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An Accurate and Efficient Modified Fuzzy C-Means Algorithm for Three-Dimensional Analysis of MRI Brain Image Segmentation

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ABSTRACT

It presents an approach for the segmentation of three-dimensional images and extraction Direct surface mesh, which has been used for segmentation and visualization of different types of images, primarily CT scans and MRIs. The algorithm is based on the integration of an initial detection of each region of interest and a subsequent Surface refinement using active contours. When working on a discrete domain, the surface obtained by segmentation of regions has a stepped appearance, with triangles orthogonally arranged; yet provides a robust way initialization and Automatic for the deformable contour, which can evolve to adapt to the topology of objects to achieve the adjustment from the actual surface contour. This integration poses an interesting segmentation approach which combines the robustness of region growing method to the final quality of the surfaces generated with T-Snakes. The proposed method was initially applied in 2 dimensions and then extended to 3D in order to generate surface meshes corresponding to the detected objects. Besides the description of the algorithms discussed, include examples where managed high quality segmentations.

Index Terms— Image Processing, Optimization Contour Segmentation**.**

1. INTRODUCTION

Segmentation of three-dimensional (3D) representations and generating geometric associated with the detected components is one of the critical problems within the field of image processing and computer visualization. Segmentation of an image is either divide it into fragments that form. each fragment contain pixels with a characteristic common, such as the intensity value, the object forming part of or position in the image. It is the initial stage in some image investigation procedure. The algorithms are constructed image segmentation commonly in one of two basic properties of the intensity values: disjointedness and resemblance. In the first category, the idea is to divide the image based abrupt changes in intensity, for example, the edges of an image. The main approximations in the second category are based on dividing the image into similar regions according to a number of criteria predefined. The thresholding growth classification regions or blocks are examples of methods in this category. The difficulty is even greater when it comes to the identification of complex components, like in case of anatomical structures in medical images. In many cases also occur various factors (such as noise, intensity variation, etc.) that affect the process detection limits of these structures and the consequent creation of a model surface consistent. Different techniques have been proposed in order to carry out this process. Among them, based schemes regions growth have shown be simple algorithms, but at the same time robust and flexible, allowing incorporate different criteria to guide the process of incorporating new information in the growth.

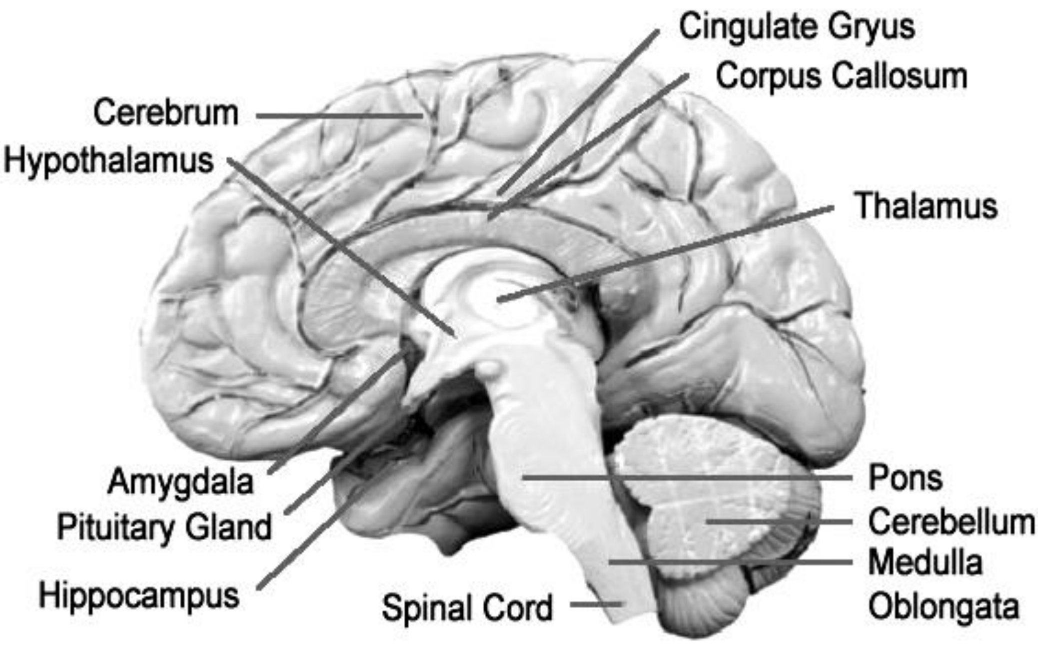

Fig 1 Major Parts of the Brain

The disadvantage they have, as any scheme that works in a domain discreet, is that the surface model reconstructed from the segmentation obtained has a stepped appearance, which must be post-processed by an algorithm smoothing before rendering. Deformable models or active contours are a powerful approach to image segmentation based on the evolution of surface of the object by the influence of a system of internal forces (which shape elasticity of the surface) and external (leading the model to the characteristics projections of the image). Its main advantages are the ability to generate directly smooth and closed surfaces associated with the components of interest within the image and Incorporation of constraints that control the smoothness of the surfaces, providing robustness against noise and the appearance of spurious edges, typical problems affecting the results of numerous segmentation algorithms. A shortcoming of these methods, without however, is their dependence on the contour or surface initialization from which changes the boundaries of an object is performed as effectively to outline is required to locate the initial contour closest to the desired limit. Given the shortcomings outlined above regarding the weaknesses of the methods based on regions and deformable models, proposed in this work, the integration of both approaches, in order to combine and enhance its aspects most favorable, thereby achieving a method of segmentation in two phases. In a first stage a segmentation algorithm based on region growing applied previously developed, which is able to detect memorabilia properly through minimal user interaction. In the general characteristics of the algorithm are explained next section.

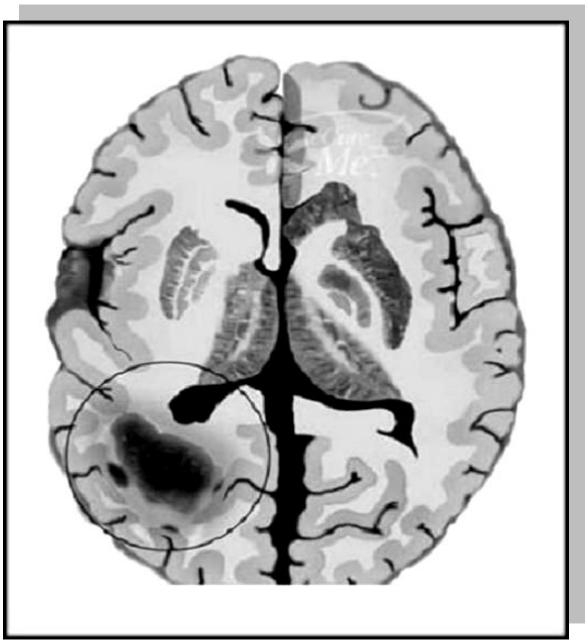

Fig 2 Brain Tumor Diagram

Surface resulting from the first phase of growth, despite the stepped aspect can provide initial contour required by the deformable model, conveniently located within the object to be segmented and about the actual edges. In this, an approach is provided to the problem solution of this type of dependence methods on initialization. This integration presents an efficient approach to segmentation and direct extraction of a mesh size, which has been used for segmentation and visualization of different kinds of images, mainly computed tomography (CT) and magnetic resonance imaging (MRI). Finally, expose some preliminary results and conclusions.

2. LITERATURE SURVEY

MR Imaging systems have a place very important in the long list of procedures that make specialty Imaging. Unlike many other methods, MRI requires specialist knowledge relatively full of phenomena that occur when different tissues placed in powerful magnetic fields and simultaneously subjected to the action of radiofrequency waves. The physics of MRI is very complex and there are numerous texts and works help the understanding of the phenomena involved in it. This paper describes the foundations of the subject in order to understand why processes and orient a better utilization of the technique in different tissues. However, since it is not the aim of this thesis, it is not possible herein include the huge amount of progress since developed Birth of MR. This not only confirms the dizzying speed of technological progress. To further this work should be utilized specialized. In conventional radiology and computed tomography (CT), the structures that appear white, black or gray is easy understanding and originates in a very simple law: "the intensity of the image is proportional to the intensity of X-rays that have traversed tissue missed". In MR, any fabric, such as a liquid, it may appear white or black according to the parameters chosen. This particularly complicates understanding and image analysis, against which there is no other solution than trying to understand what happens. Systems of digital image processing are currently an almost indispensable tool in the practice of modern medicine. The acquisition systems show enormous growth that increases day. However, the evolution of the equipment sometimes is not reflected in the process image interpretation. Therefore, it is of fundamental importance the development new paradigms and methodologies so as to have a large spectrum options for processing and display them. One of the most important tasks in medical image analysis is the segmentation, understood as the process of according to their major structural components in homogeneous regions with respect to some of its features, such as texture or intensity. A Segmentation technique hunt a divider such that the regions gained resemble to diverse anatomical structures or regions of interest of the image. An accurate segmentation is an essential requirement for large numbers of applications, such as volume calculation of certain tissues and subsequent dimensional representation, radiation therapy, surgery planning, detection of abnormal tissues. After the segmentation, the information can be used by specialists to compare volumes, morphology and tissue characteristics with normal studies or other regions in the same image. This can be determined normal parameters with the idea of detecting pathologies and assist decisions in diagnosis and therapy. This paper emerges from a systematic work with digital images together an interdisciplinary group of physicians includes specialists in Imaging, pathologists, an orthopedist, an anesthesiologist and psychiatrist. Manual image segmentation is a task that, depending on the complexity thereof, can be extremely tedious and require a great deal of time, up to several hours for each case analyzed. The thus obtained segmentation are often subjective, dependent operator and its results are not always repeatable. In some cases it requires a great anatomical knowledge to avoid mistakes. However, one appropriate segmentation by specialists is a necessary task for evaluating methods of automatic or semi-automatic classification. In segmented MRI brain tissue is essential to remove what not correspond to the region of the brain (mainly skull and meninges). Even this task appears to be simple can take considerable time. Segmentation tissue should be cut for cutting and may require more than two hours to reach an outcome.

3. SEGMENTATION

Methods based on growing regions are a flexible approach and powerful tool for image segmentation, aimed at finding regions homogeneous. The criteria used for the integration of elements is based on two aspects Main: proximity and similarity of groups of voxels. For each region that you want to target, growth starts from one or more initials, known as seed points. After growth algorithm progresses iteratively in order to incorporate those points immediate neighbors previously including meeting predetermined acceptance criteria. This process stops when there are items that meet the condition. The output of the segmentation process is a connected and labeling of image points that have been included in each set one of the regions of interest. It should set an appropriate criterion to extract the components of interest from the set of initial points defining voxels properties must meet to be incorporated into the region. This criterion is usually based on proximity and homogeneity of elements. Due to the characteristics of the images from tomographic reconstruction or MRI, assessment of homogeneity criterion should consider the possibility of some variation of intensities within the same region or even the presence of values similar in different anatomical structures. In addition, you should consider the possible presence of noise, originated in the process of acquisition or image reconstruction. Therefore, the choice of approach to use for evaluation of candidate voxels is critical to the proper performance of the algorithm. A simple criterion for comparison is based on the analysis of the intensity value of the voxel candidate with respect to the specified seed, getting a measure of distance where I (v) is the intensity value shown candidate voxel I (s) refers to the intensity of each s one of the points of the set S of seeds specified for the region. So Similarly, voxels corresponding to v 'in the vicinity of d values v (v') are calculated. It's for a given percentage p of the evaluated points is satisfied that the value d lies within a certain tolerance limit T, the voxel v to the integrated region of the otherwise discard it. This consideration allows for a more robust approach growth, which helps prevent overflow situations to other components by thin tubes and sub-segmentation problems, usually due to noise.

4. FUZZY CLUSTERING ALGORITHM

The theory of fuzzy sets is a generalization of the theory of classical ensembles, introducing the notion that membership of an element to a set is not only true or false. Approach briefly explain enabling practical use fuzzy sets as a tool for quantification of truth values of predicates. Let X be a set of objects, called the universe, whose elements are denoted by x, the membership of these objects to a set A can be represented by a function $\mu_A(x)$, as follows:

$$\mu_A(x) = \begin{cases} 1 & si\ y\ sólo\ si \quad x \in A \\ 0 & si\ y\ sólo\ si \quad x \notin A' \end{cases} \tag{1}$$

Where the image $\mu_A(x)$ of the set {0,1}, is the set of evaluation. From this it comes down to the definition of fuzzy set, when the set Evaluation of u_A (x) is the interval [0,1], using properties spaces of possibility, which must be distinguished from the probability spaces

Formally we must find a **w** to maximize

$$J_F = \frac{\left|\mathbf{w}^T(\mathbf{m}_L - \mathbf{m}_R)\right|^2}{\left|\mathbf{w}^T\mathbf{S}_w\mathbf{w}\right|} \tag{2}$$

Where $\mathbf{m}_L$ and $\mathbf{m}_R$ are the two left and right groups means

$$\mathbf{m}_L = \frac{1}{\mathrm{n}_L}\sum_{\mathbf{x}\in C_L}\mathbf{x},\ \mathbf{m}_R = \frac{1}{\mathrm{n}_R}\sum_{\mathbf{x}\in C_R}\mathbf{x} \tag{3}$$

And $\mathbf{S}_w$ is within-class covariance matrix, which is bias corrected as

$$\frac{1}{n_L + n_R}(n_L\mathbf{\Sigma}_L + n_R\mathbf{\Sigma}_R) \tag{4}$$

Where Σ_L and Σ_R are the covariance matrices of class groups C_L and C_R respectively.

$$\mathbf{\Sigma}_L = \sum_{\mathbf{x}\in C_L}(\mathbf{x} - \mathbf{m}_L)(\mathbf{x} - \mathbf{m}_L)^T \tag{5}$$

$$\mathbf{\Sigma}_L = \sum_{\mathbf{x}\in C_R}(\mathbf{x} - \mathbf{m}_R)(\mathbf{x} - \mathbf{m}_R)^T \tag{6}$$

$$\mathbf{w} = \mathbf{S}_w^{-1}(\mathbf{m}_L - \mathbf{m}_R) \tag{7}$$

$$\mathbf{w}_0 = -\frac{1}{2}(\mathbf{m}_L + \mathbf{m}_R)^T\mathbf{S}_w^{-1}(\mathbf{m}_L - \mathbf{m}_R) - \log(\frac{n_R}{n_L}) \tag{8}$$

$$\frac{\lambda_1 + \ldots + \lambda_k}{\lambda_1 + \ldots + \lambda_k + \ldots + \lambda f} > \varepsilon \tag{9}$$

$$s(X) = \frac{\left|\{T \in D \middle| X \subseteq T\}\right|}{|D|}. \tag{10}$$

$$c(XY) = \frac{s(X \cup Y)}{s(X)} \tag{11}$$

$$J(M, c_1, c_2, \ldots, c_c) = \sum_{i=j}^{c} J_i = \sum_{i=1}^{e} \sum_{k=1}^{K} m_{ik}^q d_{ik}^2, \tag{12}$$

There are two necessary conditions for J to reach a minimum:

$$m_{ik} = \frac{1}{\sum_{j=1}^{c} \left(\frac{d_{ik}}{d_{jk}} \right)^{2/(q-1)}} \tag{13}$$

$$\bar{y} = \frac{\sum_{k=1}^{N} \tau^{(k)} \bar{y}^{(k)}}{\sum_{k=1}^{N} \tau^{(k)}} \tag{14}$$

that is most frequently employed as a basis function. It is represented as

$$Z_1(x) = \exp(-\frac{\|x - \mu\|^2}{\delta_j^2} \tag{15}$$

The response of the output unit is calculated using equation

$$y = \sum_{j=1}^{J} W_{ij} Z_j(x), \tag{16}$$

$$\begin{bmatrix} average\ rate\ of\ change\ of\ f(x) \\ over\ the\ interval\ a \le x \le b \end{bmatrix} = \frac{\Delta y}{\Delta x} = \frac{f(b) - f(a)}{b - a}$$

$$\frac{f(a+h) - f(a)}{h} \tag{17}$$

5. METHODOLOGY

Before applying the segmentation algorithm is necessary to separate the brain from other tissues extra cranial (skin, scalp ...) and tissues brain (meninges, skull ...). This preliminary step known as "skull stripping" prevents these tissues confused with interest (white matter, gray matter and cerebrospinal fluid), facilitating segmentation of the latter. The extraction process comprises three skull phases. First, the MRI image is smoothed with filter that smoothers no significant gradients and preserves the strongest image edges. Then, it applied to the smoothed image Marr-Hildreth filter edge detection to identify the boundaries important anatomical [6]. Among the objects defined by these boundaries is identified corresponding to the white matter and refined using a sequence of morphological operations and connected components, to obtain a mask that separates the brain itself from other tissues.

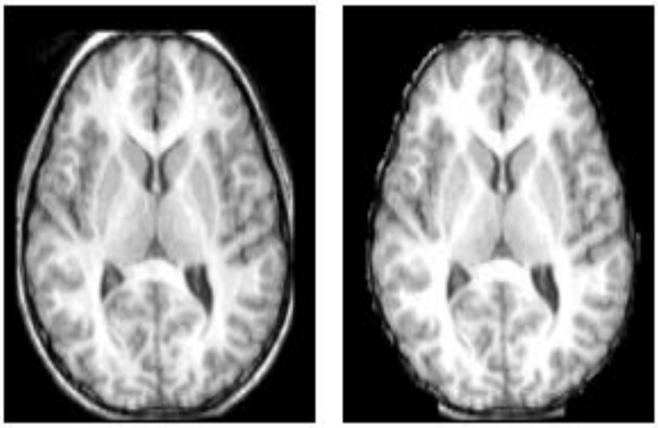

Fig 3. Result of the extraction of the skull image

After removing the skull, an anisotropic filter is applied diffusion to reduce noise present in the image [8]. The parameters chosen for the filter are κ_d= 15, τ_0 = 0.125 and 2 = number of iterations.

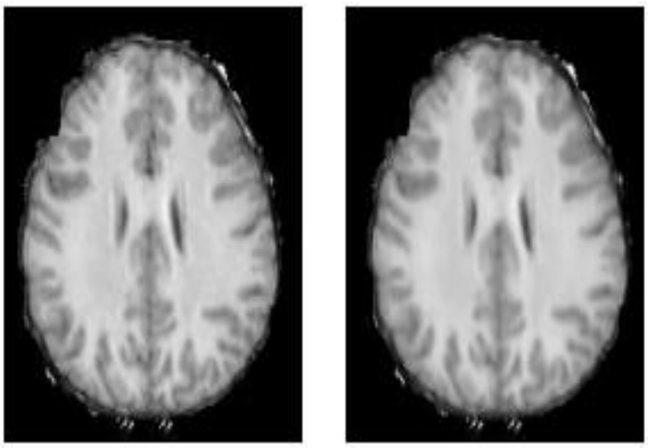

Fig 4. RM before and after anisotropic filtering

To implement the fuzzy C-means algorithm, is necessary to make a number of initial choices. The most important is the number of segments to be obtain. As the algorithm is applied on the image without skull, just 4 blocks that correspond to white matter, gray matter, cerebrospinal fluid and background. Second, determine the condition of termination. For this purpose, impose two condition. Firstly, a threshold is used for variation membership matrix U between two consecutive iterations, ie:

$$\max_{ij}\left|u_{ij}(t+1) - u_{ij}(t)\right| < \varepsilon \tag{18}$$

A maximum number of iterations is furthermore required, considering that the algorithm converges. Normally the number of iterations is limited 100. Finally, the weight exponent is chosen m measured typical value is m = 2. Once you have chosen all the parameters of the algorithm diffuse, decide how they will initialize matrices and vectors involved. You can initialize the membership matrix U or the V. The center vector first involves a unique tour of the image each iteration, while the second involves two paths, doubling the runtime. Thus, must initialize the membership matrix U, and for this is assigned to each matrix position one of these membership vectors randomly: [1,0,0,0] [0,1,0,0], [0,0,1,0] and [0,0,0,1].

Thus, the outline of the algorithm is as follows form:

1. Initialize the membership matrix U_0 for t=0
2. Repeat

a. $V_t = G_a(U_{t-1})$

b. $U_t = F_a(V_{t-1})$

c. $t \leftarrow t+1$

3. Until it $t=100 \text{ o } \max_{ij}\left|u_{ij}(t+1) - u_{ij}(t)\right| < 0.02$
4. $(U,V) \leftarrow (U_t,V_t)$

Once completed a post-processing algorithm is performed to adjust the final result. The purpose of this processing is to eliminate the remains of tissues brain that have not been suppressed by the algorithm skull removal and have been identified as gray or white matter. For this, a mask is created with those pixels that have resulted belonging to one those two segments and said mask is cleaned removing unconnected regions and holes. This mask is applied to the result of the algorithm in C averages. Since it is a very advanced programming model extraordinarily flexible (purpose language general). For the pre-processing and post-processing of the image, Seller has used ITK (Insight Toolkit) code open and free, designed for processing, segmentation and image registration and focused on medical applications.

6. EXPERIMENTAL RESULT

To evaluate this method of segmentation, it is applied about 16 MRIs of subject normal, available database IBSR (Brain Segmentation Internet Repository) [7]. This is a database that provides MRI images along with the results of manual segmentation by experts. These data are offered to researchers and segmentation algorithm developers with order to have a pool of images on to evaluate the results. The data on which has worked correspond to T1-weighted MR images. The images presented varying degrees of difficulty, that is, different levels of contrast and intensity gradient. The images have a size of 256x128x256 voxels and their data are 16-bit integer. Studies are standardized spatially according coordinates [10]. For each image, there are between 15 and 25 iterations until the algorithm is stabilized, each iteration approximately 2 minutes duration. Furthermore, need 3 minutes to pre-processing and 1 minute for post-processing. Thus, the total time of time is about 45 minutes per image (times measured for an Intel Pentium 4 processor at 1.7GHz, with 256MB of RAM). In Figure 5, one image is represented used together with expert hand segmentation provided by IBSR and segmentation obtained using the fuzzy algorithm C averages:

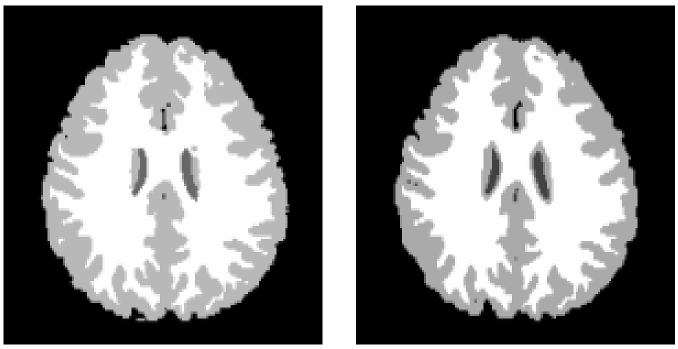

Fig 5 Original image, manual segmentation and fuzzy

To carry out the comparison between the results of segmenting the two methods are defined three parameters assessing the error rate for each classified together. Therefore, the segmentation is better the smaller these values are:

$$\text{Rate sub segmentation} = \frac{N_{fp}}{N_n} \quad (19)$$

$$\text{Rate on Segmentation} = \frac{N_{fn}}{N_p} \quad (20)$$

$$\text{Incorrect segmentation rate} = \frac{N_{fp} + N_{fn}}{N_n + N_p} \quad (21)$$

Where N_{fp} is the number of false positives, N_{fn} is the number of false negatives, N_p is the number of pixels belonging to the class and N_n is the total number of pixels that do not belong to the class. Furthermore, it has been calculated for each different set metric parameter called overlap. This parameter is more critical than the above, since no depends on the total volume of the image. A and B being the sets rated for a given segment for each one of two segmentation methods to compare the overlap metric is defined as:

$$\text{Overlapping metric} = \frac{\sum(A \cap B)}{\sum(A \cup B)} \tag{22}$$

It is equivalent to the coefficient of similarity. This metric is close to 100% for the same results and is close to zero if not shared no similarity in the voxels classified. The results of the four are represented parameters described for the gray matter:

7. DISCUSSION AND CONCLUSION

In medical imaging, segmentation is a stage extremely important for subsequent quantification. Objectivity and repeatability of the analysis to determine patterns of evolution or changes in patients and thus take a step towards the development of guidelines for assistance early diagnosis of disease, treatment and evolution. It is also an important step in improving routine reports and to distinguish between normal and pathological values of the different structures present. A number of studies of diseases of cerebral origin are based on the information obtained neuroimaging, particularly MRI, and specifically in tissue differentiation and quantitation. This makes the task of segmenting such images is a topic of constant interest and development. Manual segmentation is a method that is in use due to the high amount of time required and the visual tiredness produced, taking into a volume that may involve more than one hundred images. Methods proposed segmentation based on different computer they are solved aspects of the subject, such as ensuring the repeatability of the results obtained, but none has proven to be ideal. In medical image analysis, segmentation is a requirement always effective, whereas the technology for obtaining them varies constantly. Any new development in this regard is a contribution to the analysis and systematization of knowledge discovery images containing medical. These developments are improvements in the study, diagnosis and monitoring of various diseases, resulting directly or indirectly in a better quality of life we all deserve.

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