Medical Image Segmentation Using Genetic Algorithms

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***Abstract*—Genetic algorithms (GAs) have been found to be effective in the domain of medical image segmentation, since the problem can often be mapped to one of search in a complex and multimodal landscape. The challenges in medical image segmentation arise due to poor image contrast and artifacts that result in missing or diffuse organ/tissue boundaries. The resulting search space is therefore often noisy with a multitude of local optima. Not only does the genetic algorithmic framework prove to be effective in coming out of local optima, it also brings considerable flexibility into the segmentation procedure. In this paper, an attempt has been made to review the major applications of GAs to the domain of medical image segmentation.**

***Index Terms*—Active contour, genetic algorithms (GAs), medical image, optimization, segmentation, texture.**

I. Introduction

A LARGE part of the modern medical data is expressed as images or other types of digital signals, such as X-Rays, MRI, computer tomography (CT), positron emission tomography, single-photon emission computed tomography, electrical impedance tomography, and ultrasound [1], [2]. The acquisition of huge amount of such sophisticated image data has given rise to the development of automatic processing and analysis of medical images. Digital image processing [3]–[5] deals with the manipulation and analysis of images that are generated by discretizing the continuous signals. Segmentation of structures from 2-D and 3-D images is an important step for medical data analysis that can help in visualization, automatic feature detection, image-guided surgery, and also for registration of different images.

Segmentation of medical images is challenging due to the poor image contrast and artifacts that result in missing or diffuse organ/tissue boundaries. Consequently, this task involves incorporating as much prior information as possible, e.g, texture, shape, spatial location of organs, etc. The manual segmentation is not only tedious and time consuming, sometimes it is also inaccurate. Segmentation by experts has been found to be variable up to 20% [6]. Therefore, many automatic and semiautomatic techniques have been proposed. Although the performance of such techniques is generally good when the contrast-to-noise ratio is high, it decreases rapidly when the structures are insufficiently delineated and have low contrast like the neuroanatomic structures, such as thalamus, globus pallidus, putamen, etc.

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The problem of medical image segmentation can often be posed as one of optimization of an appropriately defined objective function. The objective function is usually complex, multimodal, discontinuous, and cannot be described in a closed mathematical form that can be analytically solved. Thus, application of several classical techniques becomes limited. Heuristic search methods that are not bound by the stringent restrictions of classical methods gain importance in such situations. In this regard, application of genetic algorithms (GAs), a search and optimization method that is capable of handling huge, complicated, and multimodal search spaces, seems to be appropriate and natural. Moreover, incorporation of domain knowledge about the image brings considerable flexibility in the segmentation procedure [7]. This paper provides a state-of-the-art survey in the application of the principles of GAs to the domain of medical image segmentation.

II. Optimization Problems and Solution Techniques

Search techniques can be broadly classified as numerical or calculus based, enumerative, and guided random search. While the calculus-based methods assume the existence of derivatives and are also local in scope making their application severely restricted, the enumerative techniques fail when the size of the search space is large as in medical image segmentation. Guided search techniques are based on enumerative methods, but use additional information about the search space. These can be further divided into single-point search and multiple-point search, depending on whether it is searching just with one point or with several points at a time. The classical gradient search techniques perform efficiently when the problems under consideration satisfy tight constraints. But when the search space is discontinuous, noisy, high dimensional, and multimodal, then GAs and related methods have been found to consistently outperform both the gradient descent method and various forms of random search [8]. Thus, such search and optimization techniques find widespread applications [9], [10].

Simulated annealing (SA) [11] is a popular single-point search technique based on the principles of statistical mechanics. Evolutionary algorithms like GAs, differential evolutions [12], tabu search [13], particle swarm optimization [14], evolutionary strategies [15], genetic programming [16], and ant colony optimization [17], etc., are popular examples of multipoint search, where a random choice is used as a tool to guide a highly explorative search through a coding of the parameter space.

III. Overview Of GAs

GAs [18]–[20] are efficient, adaptive, and robust search and optimization techniques guided by the principles of evolution and natural genetics, and have implicit parallelism. The essential components of GAs are the following: 1) a representation strategy called *chromosomes*; 2) a population of *chromosomes*; 3) mechanism for evaluating each string (*fitness function*); (iv) selection/reproduction procedure; and (v) genetic operators (*crossover* and *mutation*). The different steps of a GA process are as follows:

1) Initialize the population.
2) Decode the strings and compute their fitness values.
3) If (termination criterion is attained), then stop the process.
4) Reproduce/select strings to create new mating pool.
5) Generate new population by crossover and mutation.
6) Go to Step 2.

The different components of GAs are discussed as follows.

1) *Encoding Strategy and Population:* GAs start with the chromosomal representation of a parameter set that is to be encoded as a finite-size string over an alphabet of finite length. Although traditionally binary encoding is used, other forms like real point encoding, integer encoding, etc., are also common [19]. A set of such chromosomes in a generation is called a *population*, the size of which may be constant or may vary from one generation to another. The chromosomes in the initial population are either generated randomly or using domain-specific information.
2) *Evaluation Technique:* The fitness/objective function is chosen depending on the problem to be solved, in such a way that the strings (possible solutions) representing good points in the search space have high fitness values. This is the only information (also known as the payoff information) that GAs use while searching for possible solutions.
3) *Selection:* The selection/reproduction process copies individual strings into a tentative new population, the mating pool, for genetic operations. The number of copies that an individual receives for the next generation is usually taken to be directly proportional to its fitness value; thereby mimicking the natural selection procedure. This scheme is commonly called the *proportional selection scheme*. *Roulette wheel parent selection*, *stochastic universal selection*, and *binary tournament selection* [18], [19] are some of the most frequently used selection procedures. In the commonly used *elitist* model of GAs, the best chromosome seen up to the last generation is retained either in the population, or in a location outside it.
4) *Crossover:* The main purpose of crossover is to exchange information between randomly selected parent chromosomes by recombining parts of their genetic information. Some other common crossover techniques are two-point crossover, multiple-point crossover, shuffle-exchange crossover, and uniform crossover [21]. The successful operation of GAs depends a lot on the coding technique used to represent the problem variables. The *building block hypothesis* indicates that GAs work by identifying good building blocks, and by eventually combining them to get larger building blocks [18]. Unless good building blocks are coded tightly, the crossover operation cannot combine them together. Thus coding–crossover interaction is important for the successful operation of GAs.
5) *Mutation:* Mutation is the process by which a random alteration in the genetic structure of a chromosome takes place. Its main objective is to introduce genetic diversity into the population. Mutating a binary gene involves simple negation of the bit, while that for real coded genes is defined in a variety of ways [19].
6) *Parameters of GA:* There are several parameters in GAs that have to be tuned by the user. Some among these are the population size, probabilities of performing crossover and mutation (usually in the range [0.6–0.8] and less than 0.1, respectively), and the termination criteria. Most of such parameters in GAs are problem dependent, and no guidelines for their choice exist in the literature. Therefore, several researchers have also kept some of the GA parameters variable and/or adaptive.

IV. GA for Segmentation of Medical Images

Processing and analysis of medical images using computer comprises the following: image formation and reconstruction, image restoration, image enhancement, image compression and storage, image-based visualization, feature identification, image segmentation, shape recognition, image matching/registration, and measurement of anatomical and physiological parameters. Here, we focus on medical image segmentation [22] where application of GAs has been investigated.

A. Contour-Based Technique

Contours are the boundaries of regions in an image. Contour-based image segmentation is generally computationally efficient, but for real images often lack robustness due to their sensitivity to noise and data variability. The reliability of such methods can be improved by using techniques based on data-driven elastic models, such as *snakes* [23], [24] and deformable surface models [25], [26], which have been applied successfully in the field of medical imaging [27], [28]. However, there are a number of problems associated with contour-based techniques in extracting the region of interest (ROI), such as initialization, existence of multiple minima, and selection of elastic parameters. GAs can alleviate typical deformable model weaknesses pertaining to model initialization, deformable parameter selection, and energy functional local minima through the simultaneous evolution of a large number of models.

Grzeszczuk *et al.* in [29] have used SA for contour-based segmentation of MR images. They have defined a nonparametric energy function that is derived from statistical properties of previously segmented images, thereby incorporating knowledge from prior experience. Cagnoni *et al.* [30], on the other hand, used GA for segmenting specific anatomical structures in 3-D medical datasets. The method uses a small set of manually traced contours of the structure of interest and two cascaded modules: a nonlinear edge detector and an interpolator based on an elastic

contour model. The application of GAs is twofold. First, in the interactive specification of reference contours, and then, in optimization of the parameter of the edge detector and the interpolator. GAs have been used in [31] to guide active contours or snakes to estimate a closed contour for segmenting medical image. Here, the initial contour is estimated using a circle by providing its radius as an input parameter. Subsequently, the final boundary of the ROI is delineated by minimizing the energy of the active contour using GAs.

GAs have also been used in [32] to formulate a segmentation technique that uses the benefits of deformable templates [33] and the Markov random field (MRF) [34] model. The main problem with deformable models is that the likelihood energy is heuristically designed and does not statistically segment the image. As for MRF models, they cannot incorporate any global shape constraints in the segmentation process. Nevertheless, the likelihood model of an MRF-based approach exploits an accurate statistical modeling of the gray-level distribution of each class present in the image [35]. Since it seems that deformable templates and MRF models provide an interesting framework for structural and statistical analysis of an image, respectively, a technique that capitalizes on the benefits of both methods would provide better performance. In this regard, in [32], a deformable template-based Bayesian approach that uses GAs for the segmentation and tracking of the endocardial contour in the echographic image sequence has been proposed. A prototype template along with a set of admissible transformations is defined to capture the available global *a priori* shape knowledge of the endocardial contour with its inherent natural variability over time. In this Bayesian segmentation, the likelihood model relies on an accurate Markovian statistical modeling of the gray-level distribution of each class present in the image. The parameters of this distribution mixture are given by a preliminary statistical estimation method called iterative condition estimation (ICE) [36]. Subsequently, the detection and the tracking problem are stated in a Bayesian framework as the estimation of the deformation parameters of the template that maximize the posterior PDF. In order to maximize the function efficiently, GA along with a steepest ascent procedure has been used to segment both synthetic images and a real echocardiographic image sequence.

The GA has been used in [37] to evolve a segmenting contour by incorporating both texture and shape information. Each chromosome (of length $k+4$) represents a vector of k shape and four pose parameters. The pose parameters are incorporated using an affine transform which is the product of the translation, the scaling, and the rotation matrices, respectively. Formally, $[\widetilde{x} \quad \widetilde{y} \quad 1]^T$ can be written as

$$\begin{bmatrix} 1 & 0 & a \\ 0 & 1 & b \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} h & 0 & 0 \\ 0 & h & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \cos\theta & -\sin\theta & 0 \\ \sin\theta & \cos\theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

where (x, y) and $(\widetilde{x}, \widetilde{y})$ are the pixel coordinates of the input image and of the affine-transformed image, respectively. The four pose parameters are the translation parameters a and b, scaling factor h, and degree of rotation θ. The shape parameters are obtained from the level set function that represents the segmenting curve [38]. It is defined using the mean shape and shape variability derived from the training phase.

The method in [37] uses an initial training state and a subsequent segmentation state. A set of manually segmented images is used to derive the fitness of each chromosome by comparing the textural properties of the region segmented by that individual to the desired texture derived from the training images. Subsequently, when a new image is provided, GA is used to evolve a segmenting contour for delineating the desired object in the image. The proposed technique is used for automatically segmenting the prostate on 2-D slices of pelvic CT images. To demonstrate the effectiveness of their approach, a goodness measure G is used in [37], which is defined as $G = (1 - (H/N)) \times 1000$, where H is the Hamming distance between two binary images corresponding to the human-drawn contour and the contour derived from the GA, and N is the total number of pixels in the image. The technique, which uses both texture and shape information, was found to significantly outperform a classical texture-based segmentation technique [39] by 15.88% for training data and 70.86% for test data. It also outperformed another genetic approach called GENIE [40], which is described in Section IV-D, by 3.68% for training data and 39.97% for test data. The results indicate that incorporation of domain knowledge in the form of shape and texture information improves the performance of the genetic scheme.

GA in [41] is used for model initialization, deformable parameter selection, as well as avoiding local optima so as to overcome the problems associated with both traditional and statistical deformable models. It is also demonstrated how GAs can be combined with constrained shape deformations to effectively explore the search space. The proposed GA-based technique is used for the segmentation of the corpus callosum in midsagittal brain magnetic resonance images.

A two-stage model is employed in [42] for volumetric segmentation of lateral ventricles from brain images using parallel GAs with active model-based method. In the first stage, a coarse approximation of the object surface is captured using the finite-difference-method-based dynamic equations. Since such dynamic surfaces may easily get trapped to local minima, parallel GAs are used for further energy minimization.

Segmentation of the cardiac chambers is the first step for almost any kind of automatic high-level analysis of heart shape and its function. However, due to the presence of noise, masking structures, biological shape variability, tissue inhomogeneity, imaging-chain anisotropy, etc., segmenting these images is a difficult task. In order to overcome these problems, most researchers have adopted the strategy of exploiting anatomical knowledge about the image structure. Artificial neural networks (ANNs) with supervised training [43] have been found to be particularly suited to implement this strategy [44], [45]. Their advantages are robustness and flexibility. However, the problems that reduce the practical applicability of ANN are: 1) the complexity of setting up a training set containing the correct training data for each output neuron and 2) the constraint of using feedforward connection topologies. An approach to cardiac image segmentation that can overcome the aforementioned

drawbacks is presented in [46]. The proposed technique is based on the idea of selecting artificial creatures by means of GA on the basis of their fitness to the surrounding environment. Genetic networks (Gnets) are basically a kind of recurrent ANNs that "live" inside the image to be segmented and can recognize the structural boundaries that are used. Their behavior is developed through a GA which keeps a population of Gnets and mates the individuals that show the best performance on a set of test images of known segmentation.

B. Texture-Based Technique

Several techniques based on texture-based image segmentation are reported in Sonka *et al.* [4]. Haralick *et al.* [47] used cooccurrence matrices to calculate a set of 14 scalar features, collectively known as the Haralick transform, in order to classify terrain in aerial photographs. Richard *et al.* [48] used GA with specific adaptation, which could include texture analysis as part of its evaluation module, for medical image segmentation. Here, GA-based optimization algorithm is used to produce a population of individual subimages that are tested via a quantitative objective function, ranked using a linear fitness and decrement scheme, and modified using crossover.

GA has been used in [49] for designing texture filters for regular/structured patterns with rotational invariance, angular discrimination, and sensitivity to scale and intensity. An extension of the study may be found in [50], which extends the GA approach to real texture and the task of image classification and segmentation. It exploits the well-established Fourier spectral properties of the texture. During the training phase, for a given number of pattern classes, each with an arbitrary number of members, a mask is designed. This is configured to determine different classes of texture by response of its correlation with the Fourier spectrum of training image templates. GA is used as the optimization tool for evolving a proper mask over all possible sets of masks. The chromosomes considered in [50] are 2-D, each gene encoding (in binary) the logarithmic spectral magnitude. Crossover with two breakpoints in each dimension is used. Population size, crossover, and mutation probabilities are chosen as 100, 0.8, and 0.005, respectively. The proposed technique is tested on a real, but standardized, Brodatz texture with 32×32 pixel training segments. The results are compared qualitatively with those obtained by the cohistogram method of Unser [51] and the method of Laws [39] for three montages of texture type and smoothed using a 9×9 median filter. The segmentation result obtained by the proposed method is found to be comparable to or better than the others. The technique is then applied to MRI brain image to segment the cerebellum from surrounding white (wm) and gray matter (gm). Transaxial slices from an MRI dataset of size 236×176 pixels at 1 mm resolution are used. For training, 16×16 pixel windows are extracted from the cerebellum region as well as from the surroundingwm and gm. Three descriptors derived from the gray-level spatial dependency matrices, namely the contrast, entropy, and energy are used for demonstrating the effectiveness of the proposed technique. It is found that the quality of the results provided by the proposed technique is as good as, or better than, traditional techniques. Moreover, it has the advantage of not having to decide which texture measure to use for a specific image structure.

A further extension of the study in [50] is provided in [52] where two GA-based pattern detection techniques, one involving structured texture and other random noise, have been described. The objective in both these cases is to discriminate between regions based on their texture properties. Both these methods have been formulated as large-scale optimization problems and GAs are used to solve them. For structured texture, the approach followed is the same as the one described in [50]. For random texture, the proposed technique starts from a "ground-truth" image and a corresponding image corrupted with a specific type and level of noise. Training is performed by selecting a window (taken to be 1/16th area of the full image in [52]) over which to configure a stack filter. For this purpose, GA is used to determine the sequence of rank-order functions to use in the stack filter design which minimizes an objective function over the training window. The objective function that has been used in [52] is due to [53], which measures the mean absolute error (MAE) between the noise-free image I_0 and the restored image I_1 and is defined as $\text{MAE} = \frac{1}{n} \sum_{\text{image}} |I_0(i,j) - I_1(i,j)|$, where n is the number of pixels over which the calculation is performed. Note that MAE has to be minimized by GAs for realizing the task of restoring a corrupted image. For cases where "ground truth" images are unavailable, a training method based on simulation is used to realize a filter that can suppress noise and retain contrast. The method is demonstrated on a nuclear medicine bone scan image. The main difference between the techniques described in [50] and [52] and other texture classification techniques lies in the fact that the former approach searches the frequency spectrum of the given textures, extracting characteristic relationships that are difficult to discover analytically. Although the proposed technique requires an initial training phase, it does not use any specific texture technique and parameter. In this regard, it may be interesting to investigate the effectiveness of using wavelet transform [54] instead of Fourier transform of each template image in order to encode the resulting spectra in the chromosomes of GAs. As wavelets provide localization in both the frequency and spatial domains, this might further improve the medical image segmentation performance.

C. Knowledge-Based Technique

Knowledge about the human anatomy and imaging parameters can often be effectively incorporated in the segmentation process to improve its efficiency. In [55] and [56], a CT image segmentation technique based on template matching and knowledge-based approach has been developed. Region growing technique along with knowledge-based classification [57], [58], and edge-based technique along with knowledge-based interpretation [59] have been proposed by researchers for MRI segmentation.

While the performance of the aforesaid automatic segmentation techniques is generally good for images with high contrast-to-noise ratio, they are not suitable for segmentation

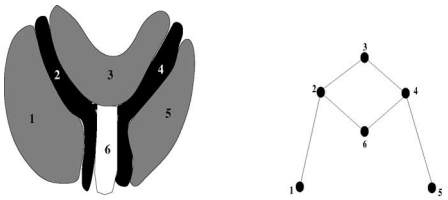

Fig. 1. (a) Example of six neuroanatomic structures present in a portion of cross-sectional brain anatomy ([16]).(b) The corresponding region adjacency graph.

of insufficiently delineated, low-contrast neuroanatomic structures, such as thalamus, putamen, globus pallidus, etc., in the human brain. In order to overcome this limitation, Sonka *et al.* [60] proposed a GA-based method that utilizes *a priori* knowledge about the human brain anatomy. Here, initially an edge-based region growing method [61], [62] is adopted, which uses edge information to accurately specify boundaries between homogeneous regions. In the primary segmentation step, an intentionally oversegmented image is generated such that further processing only deals with merging primary regions. Subsequently, a region adjacency graph (RAG) is constructed, to describe region properties and region interrelationships in the primary regions resulting from primary image segmentation. Fig. 1(a) and (b) demonstrates an example of the brain anatomy and the corresponding RAG, respectively, as shown in [60].

At the beginning of the segmentation/interpretation process, each primary region in the RAG is numbered and a one-to-one correspondence between primary regions and the position in a chromosome used by the GA is established. The objective function used by the GA represents *a priori* knowledge about human brain anatomy and imaging parameters. This is defined in [60] as the image interpretation confidence, C_{image}

$$C_{\text{image}} = \frac{\sum_{i=1}^{N_R} C(\theta_i)}{N_R} \tag{1}$$

where $C(\theta_i)$ represents the confidence in the interpretation of θ_i of a region R_i and N_R is the number of regions in the corresponding RAG. Now $C(\theta_i)$ is computed as

$$C(\theta_i) = \frac{C(\theta_i|X_i)\sum_{j=1}^{N_A}[r(\theta_i,\theta_j)C(\theta_j|X_j)]}{N_A} \tag{2}$$

where $r(\theta_i,\theta_j)$ is the value of the compatibility function of two adjacent regions R_i and R_j with labels θ_i and θ_j, and N_A is the number of regions adjacent to the region R_i. Confidence $C(\theta_i|X_j)$ is the interpretation θ_i of the region R_i with region property X_i calculated as $C(\theta_i|X_i) = P(\theta_i|X_i)$, where $P(\theta_i|X_i)$ is the conditional probability evaluating the confidence that a region R_i is correctly labeled θ_i considering only the unary properties X_i. Both the unary confidences $C(\theta_i|X_i)$ and the binary compatibility relations $r(\theta_i,\theta_j)$ are computed using *a priori* knowledge about the human brain anatomy. Twenty out of 28 MR brain images are used to form the training set from which specific knowledge is acquired, and this is used in the proposed interpretation method. The GA-based technique [60] is able to segment 17 neuroanatomic structures, such as corpus callosum, fornix, third ventricle, cistern, pineal gland, left/right ventricles, left/right caudate nucleus, left/right internal capsule, left/right putamen, left/right globus pallidus, and left/right thalamus from MR brain images. The signed percent area error, labeling error, and the object positioning error in the identification of the neuroanatomic structures in the test set are reported to be 8 $\pm$ 17%, 12 $\pm$ 12%, and 2.3 $\pm$ 1.6 pixels, respectively. The average border positioning error is 1.1 $\pm$ 0.5 pixels, root-mean-squared border positioning error is 1.5 $\pm$ 0.6 pixels, and maximum border positioning error is 4.5 $\pm$ 2.7 pixels. The correlation coefficient of the computer-identified and observer-defined neuroanatomic structure areas is found to be 0.99, which indicates a high correlation.

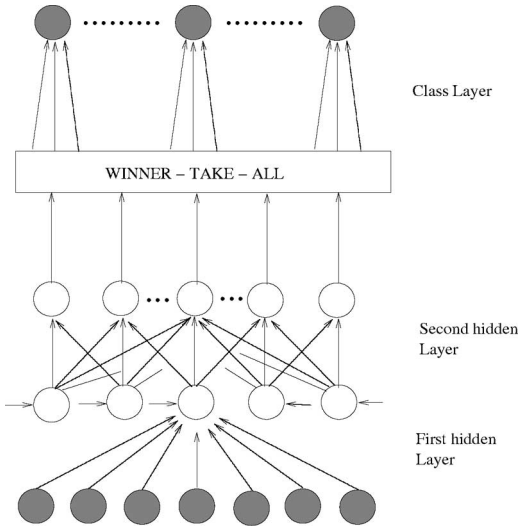

Fig. 2. MoRCE network ([65]).

D. Learning-Based Technique

Among learning-from-examples techniques, in which the problem of image segmentation can be reformulated as an optimization problem, GA has been used for segmentation by defining the objective function as a multiterm cost function. An adaptive approach in which GAs are used to optimize the performances of the Phoenix segmentation algorithm is described in [7]. A region-based segmentation in [63] is mapped onto a chromosome represented as a binary string and evolved a population of segmentations using a fuzzy fitness function. GAs have been used in [46] to optimize the parameters of recurrent neural networks to segment echocardiographic images. A fairly comprehensive review of other approaches is available in [64].

A modified restricted Coulomb energy (MoRCE) network trained by GAs is presented in [65]. Each neuron of the network forms a closed region in the input space. Fig. 2 shows a MoRCE network. GAs are used to improve the classification performance of the MR and CT images with minimized number of neurons. Both MR and CT head images with tumor are classified by MLP, restricted Coulomb energy (RCE), and MoRCE networks. The MR head image is segmented into five categories: background

or soft tissue, light grey brain, dark grey brain, tumor, and bone. Whereas, the CT head image is segmented into four classes: background, soft tissue, tumor, and bone. Elements of a 9-D vector in the training set are formed by the gray levels that are at one neighborhood of the center point. For training 50 center points (or, feature vectors) are selected for each class by the user. Thus, the size of the 9-D training data is $N \times 50$, where N is the number of classes. Similarly, the test set is created with 50 other feature vectors for each class, to result in a test data size of $N \times 50$. The results show that for MR image, while MLP and RCE provide classification accuracies of 67.2% and 82.8%, MoRCE gives a much better score of 94%. Again, for the CT image, MoRCE provides a significantly superior score of 96%, while MLP and RCE provide scores of 89% and 90%. From the results, it is also evident that RCE provides better performance than the standard MLP. In terms of the number of neurons, MoRCE requires fewer neurons than the MLP and RCE. Although the time for training required by MoRCE is more than that required by RCE, it is still much less than the training time of MLP. From the training and test performance on MR and CT images, it is observed that classifying a CT image is relatively easier than classifying an MR image.

Perkins *et al.* in [40] tackle the problem of pixel-by-pixel classification of a multispectral image using supervised learning. Instead of taking only the spectral components of each pixel, they use a genetic approach for searching a space of image processing operations for a set that can produce suitable feature planes. A discriminant-function-based classifier that uses these feature planes outputs a final classification of the full image. This hybrid genetic learning systems is called GENIE. Harvey *et al.* in [66] use GENIE for identifying cancerous cells on images of breast cancer tissue. The results demonstrate that the GENIE system is able to identify the benign and malignant cells from a variety of samples.

E. Model-Based Technique

One approach to segmentation of an MR image involves fitting a model PDF to the PDF obtained from the data [67], [68]. The method proposed in [68] uses GAs to optimize a complex PDF to fit the histogram derived from the data. This technique is based on a previous quantification method that used a statistical model and partial volume effect [67] while utilizing tree annealing, a technique based on simulated annealing, as the optimization tool. The GA-based method [68] assumes the brain material is composed of three matter types: cerebrospinal fluid (csf), gm, and wm. Here, two models are considered. In the first model, it is assumed that each pixel contains a single matter type that is determined by pixel intensity, i.e., wm pixels have higher intensity than gm, and gm pixels have higher intensity than csf. The matter types are assumed to have a Gaussian density function with means $\mu_{\rm gm}$, $\mu_{\rm wm}$, and $\mu_{\rm csf}$, amplitude factors $a_{\rm gm}$, $a_{\rm wm}$, and $a_{\rm csf}$, and a common variance value σ. The mixture PDF is a sum of these three Gaussian distributions and given by

$$y_i = \sum_{k={\rm gm,wm,csf}} \frac{a_k}{\sqrt{2\pi} * \sigma} * e^{-(x_i-\mu_k)^2/2\sigma^2}. \qquad (3)$$

In the second model, it is assumed that a pixel can be a single matter or composed of two matter types; thereby giving up to six possible combinations (gm, wm, csf, gm_wm, gm_csf, wm_csf) for each pixel. The means and variances of the combinational pixels depend on those of the individual matter pixels. For example, the mean and variance of pixels of class gm-wm are given by $\mu_{\rm gm\_wm} = (\mu_{\rm gm} + \mu_{\rm wm})/2$ and $\sigma_{\rm gm\_wm} = \sqrt{2\sigma^2/3 + (\mu_{\rm gm} - \mu_{\rm wm})^2/12}$, respectively. The mixture PDF in this model is a sum of six Gaussian distributions, and is given by

$$y_i = \sum_{k={\rm gm,wm,csf}} \frac{a_k}{\sqrt{2\pi} * \sigma} * e^{-(x_i-\mu_k)^2/2\sigma^2} + \sum_{l={\rm gm\_wm,gm\_csf,wm\_csf}} \frac{a_l}{\sqrt{2\pi} * \sigma_l} * e^{-(x_i-\mu_l)^2/2{\sigma_l}^2}. \qquad (4)$$

Therefore, the task of optimization involves evolution of the density function parameters such that the mixture PDF optimally fits the histogram plot derived from the image. This requires optimization of seven parameters in (3) (first model) and ten parameters in (4) (second model). For this purpose, GAs have been used where the parameters are encoded in a chromosome. The error function that needs to be minimized is $E = \sqrt{\sum_{i=0,255}(z_i - z_i^*)^2}$, where, z_i and z_i^* are the actual and computed data points, respectively. Initially, the fitness is taken as $\frac{1}{E}$, which is subsequently modified to $\frac{\text{no of matched points}}{E}$, where a point is considered to be matched if it lies within a specified tolerance. Roulette wheel selection, single-point crossover with probability 0.6, and mutation rate of 0.01 are used. The results of the GA-based scheme are compared to those obtained using tree annealing [67] for both the models with two different histograms. It is observed that the error value of both the approaches using the first model are exactly the same, viz., 0.029 and 0.027 for the first and the second histograms, respectively. Similarly, for the second model, the values of the two approaches are almost the same. A single run of the GA-based method [68], which takes less than 15 min on a DEC 3100, shows an improvement with respect to time as compared to the tree annealing [67] approach. It may be noted that the aforementioned task appears to be multiobjective in nature, and therefore, application of multiobjective GAs [69] is expected to yield better results.

An automatic MRI brain image segmentation technique using a new fuzzy-point-symmetry-based genetic clustering technique (Fuzzy-VGAPS) is proposed in [70] with encoding of the cluster centers in the chromosomes [71]. Fuzzy-VGAPS is able to evolve the number of clusters present in the dataset automatically. A newly developed fuzzy-point-symmetry-based cluster validity index, FSym-index, is used as a measure of "goodness" of the corresponding partition. A Kd-tree-based data structure is used to reduce the complexity of computing the symmetry distance. Adaptive probabilities of crossover and mutation are applied. The population size is kept fixed at 20. It is observed that Fuzzy-VGAPS provides an improvement in the range [2.94%–35.17%] and [10.14%–61.25%] over fuzzy

C-means and [2.898%–52.066%] and [1.587%–61.73%] over the expectation maximization algorithm for MRI with normal brain and multiple sclerosis lesions, respectively. The improvement is in terms of Minkowski value, which is a measure of the quality of a solution given true clustering. The improvement of Fuzzy-VGAPS over Fuzzy-VGA [72] for MRI with multiple sclerosis lesions is reported to be in the range [2.898%–52.066%]. The results establish the effectiveness of integrating GAs with the point symmetry property for efficient segmentation of MRI images, though other models of symmetry like line symmetry, plane symmetry, are likely to further improve the performance.

V. Conclusion

In this paper, a detailed survey of the applications of GAs to medical image segmentation is reported. The classical image segmentation techniques that use information regarding texture, shape, contours, etc., perform well when the images are simple, less noisy, and the problem can be described in some closed mathematical form that can be solved analytically. However, in the domain of medical images, it is found that the objective function is usually much complex, multimodal, and discontinuous. As a result, application of GAs and other evolutionary techniques become attractive and is also quite effective.

The main challenges and issues in integrating GAs for solving the optimization problems in medical image segmentation are manifold. First, the encoding strategy must be suitably defined so that it conforms to the building block hypothesis. Any adhoc encoding strategy may not follow this hypothesis, and GAs may often yield poor result in such situations. Since fitness computation is the most time-consuming part, its efficient design is crucial for a successful application of GAs. The choice of the different genetic operators as well as the termination criteria are also important issues in GAs. Often, these are tuned manually, and require a large amount of expertise as well as experience. Alternatively, the parameters can be kept variable and/or adaptive so as to be able to self-modify in response to the population statistics. Ways of avoiding premature convergence are also critical in any application of GAs. A common approach in this regard is fitness scaling [18]. Another important consideration in medical image analysis is the reduction of the computation time of GAs, which is, usually, time-consuming in nature. Incorporation of expert knowledge and integration with local search are ways to enhance the convergence rate.

In medical image segmentation, sometimes it is possible to define multiple criteria that need to be optimized simultaneously. Hence, another major issue in this regard is the application of multiobjective optimization (MOO) techniques [69], [73] that can be effectively utilized to yield a set of Pareto optimal solutions that the domain expert can then analyze. Moreover, hybridizations of MOO techniques with other computational intelligence techniques like rough sets, fuzzy sets, neural networks, etc., are interesting directions of future research in this domain.

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