A FUZZY-BASED LEARNING VECTOR QUANTIZATION NEURAL NETWORK FOR RECURRENT NASAL PAPILLOMA DETECTION

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ABSTRACT

The objective of the paper is to develop a suite of effective and prompt methods for recurrent nasal papilloma (RNP) detection. The magnetic resonance image (MRI) is one of the common auxiliary tools utilized to clinically diagnose recurrent nasal papilloma nowadays. Owing to the response of RNP regions in Gadolinium-enhanced magnetic resonance images is different from the response of normal tissues, the difference between the dynamic-MR images before and after administering contrast material can be calculated and extract the suspicious RNP regions automatically with image processing techniques. Then, a fuzzy algorithm for learning vector quantization (FALVQ) neural network is used to pick the actual RNP regions. Finally, the RNP regions are detected integrally by region growing method based on the features of pixels in actual RNP regions. The experimental results show that the proposed method can detect RNP regions automatically, correctly and fast.

1. INTRODUCTION

Since the environment pollution, the portion of human in Asia suffers from nasal papilloma is increasing gradually. Therefore, it is important to obtain better detection results for surgery. Recently, a new image modality called Gadolinium-enhanced dynamic magnetic resonance images (MRIs) has been developed and is widely used in the diagnosis of recurrent nasal papilloma (RNP) [1-2].

The dynamic-MRIs are taken in the same location at particular time (0, 5, 30, 60, 90, 120, 300 seconds) after injecting into the patient with Gadolinium. After injection, the graylevel responses in RNP regions will increase as time increases. The responses will reach a stable status after a certain time period. The continuously acquisition images technique causes different variations of graylevel between tumor and normal tissues and the tumor regions can be found out according to the characteristic, nevertheless, it is hardly to identify the area as tumor by means of human eyesight.

In order to solve this problem, Brix et al. [1-2] proposed to construct the temporal intensities into a curve called the relative signal intensity (RSI). They further developed a mathematical pharmacokinetic model to fit the RSI curves with three adjustable parameters: $A$ (enhancement amplitude), $T_c$ (tissue distribution time), and $C$ (first-order washout rate). According to the $A$ and $T_c$ values, the possibility that pixel associated with the RSI curve is a tumor pixel can be estimate. However, this procedure is very time-consuming. Therefore, Huang et al. [8] developed a computer-aided system, which allows users to delineate an initial region of interest (ROI). Then, through an active contour technique, the system automatically extracts a more precise ROI. For each pixel inside the ROI region, its temporal intensity values are converted into an RSI curve [1], which is then fitted into the three-parameter mathematical pharmacokinetic model proposed by Brix et al. To facilitate visual interpretation, each pair of $A$ and $T_c$ values is also mapped into a colored image representation of the recurrent nasal tumor. While these contributions have facilitated the recognition of tumor characteristics in the dynamic MR images, this approach is still limited in two respects: First, finding the ROI is done in a semiautomatic manner, which implies that physicians must identify the suspicious lesion a priori; that is, lesion detection is actually not conducted in their work. Second, the RSI curves in the same region vary considerably, making the identification of the tumor less accurate. Due to the difference of RSI curves of nasal papilloma area is too large to represent the information of tumor; Chang et al. [3] proposed a novel curve called Relative Intensity Change (RIC) to diminish the difference of curves.

Therefore, the motivation of this paper is to propose a RIC-based fuzzy algorithm for learning vectors quantization (FALVQ) neural network to detect the recurrent nasal papilloma automatically. Figure 1 shows the schematic block of the proposed method.
In the proposed method, instead of identifying the ROI by physicians, we extract the suspicious recurrent nasal papilloma regions from the MRI sequences automatically. Secondly, we apply the fuzzy clustering algorithm [6-7] and fuzzy algorithms for learning vectors quantization (FALVQ) neural network [4-5] to segment the suspicious recurrent nasal papilloma regions and classify them according to the property of RIC curves. Thirdly, we identify the absolute position of recurrent nasal papilloma in terms of the pathological characteristic of the scope where nasal papillma occurred. Finally, a feature-based region growing is executed to retrieve the shape of RNP completely. Experimental results show that the RNP regions can be extracted accurately.

The remainder of this paper is organized as follows. In Section II, the proposed method and the architecture of classification model contained fuzzy c-Means algorithm and FAVLQ neural network is introduced. The experimental results of the proposed method are presented in Section III. Finally, conclusions are drawn in Section IV.

2. METHOD

2.1 Extracting Suspicious RNP Regions

In MRIs, there is some artifact noise contained in background inevitably. Therefore, a region growing method is applying to extract the region of head in images and remove the noise in background from head region mask images [11]. Then we define the head region image difference as follows:

\[ D_i = S_i - S_0 \]  

where \( S_i \) is the \( i \)-th dynamic-MRI obtained at different acquisition time, \( S_0 \) is the first MRI before injection. Therefore, the average difference of head region image is defined as

\[ D_m = \frac{1}{N} \sum_{i=1}^{N} D_i \]  

where \( N \) is the number of dynamic-MRIs sequences.

Since the influence of artifact in MRIs, we use a median filter to deal with the average difference image in order to remove the artifact noise. The median filter can be represented as follows:

\[ M(x, y) = \text{median}_{(i,j) \in B_{xy}}[D_m(s, t)] \]  

where \( B_{xy} \) is a \( n \times n \) mask whose center is \((x, y)\). Relative to the image before injection, the image \( M \) obtained by Eq. (1-3) only retains regions with difference of graylevel values. According to the property of RSI curves, the graylevel values of recurrent nasal papilloma area are about one and half times of these values before injection, therefore, the threshold \( T \) value is defined as:

\[ T = 1.5 \cdot \frac{Q(M_T) - \delta(M_T)}{2} \]  

\[ M_T = |M(x, y) - M(x, y) > 0| \]  

where \( Q \) is the mean value and \( \delta \) is the standard deviation of the image \( M \). Hence, we utilize thresholding to deal with image \( M \) in order to remove the influence of noise.

Injection into the patient with Gadolinium is expected that recurrent nasal papilloma region has unusual response in dynamic MRIs, however, Gadolinium has response not merely in tumor but also in the region around tumor. Therefore, results of thresholding appear the phenomenon of over-detection. In order to isolate the tumor region, we...
use opening morphologic operators to clear up redundant fragments.

The schematic block diagram of the proposed method to extract suspicious regions is summarized as Fig. 2.

![Schematic block diagram](image)

**Fig. 2** The schematic block diagram to extract the regions of suspicious RNP

The dynamic-MRIs are handled according to the flowchart step by step to extract suspicious regions of recurrent nasal papilloma.

### 2.2 Classification Model

After previous processes, we can obtain the region of suspicious recurrent nasal papilloma. However, not only tumor but also some other normal tissues are extracted. Therefore the FALVQ neural network is used to classify these suspicious regions into two categories (tumor and normal region). The input vector set of the classification model is shown as Fig. 3.

![Input vector set](image)

**Fig. 3** The diagram of input vector set of the classification model

The graylevel value in the MRI before injection and associate RIC values of each pixel in suspicious regions is adopted as input vector in fuzzy c-means algorithm [6-7], the i-th suspicious input vector can be represented as:

\[
x_i = [g_i(1), RIC_{i2}, \ldots, RIC_{i7}] = [x_{i1}, x_{i2}, \ldots, x_{i7}]\]

where \(g_i(k)\) is the graylevel of the i-th pixel at k-th image, \(k=1,2,\ldots,7\). These RIC values of the i-th pixel are represented as:

\[
R_i = \left[\begin{array}{c} g_i(1) \\ g_i(2) \\ \vdots \\ g_i(7) \end{array} \right] = [RIC_{i1}, RIC_{i2}, \ldots, RIC_{i7}]\]

Hence, the suspicious RNP regions can be defined as \(X = \{x_1, x_2, \ldots, x_n\}\). According to the membership functions matrix \(U = [\mu_{ij}]\), the suspicious regions are categorized into two clusters \(c_1\) and \(c_2\). The element \(\mu_{ij}\) denotes the degree of possibility that a suspicious RNP region \(x_i\) belongs to \(j\)-th cluster. The clustering algorithm is summarized as follows.

**Step (1)** Initialize the number of classes \(c=2\) and \(U(t)\), the fuzzification parameter \(m\) (\(1 \leq m \leq \infty\)), and the threshold of converge \(\varepsilon > 0\). Set \(t=0\);

**Step (2)** Calculate the class center matrix \(U(t) = [w_1, w_2]\) using:

\[
w_j = \frac{1}{\sum_{i=1}^{n} (\mu_{ij})^{2}} \sum_{i=1}^{n} (\mu_{ij})^{m} x_i \quad \text{for every } j
\]

**Step (3)** Calculate the membership matrix \(U(t+1) = [\mu_{ij}]\) using:

\[
\mu_{ij} = \left( \sum_{j=1}^{2} \left( \frac{|x_j-w_j|}{|K_j-w_j|} \right)^{2(m-1)} \right)^{-1}
\]

for every \(i\) and \(j\)

**Step (4)** Calculate \(\Delta = \max|U(t+1) - U(t)|\). If \(\Delta > \varepsilon\), then go to Step (2) and set \(t = t+1\); otherwise stop the process.

Since the objective of the proposed method is to distinguish between the RNP regions and normal tissue, therefore the suspicious RNP regions will be classified into two categories: the normal and the RNP. The two cluster centers are set to the initial vectors of prototype of FALVQ which are represented as \(u = \{v_1, v_2\}\). Each input vector of FALVQ can be represented as \(x_i = [g_i(1), RIC_{i2}, \ldots, RIC_{i7}]\); and only the pixels in the suspicious RNP regions are fed into the FALVQ.

During the FALVQ process, \(u(x)\) represents membership function that regulates the competition between the prototypes \(v_1\) and \(v_2\) for the input \(x\). The specific form of the membership functions determines the strength of attraction between input and the prototypes during the learning process. Assuming that \(v_1\) is the
winning prototype and \( v_j \) is the losing prototype corresponding to the input vector \( x \) in the Euclidean distance sense, we define the winning membership \( u_{\text{win}}(x) = 1 \), and the losing membership as:

\[
u_{\text{lose}}(x) = \frac{\|x - v_i\|^2}{\|x - v_j\|^2},
\]

where \( u(x) = x(1 + x)^{-1} \).

The winning prototype \( v_i \) can be updated by:

\[
\Delta v_i = \eta (x - v_i)(1 + w_{\text{lose}}(x)),
\]

where \( \eta \) is the learning rate and

\[
w_{\text{lose}}(x) = w\left(\frac{\|x - v_i\|^2}{\|x - v_j\|^2}\right)
\]

with \( w(\cdot) = u'(\cdot) \).

Each losing prototype \( v_j \neq v_i \) can be updated by:

\[
\Delta v_j = \eta (x - v_j)w_{\text{lose}}(x)
\]

where \( n_{\text{lose}}(x) = n\left(\frac{\|x - v_i\|^2}{\|x - v_j\|^2}\right) \) with

\[
n(\cdot) = u(\cdot) - z u'(\cdot).
\]

The learning rate \( \eta \) should be time varying. It should start at a relative large initial learning rate \( \eta_0 \), and then shrink monotonically with increasing iteration \( \nu \). This can be defined as:

\[
\eta = \eta_0 \left(1 - \nu / N\right)
\]

where \( N \) is the total number of iterations predetermined for the learning process. The membership functions \( u(\cdot) \) generated the corresponding interference functions \( w(\cdot) \) and \( n(\cdot) \).

The proposed FALVQ algorithm can be summarized as follows:

Step (1) Set \( c = 2, \eta_0, N\); and \( \nu = 0 \); receive an initial prototype

\[\mathcal{U}_0 = \{v_{1,0}, v_{2,0}\}\] from clustering algorithm.

Step (2) Use Eq. (14) to calculate the learning rate \( \eta \).

Step (3) Set \( \nu = \nu + 1 \).

Step (4) For each input vector \( x \): find winning prototype \( i \) such that

\[
\|x - v_{i,\nu-1}\|^2 < \|x - v_{j,\nu-1}\|^2;
\]

use Eq. (9) to calculate \( u_{\text{lose}}(x) \),

use Eq. (11) to calculate \( w_{\text{lose}}(x) \),

use Eq. (13) to calculate \( n_{\text{lose}}(x) \),

update \( v_i \) by Eq. (10),

update \( v_j \neq v_i \) by Eq. (12).

Step (5) If \( \nu < N \), then go to 2. Otherwise, we stop the algorithm.

Fig. 4 illustrates the architecture of the proposed classification model.

Fig. 4 The architecture of the proposed classification model

2.3 Characteristic of RNP

The major objective of the third phase is to extract the actual region of RNP from classified results. According to medical reports, the scope of most RNP occurred is located at the region between the nasal cavity and skull, only in a few serious cases does the skull suffer from invasion by the RNP. Base on this pathological characteristic, we draw a semicircular region centered at the center of the head contour region \( C \), within a radius of \( 1/3 \|C, Top\| \), where \( Top \) is the highest point of the head contour [9]. RNP will
occurs in the scope of semicircle. Therefore, the correct position of RNP is the largest detected region connected with the semicircle. Fig. 5 shows the search region of possible recurrent nasal papilloma.

### 2.4 Recovery of RNP Region

Through all procedures proposed above, we can extract an almost actual region of RNP without pixels belonged to normal tissues practically, but some pixels of actual RNP located at the boundary or suburb of RNP region are eliminated by the morphological operation. Hence, a retrieval procedure is indispensable to recover the true shape of RNP region. Therefore, a feature-based region growing method is proposed to recover the complete shape of RNP. The feature vectors of all the pixels belonged to detected true RNP region are formed by combining the graylevel and RIC2 values, respectively. The feature vectors are quantized and mapped into a two-dimensional feature space. Each feature vector mapped into a grid of the feature space according to the graylevel and RIC scales.

![Image of histogram]

**Fig. 6 Histogram of all the feature vectors mapped into 2-dimensional feature space.**

Figure 6 shows the histogram of all the feature vectors mapped into two-dimensional feature space. Then, the result of histogram of all feature vectors quantized and mapped into the feature space is translated into the interval between 0 and 1 with a shift sigmoid function to represent the probability degree of pixel belonged to actual RNP region. The shift sigmoid function is defined as:

\[
P_i = \frac{1}{1 + e^{-\alpha(F - shf)}}
\]

where \(P_i\) is the probability degree of pixel belonged to actual RNP region, where the feature vector of pixel mapped into the grid \(i\) of feature space, \(F\) is the times of grid \(i\) is mapped, \(\alpha\) is slope parameter, and \(shf\) is the shift quantity. In this equation, \(\alpha\) and \(shf\) are adjustable parameters. The criterion of region growing is the average of probability degree of all the pixels located in the mask whose center is the considered pixel.

After the region growing procedure, the pixels located at boundary of RNP and eliminated by morphological operation are retrieved. The RNP region is extracted completely throughout the proposed method.

### 3. THE EXPERIMENTAL RESULTS

To show the capacity of the method we proposed, the Gd-enhanced MRIs for these experiments were taken from the radiology departments of Kaohsiung Veteran General Hospital. These dynamic MRIs were obtained with fast spin-echo technique with the following parameters: TR/effective TE/excitation=400/17/1, echo train length=4, matrix= 256 × 192, field of view=24 × 18cm, and slice thickness=5mm. The injection was performed through a 20-gauge catheter inserted in an antecubital vein before the start of the study. The first dynamic image \(t=0\) s was obtained before bolus injection of gadolinium diethylene-triamine pentaacetic (Gd-DTPA). Dynamic images were repeated 5 and 30s after rapid manual bolus injection (2mL/s) of 0.1-mmol/kg gadolinium DTPA followed by a 10-mL flush of normal saline. A total of seven images were obtained in each case at specific time \(t\) (\(t=0, 5, 30, 60, 90, 120, 300\)).

Fig. 7 shows the detection results of the proposed method step by step. Obviously, we can discern that the background exist serious artifact, this is the reason why we need the “head region extraction” process to remove the influence of the artifact noise. All the dynamic MR images are performed the process of head region extraction. Then, the difference images of dynamic MRI sequence can be computed by subtracting the original image from the \(i\)-th dynamic MRI, where \(i = 2, 3, ..., 7\). Accordingly, the average of image difference can be calculated immediately. Figure 7(a) shows the result of the average difference image; we can discover that the area nearby recurrent nasal papilloma is brighter than others. According to the value of the threshold calculated by Eq. (4-5), thresholding is applied to the average difference image, the result of thresholding is shown in Fig. 7(b). We can easily notice that there are a lot of fragments in thresholding image. In order to diminish the influence of the fragmental redundancies, a morphological open operation is used to remove trivial fragments from the result of thresholding. Figure 7(c) shows the extracted suspicious regions of the recurrent nasal papilloma by thresholding and morphological operation.
Fig. 7 (a) The average difference image; (b) Result of thresholding with average difference image; (c) Result of morphological operation with thresholding image; (d) Classified result of suspicious RNP regions; (e) Actual RNP decided by pathological characteristic; (f) Result of region growing.

Since the suspicious RNP regions are extracted, the classification model would be used to classify the extracted result into two categories (normal tissues and recurrent nasal papilloma). Then, according to the pathological characteristic of RNP, the real RNP region can be decided correctly. Fig. 7(d) shows the classified result by classification model. According to Fig. 7(d), although over-detection phenomenon in the surrounding tissues of nasal cavity is obvious, the over-detected regions are disconnected from the detected recurrent nasal papilloma. Thus they can be easily removed by a knowledge-based refinement method and the actual RNP decided by the pathological characteristic of RNP is shown in Fig. 7(e). The recurrent nasal papilloma detected result after the feature-based region growing is fused into the first slice of Gd-enhanced MR image sequences, as shown in Fig. 7(f).

It clearly shows that a precise RNP boundary was detected in the proposed method.

Figure 8(a) is the original T1-weighted MR image, which shows isointense mass in the right ethmoid sinus. The contour of the detected recurrent nasal papilloma is superposed onto the original MR image as shown in Figure 8(c). Figure 8(b) is the original T1-weighted MR image, which shows mass in the left paranasal maxillary sinus and ostiomeatal complex region. The detected recurrent nasal papilloma is superposed onto the original MR image as shown in Figure 8(d). From the Fig. 8(c) and Fig. 8(d), we can conclude that the experimental results show that the proposed method is robust and accurate for detect the recurrent nasal papilloma region automatically.

In order to illustrate the diagnostic performance of the proposed method, we adopt the criteria suggested in [10] to define sensitivity and specificity for accuracy evaluation. Let \( A_p \) be the total number of positive pixels and \( A_n \) denote the total number of negative pixels. We also define \( A_p \) be the number of pixels in actual tumor region and detected by proposed method and \( A_n \) be the number of pixels detected but in normal tissue. Hence, the true negatives pixels \( A_{tn} \) and false negative pixels \( A_{fn} \) can be defined by

\[
A_{tn} = A_n - A_p \quad \text{and} \quad A_{fn} = A_p - A_n
\]

respectively. The sensitivity and specificity are defined as:

\[
\text{Sensitivity} = \frac{A_{tn}}{A_n} \quad \text{and} \quad \text{Specificity} = \frac{A_{tn}}{A_p}
\]
False-Positive Fraction
True-Positive Fraction

\[
\text{Sensitivity} = \frac{A_{tp}}{A_p} \quad (16)
\]

\[
\text{Specificity} = \frac{A_{tn}}{A_n} \quad (17)
\]

Table I shows the accuracy measure of the proposed method. The average sensitivity and specificity are 0.9039 and 1.000, respectively. These values demonstrate the effectiveness of the proposed method.

The receiver operating characteristic (ROC) curves [10] are widely used for evaluating diagnosis systems. The ROC curve of Case 1 with the proposed method is shown as Fig. 9. We can see that the value of true-positive-fraction almost reached 1 with tiny loss of false-positive fraction and the value of Az equals to 0.97. The values of Az in some cases are displayed in Table II, and the average value of Az is 0.953.

TABLE I

<table>
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<tr>
<th></th>
<th>Case1</th>
<th>Case2</th>
<th>Case3</th>
<th>Case4</th>
<th>Case5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sensitivity</td>
<td>0.9231</td>
<td>0.8939</td>
<td>0.8546</td>
<td>0.9199</td>
<td>0.9280</td>
</tr>
<tr>
<td>Specificity</td>
<td>0.9992</td>
<td>0.9982</td>
<td>0.9987</td>
<td>0.9985</td>
<td>0.9949</td>
</tr>
</tbody>
</table>

Fig. 9 ROC curve of the proposed method in Case 1

TABLE II

<table>
<thead>
<tr>
<th></th>
<th>Case1</th>
<th>Case2</th>
<th>Case3</th>
<th>Case4</th>
<th>Case5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Az</td>
<td>0.9700</td>
<td>0.9498</td>
<td>0.9519</td>
<td>0.9462</td>
<td>0.9452</td>
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</table>

4. CONCLUSIONS

Nowadays, the dynamic-MRIs are the most powerful tool for detecting recurrent nasal papilloma. However, it is hardly to identify the tumor area by means of human eyesight. Thus, an efficient diagnostic system is necessary to assist physicians for diagnosing RNP accurately. Although the dynamic-MRI is a useful tool for detecting recurrent nasal papilloma, it is inevitable that there is some noise contained in each MRI slice. The influence of the noise causes the computer-aided detection of recurrent nasal papilloma inefficiency and inaccuracy. Therefore, the diagnostic system includes a series of image processing skills to remove the noise in the first, no matter noise contained in background or head region. Simultaneously, we extract the suspicious nasal papilloma regions from the MRIs sequences, instead of delineating the region of interest by physicians, the suspicious recurrent nasal papilloma regions are extracted automatically in proposed method. Secondely we utilize FALVQ to classify them according to the property of RIC curves. Thirdly, we identify the absolute position of recurrent nasal papilloma in terms of the pathological characteristic of the scope where recurrent nasal papilloma occurred. Finally, region growing is applied to recovery the integral shape of recurrent nasal papilloma in practice. After all proposed procedures in this thesis, we have successfully detected the recurrent nasal papilloma from dynamic-MRIs and the experimental results enhance clinical diagnosis and greatly increase the accuracy of recurrent nasal papilloma detection. Compared with the traditional methods, the proposed method achieves three important improvements: 1. it can detect the RNP in any acquisition time parameters, 2. it takes less computation time, 3. it can detect the RNP regions automatically without physicians delineate the suspicious region of interest (ROI) a priori to avoid miss diagnosis caused by manually mistakes. The proposed methods can detect RNP regions automatically, correctly and fast.

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