A Generic Approach for Pathological Lung Segmentation

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This is a short description of the methodology we used to segment pathological lungs. Our accompanying paper with full details is under review currently. The full paper will be replaced with this document once the review process is finished.

We developed a generic method for automatically segmenting lungs with a diverse range of lung abnormalities. Our algorithm uses *fuzzy-connectedness (FC)* image segmentation for initial delineation followed by multi-stage refinements. Refinement steps are conducted in an intelligent fashion through an another algorithm which detects the existence of pathology using anatomical information. Our method is fully automated and does not require any input from the user at any stage.

The Algorithm

The proposed algorithm consists of following steps:

1. Automatic seed selection for initial FC segmentation using anatomical information.
2. FC initial segmentation.
3. Disease detection based on segmentation evaluation and anatomical information.
4. Learning-based pathological area segmentation through random forest classifications.
5. Context-aware classification of pleural effusion[1].
6. Automatic trachea extraction for lung separation (left and right) and labeling.

Results

Patient scans and quantitative analysis

We tested our algorithm for publicly available LObe and Lung Analysis 2011 (LOLA11) Challenge dataset. Evaluations of the other data sets along with LOLA challenge that we have used in our evaluation for severe lung diseases can be found in our paper. Overall, more than 400 CT scans were analyzed to demonstrate the high sensitivity and specificity of our proposed generic algorithm. However, we herein briefly present the LOLA11 results only.

Segmentation performance

The segmentation performance of our method on in-house images are described in our paper mentioned before. For LOLA dataset we made enteries to the challeng (i) lung-field including the pleural areas and (ii) lung-field not including the pleural areas; the evaulations from both submissions are reproduced in Table 1.

[1] *Optional*: Some studies in the literature consider pleural effusions as not a part of lung fields. Although lung field and pleural area has distinct tissue in between, this fluid may invade and constrained the lung field, which changes the capacity calculations. Therefore, our method has the ability to segment lung with or without considering the pleural fluid as a part of lung field.

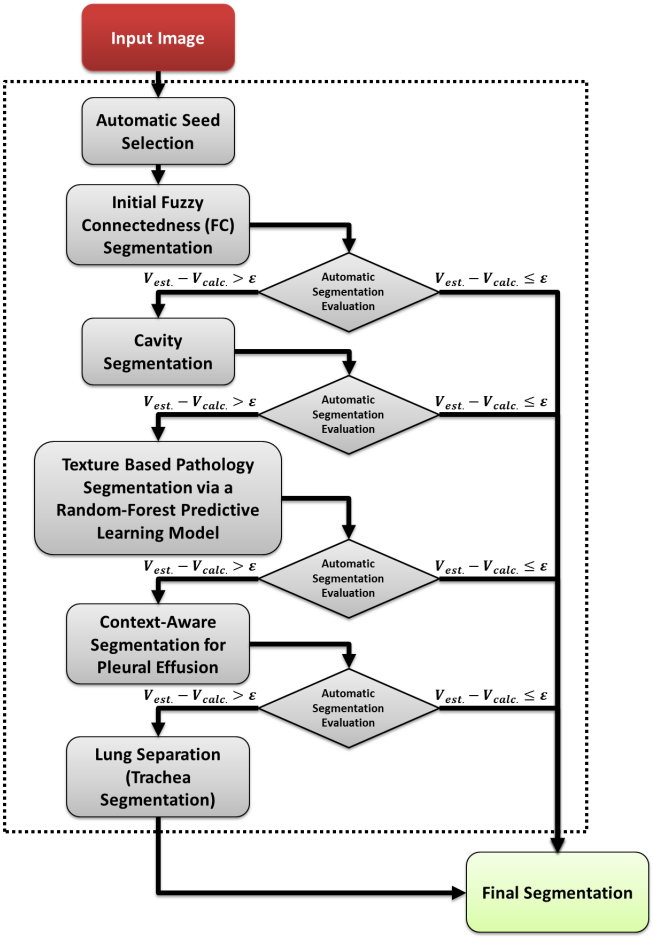

Figure 1: *Block diagram of the proposed method.*

Conclusions

We presented a novel method for fully automated segmentation of lung with and without abnormalities. To the best of our knowledge, the proposed method is the first fully automated technique for segmenting lungs with a diverse range of abnormalities seen in lung CTs. In this sense, our method is different from others which focus on a few or only one type of abnormality; hence, the proposed method is generic. The core of our method is the region-based FC method for initial rough segmentation. The initial segmentation covers the normal lung parenchyma inside the lung field. The algorithm is further equipped with multiple refinement stages including random forest classifier design for abnormal imaging pattern detection and a novel context-aware learning method to handle extreme cases such as pleural effusion. The robustness and the effectiveness of our proposed method is tested on more than 400 lung CT scans acquired through various sources containing wide range of abnormalities including LOLA challange data sets. High accuracy and efficiency were achieved in all the cases spanning from minimal to high pathology existence.

(a) *Pleural fluid included inside the lung field.*

obj	mean	std	min	Q1	median	Q3	max
LL	0.957	0.137	0.034	0.979	0.987	0.995	0.999
RL	0.952	0.151	0.000	0.984	0.990	0.997	0.999
score	0.955						

(b) *Pleural fluid excluded from the lung field.*

obj	mean	std	min	Q1	median	Q3	max
LL	0.968	0.097	0.316	0.979	0.987	0.995	0.999
RL	0.968	0.134	0.000	0.984	0.990	0.997	0.999
score	0.968						

Table 1: *Overlap scores for the Automated Lung Segmentation for the 55 scans in LOLA11.*