LIVER SEGMENTATION USING LEVEL SETS AND GENETIC ALGORITHMS

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Abstract: This paper presents a method based on level sets to segment the liver using Computer Tomography (CT) images. Initially, the liver boundary is manually set in one slice as an initial solution, and then the method automatically segments the liver in all other slices, sequentially. In each step of iteration it fits a Gaussian curve to the liver histogram to model the speed image in which the level sets propagates. The parameters of our method were estimated using Genetic Algorithms (GA) and a database of reference segmentations. The method was tested using 20 different exams and five different measures of performance, and the results obtained confirm the potential of the method. The cases in which the method presented a poor performance are also discussed in order to instigate further research.

1 INTRODUCTION

In medical imaging analysis, image-guided surgery and organs visualization, segmentation is a crucial step. This step is particularly arduous in abdominal CT images because different organs lie within overlaping intensity value ranges and are often near to each other anatomically.

Numerous techniques have been proposed in the literature for extraction of organs contours in abdominal CT scans. They can be roughly divided in two main groups: model driven and data driven approaches.

Model driven techniques (e.g. Lamecker et al., 2004) use pre-defined models to segment the desired object from the available images. This kind of technique basically searches the images for instances that fit a given model described in terms of object characteristics such as position, texture and spatial relation to other objects.

Data driven techniques (e.g. Fujimoto et al., 2001) try to emulate the human capacity to identify objects using some similarity information present on image data, automatically detecting and classifying objects and features in images. Many of them use known techniques such as region growing and thresholding, combined with some prior knowledge about the object being analised.

This paper proposes a model driven method based on level sets to segment the liver with an evolutionary approach to select its paremeters. Using an initial user-defined liver segment in one slice, the method segments the liver through all other slices. It uses a Gaussian fit to define the speed image where the level sets propagates. The initial solution at each slice is defined as the region previously segmented on an adjacent slice. Experiments using five exams as training set and other 15 exams for validation indicate the outcome of our method.

The subsequent text is organised in the following way. Section 2 presents theorectical fundamentals of level sets and genetic algorithms. Section 3 presents the proposed segmentation method in details, section 4 presents the parameters estimation experiments, section 5 reports some results, and the main conclusions are presented in section 6.

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2 THEORETICAL FUNDAMENTALS

In this section we introduce theoretical fundamentals related to the level sets method and present then an overall description of genetic algorithms.

2.1 Level Sets

Level set methods were developed by Sethian and Osher (Osher and Sethian, 1998) and firstly introduced in medical imaging by Malladi et al. (Malladi et al, 1995).

Level set is a continuous deformable model method with implicit representation. Its main idea is to embed the deformable model in a d+1 dimensional space, to segment iteratively an object in a d dimensional space, using partial differential equations. The main advantage of level sets is that it allows changes of surface topology implicitly. As it embeds the evolving surface, also called interface, in a higher dimensional function, this interface can split into several connected components or merge from different connected components naturally, and the embedding level sets function remains continuous.

Considering $\psi(x,t)$ the level sets function, x the position vector and t the time step of the level set evolution, the evolving surface is represented as the zero level set of $\psi(x,t)$=0. The segmentation result is achieved when the RMS difference between $\psi(x,t)$=0 and $\psi(x,t$-1)=0 is less than a pre-defined minimum RMS value.

The level sets function is normally a smooth well behaved function, in our work the signed distance function. This function calculates, for each voxel, the distance to the closest voxel in the interface. This distance is negative inside the interface, and positive outside.

Given an initial surface S_0 and consequently $\psi(x,t=0)$, the level set function is evolved under the control of the differential equation 1, as proposed in ITK library (Yoo et al, 2002), that defines the displacement of the interface in a time step.

$$\frac{d}{dt}\psi = -\alpha A(x)\nabla\psi - \beta P(x)|\nabla\psi| + \gamma Z(x)\kappa|\nabla\psi| \qquad (1)$$

The gradient (or its module) of $\psi(x,t)$ appears in each term of the equation. As we defined $\psi(x,t)$ as a signed distance function, the gradient of $\psi(x,t)$ points from inside to outside considering the interface $\psi(x,t)$=0, and $|\psi|$ = 1, by definition.

A, P and Z, are usually calculated from the input image. A is the advection term. This term is a vector field responsible for attracting the evolving surface to determinate features, usually related to boundaries of objects, and pre-defined barriers. It is weighted by the constant advection weight α, and multiplied by the gradient of $\psi(x,t)$.

P is the propagation term. This term is a propagation image, also called speed image, where the level sets propagates. This image normally has high values in regions where the interface can expand quickly, and values close to zero in regions where it should move slowly or stop, normally close to important features. It is weighted by the constant propagation weight β and multiplied by the module of the gradient of $\psi(x,t)$.

K is the mean curvature of the interface, and is defined as the divergence of the normal to the interface, usually being calculated using first and second derivatives of the interface, based on finite differences. In this way, $K > 0$ for convex regions, and $K < 0$ for concave regions. Z is a spatial modifier for the mean curvature K, and modifies the value of K in a determinate spatial position. In this work it was defined as P, in such a way that the curvature has less importance when close to important features. It is weighted by the constant mean curvature weight γ and multiplied by the module of the gradient of $\psi(x,t)$.

A segmentation algorithm based on level sets may use all these terms, or it may omit one or more terms.

Many of the parameters mentioned until now must be properly adjusted for the level sets method to produce accurate result. The determination of appropriate parameter values can usually not be done by heuristics mainly due to the complexity of the target application. Multiple local minima frequently found in such problems make it difficult to use non-linear optimization methods for parameter adjustment.

A well known alternative to estimate segmentation parameters of complex functions, usually hard to model analytically or with many local minima, are Genetic Algorithms.

2.2 Genetic Algorithms

Genetic Algorithms are a computational search technique to find approximate solutions to optimization problems. They are based in the biological evolution of species as presented by Charles Darwin. The main principle of the Darwin's Theory of Evolution is that individual characteristics

are transmitted from parents to children over generations, and individuals more adapted to the environment have greater chances to survive and pass on particular characteristics to their offspring.

In evolutionary computing terms an individual represents a potential solution for a given problem, and its relevant characteristics with respect to the problem are called genes.

A population is a set of individuals in a particular generation, and individuals in a population are graded as to their capacity to solve the problem. That capacity is determined by a fitness function, which indicates numerically how good an individual is as a solution to the problem (Michalewicz, 1994).

GAs propose an evolutionary process to search for solutions that maximize or minimize a fitness function. This search is performed iteratively over generations of individuals. For each generation the less fitted individuals are discarded and new individuals are generated by the reproduction of the fittest. The creation of the new individuals is done by the use of genetic operators.

A genetic operator represents a rule for the generation of new individuals. The classical genetic operators are crossover and mutation. Mutation changes gene values in a random fashion, respecting the genes' search spaces. Mutation is important to introduce a random component in the search of a solution in order to avoid convergence to local minima.

Crossover operators act by mixing genes between two individuals to create new ones that inherit characteristics of the original individuals. The general idea is that an individual's fitness is a function of its characteristics, and the exchange of good genes may produce better fitted individuals depending on the genes inherited from their parents. Although less fitted individuals can also be generated by this process, they will have a lower chance of being selected for reproduction.

Other genetic operators can be found in the literature (Michalewicz, 1994). Most of them are variants of crossover and mutation, adapted for specific types of problems.

3 SEGMENTATION METHOD

The proposed method relies on two heuristics: the liver parenchyma is roughly homogeneous, and liver veins are mainly inside the liver, as well as liver nodules. The impact of these heuristics on cases where peripheral nodules and veins are present is discussed in details in section 6.

The first step is to define, at a slice N, an initial solution that is expected to contain great part of the liver. This solution does not need to be accurate, as it will be later deformed too. Then, an iterative process takes place, both upwards and downwards, processing sequentially the whole stack of slices. In this process the initial solution of a slice to be processed is defined as the result previously computed at the adjacent slice.

The same segmentation algorithm is applied in each iteration step. It receives as input data, the image slice and the result obtained in the adjacent slice. This initial solution is then deformed towards the liver boundaries using an approach based on level sets.

As seen in section 2.1, one needs to define the propagation, advection and mean curvature terms, to create the level set function. However, in this work the advection term was not used, because the boundaries of the liver cannot be robustly detected as the liver usually share similar pixel intensity values with some of its anatomical neighbouring structures.

The speed image of the propagation term is defined by a model based on two automatically defined thresholds TL and TH ($TL<TH$) and the input image $g(x)$. This model is expressed by equation 2:

$$P(x) = \begin{cases} g(x) - TL & if \;\; g(x) < (TH - TL)/2 + TL \\ TH - g(x) & otherwise \end{cases} \quad (2)$$

One can notice that $P(x)$ assumes positive values when the pixel intensity relies inside the range $[TL,TH]$ and negative values when it is outside the range. In this way, the surface expands where pixel values are inside the range, and shrinks otherwise.

The computation of TL and TH is based on the assumption that the histogram of voxels inside the liver is usually Gaussian like shaped.

Initially the histogram of the region inside the initial solution is calculated. Then a Gaussian curve is fitted to the histogram, using a non-linear minimization estimator, and two thresholds TL and TH are computed as the values where the Gaussian achieves two pre-defined values GL and GH. This range $[TL,TH]$ of grey level values is expected to be characteristic of liver parenchyma.

The spatial modifier $Z(x)$ of the mean curvature K is set as $P(x)$. So $Z(x) = P(x)$.

At this point the level sets process takes place, deforming the given initial solution towards the liver boundaries using all the terms just defined, until the convergence criteria is achieved (minimum RMS).

This level sets approach segments the liver parenchyma, but nodules and veins, which normally appear respectively as darker and brighter regions, are not segmented. This problem is partially eliminated by the use of a 'fill-holes' morphologic algorithm, that merges veins and nodules that are totally inside the liver. When a nodule or vein is at the periphery, though, they usually do not appear in the final result.

The process ends when it achieves the first and last slices, or when an initial segment is vanished by the level sets algorithm in a given slice.

In this section it was possible to observe that the method needs five different parameters to run, which were tuned using an evolutionary approach:

1. Minimum RMS: the convergence criteria of level sets function, defined in terms of the root mean squared (RMS) change in the level set function.
2. *GL*: Gaussian low factor
3. *GH*: Gaussian high factor
4. β: level set propagation weight
5. γ: level set mean curvature weight

4 PARAMETERS ADAPTATION

4.1 Processing Scheme

In the devised GA each individual consists of a set of segmentation parameter values; each parameter is represented by a gene. The fitness of each solution (individual) is calculated by comparing the segmentation produced by the solution with the reference segmentation, using five different measures of performance (Heimann et al, 2007), as described in section 4.3.

As described in section 3, the segmentation method has a set of five parameters to be optimized: Minimum RMS, GL, GH, β and γ.

Each parameter value (genes) of the initial set of solutions (initial population) is generated randomly, in given ranges. As the evolutionary process advances, the best solutions (fittest individuals) are selected and new solutions (generations) are created from them (reproduction).

The selection of individuals for reproduction takes the fitness values into consideration, so that the fittest individuals have a larger probability of being selected. Furthermore, the best individuals from one generation are kept in the next generation. The evolutionary process stops after a fixed number of generations, and the gene values of the fittest individual are taken as the final (adapted) segmentation parameter values.

4.2 Reproduction Procedure

As stated before, the initial population is created by setting random values for the genes of each individual. After fitness evaluation a new population is created by replacing the Q worst individuals of the prior population, being Q a positive integer value smaller than the population size.

The new individuals are created by genetic operations over selected individuals of the prior population. The selection of individuals is done by a roulette mechanism, which takes into consideration normalized fitness values (Davis, 1990).

The following genetic operators were used (Davis, 1990; Michalewicz, 1994). One point crossover: two individuals exchange genes; arithmetic crossover: a linear combination of a set of genes of two individuals is per-formed; mutation: the value of a gene is substituted by a random value.

The selection of the reproduction operation is also done by a roulette mechanism, considering a predefined probability value for each operator. To help preventing convergence to local minima, the operators' application probabilities are interpolated during the evolution process (Davis, 1990), decreasing crossover probability while increasing mutation probabilities.

In each generation the best individuals can be saved to the preceding generation, according to a Steady State rate. This rate specifies the amount of individuals that will be saved to the next generation.

It is also possible to make more than one experiment in sequel, and the best individuals of one experiment are saved to the next experiment, guiding the following experiment to good solutions.

In this work, the GA was configured as the following: number of generations = 30; population size = 30; initial crossover rate = 0.8; final crossover rate = 0.65; initial mutation rate = 0.1; final crossover rate = 0.8; initial steady state rate = 0.8; final steady state rate = 0.2; number of sequenced experiments = 2; rate of seed from the first experiment to the second = 0.1.

4.3 Fitness Evaluation

The fitness of an individual should indicate how good the segmentation result in relation to the reference segmentation is. In mathematical terms, given a set of reference segments M and a parameter vector N a fitness function $F(M,N)$ that properly

expresses the goodness of a segmentation outcome must be defined.

Once the fitness function F is chosen, the task of the GA consists in searching for the parameter vector Wopt, for which the value of F is minimum:

$$W_{opt} = \arg_P(\min[F(M,N)]) \quad (3)$$

The fitness function devised in this work is defined as the mean of five score measures that evaluate the differences between two different surfaces: the one obtained by the segmentation method using the parameters of the evaluated individual and a given reference.

These score measures were defined taking into account the variability of the results obtained manually with different specialists. In this way, it considers that a high-scored method is as precise as a human specialist.

To implement this idea, values of the mean error usually obtained in human manual segmentation were estimated for each of the five metrics defined. In this way the score is high when the differences (errors) between the result and the reference are similar to the ones usually obtained by the specialists, and low if the differences are bigger than that.

The reference and the evaluation metrics are provided by SLiver07 conference (Heimann et al, 2007), and the evaluation metrics used are:

1. Volumetric overlap (VOE): is the number of voxels in the intersection of segmentation and reference, divided by the number of voxels in the union of segmentation and reference.
2. Relative absolute volume difference, in percent (RVD): 1 minus the total volume of the segmentation divided by the total volume of the reference
3. Average symmetric absolute surface distance, in millimetres (ASD): the border voxels of segmentation and reference are determined and for each voxel in these sets, the closest voxel in the other set is determined (using Euclidean distance). All these distances are stored, for border voxels from both reference and segmentation. The average of all these distances gives the averages symmetric absolute surface distance.
4. Symmetric RMS surface distance, in millimetres (RMSSD): is similar to the previous measure, but stores the squared distances between the two sets of border voxels. After averaging the squared values, the root is extracted and gives the symmetric RMS surface distance.
5. Maximum symmetric absolute surface distance, in millimetres (MSD): is similar to the previous two, but only the maximum of all voxel distances is taken instead of the average.

5 EXPERIMENTAL EVALUATION

In order to evaluate the performance of the proposed method a software prototype was developed in C++/C#. The prototype includes the library that implements the GA, and the ITK library which implements the level sets framework used in the segmentation method.

To estimate the optimal set of parameters, the prototype allows the user to define the search ranges of each parameter. In our experiment a set of five exams was used for training, i.e., for estimation of segmentation parameter values, using the evolutionary approach. Then, using the optimal segmentation parameters found, the other 15 exams available on the dataset were evaluated.

Table 1: Liver segmentation results.

Evaluation	Best	Worst	Mean
VOE (Score)	5.45 (78.70)	12.07 (52.82)	7.35 (71.29)
RVD (Score)	-0.63 (96.63)	8.12 (56.80)	-2.19 (82.27)
ASD (Score)	0.76 (80.85)	3.57 (10.70)	1.35 (66.25)
RMSSD (Score)	1.69 (76.46)	8.22 (0)	3.05 (58.58)
MSD (Score)	17.03 (77.59)	55.09 (27.21)	26.81 (64.72)
Overall Score	82.05	29.57	68.62

Table 1 illustrates the results obtained in the evaluation phase. We compiled our results, depicting the best, worst, and mean results for all test set. The overall score was computed as the simple mean of the five different metric scores.

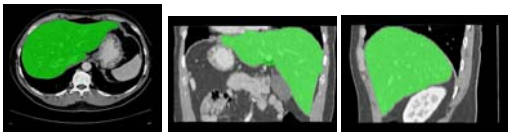

Figure 1: Best result obtained (left) axial view; (center) coronal view; (right) sagittal view.

The method attained a good performance in 17 of the 20 exams, in which the overall score is above 65. Figure 1 shows the result obtained in the best case, with overall score of 82.05. It is possible to observe that the liver boundaries are accurately defined.

In 3 exams, though, the results contain some significant errors that can be verified visually. The exam with the lowest score among all exams tested has an overall score of 29.57. In this exam the liver has a huge nodule, and it causes a leak of the segmented region towards adjacent darker structures. Considering the size of the nodule, the result is reasonable, though.

On another exam with low score (46.18) it is possible to observe a single major error, caused by a peripheral nodule not classified as liver. This is explained by the heuristic adopted, that considers a single Gaussian curve to model liver tissue. Once the nodule in this exam appears much darker than the liver parenchyma, its voxel intensities lie outside the range [*TL,TH*] defined by the Gaussian fit. As the nodule is peripheral, it wasn't possible to correct this error with morphological fill holes, and therefore the nodule region was not included in the final result.

Our results can be easily compared with many other approaches, since the data and evaluation metrics were obtained from the website of the liver segmentation competition held in the Sliver07 conference, and the results of other approaches are also available there. Thus, this comparison with other works is straightforward once one visits the conference's website. If compared with other automatic and semi-automatic methods, our method has a good performance being ranked among the top 5 score.

6 CONCLUSIONS

We have presented a method to segment the liver based on a level sets approach, using an evolutionary method to estimate its optimal parameters. These parameters were coded into genes of the individuals of a GA, and the fitness evaluation was defined to measure the similarity between a user defined reference and the segmentation result.

Trough all the experiments it was possible to verify the potential of the presented methodology. The use of level sets, which is a consolidate alternative to segment medical images, achieved good performances in the tested exams, and the use of GA to estimate its optimal parameters produced robust parameters.

The method has, though, some limitations. It presented some low performances in the presence of peripheral nodules and veins, and also when nodules with volume similar to the liver parenchyma were observed. These cases were presented in details in section 5.

It is important to notice that the method can be applied to segment other organs beside the liver, especially considering the ones roughly homogeneous. In this case the GA would estimate other parameters based on the input reference of the organ to be segmented.

Some suggestions for further research would be a better modelling to build the speed image considering also the information of liver internal structures, such as vessels and nodules. Another possibility would be use the advection term to suppress or reinforce some specific barriers, which could be used to avoid leaking and also enable the inclusion of peripheral nodules and veins in the final result.

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