

# A Similarity Retrieval Method in Brain Image Sequence Database

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**Abstract.** Image mining is more than just an extension of data mining to image domain but an interdisciplinary endeavor. Very few people have systematically investigated this field. Similarity Retrieval in medical image sequence database is an important part in domain-specific application because there are several technical aspects which make this problem challenging. In this paper, we introduce a notion of image sequence similarity patterns (ISSP) for medical image database. These patterns are significant in medical images because the similarity for two medical images is not important, but rather, it is the similarity of objects each of which has an image sequence that is meaningful. We design the new algorithms with the guidance of the domain knowledge to discover the possible Space-Occupying Lesion (PSO) in brain images and ISSP for similarity retrieval. Our experiments demonstrate that the results of similarity retrieval are meaningful and interesting to medical doctors.

## 1 Introduction

Advances in image acquisition and storage technology have led to tremendous growth in very large and detailed image databases [1]. A vast amount of image data is generated in our daily life and each field, such as medical image (CT images, ECT images and MR images etc), satellite images and all kinds of digital photographs. These images involve a great number of useful and implicit information that is difficult for users to discover.

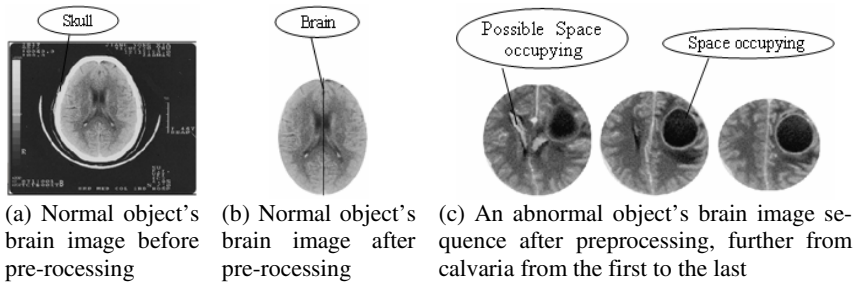
Image mining can automatically discover these implicit information and patterns from the high volume of images and is rapidly gaining attention in the field of data mining. Image mining is more than just an extension of data mining to image domain. It is an interdisciplinary endeavor that draws upon computer vision, image processing, image retrieval, machine learning, artificial intelligence, database and data mining, etc. While some of individual fields in themselves may be quite matured, image mining, to date, is just a growing research focus and is still at an experimental stage. Research in image mining can be broadly classified to two main directions: (1) domain-specific applications; (2) general applications [2]. The focus in the first direction is to extract the most relevant image features into a form suitable for data mining [4,8,9] and the latter is to generate image patterns that may be helpful in understanding

of the interaction between high level human perceptions of image and low level image features [1,10,14,15]. Data mining in medical images belongs to the first direction.

Brain tissue is human's advanced nerve center, so its function is particularly important. The disease affecting the brain has received much attention in the domain of medicine. That is why data mining in medical images for assisting medical staff is so significant. Computerized Tomography (CT) is one of the most important techniques that are used to diagnose by medical doctors. Brain CT scan of each patient (as an object below) is an image sequence in which each one is an image of a layer every a few millimeters from calvaria. There exists a certain spatial relationship between images in the sequence.

This paper presents a new method to retrieve similar objects each of which includes an image sequence. The novelty includes three directions. The first is to make use of medical domain knowledge efficiently to guide data mining. The second is that we utilize two different clustering algorithms on pixels to discover the possible brain diseases that are called Space-Occupying Lesion (SO) by doctors, as shown in figure 1(c). The third is that we introduce a notion of image sequence similarity patterns ISSP for similarity retrieval.

The rest of the paper is organized as follows: section 2 is the statement of problem. Pixel clustering for detecting PSO is introduced in section 3. Section 4 presents similarity retrieval method based on ISSP. Section 5 is experimental result. Conclusions and future research are presented in section 6.



**Fig. 1.** An example of normal and abnormal brain image

## 2 Statement of Problem

At present, the main work of data mining on medical images [3,4,5,6,7,12,13] has two characteristics: (1) research content is the images in the medical image database, not the objects with medical images. For example, it is possible to classify images in the same object into the different class because they always have different morphological SO. This determines the type of knowledge that will be mined; (2) research method is to extract features from images to form feature attributes and use data mining on these attributes, not to consider the fundamental element – pixel's significance. In fact, medical doctors make a diagnosis mainly according to medical knowledge and the tone of pixels. Figure 2 shows the framework of these precious works, where  $IM_i$  is an

image and  $F_{ij}$  is a feature in  $IM_i$ . Also, these work paid little attention to the guidance effect of domain knowledge to data mining.

Our research content is objects each of which contains a series of images and the images from different objects maybe have different intensity, see figure 3. The images from one object have the same structure but come from the different layers of a brain.

They have similar pixel density distribution and it is possible for two spatial-adjacent images to be similar in one object, see figure 1(c). Each image contains some PSOs that also have a spatial relationship in an image. Therefore, the objects with the similar image sequence patterns (ISP) should have similar clinical manifestations. It is very helpful to assist medical doctors to make a diagnosis.

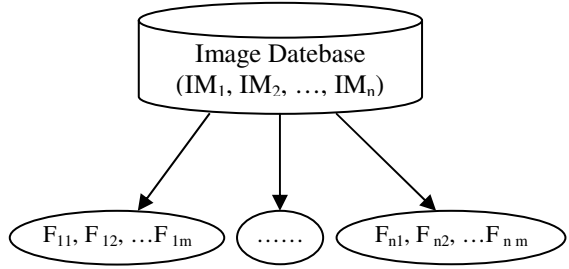


Fig. 2. Framework of Precious Works.  $IM_n$  is an image and  $F_{n,m}$  is one of the features extracted from  $IM_n$ .

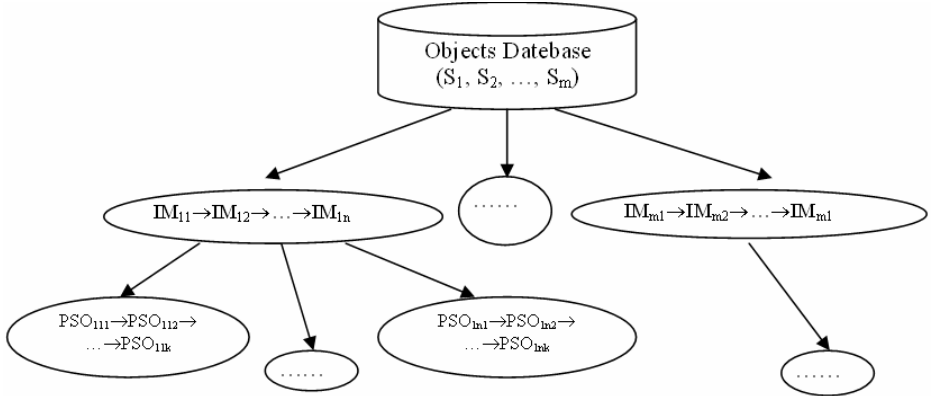


Fig. 3. Framework of Our Work

### 3 Pixel Clustering for Detecting Possible SO (PSO)

In preprocessing, our work uses domain knowledge effectively to remove the noisy data. A brain CT image mainly consists of three parts: noisy data, skull and cerebrum. The noisy data includes the black background and some additive information on it, such as CT identification, date and patient's name etc. This information is not only helpless but revealing patient's privacy. We are only interested in cerebrum. So we use domain knowledge (DK1) and cropping technique of image processing to gain it.

**DK1** --- human's brain skull has the highest density and surrounds the cerebrum. That is, the skull is a cricoid area with the whitest pixels that separate cerebrum from

the noisy data, see figure 1(a). It becomes easy to remove the noisy data by using cropping technique and keep the interesting region with the guidance of DK1.

After image preprocessing, all the objects are formed as follows, see table 1. Each object has a unique identification (ID) and its image part (IM) is a preprocessed image sequence where every code is composed of id and the image sequence number. The arrow represents the spatial relationship.

**Table 1.** Each object is formed as a record in the table after its images are preprocessed

ID	IM
001	001.01→001.02→001.03→...→001.07
002	002.01→002.02→002.03→...→002.13
...	.....
n	n.01→n.02→n.03→...→n.10

The following domain knowledge (DK2) is used to direct clustering algorithm.

(1) The normal persons have nearly the same brain structure that is evident to be lateral symmetry. That is, the distribution of density in the left hemisphere of the brain is almost identical with the right, see figure 1 (b). If there is SO in either side, its density will change and destroy the symmetry;

(2) If one object has SO, it is more possible that this SO will be shown in some continuous images, see figure 1 (c).

### 3.1 Basic Definitions

Let  $S = \{S_i \mid i=1 \dots m\}$  be object set; Let  $S_i = \{IM_{i1}, IM_{i2}, \dots, IM_{in}\}$  be object or ordered image set, where (1)  $IM_{i1}$  and  $IM_{in}$  are the nearest and farthest image from calvaria; (2) For any  $IM_{i1}, IM_{i2}, \dots, IM_{ip}, IM_{ip}$  must be the farthest image from calvaria;

For any preprocessed image  $IM_p$ , it is halved by brain midline (shown as figure 1(b)) and is composed of two parts:  $IM_p(L)$  and  $IM_p(R)$  present the left and right hemisphere image respectively. For any  $IM_p$  and  $IM_j$ , they are adjacent if (1)  $IM_p \in S_i$  and  $IM_j \in S_i$ ; (2)  $p=j+1$  or  $p=j-1$ ;

**Definition 1.** Pixel set of  $IM_p$  is defined as  $P = \{p_i \mid p_i$  is the pixel with coordinate  $(x_i, y_i)$  in the image  $IM_p\}$ ,  $P(L)$  and  $P(R)$  are pixel set of  $IM_p(L)$  and  $IM_p(R)$  respectively.

According to the symmetry of the brain structure in DK2, we assume that the number of pixels in  $IM_p(L)$  and  $IM_p(R)$  are equal. That is,  $|P(L)| = |P(R)| = |P|/2$ . For any  $p_{li} \in P(L)$ ,  $p_{ri} \in P(R)$ , they are symmetric pixel if the line between  $p_{li}$  and  $p_{ri}$  is halved vertically by brain midline. They are denoted as  $p_{li}$  and  $p_{ri}$  below.

**Definition 2.** We partition all pixels in pixel set  $P$  into  $m$  blocks. Pixels in the same block have the same grey level and pixels in the different blocks have the different grey level. Let  $G(P) = \{g_1, g_2, \dots, g_m\}$  be  $P$ 's grey-scale (GS) set if  $G(P)$  is an ascending sort set of  $g_1', g_2', \dots, g_m'$  and  $g_i'$  is grey level of pixels in the  $i^{th}$  block, where

$g_i$  ( $i=1, \dots, m$ ) is the  $i^{\text{th}}$  GS,  $g_1'$  and  $g_m'$  are  $P$ 's minimum and maximum GS respectively. The GS of pixel  $p_i$  is denoted as  $g(p_i)$ . we call  $g_{\text{mean}}(P)$  the mean GS if

$$g_{\text{mean}}(P) = \frac{\sum_{i=1}^{|P|} g(p_i)}{|P|}$$

**Definition 3.** For any  $P$  and distance function  $\text{DisA} = |g_k - g_{\text{mean}}(P)|$ , mid-value GS is a middle value in the GS set that minimizes  $\text{DisA}$ .

**Theorem 1.** Mid-value GS set includes not more than two values.

**Proof.** The value of  $\text{DisA}$  has two possibilities:

- (1) If  $g_k - g_{\text{mean}}(P) < 0$ , then  $\text{DisA} = g_{\text{mean}}(P) - g_k$ ;
- (2) If  $g_k - g_{\text{mean}}(P) \geq 0$ , then  $\text{DisA} = g_k - g_{\text{mean}}(P)$ ;

In the first case, if there exist more than two GS that make the value of  $\text{DisA}$  be a certain minimum  $\Upsilon$ :  $g_1', g_2', \dots, g_k'$  ( $k > 2$ ), then they must satisfy the equation  $g_1' = g_2' = \dots = g_k'$ . This doesn't agree with the definition of GS set. Therefore, it is only one GS that minimizes  $\text{DisA}$  in the first case, denoted as  $g_{\text{mida}}$ .

Case 2 is proved similarly and thus it is also only one GS that minimizes  $\text{DisA}$ , denoted as  $g_{\text{midb}}$ .

If  $g_{\text{mean}}(P) - g_{\text{mida}} = g_{\text{midb}} - g_{\text{mean}}(P)$ , then mid-value set includes two elements. Otherwise, it only includes one of  $g_{\text{mida}}$  and  $g_{\text{midb}}$  that minimizes  $\text{DisA}$ .

For any  $P$ ,  $g_s$  is called Benchmark GS and another one is denoted as  $g_s'$ , if

- (1) Mid-value GS set includes one element  $g_{\text{mid}}$ , and  $g_s$  is the minimum value between  $g_{\text{mean}}$  and  $g_{\text{mid}}$ ;
- (2) Mid GS set includes two elements,  $g_s$  is the minimum value between these two values.

**Definition 4.** For pixel set  $P$ , let  $g^{(l)} = \{g_i \mid g_i \leq g_1 \leq g_i + |g_1 - g_s|/2\}$  be low bound GS;  $g^{(h)} = \{g_i \mid g_m - |g_m - g_s|/2 \leq g_i \leq g_m\}$  be high bound GS;  $g^{(b)} = g^{(l)} \cup g^{(h)}$  be bound GS.

For pixel set  $P$ , let

$P^{(l)} = \{p_i \mid g(p_i) \in g^{(l)}\}$  be low bound pixel set;

$P^{(h)} = \{p_i \mid g(p_i) \in g^{(h)}\}$  be high bound pixel set;

$P^{(b)} = P^{(l)} \cup P^{(h)}$  be bound pixel set and pixels in  $P^{(b)}$  are bound pixels.

**Definition 5.**  $\Delta g(P)$  is  $IM_p$ 's difference set if for any symmetrical pixel  $p_{li}$  and  $p_{ri}$  in  $P$ ,  $\Delta g(P) = \{ \Delta g_i \mid \Delta g_i = g(p_{li}) - g(p_{ri}), i=1, 2, \dots, |p|/2 \}$ .

**Definition 6.** For any image sequence  $\langle IM_{ij}, \dots, IM_{ik} \rangle$ , if

- (1) only the first and last image  $IM_{ij}$  and  $IM_{ik}$  have one adjacent  $IM$ ;
  - (2) other  $IM_{ip}$  (if existed) has two adjacent  $IM$ ;
- we called that it has the property of continuity. Image sequence  $\langle IM_{ij}, \dots, IM_{ik} \rangle$  has the property of discontinuity if it can't satisfy the property of continuity.

**Definition 7.** For any pixel  $p_i$  and a certain integer  $\mathcal{E}$ , the assemble of pixels is called  $\mathcal{E}$ -adjacent area ( $\mathcal{E}$ -AA) if distance between  $p_i$  and pixels in the assemble is not more than  $\mathcal{E}$ .  $P_i$  is *core pixel* (c-pixel) if its  $\mathcal{E}$ -AA involves no less than  $MP$  pixels that satisfy some conditions.  $P_i$  is *immediate density reachable* from  $p_j$  if  $p_i$  is in the  $\mathcal{E}$ -AA of

$p_j$  and  $p_j$  is c-pixel.  $P_i$  and  $p_k$  are *density reachable* if for some pixels  $p_1, p_2, \dots, p_k$ , any pixel  $p_{i+1}$  is immediate density reachable from  $p_i$ .  $P_i$  and  $p_j$  are *density connective* if there exists pixel  $p_k$  that is density reachable from not only  $p_i$  but also  $p_j$ .

### 3.2 Pixel Clustering with the Guidance of DK2

It is very crucial step for medical doctors to determine whether there is a Space-Occupying Lesion or not in the brain images. In this paper, we use clustering method on the pixels of images to detect the PSO. Firstly, for any  $IM_p$ , we compute to get the  $IM_p$ 's difference set  $\Delta g(P)$ , then sort the absolute value of each element in  $\Delta g(P)$  to yield the set  $\Delta g'(P) = \{|\Delta g_i| \mid \Delta g_i \in \Delta g(P) \text{ and for any } |\Delta g_i|, \text{ it must be maximal in the former } i \text{ elements}\}$ . Each element of  $\Delta g'(P)$  is regarded as an atomic cluster and hierarchical clustering from bottom to top will not stop in the light of the following similarity function of difference between pixels' GS until the number of clusters is equal to a specified value  $k$ .

Similarity( $C_i, C_j$ ) =  $\min|T_i - T_j|$ , where  $T_i$  and  $T_j$  are mean value of all  $|\Delta g_i|$  in cluster  $C_i$  and  $C_j$  respectively. The algorithm is as follows:

#### Clustering algorithm I:

**Input:** the set  $\Delta g'(P)$  and the number of clusters  $k$

**Output:**  $k$  clusters that satisfy the similarity function similarity( $C_i, C_j$ )

1. Each element of  $\Delta g'(P)$  is regarded as an atomic cluster and compute  $|T_i - T_j|$  of the adjacent clusters;
2. Clustering in terms of similarity( $C_i, C_j$ );
3. While (the number of clusters is not equal to  $k$ ) {
4.     Compute  $|T_i - T_j|$  of the adjacent clusters;
5.     Clustering in terms of similarity( $C_i, C_j$ ); }

According to "If there is SO in either side, its density will change and destroy the symmetry", we can deduce that if there exists SO in the image, then pixels' GS of SO should change and the value of the elements corresponding to these pixels in  $\Delta g'(P)$  will be much greater than zero. Otherwise, the value of these corresponding elements in  $\Delta g'(P)$  will approximate zero. Therefore, we set the number of clusters to 2 as the termination condition. The first step of Clustering algorithm I scans  $|P|/2$  elements in the set  $\Delta g'(P)$  one time and time complexity is  $O(|P|/2)$ . The second step is to select the minimum and time complexity is  $O(|P|/2)$ , too. In the third step, the loop times is related to the speed of clustering. The worst case, only two clusters is clustered to a bigger cluster in each loop. The number of time is  $|P|/2-3$  and time complexity of the 4<sup>th</sup> and 5<sup>th</sup> step is  $O(|P|/2-i)$ , where  $i$  is the  $i^{\text{th}}$  loop. Accordingly, the 3<sup>rd</sup> and 5<sup>th</sup> step for the worst case need  $(n-3)(n+2)/2$  operations and time complexity is  $O(n^2)$ .

According to the symmetry of the brain structure, we single out the cluster with the greater  $|\Delta g_i|$  from clustering algorithm I (denoted as high difference cluster) to be the main study objects of the next step. It means that data size to be processed may be reduced. For Each  $\Delta g_i$ , there are two corresponding symmetric pixels  $p_{li}$  and  $p_{ri}$ . All symmetric pixels  $g(p_{li})$  and  $g(p_{ri})$  in the high difference cluster are judged to be whether bound GS or not, then bound pixel set is generated.

Next, the based-on density clustering method is utilized to re-cluster these bound pixel set and determine the location and size of SO in each brain image. The algorithm is as follows:

**Clustering algorithm II:**  
**Input:** all bound pixel set,  $\epsilon$  and MP  
**Output:** k clusters

1. Assume that the pixel count of any bound pixel set is  $b_n$  and examine  $\epsilon$ -AA of these  $b_n$  pixels;
2. If ( $\epsilon$ -AA of  $p_i$  involves more than MP bound pixels)
3. Then mark  $p_i$  as the c-pixel;
4. While (all c-pixels) {
5. Clustering all *density reachable* pixels; }

For  $\epsilon$  and MP in clustering algorithm II, we specify their value through learning on the normal object’s brain images. The learning process is as follows: (1) run the first clustering on the normal object’s  $IM_p$  and achieve the bound pixel set; (2) count (not clustering) on the bound pixel sets which, in fact, are noisy data but not SO, and compute the maximum of the radius and the count of all bound pixel set which are the greatest lower bound of  $\epsilon$  and MP. Time complexity of this algorithm is  $O(n \log n)$ . The k clusters generated from this algorithm are k PSOs.

## 4 Similarity Retrieval Method

In this section, we will: (1) discover the image sequence pattern (ISP) of one object; (2) discover the image sequence similarity patterns (ISSP) of two objects.

### 4.1 Discovering ISP Algorithm

The whole PSO in an image can be found using the above algorithm. For these PSOs, we denote each PSO as the following:  $\langle H(L), (x_i, y_i), (x_{a1}, x_{a2}), (y_{b1}, y_{b2}) \rangle$ , where H (L) represents the high (low) bound GS,  $(x_i, y_i)$  is the coordinate of the center of this PSO,  $(x_{a1}, x_{a2})$  and  $(y_{b1}, y_{b2})$  are the max and min x and y coordinate of the PSO. They are computed by the following formula:

$$x_i = \frac{1}{k} \sum_{j=1}^k x_j \tag{1} \qquad y_i = \frac{1}{k} \sum_{j=1}^k y_j \tag{2}$$

$$x_{a1} = \max_{j=1}^k (x_j) \tag{3} \qquad x_{a2} = \min_{j=1}^k (x_j) \tag{4}$$

$$y_{b1} = \max_{j=1}^k (y_j) \tag{5} \qquad y_{b2} = \min_{j=1}^k (y_j) \tag{6}$$

We take the center of the brain as the origin of coordinates. If  $x_i \leq 0$ , then this PSO is in  $IM(L)$ . Otherwise, it is in  $IM(R)$ .

**Definition 8.**  $PSO_k$  is prior to  $PSO_j$  if for  $PSO_k = \langle H(L), (x_k, y_k), (x_{ka1}, x_{ka2}), (y_{kb1}, y_{kb2}) \rangle$  and  $PSO_j = \langle H(L), (x_j, y_j), (x_{ja1}, x_{ja2}), (y_{jb1}, y_{jb2}) \rangle$ , they satisfy one of the three prior conditions:

- (a)  $x_k < x_j$ ; (b)  $x_k = x_j$  and  $y_k > y_j$ ; (c)  $x_{ka1} \leq x_{ja1}$  and  $x_{ka2} \geq x_{ja2}$ ; (d)  $y_{kb1} \leq y_{jb1}$  and  $y_{kb2} \geq y_{jb2}$ ;  
 We denote it as  $PSO_k \gg PSO_j$ .

According to this priority, we describe PSO pattern (PSOP) of each image as the following form:

$$PSOP(IM_i) = \langle L_{i1}, L_{i2}, \dots, L_{im}; R_{i1}, R_{i2}, \dots, R_{in} \rangle$$

Where  $L_{im}$  and  $R_{in}$  represent a PSO in  $IM_i(L)$  and  $IM_i(R)$  respectively.

**Definition 9.** PSOP of two images is complete similar if  $|PSOP(IM_i)| = |PSOP(IM_j)|$ , and the corresponding  $L_{ik}$  and  $L_{jk}$  (or  $R_{ik}$  and  $R_{jk}$ ) have the same bound GS, locate the same part of the image (IM(L) or IM(R)) and satisfy the same prior condition. That is, if  $L_{ik}$  and  $L_{i(k+1)}$  satisfy the prior condition (a) or (b), then  $L_{jk}$  and  $L_{j(k+1)}$  must satisfy (a) or (b).

**Definition 10.** PSOP of two images is incomplete similar if cut one or more discontinuous PSO from one or both of these two images, then  $|PSOP(IM_i)| = |PSOP(IM_j)|$ , and the corresponding  $L_{ik}$  and  $L_{jk}$  (or  $R_{ik}$  and  $R_{jk}$ ) have the same bound GS, locate the same part of the image (IM(L) or IM(R)) and satisfy the same prior condition.

For each image of one object, it has a PSOP and maybe is different from the PSOP of the adjacent image. We compare the PSOP of all adjacent images and get a pattern sequence in which two adjacent patterns are not same. This pattern sequence is called image sequence pattern (ISP).

The algorithm of discovering ISP is as follows.

**DISP Algorithm:**

**Input:** m images of one object

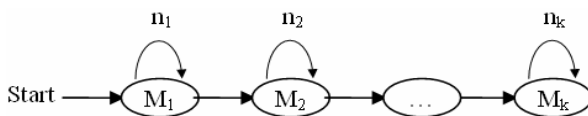
**Output:** Image sequence patterns (ISP)

1. Initialization:  $j=1, n_j=1, k=1$ ;
2. For  $i = 1$  to  $m$  {
3. Compare the pattern  $PSOP(IM_i)$  and  $PSOP(IM_{i+1})$  of  $i_{th}$  and  $(i+1)_{th}$  image;
4. If complete similar
5. Then record the pattern as  $\langle PSOP(IM_k), n_j = n_j + 1 \rangle$ ;
6. Else if  $j = i$
7. Then  $k=i$  and record the pattern as  $\langle PSOP(IM_k), n_j = 1 \rangle$ ;  $j=j+1$ ;
8. Else  $k=i+1$  and record the pattern as  $\langle PSOP(IM_k), n_j = 1 \rangle$ ;  $j=j+1$ ;

We use an example to illustrate ISP from DISP algorithm, see figure 4. Convenient for description, we denote ISP as the following form:

$$ISP(S_i) = \{ \langle M_i(IM_{i1}), n_1 \rangle, \langle M_i(IM_{i2}), n_2 \rangle, \dots, \langle M_i(IM_{ik}), n_k \rangle \}, \text{ or } \{ \langle M_i, n_1 \rangle, \langle M_i, n_2 \rangle, \dots, \langle M_i, n_k \rangle \}$$

Where for  $j=1 \dots k$ ,  $M_j$  and  $M_{j+1}$  are the distinct PSOP.  $IM_{ij}$  is the first image with the PSOP  $M_j$  and  $n_j$  is the number of the adjacent images with the same PSOP  $M_j$ .



**Fig. 4.** Patterns from Discovering ISP Algorithm



## 4.2 Discovering ISSP Algorithm

For  $ISP(S_i)$  and  $ISP(S_j)$ , ISSP of two objects refers to the longest similar and continuous sub-patterns that belongs to the ISP of each object. For example,  $ISP(S_i) = \{ \langle M_1, 1 \rangle, \langle M_2, 2 \rangle, \langle M_3, 2 \rangle, \langle M_4, 1 \rangle, \langle M_5, 1 \rangle \}$  and  $ISP(S_j) = \{ \langle M_1, 1 \rangle, \langle M_2, 3 \rangle, \langle M_3, 3 \rangle, \langle M_4, 2 \rangle, \langle M_5, 1 \rangle, \langle M_6, 1 \rangle \}$ , if  $M_1$  is similar to  $M_1$ ,  $M_3$  similar to  $M_3$ ,  $M_4$  similar to  $M_4$  and  $M_5$  similar to  $M_6$ , then ISSP of these two objects is  $\langle M_1, M_3, M_4, M_6 \rangle$ . Here,  $M_3$  and  $M_4$  are called continuous sup-pattern, and  $M_1$  and  $M_5$  are discontinuous sup-pattern.

Since there are spatial relationship between all images in  $S_i$ , that is, for any  $IM_{i1}, IM_{i2}, \dots, IM_{in}, IM_{i(j+1)}$  must be farther from calvaria than  $IM_{ij}$ , it is not necessary to retrieve the whole PSOPs of one object to find the similar pattern of a given  $M_i$ . For example,  $M_1$  is PSOP of the farthest image from calvaria of one object and  $M_p$  is PSOP of the nearest image of another different object, it is not meaningful to compare  $M_1$  and  $M_p$  to find whether they are similar or not because  $M_1$  and  $M_p$  show the different parts of the brain. According to this, two rules are introduced to reduce the retrieval space and enhance the efficiency. For two objects  $S_i$  and  $S_j$ , assumed that  $ISP(S_i) = m$  and  $ISP(S_j) = n$ ,

- (1) if  $m=n$ , that is, the number of the PSOPs in these two objects is equal, then we only need to retrieve  $M_{i-1}, M_i$  and  $M_{i+1}$  in  $ISP(S_i)$  to discover the similar patterns of  $M_i$  in  $ISP(S_j)$ .
- (2) If  $m < n$ , then we only need to retrieve  $M_i, M_{i+1}, \dots, M_{i+n-m}$  in  $ISP(S_i)$  to discover the similar patterns of  $M_i$  in  $ISP(S_j)$ .

The algorithm of discovering ISSP is as follows.

### DISSP Algorithm:

**Input:** ISP of two objects

**Output:** Image sequence similarity patterns (ISSP)

1. Initialization:  $C=NULL, NC=NULL$ ;
2. Assumed that  $ISP(S_i)=m$  and  $ISP(S_j)=n$ , if  $m \leq n$ , start the following steps:
3. For  $i = 1$  to  $m$  {
4. if  $m=n$ , then goto step (5); if  $m < n$ , then goto step(7);
5. Compare  $M_i$  in  $ISP(S_i)$  with  $M_{i-1}, M_i$  and  $M_{i+1}$  in  $ISP(S_j)$ . If discover a complete similar PSOP,  $C=C \cup (M_i \rightarrow M_j)$ . If there is no PSOP to compare in  $ISP(S_j)$ , return step (3) to start the next iteration. If there is no complete similar PSOP to be discovered, goto step (6);
6. Compare  $M_i$  in  $ISP(S_i)$  with  $M_{i-1}, M_i$  and  $M_{i+1}$  in  $ISP(S_j)$ . If discover a incomplete similar PSOP,  $NC=NC \cup (M_i \rightarrow M_j)$ . If there is no PSOP to compare in  $ISP(S_j)$ , return step (3) to start the next iteration;
7. Compare  $M_i$  in  $ISP(S_i)$  with  $M_i, M_{i+1}, \dots, M_{i+n-m}$  in  $ISP(S_j)$ . If discover a complete similar PSOP,  $C=C \cup (M_i \rightarrow M_j)$ . If there is no PSOP to compare in  $ISP(S_j)$ , return step (3) to start the next iteration. If there is no complete similar PSOP to be discovered, goto step (8);
8. Compare  $M_i$  in  $ISP(S_i)$  with  $M_i, M_{i+1}, \dots, M_{i+n-m}$  in  $ISP(S_j)$ . If discover a incomplete similar PSOP,  $NC=NC \cup (M_i \rightarrow M_j)$ . If there is no PSOP to compare in  $ISP(S_j)$ , return step (3) to start the next iteration; }
9. Order the whole patterns in  $C \cup NC$  by the spatial relationship of  $M_i$  and use the exhausting method to discover the ISSP;

Since the above rules reduce the number of the PSOPs to be retrieved efficiently, the time cost of this algorithm mainly lies on the procedure of comparing the similarity of two PSOPs that depends on the count of the PSOs. Therefore, the time complexity of this algorithm is  $O(km)$ , where  $k$  is the number of the PSOs.

**Definition 11.** Two objects are similar if there exists ISSP in two objects.

We give an example to illustrate this algorithm. For two objects  $S_i$  and  $S_j$ ,  $ISP(S_i) = \{ \langle M_1, 1 \rangle, \langle M_2, 2 \rangle, \langle M_3, 2 \rangle, \langle M_4, 1 \rangle, \langle M_5, 1 \rangle, \langle M_6, 1 \rangle \}$  and  $ISP(S_j) = \{ \langle M_1, 1 \rangle, \langle M_2, 3 \rangle, \langle M_3, 1 \rangle \}$ , we use DISSP algorithm to get the results:  $C = (M_2 \rightarrow M_2, M_4)$  and  $NC = (M_1 \rightarrow M_1, M_3) \cup (M_3 \rightarrow M_6)$ , where  $C$  and  $NC$  includes the complete and incomplete similar patterns respectively. Notice that  $|ISP(S_j)| < |ISP(S_i)|$ , we order  $C \cup NC$  by the spatial relationship of  $M_j$  in  $ISP(S_j)$ . The result is  $(M_1 \rightarrow M_1, M_3) \cup (M_2 \rightarrow M_2, M_4) \cup (M_3 \rightarrow M_6)$ . By means of exhausting method, the final ISSP is  $\langle M_1, M_2, M_6 \rangle$  and  $\langle M_3, M_4, M_6 \rangle$ . Therefore,  $S_i$  is similar to  $S_j$ .

### 5 Experiments

The dataset utilized in our experiments was real data from hospital. The main reason that we study on real brain CT images instead of any simulative data is to avoid reducing the accuracy of the similarity retrieval and the reliability of the discovered knowledge. To have access to real medical images is a very difficult undertaking due to legally privacy issues and management of hospital. But with some specialists' help and support, we got 103 pieces of precious data, which included 11 normal objects' CT scans and 92 abnormal objects data including CT scans and clinical data. Up to now, we have not found the method used on this kind of object dataset where each object has a brain image sequence. Therefore, we only give our experimental results.

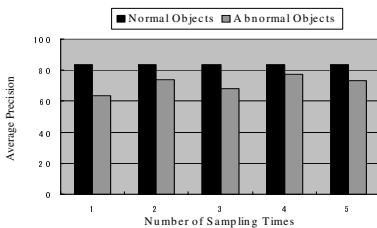
We randomly sample 10 percent of normal objects and 10 percent of abnormal objects as the targets from the dataset and use our algorithm to retrieve the similar objects of each target from the whole dataset. The formulas for precision and recall are given below to evaluate our algorithm:

$$P(p) = \frac{TP}{TP + FP}$$

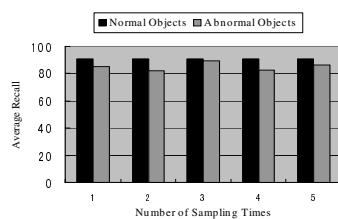
$$P(n) = \frac{TN}{TN + FN}$$

$$R(p) = \frac{TP}{TP + FN}$$

$$R(n) = \frac{TN}{TN + FP}$$



**Fig. 5.** Average Precision when the Norman and Abnormal Objects as Targets

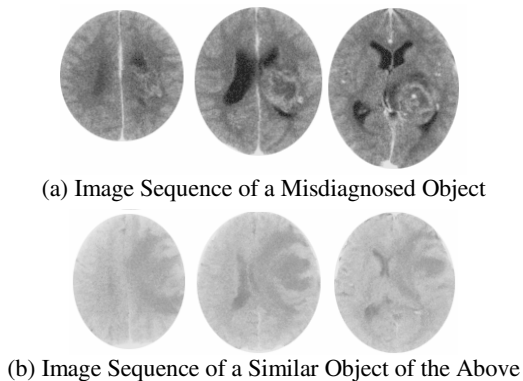


**Fig. 6.** Average Recall when the Norman and Abnormal Objects as Targets

Where TP stands for true positives, FP for false positives, FN for false negatives, TN for true negatives,  $P(p)$  and  $R(p)$  for the precision and recall of similarity retrieval of abnormal objects,  $P(n)$  and  $R(n)$  for the precision and recall of similarity retrieval of normal objects. Figure 5 and figure 6 shows the experimental results of randomly sampling 5 times. We can observe that the precision and recall are very high for normal targets. Only one abnormal object is retrieved as the similar object of normal targets for each time because the tumor in the brain of this abnormal object is laterally symmetrical. While our clustering algorithms calculate the difference set, they ignore the tumor. One normal object is not retrieved for each time because his (her) brain images are too bright and some noisy dark pixels cause the false results.

The average precision of the abnormal targets is more than 60% but not very high. All retrieved objects are certainly the abnormal objects with tumor in their brain and the image sequence of them is similar to that of the target. The reason why not very high is that their concrete tumor kind is not the same as the target and the medical doctors made a different detailed diagnosis. But this demonstrates that our similarity retrieval algorithm based on ISSP can gain the similar image sequence of the target. The average recall, however, is very high. This illustrates that the results of our similarity retrieval method based on ISSP can include most of the similar objects with the targets. For example, there are 7 objects including the target itself that are actually similar to the target in the dataset and our method can find 10 similar objects in which 6 objects belong to the actually similar objects.

In addition, there are two abnormal objects in the dataset who were misdiagnosed in the first visit to the doctor. Their final diagnosis had to resort to the biopsy techniques that are costly and need to remove the tissue from the patient. Our algorithm succeeds in retrieving the similar objects whose clinical diagnosis are the same as these two abnormal objects. Figure 7 shows one of these two misdiagnosed objects and one of the similar objects with it. This result can provide significant information to the medical doctors to make a right diagnosis.



**Fig. 7.** Two objects with the similar image sequence pattern have a same clinical diagnosis

## 6 Conclusions

In this paper, we firstly use two clustering algorithms to generate the possible Space-Occupying Lesion, and then discover ISP for each object. Next, we introduce a notion of image sequence similarity patterns (ISSP) for medical image database. ISSP refer to the longest similar and continuous sub-patterns hidden in two objects each of which contains an image sequence. These patterns are significant in medical images because the similarity for most medical images is not important, but rather, it is the similarity of objects each of which has an image sequence that is meaningful. We design a new algorithm with the guidance of the domain knowledge to generate ISSP for similarity retrieval. Our experiments demonstrate that the guidance of domain knowledge is meaningful and the results are interesting to medical doctors.

## References

- [1] Zaiane, O.R., et al.: Mining MultiMedia Data. Meeting of Minds, CASCON (1998)
- [2] Hsu, W., Lee, M.L., Zhang, J.: Image Mining: Trends and Developments. *Journal of Intelligent Information Systems* 19(1), 7–23 (2002)
- [3] Megalooikonomou, V., Davatzikos, C., Herskovits, E.H.: Mining Lesion-Deficit Associations in a Brain Image Database. In: *KDD-99*, San Diego, CA (1999)
- [4] Hsu, W., Lee, M.L., Goh, K.G.: Image Mining in IRIS: Integrated Retinal Information System. In: *Proceedings of the ACM SIGMOD*, Dallas, Texas, May 2000, p. 593 (2000)
- [5] Liu, Y., Dellaert, F., Rothfus, W.E., Moore, A., Schneider, J., Kanade, T.: Classification-Driven Pathological Neuroimage Retrieval Using Statistical Asymmetry Measures. In: Niessen, W.J., Viergever, M.A. (eds.) *MICCAI 2001*. LNCS, vol. 2208, Springer, Heidelberg (2001)
- [6] Antonie, M.-L., Zaiane, O.R., Coman, A.: Application of Data Mining Techniques for Medical Image Classification. In: Perner, P. (ed.) *MLDM 2001*. LNCS (LNAI), vol. 2123, Springer, Heidelberg (2001)
- [7] Zaiane, O.R., Antonie, M.-L., Coman, A.: Mammography Classification by an Association Rule-based Classifier. In: Zaiane, O.R., Simoff, S.J., Djeraba, C. (eds.) *MDM/KDD 2002 and KDMCD 2002*. LNCS (LNAI), vol. 2797, Springer, Heidelberg (2003)
- [8] Fayyad, U.M., Djorgovski, S.G., Weir, N.: Automating the Analysis and Cataloging of Sky Surveys. In: *Advances in Knowledge Discovery and Data Mining*, pp. 471–493 (1996)
- [9] Kitamoto, A.: Data Mining for Typhoon Image Collection. In: Perner, P. (ed.) *MLDM 2001*. LNCS (LNAI), vol. 2123, Springer, Heidelberg (2001)
- [10] Ordonez, C., Omiecinski, E.: Discovering Association Rules Based on Image Content. In: *IEEE Advances in Digital Libraries Conference*, IEEE Computer Society Press, Los Alamitos (1999)
- [11] Burl, M.C., et al.: Mining For Image Content. In *systems, Cybernetics, and Informatics / Information Systems: Analysis and Synthesis* (1999)
- [12] Soltanian-Zadeh, H., Nezafat, R., Windham, J.P.: Is There Texture Information in Standard Brain MRI? In: *Proceedings of SPIE Medical Imaging 1999: Image Processing conference*, San Diego, CA (1999)

- [13] Barra, V., Boire, J-Y.: Tissue segmentation on MR Images of the Brain by Positivistic Clustering on a 3D Wavelet Representation. *J. of Magnetic resonance Imaging* 11, 267–278 (2000)
- [14] Yanai, K.: Image Classification by a Probabilistic Model Learned from Imperfect Training Data on the Web. In: *Seventh International Workshop on Multimedia Data Mining*, pp. 75–81 (2006)
- [15] Walter, J.A., WeBling, D., Essig, K., Ritter, H.: Interactive Hyperbolic Image Browsing-Towards an Integrated Multimedia Navigator. In: *MDM2006. Seventh International Workshop on Multimedia Data Mining*, pp. 101–108 (2006)