Multi-mode Narrow-band Thresholding with Application in Liver Segmentation from Low-contrast CT Images

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Abstract

Segmentation of liver in CT images is regarded as a challenge in image processing due to low-contrast of datasets, variety of liver shape, and its non-uniform texture; especially for abnormal cases. In this paper, we deal with normal and abnormal datasets as images containing two or more Gaussian components. We threshold a slice in a narrow band of each mode, find liver pixels based on a priori knowledge, prepare a probability map, and threshold the map to find initial liver border. Final boundary of liver is obtained through a few iterations of ‘Geodesic Active Contour’. The proposed method was tested on 30 normal and 17 abnormal datasets each containing 159-263 slices; acquired from different CT machines. The results for normal and abnormal datasets are completely acceptable, according to the evaluation done by a specialist. However, for severely abnormal datasets, the proposed method is regarded as a promising algorithm for liver segmentation.

1. Introduction

Development of medical imaging technologies has made it a necessity to analyze patient datasets before taking any decision on treatment planning. In case of liver, its size, volume, and shape; structure of its vessels; and tumors sizes and locations are important [1].

The initial step of liver image analysis is segmentation. Due to variety of liver’s shape, size, and location; and low contrast of CT images; liver segmentation is still considered as a challenge. Many image processing techniques have been proposed to develop semi-automatic/automatic, low-level/high-level, and 2D/3D liver segmentation algorithms. The techniques which have been employed include probabilistic atlases [2], active contours [3], statistical shape models [4], intensity-based [5], and texture-based methods [6]. High-level techniques and 3D approaches are robust but they usually need a training step. They are sensitive to initialization or registration step and cannot segment datasets that substantially differ from the training set. Low-level and 2D techniques consider variations of liver in different datasets but are not robust enough and may lead to over-segmentation or under-segmentation.

In this paper, we propose a novel liver segmentation algorithm which exploits a 2D technique to consider variations and uses a 3D technique to establish robustness for low contrast CT images. In the proposed method, we first use K-means clustering and a priori knowledge to find a rough liver boundary in each slice of the low-contrast CT image. Then the liver boundaries of all slices are used as the initial surface input of a 3D geodesic active contour algorithm to find the accurate liver surface.

2. Narrow band thresholding

The proposed algorithm consists of three steps: preprocessing, initial boundary extraction, and final boundary tuning.

Preprocessing includes region extraction, interpolation, smoothing, ROI definition, and initial slice segmentation. In order to decrease the run-time of the algorithm and reduce the required memory size, we
extract the region that includes the bounding box of the
trunk in the axial plane, and the bounding box of liver
in the coronal plane. This leads to a reduction of 60%
percent in number of pixels, approximately. The inter-
slice spacing of a dataset is sometimes more than twice
the intra-slice spacing. In such a case, we employ a
cubic interpolator filter to prepare a homogenously-
spaced dataset. Since ribs’ muscles have the same
intensity range as that of liver and they are in contact
with liver, this may lead to over-segmentation in the
result. We extract bones by thresholding and connect
them together by a spline curve to delineate liver and
muscles. Finally, it is needed to segment a slice
manually, which we call it initial slice; in this paper.
This slice should have a large cross-section and
contain the major components of liver intensity. We
adopted the approach used in [5] to segment liver from
the initial slice up to the first slice, then from the initial
slice down to the last slice. Thus, we do not miss any
separate part of liver.

Initial boundary extraction starts with an analysis of
the initial slice. We employ “Expectation
Maximization” algorithm with four Gaussian modes to
estimate mean and standard deviation of major
components which make up the intensity range of
liver. In this analysis, we only consider those
components of the mixture model which have a share
of 5% or more as major liver components. For each
mode, we threshold a slice in narrow region around its
mean value to find liver candidate pixels (Fig. 1(a)).
Let’s intensity range of liver be composed of three
Gaussian component, \( G(x| \mu_i, \sigma_i) \), \( i = 1, 2, 3 \). We
threshold a slice in the range \([\mu_i - \alpha \sigma_i, \mu_i + \alpha \sigma_i]\).
The width of this region, i.e. \( 2\alpha \sigma_i \), which is a fraction
of standard deviation of the corresponding mode, can
be tuned for high-contrast and low-contrast datasets,
individually. For high-contrast datasets, we select the
fraction in the range \([0.3 \sigma, 0.5 \sigma]\) and for low-contrast
datasets, it is in the range \([0.1 \sigma, 0.3 \sigma]\). After
thresholding a slice, we use a priori knowledge of the
previous slice to remove outlier pixels. The remaining
pixels are then clustered by K-means clustering. We
decide to label each cluster as a liver or non-liver
cluster, based on the location of its center (Fig. 1(b)).
If the center of a cluster is inside liver of previous
slice, it is regarded as a liver cluster. We remain all the
members of liver clusters and call them as liver index
pixels. We then threshold the original image in the
whole range of each mode \( i \) \( ([\mu_i - 3 \sigma_i, \mu_i + 3 \sigma_i]) \), so
that more pixels are involved. We assign a probability
measure \( p(x) = 1/d(x) \) to each pixel based on their
distance (\( d(x) \)) to the index pixels of the object. The
probability map is shown in Fig. 1(c). The pixels in
liver region have higher probability. We threshold the
probability map by half of its maximum value to find
initial liver border (Fig. 1(d)).

Finally, the initial liver boundaries of all slices are
used as the initial surface input of a 3D geodesic active
contour algorithm [7]. The final liver boundary is
attained by a few iteration of active contour algorithm.
We tune the number of iterations to a low value so that
the contour is prevented from leakage to nearby
organs.

Fig. 1 Steps of initial liver extraction. (a) Narrow-band
thresholded image, (b) Clustering liver candidate pixels
(Cluster centers are shown in yellow), (c) Probability map,
(d) Initial liver border.

3. Results

We applied the proposed method to 30 normal
datasets and 17 abnormal datasets, each containing
159-263 images. Datasets belong to Shiga University
of Medical Science and Osaka University with a
resolution of 0.6836 x 0.6836 x 1 mm³ and 0.5859 x
0.5859 x 1.25, respectively.

Preprocessing and active contour parts of the
algorithm were coded in C++ to decrease the run-time
of the algorithm. Initial liver extraction was
implemented in MATLAB 7 to benefit from its rich
image processing toolbox. The platform, on which we
run the algorithm, is an Intel® Core™ 2 Duo with
2GBytes of RAM. The whole algorithm takes 18-22
minutes to segment liver in a dataset.

Segmentation results of sample slices for different
normal and abnormal datasets are shown in Fig. 2
and Fig. 3, respectively. Iso-surface visualizations of
six livers that are segmented by the proposed algorithm are shown in Fig. 4.

![Fig. 2 Segmentation results of sample slices for different normal datasets.](image)

![Fig. 3 Segmentation results of sample slices for different abnormal datasets.](image)

In order to evaluate our method quantitatively, we utilized several measures which are used in MICCAI 2007 Grand Challenge workshop [8]. Quantitative evaluations for several datasets are shown in Table 1.

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![Fig. 4 Iso-surface visualization of liver for six different datasets.](image)

### 4. Discussion

The results of liver segmentation, which are shown in Fig. 2, correspond to low-contrast datasets. We included upper slices (Fig. 2(a)), middle slices (Fig. 2(b), (d), (e), (g), (h)), Fig. 3(a), (c), (e), (f)), and lower slices (Fig. 2(c), (f), Fig. 3(b), (d)). Since we use narrow-band thresholding to select liver pixels and combine it with a priori knowledge of previously segmented slice, error of over-segmentation is reduced.
to a large extent. If there is leakage in some slices, due to k-means clustering, the algorithm can compensate for it in next slices. Due to small cross-section of liver in upper and lower slices, initial boundary of liver is not detected there. However, since we use active contour algorithm to find final boundary, it improves the results. For normal datasets, selection of initial slice has minimum effect on final result. To choose initial slice, it only suffices to select a slice in which liver has a large cross-section which is usually found in the middle of a dataset. To test sensitivity of the proposed algorithm to the selection of initial slice, we ran it twice with two different initial slices. The cross-section of liver in the first initial slice was twice the first one. However, the results were affected slightly. Regarding Table 1, segmented volumes have an absolute relative volume difference of 3.28%. Maximum surface distance is 30 mm, on average, and it is used usually by very narrow regions of liver that are not detected by the algorithm. Another source of error is segmentation of Inferior Vena Cava (IVC). Physicians regard it as part of liver only in slices where it is completely enclosed by liver. We need a rule-based algorithm to segment IVC separately and decide on whether it should be attached to the result or not.

As can be seen in Fig. 3, the algorithm has acceptable results for abnormal datasets. If liver’s texture changes severely for different slices of an abnormal dataset, the algorithm will lose liver in these slices since it cannot detect available modes of intensity correctly. We need to consider variations of statistical parameters to have good results for such cases. Fig. 4 shows that the proposed algorithm can segment liver with arbitrary shapes and it does not need a training step.

We also applied our method to high-contrast datasets in which we need a different set of parameters, with respect to low-contrast datasets. The switching mechanism between two sets of parameters is done by user. We intend to use an automatic mechanism to grade liver datasets based on the contrast of images. Since we find initial boundary of liver through a 3D algorithm, it exploits robustness of 3D approaches, too.

By starting the task of segmentation from a middle slice in which liver has a single cross-section, we do not miss any separate part of liver in next slices.

5. Conclusion and future works

In this paper, we presented a new method for segmentation of liver from low-contrast CT datasets. We proved the ability of the method by applying it on low-contrast CT datasets. The results of segmentation for normal datasets are good and those for abnormal datasets are promising. In future, we try to expand the proposed method to include more abnormal datasets from different imaging machines. Also, we decide to grade liver datasets based on their contrast into two or more groups and use an appropriate set of parameters for each.

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7. References


