a continuous scan which is taken in a spiral fashion. It is a much quicker process and the scanned images are contiguous.

Once we got medical image after reconstruction, we proceed to treat it using PCNN before screen visualization.

3 PULSE COUPLED NEURAL NETWORKS MODEL

The PCNN is a two-dimensional neural network with a single layer. Each network neuron corresponds to an input image pixel. Because of this, the structure of the PCNN comes out from the structure of input image [4].

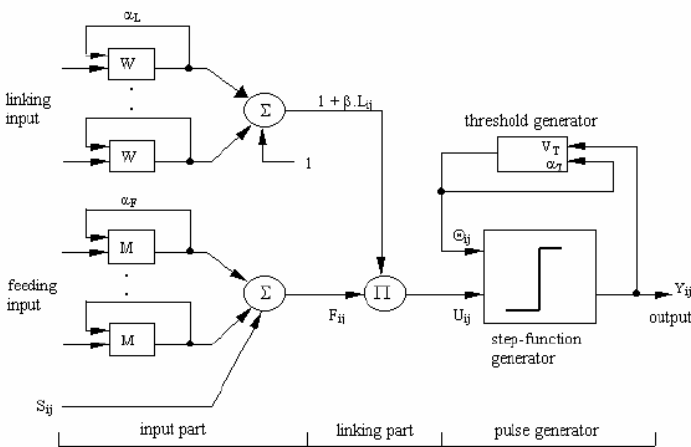


Fig. 2. Pulse Coupled Neural Networks Structure

The PCNN's neuron structure is shown in Fig. 2. There are three parts that form a neuron: a feeding field, a linking modulation, and a pulse generator. The neuron's operation is described as iteration by the following equations.

$$F_{ij}(n) = S_{ij} + F_{ij}(n - 1) \cdot e^{-\alpha_F} + V_F \cdot (M * Y(n - 1))_{ij} \quad (3)$$

$$L_{ij}(n) = L_{ij}(n - 1) \cdot e^{-\alpha_L} + V_L \cdot (W * Y(n - 1))_{ij} \quad (4)$$

$$U_{ij}(n) = F_{ij}(n) \cdot (1 + \beta \cdot L_{ij}(n)) \quad (5)$$

$$\theta_{ij}(n) = \theta_{ij}(n - 1) \cdot e^{-\alpha_\theta} + V_\theta \cdot Y_{ij}(n - 1) \quad (6)$$

$$Y_{ij}(n) = \begin{cases} 1, & \text{if } U_{ij}(n) > \theta_{ij}(n) \\ 0, & \text{sinon} \end{cases} \quad (7)$$

In these equations, (i,j) is the position of a neuron in the network and a pixel in the input image. For example, if the input image is 128x128 pixels, the range of indexes (i,j) will be between (1,1) and (128,128). n is the iterative step number; and S_{ij} is the gray level of the input image pixel. F_{ij}[n], L_{ij}[n], U_{ij}[n], θ_{ij}[n] is the feeding input, linking input, internal activities, and dynamic threshold, respectively. The pulse output of a neuron, Y_{ij}[n] is the binary value which indicates the status of the neuron. Y_{ij}[n] equals to 1 means the

neuron is activated [3][4]. M and W are the constant synaptic weight matrices and depended on the field of the surrounding neurons, i.e. the linking field. For example, if each neuron is only connected by eight neurons surrounding it, the linking field is a 3x3 matrix. As a result, M and W are 3x3 matrices, too. M and W refer to the Gaussian weight functions with distance and they are usually chosen as the same. β is the linking coefficient constant; α_F, α_L and α_θ are the attenuation time constants; and the V_F, V_L and V_θ are the inherent voltage potential of the feeding signal, linking signal, and dynamic threshold, respectively. In conclusion, the operation of a neuron at step n depends on its corresponding pixel value (i.e. S_{ij}), the pulse output from the surrounding neurons at the previous step, and the internal signals of the neuron itself (i.e. F_{ij}[n - 1], L_{ij}[n - 1], U_{ij}[n - 1], θ_{ij}[n - 1]). All of the network pulses Y_{ij}[n] form a binary image which contains important information such as regional information, edge information, and features of an object in the input image [4].

4 SUPPLEMENTARY MODULE

The new module is implemented between system image reconstruction and image display system (Fig. 3). All previous patient scan images are stored on separate database. Only one image from this database is required to be compared with x-ray reconstructed image output. Two PCNN start to segment each of image and at the end of process, we count the number of pixel which has a white color (value 1). Depending on this value, we calculate the difference between the PCNN outputs, then the percentage of alteration (cure or deterioration). On the screen, the doctor can see directly the impacted/cured region. The Fig. 4 explains with more details the chart of the algorithm.

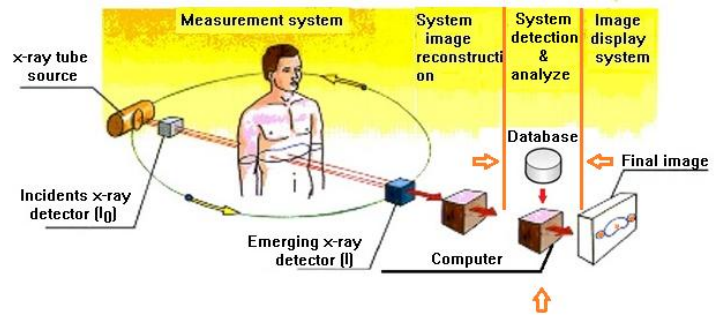


Fig. 3. Fundamental principles of x-ray scanner with new module

Mainly, this simple method helps the doctor to follow the evolution of his patient illness. In case, he wants to compare some image from database, the algorithm is still valid but used offline i.e. the reconstructed image is replaced by another image from database.

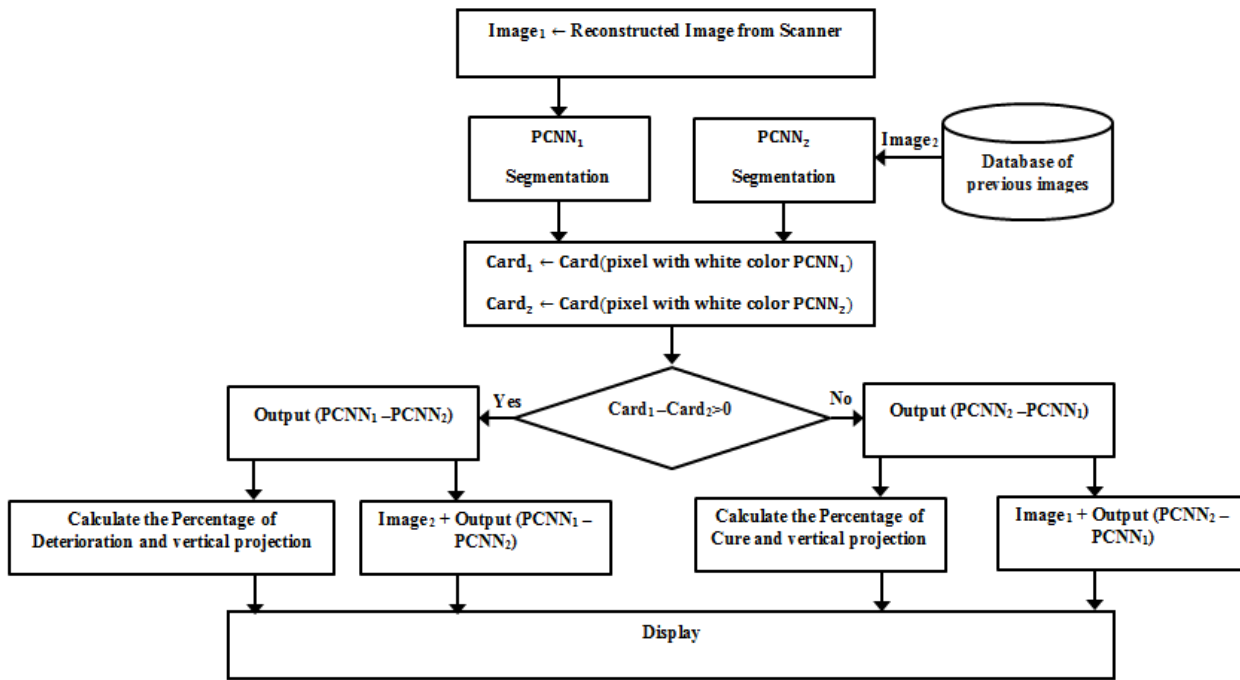


Fig. 4. Supplementary module method

PCNN configuration is very important here because it will ensure the good performance of image segmentation. In our case, the neural network uses the following parameters:

- Weights matrix:

$$M = W = \begin{bmatrix} \sqrt{2}/2 & 1 & \sqrt{2}/2 \\ 1 & 1 & 1 \\ \sqrt{2}/2 & 1 & \sqrt{2}/2 \end{bmatrix} \quad (8)$$

- Initial values of matrix:

The initial values of linking L, feeding F matrix and the stimulus S are the same as the input image $R \times C$. The convolution between null matrix which has the same size as the input image and weights matrix initiates the output value Y of PCNN. The first value of dynamic threshold Θ is an R -by- C matrix of two.

- Delay constants:

$$\alpha_F = 0.1, \alpha_L = 0.3 \text{ and } \alpha_\Theta = 0.2$$

- Normalizing constants:

$$V_F = 1.5, V_L = 0.2, V_\Theta = 20 \text{ and } \beta = 0.1$$

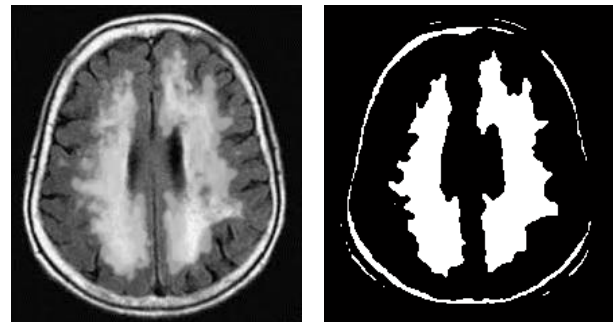


Fig. 5. Image original and segmented – Scanner

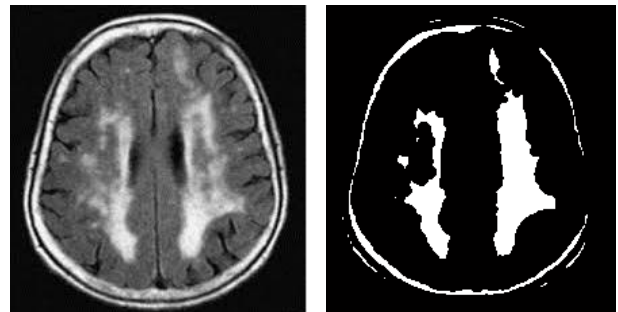


Fig. 6. Image original and segmented – Database

Three iterations are enough for image segmentation. Fig. 5 and Fig. 6 present segmented images after three iterations successive with the corresponding original image.

The brain scanner segmented image contains more white color pixel than the image from database. So we should calculate the difference between scanner and database segmented image and add it with smaller original image to be visualized on final screen.

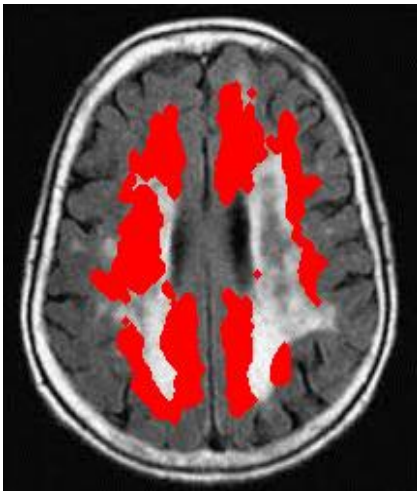


Fig. 7. Final x-ray scanner output image

The below equation shows how to calculate the region's deterioration or cure percentage:

$$\text{percentage of impacted region} = \frac{\text{Card}_1 - \text{Card}_2}{\max(\text{Card}_1, \text{Card}_2)} \times 100 \tag{9}$$

For our example, the deterioration percentage is at 41.74% (red color). Another way to analyze the image is to calculate the vertical projection as following:

$$I_{pv_x} = \sum_{x=1}^c I(x, y) \tag{10}$$

We just plot the vertical projection for the both output of PCNN on the same figure and compare.

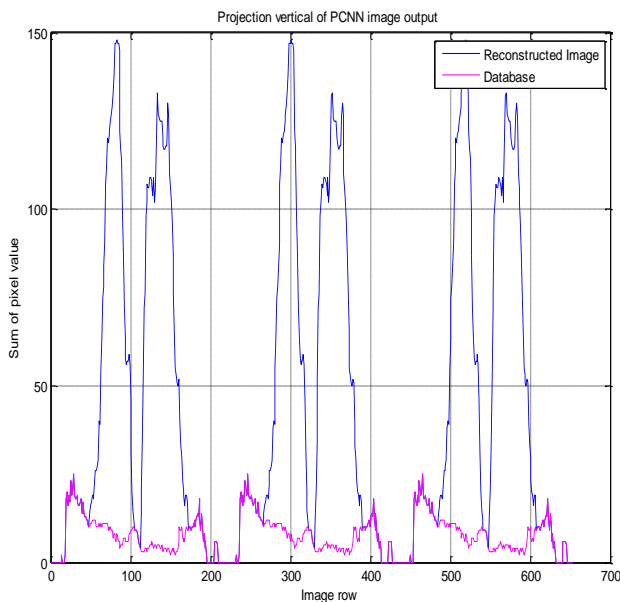


Fig. 8. Comparison with vertical projection

The reconstructed image graph has very high peak than the image from database. It means that the patient is not cured. In case these peaks become lower than the peak of image from database, it is a good indication of cure. To differentiate cured and deterioration state, we have three indications: impacted region percentage ('-' for cured and '+' for deterioration), region color (green for cured and red for deterioration), vertical projection (low peak for cured and high peak for deterioration).

5 RESULTS

For testing, we have two patients: the first one (patient 1) has a brain tumor and the second (patient 2) with subtalar arthrosis. The first scanner exam was done on 2008 for the patient 1, then on 2009 and 2011. With the new proposed module, we can notice that the patient has a positive result. The region impacted is reduced showing by the following figures. The green color describes the cured region and the only region surrounded by the last one presents a disease area.

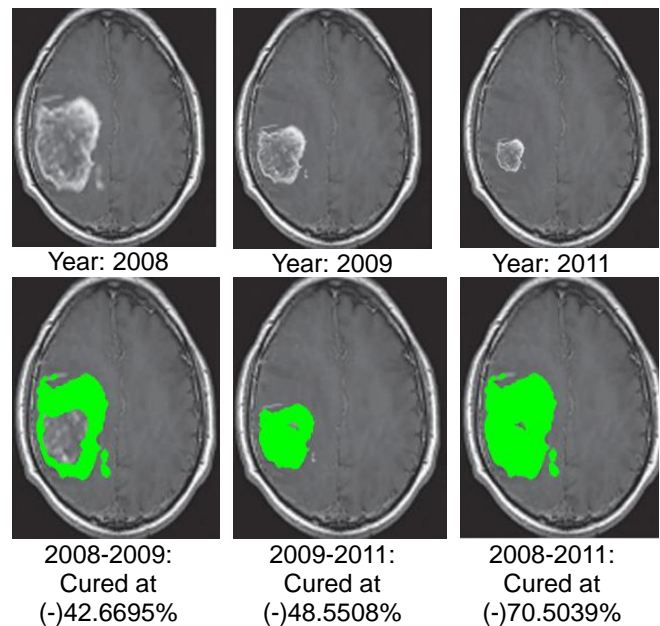


Fig. 9. Cured evolution of patient 1

For the patient 2, the medical examination was done every year. As per the supplementary module result on Fig. 10, there is a dilatation of arthrosis region (marked in red). Between 2010 and 2012, the deterioration rate is around 68.08%.

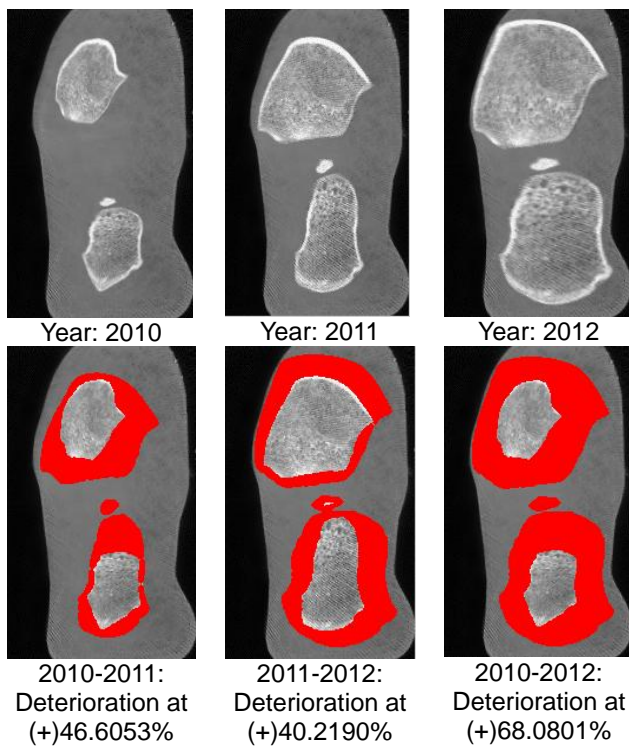


Fig. 10. Deterioration evolution of patient 2

6 CONCLUSIONS

In this paper, we proposed a supplementary module for x-ray scanner used on medical domain to follow the evolution of patient's illnesses. This module is inserted between image reconstruction system and visualization. The reconstructed image is the first input of the algorithm and the second one is from database. The both pass on segmentation step using Pulse-Coupled Neural Network which has an excellent performance on image segmentation. To obtain the analyze result, we calculate the difference between PCNN outputs and the percentage of cured/deterioration. The final screen, in which the doctor looks the result, shows in green/red color the region impacted i.e. cured/deterioration region. The percentage is prefixed by '+' in case of deterioration and by '-' for cured. This module doesn't increase the response time of the functionality of standard scanner because his response time is only around two milliseconds due of PCNN ability to segment image. The algorithm is very simple and helpful for scanner user end.

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