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# Profiling the Features of Pre-segmented Healthy Liver CT Scans: Towards Fast Detection of Liver Lesions in Emergency Scenario

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***Abstract*—Automating the detection of lesions in liver CT scans requires a high performance and robust solution. With CT-scan start to become the norm in emergency department, the need for a fast and efficient liver lesions detection method is arising. In this paper, we propose a fast and evolvable method to profile the features of pre-segmented healthy liver and use it to detect the presence of liver lesions in emergency scenario. Our preliminary experiment with the MICCAI 2007 grand challenge datasets shows promising results of a fast training time, ability to evolve the produced healthy liver profiles, and accurate detection of the liver lesions. Lastly, the future work directions are also presented.**

## I. Introduction

COMPUTED Tomography (CT) scan is a medical imaging method that uses x-rays to create a non-superimposed, cross-sectional, and multi-slices images of a particular part of body [1]. Since its inception as an application in radiological diagnostics during the seventies, CT scan has evolved to become an integral part of the medical image analysis research. In particular, research on automatic liver lesions detection and delineation using CT images has been an active and challenging sub-area of medical image analysis research.

Numerous works have been devoted to propose solutions to automatically detect liver lesions, especially tumors, using different approaches and techniques. Generally, the recent advances in liver lesions detection can be summarized into five main approaches: using machine learning methods [3-6], using region based methods [7-8], using edge detection methods [9] and using partial differential equation-based methods [10-11].

Although the output of these state of the art researches has shown to achieve satisfactory results, however, most approaches share the same limitation: it was very time-consuming and computationally expensive due to the growing number of CT-scan image slices for each studies. With the exponential growth of CT-scan usage trends in emergency department [2], a system that is able to accurately and quickly detect the presence of liver lesions in CT images immediately after the scanning process finished will help medical experts to better plan their actions because, in case emergency surgery is needed, failure to detect liver lesions can have some clinical risks [12-13]. The work presented in this paper aimed to propose an alternative solution of that could quickly analyze hundreds of CT images and detect liver lesions in emergency scenario. Specifically, our focus is towards proposing an evolvable machine learning solutions.

Evolving connectionist system (ECOS) framework, among others, is one of the most successful machine learning frameworks [14], which is evolvable in structure and offers adaptive functionalities. Motivated by the wide success of ECOS implementation applied in other domains [15-17], we propose to enhance and modify one of ECOS framework implementation called Evolving-neural-based Fuzzy Inference System (EFIS) and its online clustering methods ECMm [18] to perform fast detection of the liver lesions in CT images.

The idea of having an evolvable detection method is also an attempt to address one of the most important challenges in liver lesions detection: the fact that liver CT scans can have a wide spectrum of forms, structures, intensity distributions, as well as other properties depending on the settings of one particular scans. This may lead to problems that existing detection methods tend to produce inaccurate results when the CT scans is acquired using different settings from one it originally designed and trained to detect. Therefore, a detection method that is able to learn new images dynamically and evolve its structure is needed.

The reminder of this paper is organized as follows: Section 2 presents our proposed fast and evolvable methodology and the materials used in this work. The preliminary results of our experiments and its discussion are presented in Section 3. A conclusion and future work direction described in Section 4 ends this paper.

## II. Materials and Methods

### A. Overview

Fig.1 shows our proposed evolvable methodology to detect the presence of liver tumor in emergency scenario. The three core components are the GLCM feature extraction component, feature profiling using ECMm-Sorensen, and the liver lesions detection using EFIS. In addition, two support components such as the thin client and alerting component are basically designed to integrate the proposed

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detection methodology into existing emergency scenario diagnostic workflow.

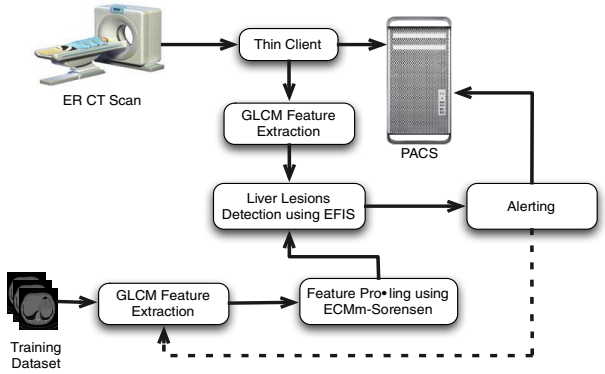


Fig. 1. Proposed methodology.

The initialization process starts with extracting the GLCM features from the healthy liver training CT images, and then create the profile of the healthy liver features using ECMm-Sorensen, and finally extract the fuzzy rules of this healthy liver features. Next the main process workflow starts whenever there is an emergency CT scans performed, the thin client component will send a copy of the produced CT images to be quickly scanned to detect the presence of liver lesions using the previously created healthy liver profiles. When liver lesions detected in the CT images, the alerting component will update the PACS details on the particular CT scans marked as containing liver lesions. Medical experts can evaluate the output of the detection and let the ECMm evolve the created profile by feeding new CT scans acquired with different settings.

### *B. GLCM Features Extraction and Selection*

The Grey Level Co-occurrence Matrix (GLCM) is a second order statistical pixel-based widely used for texture analysis on medical images. The basic idea of this second order texture extraction method is to use a matrix to keep track of each possible pairs of grey levels and the number of pixel intensity pairs at a distance given by a specific displacement vector [19].

We ran a simple test to evaluate each of GLCM feature descriptors on a few random abdominal CT images. Based on visual appearance on liver lesions visibility, we decide to first start to use 4 GLCM feature descriptors in our preliminary experiment reported in Section 3. Following are the properties of each feature descriptors:

- Energy: $\sum_{i=1}^{n}\sum_{j=1}^{m} P(i,j)^2$ (1)
- Entropy: $\sum_{i=0}^{G-1}\sum_{j=0}^{G-1} P(i,j) \times \log(P(i,j))$ (2)
- Sum of Average: $\sum_{i=0}^{2G-2} iP_{x+y}(i)$ (3)
- Maximum Probability: $\mathrm{MAX}_{i,j} P(i,j)$ (4)

In addition, the window size used to compute the 4 feature descriptors above is a 3x3 matrix.

### *C. Enhanced Evolving Clustering Method*

In order to dynamically create a profile of the extracted healthy liver features, we modify our previously designed ECMm algorithm [18]. ECMm is an enhanced evolving clustering method derived from the ECOS framework aimed to dynamically cluster an online input stream of data. It is a distance-based clustering method where no predefined number of clusters needed.

The original ECMm algorithm is using the normalized Euclidean distance measurement to calculate the distance between the new input data and the cluster center. To fits the nature of the GLCM features, we modify ECMm to use different distance measurement calculation. In our small experiments, not reported in this paper, we evaluate three other distance measurement equations such as Manhattan distance, Chebyshev distance, and Sorensen distance in addition to Euclidean distance. Our findings show that the Sorensen distance performs better than the other four distance equations including the original Euclidean distance. The ECMm with Sorensen distance retains sensitivity in more heterogeneous features data and gives less weight to outliers. Hence, in this work we propose the modified ECMm-Sorensen to profile the extracted GLCM features of healthy liver. The following summarizes the main steps in the proposed ECMm-Sorensen algorithm:

Step 1. If cluster previously produced exist, initializes the cluster center $Cc_j$, $j$ = 1,2,3,…,$n$. Else, go to Step 6 to start creating new clusters.

Step 2. Determine the membership matrix $U$ for each of its element $u_{ij}$ derived from:

$$\text{IF } \frac{|x_i - Cc_j|}{(x_i + Cc_j)} \leq \frac{|x_i - Cc_k|}{(x_i + Cc_k)}, \text{ for } k = 1,2,3,\ldots, n, j \neq k,$$
$$\text{THEN } u_{ij} = 1, \text{ ELSE } u_{ij} = 0 \quad (5)$$

Step 3. Employ the constrained minimization method to modify the cluster centers using:

$$\frac{|x_k - Cc_j|}{(x_k + Cc_j)} \leq Dthr \quad (6)$$

Step 4. To optimize the cluster, calculate the objective function $J$ which defined by the following:

$$J = \sum_{j=1}^{n} J_j \quad (7)$$

where

$$J_j = \sum_{k, xk \in C_j} \frac{|x_k - Cc_j|}{(x_k + Cc_j)} \text{ for each } j = 1,2,3,\ldots, n.$$

Step 5. If the result or the improvement is below a certain tolerance value, or the iteration number of minimizing operation is over a certain value, go to Step 7. Else, go back to Step 2.

Step 6. Create the first cluster $C_1$ by taking the position of the first input data as the first cluster center $Cc_1$, and set its cluster radius $Ru_1$ value to 0.

Step 7. If no more input data presented, the clustering processes finishes. Else, take the current input example $\boldsymbol{x}_i$, and calculate the Sorensen distance $D_{ij}$ between $\boldsymbol{x}_i$ and all existing cluster centers $Cc_j$ using:

$$D_{ij} = \frac{|x_i - Cc_j|}{(x_i + Cc_j)} \quad (8)$$

Step 8. If exist a cluster $C_m$ with a center $Cc_m$, a cluster radius $Ru_m$, and the Sorensen distance value $D_{ij}$ such that:

$$D_{im} = \frac{|x_i - Cc_m|}{(x_i + Cc_m)} = min\ \{D_{ij}\}$$
$$= min\ \{\frac{|x_i - Cc_j|}{(x_i + Cc_j)}\}\ \text{for}\ j = 1,2,3,\ldots,n; \quad (9)$$

and

$$D_{im} < Ru_m \quad (10)$$

then the current $\boldsymbol{x}_i$ belong to this cluster. Go back to Step 7. Else, continue to Step 9.

Step 9. Find a cluster $C_a$ with a center $Cc_a$, a cluster radius $Ru_a$, and a Sorensen distance value $D_{ia}$ which has a minimum $S_{ia}$ value:

$$S_{ia} = D_{ia} + Ru_a = min\{S_{ij}\}, j = 1,2,3,\ldots, n \quad (11)$$

Step 10. If $S_{ia}$ is greater than $2\times Dthr$, the example $\boldsymbol{x}_i$ does not belong to any existing cluster. Then repeat the process from Step 6 to create a new cluster.

Step 11. If $S_{ia}$ is not greater than $2\times Dthr$, then cluster $C_a$ is updated by moving its $Cc_a$ center and increasing its radius value $Ru_a$. The updated radius $Ru_a^{new}$ is set to be equal to $S_{ia}/2$ and the new center $Cc_a^{new}$ is located on the line connecting input vector $\boldsymbol{x}_i$ and the old cluster center $Cc_a$, so that the distance from the new center $Cc_a^{new}$ to the point $\boldsymbol{x}_i$ is equal to $Ru_a^{new}$. Go back to Step 7.

### D. Evolvable-neural-based Fuzzy Inference System

EFIS, Evolvable-neural-based Fuzzy Inference System, is an ECoS-based implementation of fuzzy inference system that is specifically designed to profile the normal behavior of network traffic and detect traffic anomaly in online mode [18]. EFIS offers self-ability to evolve in open space and deal with concept drift problem in online and lifelong mode. With aim to create profiles of a healthy liver, here we modify the Evolvable-neural-based Fuzzy Inference System (EFIS) to extract the profiles of the healthy liver features from clusters created using the proposed ECMm-Sorensen.

We maintain the two main parts of EFIS structure: the Profile Creation and Management (PCM) module which creates and extracts rules from the clustering results; and the Neuro-Fuzzy Model (NFM) module which is a 5 layer neural-based fuzzy inference system [18]. The PCM module connects EFIS with the proposed ECMm-Sorensen clustering method in order to dynamically partition the input space. The main purpose is to extract fuzzy rules from the clusters created by ECMm-Sorensen. These rules are basically the profile of healthy liver features. Whereas the main purpose of the NFM module is basically to use the extracted rules to determine the state of the liver.

The rule extraction algorithm used in our modified EFIS is as follows:

Step 1. Take the first data points from the features data set.

Step 2. Obtain the $m$ cluster centers of the resulted clustering using ECMm-Sorensen.

Step 3. For every cluster centers $C_i$, find all data points whose position in the input space are closest to the center, $i = 1, 2, \ldots, m$.

Step 4. Extract the fuzzy rule corresponding to a cluster center by creating the antecedents of the fuzzy rule using the position of the cluster center and the consequent part is simply a state Boolean value.

Fig. 2 illustrates how the rules are mapped with the given sample cluster A resulted from ECMm-Sorensen in terms of the membership functions. The extracted rule type itself is of a Takagi-Sugeno fuzzy rule in the following format:

IF $x_1$ is *Eng* and $x_2$ is *Ent* and $x_3$ is *SoA* and $x_4$ is *MxP*
THEN $y$ is $H$ (12)

where $x_1$, $x_2$, $x_3$, $x_4$ represent the Energy, Entropy, Sum of Average, and Max Probability Features respectively. *Eng*, *Ent*, *SoA*, and *MxP* are fuzzy values defined by the triangular fuzzy membership function $\mu_1$, $\mu_2$, $\mu_3$, $\mu_4$ respectively. And $H$ is the boolean state of the profile, either healthy or with lesions. And to further minimize the number of cluster created due to noise, we set a scheme to omit outlier clusters using the following:

IF $Ru_a \leq Dthr/5$ OR total instances in $C_a \leq 6$
THEN $C_a$ considered as outlier (13)

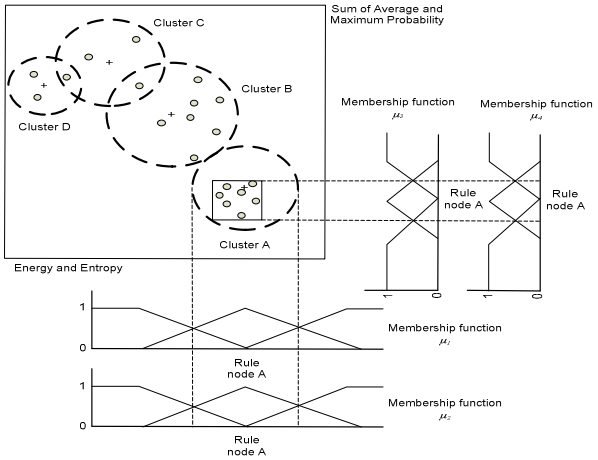


Fig. 2. An illustration of EFIS rule extraction process.

The contents of each healthy liver profiles can be manually evaluated since EFIS allows user to view all the rules in a particular profile. This would avoid black box symptoms like most connectionist systems (especially neural network based system). These profiles are then passed to the NFM module, inserted into the neuro-fuzzy inference structure, and ready to determine the liver state.

### E. Datasets

In this paper, we use the MICCAI 2007 grand challenge datasets [20] to evaluate the efficacy of our proposed evolvable methodology. The MICCAI 2007 datasets were contrast-enhanced CT images and acquired in transversal direction, with pixel sizes between 0.55 and 0.8 mm and inter-slice distance between 1 and 5 mm, on a variety of scanners from different manufacturers [20]. Both the training and testing datasets are used with its manual segmentation mask to obtain pre-segmented liver images.

## III. Experimental Results and Discussions

Here we report the results of two preliminary experiments conducted to evaluate our proposed evolvable method. At this stage, the focus of our experiments is to test the ability

of the proposed ECMm-Sorensen and the modified EFIS to profile the features of healthy liver and detect the presence of liver lesions. As such, in both experiments, we assume the liver is already segmented from the original abdominal CT images. In particular, we use the liver masks come with the MICCAI 2007 datasets and, instead of using different mask for different CT images, we overlapped these different masks provided and create a single mask to be used to obtain the pre-segmented liver region. Therefore, we can say that this mask is used as the profile healthy liver region and the pre-segmented liver region cropped using the same mask from incoming abdominal CT images is compared with the healthy liver profile to detect the presence of liver lesions.

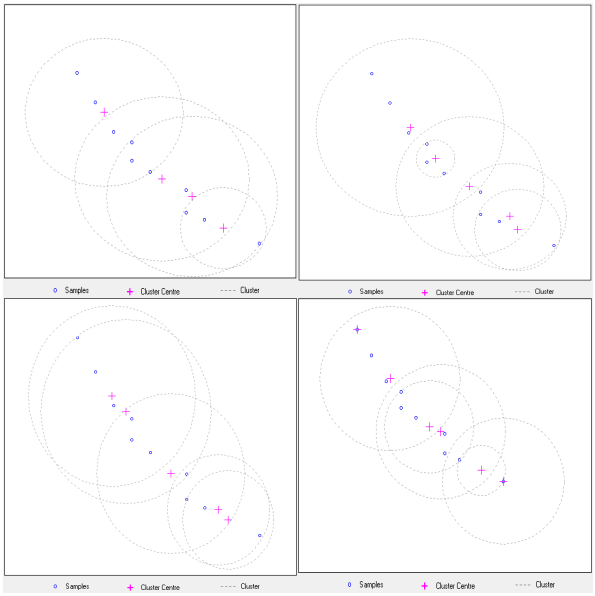


Fig. 3. ECMm-Sorensen clustering results profiling healthy liver.

### A. Training Experiment

In the first training experiment we use 10 abdominal CT images from MICCAI 2007 datasets containing healthy liver to evaluate ECMm-Sorensen in profiling the features of healthy liver. The one mask previously created is used to obtain the pre-segmented liver region from the 10 abdominal CT images before extracting its GLCM features. Fig. 3 depicts the ECMm-Sorensen clustering results for the first four pre-segmented healthy liver.

From Fig. 3 we can see that the clustering results presents similar pattern of healthy liver features. However, as the features values of each pre-segmented healthy liver is different depending on the settings used to acquire the corresponding CT image, we also can see that ECMm-Sorensen produce different clustering results for each pre-segmented liver, which indicate the evolution of the created profile to cover more healthy liver features properties as different healthy liver properties is presented.

This analysis is supported by the complete statistical results of the overall training experiments shown in Fig. 4. We can see that the objective value of the ECMm-Sorensen is decreasing and become more stable when presented with the last 3 of the pre-segmented healthy liver. This indicates the profile created becoming more and more comprehensive and the last 3 pre-segmented liver features is similar with what has been profiled before.

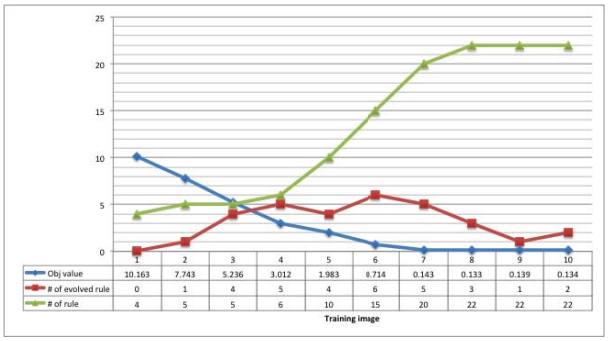


Fig. 4. ECMm-Sorensen statistical results during training experiment.

Statistics in Fig. 4 also shows the evolution of increasing number of rules inside the created healthy liver profile with 22 rules are created in the end. In addition, the statistics also report similar evolution pattern on the count of evolved/adapted rules. Lastly in terms of speed, on average, clustering each pre-segmented healthy liver took less than 6 seconds.

### B. Preliminary Evaluation

In the second of the experiment, we report a preliminary evaluation of the ability of our proposed evolvable method to quickly detect the presence of liver lesions. We use 10 different abdominal CT images containing healthy liver and another 15 abdominal CT images containing liver with lesions from MICCAI 2007 datasets. Similar to the training experiment, a pre-segmented liver region is obtained from these testing CT images first before the GLCM features being extracted. Fig. 5 shows the EFIS rule firing statistics during few of liver lesions detection session throughout the experiment.

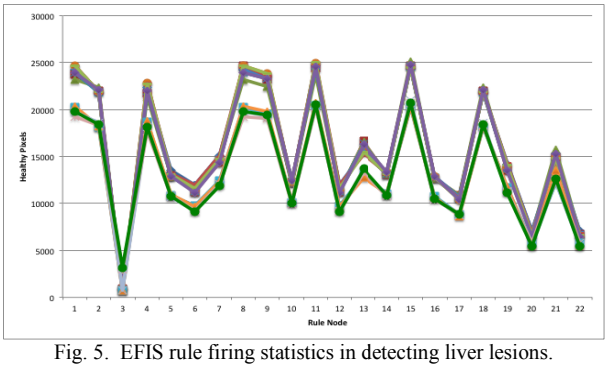


Fig. 5. EFIS rule firing statistics in detecting liver lesions.

We set the alerting component to trigger lesions detection alert when there exist a rule fired less than 5000 times. That being said, the more rules being fired, the more likely the pre-segmented liver considered to be healthy. From Fig. 5 we can observe that when presented with pre-segmented liver with lesions, one of the rule will be fired less than 5000 times and when it happens, the alerting component successfully raised an alert that there is a lesions detected in

the particular pre-segmented lesions.

With the same settings applied to the alerting components throughout the experiment, the modified EFIS, using the healthy liver profile created by ECMm-Sorensen, manage to quickly detect the presence of liver lesions regardless of its size in all the 15 pre-segmented liver containing lesions and classify the liver as healthy in all the 10 pre-segmented liver without lesions. Particularly, the proposed method is able to detect the presence of small lesions with limited visibility as seen in the left image of Fig. 6. It also manages to classify healthy liver as healthy even with the presence of some non-lesion liver texture as depicted in the right image of Fig. 6. Overall, the preliminary results obtained are very encouraging.

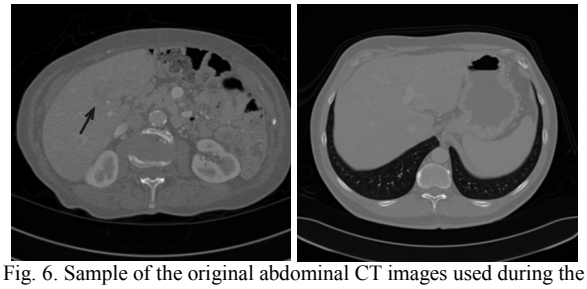

Fig. 6. Sample of the original abdominal CT images used during the preliminary evaluation.

## IV. Conclusions and Future Works

In this paper, we introduce an alternative method to dynamically create a profile of healthy liver to detect the presence of liver lesions in emergency scenario. Our preliminary experiments shows an encouraging results of the ability of the proposed ECMm-Sorensen and the modified EFIS to cluster the GLCM features extracted from pre-segmented healthy liver, create profile of fuzzy rules, and perform real-time liver lesions detection with high accuracy.

As part of an on-going project, the proposed method still needs improvements in many ways for future works. Among the improvements planned are experimenting with different window size to extract the GLCM features value, proposing an online and fast segmentation algorithm to eliminate the current limitation of using pre-segmented liver region, and further modifying the EFIS structure. Most importantly, conducting more rigorous experiments with real clinical CT scan images in emergency scenario will be carried out with our partner hospital.

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