3D LUNG SEGMENTATION USING MARKOV RANDOM FIELDS

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Abstract: In this paper, Bayesian classification with Markov random fields is used for 3D Computed Tomography (3D CT) lung image segmentation and modified metropolis dynamic is employed as optimization algorithm. Lung tissue is well separated from the other tissues like a bones, muscles, surrounding soft tissue and fat. Segmentation is necessary for subsequent lung analysis (size, shape, lung contour, etc.), and lung blood-vessels, airways (bronchi, bronchioles) segmentation and tumour studies.

Keywords: Markov Random Fields, 3D Lung Segmentation, Bayesian Classification.

1 INTRODUCTION

Thresholding is quietly sufficient method used for medical CT image segmentation, which is given by character of CT images, where specific tissues has nearly equal density. Typical peaks in grayscale histogram are formed due to this property. Optimal threshold could be placed manually between the neighbouring peaks of histogram, or some well known statistical methods as Otsu algorithm can be used. However, some errors (i.e. misclassified voxels) caused by noise and tissue inhomogeneity are presented in finally segmented image, because only isolated voxels are taken into account. The knowledge of relations between nearby voxels is much more useful and should be incorporated to minimize these errors. Markov random fields (MRFs) is method using image statistical models [1]. The simplest model consists label probabilities of isolated voxels. More complex model includes label probabilities of isolated voxels and neighbourhood dependencies. Image segmentation problem using MRFs can be expressed as the optimization process with some algorithms. Many of these are available such as Iterated Condition Modes, Graduated Non-Convexity, Mean Field Annealing, Simulated Annealing, Controlled Random Search, etc. Three heuristics are proposed in [2]; there are explained Deterministic Pseudo Annealing, Game Strategy Approach and Modified Metropolis Dynamic. The last one is used in this paper.

2 METHOD

In this paper, the MRF is defined by the Bayesian classification which can be described by statistical dependences between the connected neighbouring voxels. The MRF energy is defined by the configuration of the MRF clique. Clique is intended by voxel group exactly defined by the selected rule. The simplest clique is represented by just a single voxel. More complex clique can contain any, but clearly defined, voxel neighbourhood. The degree of similarity of estimated label to its neighbours is determined by the MRF constrain [2, 3]. The best distribution of labels which fulfils MRF constrain is searched. MRF energy and information based on an observation of the occurrence of labels is combined by Bayesian model. Label of each voxel is depending on the image intensity on the corresponding voxel coordinates and also on the voxel neighbourhood. These two energies are combined to a single merit function and segmentation is solved as an optimization problem. It means, maximum (minimum) of merit function is searched by maximizing (minimizing) both energies.

Bayesian probability of labels (Equation 1) is described by:

$$P(L/Y) = \frac{P(Y/L)P(L)}{P(Y)}, \tag{1}$$

where L is label, Y denotes image intensity and $P(Y)$ is normalization function independent on labelling. $P(Y/L)$ represents energy based on label probability depending on image voxel intensity. $P(L)$ is clique potential defined by clique order (Equation 2) which corresponds to Markov random field energy.

$$P(L) = e^{-\frac{1}{T}\Sigma V_{cL}} = e^{-\frac{1}{T}\Sigma\beta\gamma(L_{S_i},L_{S_j})} \qquad \gamma(L_{S_i},L_{S_j}) = \begin{cases} -1 & \text{if } L_{S_i} = L_{S_j} \\ +1 & \text{if } L_{S_i} \neq L_{S_j}, \end{cases} \tag{2}$$

where V_{cL} is a clique potential, T is a temperature (prevents jamming in local extrema), β denotes homogeneity parameter (higher value means higher homogeneity of regions), γ is potential of single clique and L_S are neighbouring voxels. Gaussian distribution is used to model a prior label probability (energy) (Equation 3). This function is defined for each label class L_i with standard deviation σ_{L_i} and mean value μ_{L_i} which are obtained from image histogram by curve fitting.

$$P(y_i/L_i) = \frac{1}{\sqrt{2\pi}\sigma_{L_i}} e^{\frac{-(y_i-\mu_{L_i})^2}{2\sigma_{L_i}^2}} \tag{3}$$

After that, the optimization function (Equation 4) is created:

$$L = arg\ max(\frac{1}{T} ln\ P(Y/L) + ln\ P(L)), \tag{4}$$

Optimization is performed by Modified Metropolis Dynamic (MMD) algorithm which use random generation of new labels for each voxel and the label acceptance process is defined deterministically by probabilistic model described above. Optimization process can be rewritten as local merit function maximization (Equation 5) for each voxel S_i which is solved in an iteration manner:

$$\varepsilon_i(L) = \frac{1}{T}\left(ln\ \sqrt{2\pi}\sigma_{L_i} + \frac{(y_i-\mu_{L_i})^2}{2\sigma_{L_i}^2} + \sum\beta\gamma(L_{S_i},L_{S_j}) \right), \tag{5}$$

Whole MMD algorithm can thus be described [4, 5]:

1. MRF is initialized in first iteration step k with initial temperature T and initial random label configuration L,
2. randomly picked global state L' which is different from L,
3. local energies $\varepsilon(L)$, $\varepsilon(L')$ and their difference $\Delta\varepsilon$ for each voxel are computed,
4. new state of voxel is accepted, if following condition (Equation 6) is fulfilled:

$$L_i^{k+1} = \begin{cases} L_i' & \text{if } \Delta\varepsilon_i > 0 \text{ and } \alpha \geq e^{\frac{-\Delta\varepsilon_i}{T}} \\ L_i^k & \text{otherwise,} \end{cases} \tag{6}$$

   where $\alpha \in <0,1>$ is a constant threshold parameter (higher α means higher probability of label acceptance, it also influence speed of convergence),
5. temperature T is increased and algorithm continues from step 2 or is ended if maximum number of iterations is reached or number of modified voxel labels is less than a chosen threshold.

3 RESULTS

The method described above is used for lung segmentation in three-dimensional case. The main goal is labelling the lung tissue to one class and other tissues (surrounding tissues, muscles, fat and bones) to second class. The lung tissue is reflected on histogram by the first (the smallest) peak from the left (Figure 1). The other peaks and bottoms on the right of histogram are formed by other soft and dense tissue. Proper Gaussian curves is used to model a prior label probability for each of these parts of histogram. Mean values and standard deviations are estimated automatically individually for each patient image. Label probabilities are defined by Gaussian curves fitted on histogram peaks using peak detection and least mean square (LMS) algorithm. The example of these probabilities is shown in Figure 1. Probability, that image voxel is labelled as lung tissue is defined by green curve, on the other hand, probability of labelling as other tissue is reflected by red curve. Because of the probabilities are described, the histogram is normalized to $< 0, 1 >$ interval.

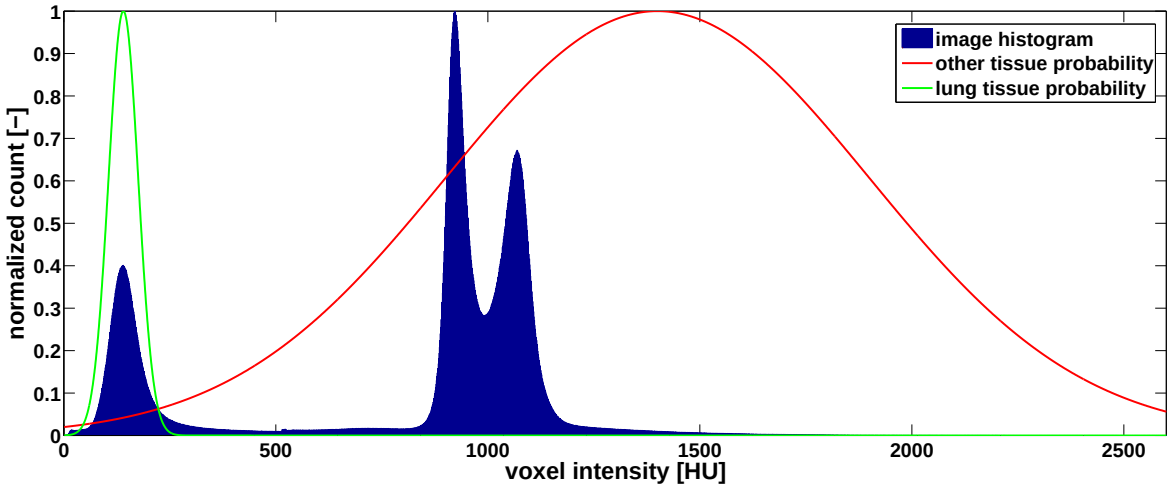

Figure 1: Normalized histogram of 3D CT lungs image (green curve - lung tissue probability, red curve - other tissue probability.)

Peak detection is performed by top-hats morphological operation of given histogram. Top-hats operation result is defined as a residue after subtraction of the original image and its opening. The values of image opening are always lower than values of the original image. Due to this, the result is always greater or equal to zero. It means, after top-hats operation only thin and tall peaks are left from the original [6]. Mean value of lung tissue is defined by position of maxima of first greater peak given by top-hats result. Mean value of the other tissue is formed by centre between lung tissue mean value and the last value of histogram. Standard deviation (STD) is obtained by LMS algorithm. First, vector of STDs is generated according to the histogram range. Further, this vector is iteratively browsed and the Gaussian curve is created with fixed mean value. Then, the difference between generated Gaussian curve and corresponding peak is measured. Finally, optimal STD is picked by minima of LMS function. Acquired curves are applied on original image; the lemma (Equation 3) is defined by a so 'transformed' images.

The lemma (Equation 2) is defined by cliques in MRF. For example, if the first order clique is accounted and 4-connected neighbourhood is taken, the result is defined by sum of these members. When all four neighbouring voxels are different from the computed voxel and the β parameter is equal to 1, the clique potential is -4, and vice versa, if all voxels has the same value, the clique potential is +4, etc. Precise tuning of MRF parameters is a difficult problem. For this reason, the MRF parameters are tuned meanwhile experimentally. Used values are listed in Table 1. The total MRF energy is defined by this scheme.

Parameter	Value
α	0.73
β	1.7
T_{init}	0.001
T_{max}	1.2
T_{iter}	1.1
clique order	1
neighbourhood	26
iterations	30

Table 1: Tuned MRF parameters

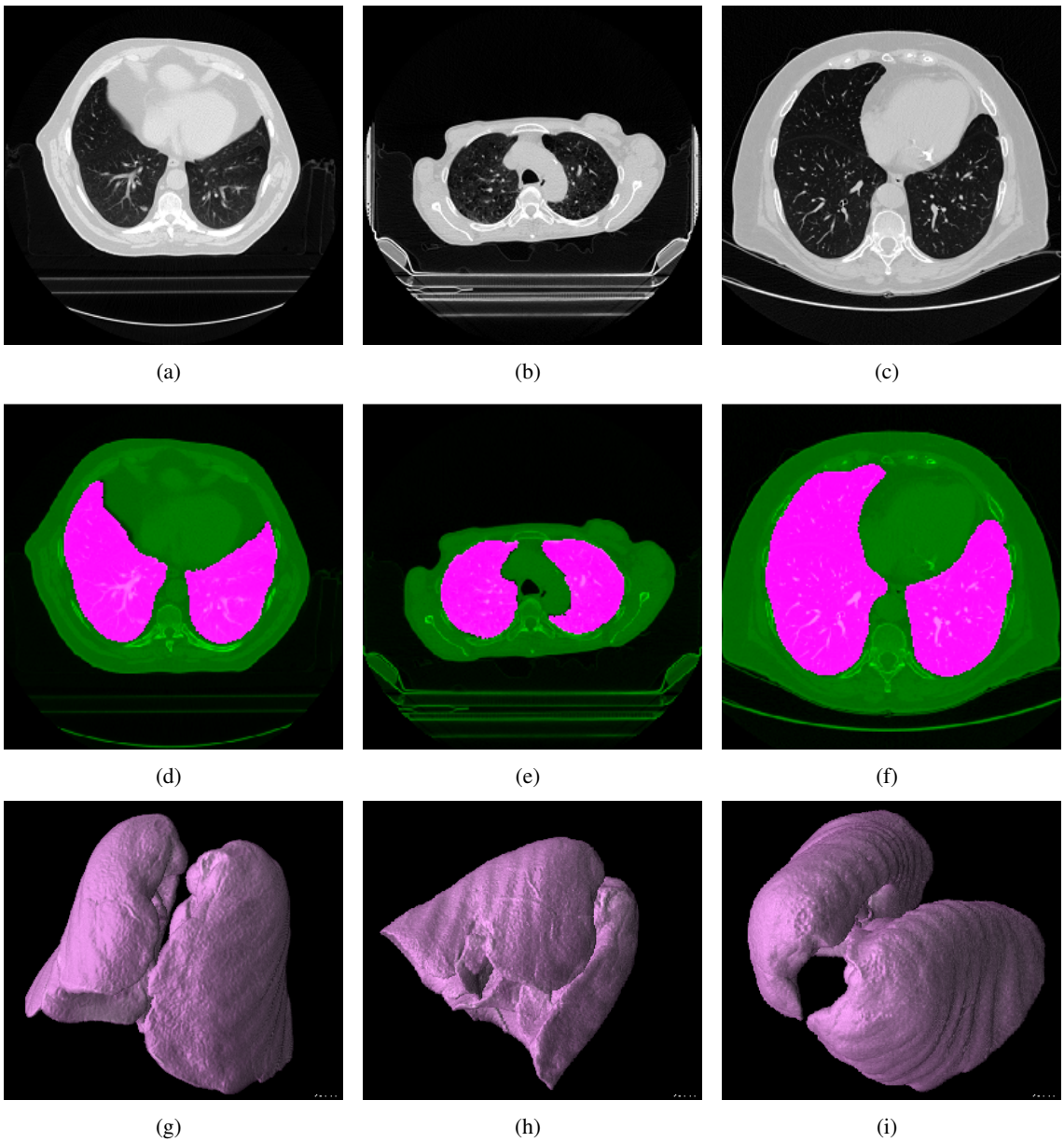

Figure 2: Result images (green (gray) - orginal image, magenta - segmentation result): patient 1 (original) (a), patient 2 (original) (b), patient 3 (original) (c), patient 1 (fuse) (d), patient 2 (fuse) (e), patient 3 (fuse) (f), patient 3 - 3D lungs rendered 1 (g), 3D lungs render 2 (h), 3D lungs render 3 (i).

Optimal segmentation output is determined by label distribution, after maximal energy (maxima of merit function (Equation 5)) is found. Segmentation results obtained by this process are shown in the transversal plain in the three different patient images (Figure 2). Original data are highlighted by green (gray) colour and segmented regions by magenta (blue) colour. 3D rendered images of segmented lungs are presented. Size of tested images is 512x512x141 for patient 1 (Figure 2(a)), 512x512x169 for patient 2 (Figure 2(b)) and 512x512x417 for patient 3 (Figure 2(c)).

4 CONCLUSION

In this paper, the 3D CT lung segmentation method was proposed. Bayesian classification utilizing MRF was used to solve segmentation problem. Statistical model of Bayesian classification was formed by histogram fitting using Gaussian probability distribution. MRF was defined by clique potentials of first order cliques with 26-connected neighbourhood. The other MRF parameters was experimentally tuned. MMD heuristic was used to optimization for its parallel computation possibility.

Proposed method was well used to lung tissue segmentation. Results are shown in Section 3. Main advantage of this approach is minimization of errors caused by noise and image inhomogeneity. Relatively simple way to parallel computing and usage of multi-dimensional convolution are the another advantages of these method.

Future work will be aimed to segmentation of other tissues during single iteration process (more label classes will be used), especially lung blood-vessel and airways will be segmented. The further step will be upgrade to bones and soft tissue segmentation and application on another body parts such as brain and abdominal.

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