Results of Applying Two-Pass Region Growing Algorithm for Airway Tree Segmentation to MDCT Chest Scans from EXACT Database

Anna Fabijańska

Department of Computer Engineering, Technical University of Lodz,
18/22 Stefanowskiego Str., 90-924 Lodz, Poland

`an_fab@kis.p.lodz.pl`

`http://www.kis.p.lodz.pl`

Abstract. This paper addresses problem of CT based investigation of pulmonary airways. Especially algorithm for airway tree segmentation is introduced. The algorithm is based on 3D seeded region growing. In the proposed method region growing is repeated twice with different settings. First, in order to avoid leakages into the lungs, algorithm is performed with very strict criteria. Next it works only in the places of interest which are found by morphological gradient and threshold. Results of applying the proposed method to several CT chest scans selected randomly from EXACT database are presented and discussed. Moreover comparision with the ground truths, provided by EXACT organisers, is given by means of the evaluation measures.

Key words: Airway Tree Segmentation, Bronchial Tree, Clinical Investigation, CT bronchography, Pulmonary Imaging, Region Growing, Multidetector Computed Tomography, MDCT, X-Ray CT

1 Introduction

Multidetector computer tomography is a powerful technique which produces detailed three-dimensional images of the inside of a human body. Due to its effectiveness computer tomography (CT) is successfully used in many clinical applications and physiological studies to investigate changes due to various diseases.

One of the examples of computer tomography usage is an investigation of pulmonary disorders. CT chest scans are especially helpful in diagnosis of chronic obstructive pulmonary disease (COPD) which is a common name for pathological changes due to different combinations of airway diseases and asthma which are characterized by airflow limitation [1][2][3]. Quantitative description of an airway wall, especially the thickness of airway walls and diameter of an airway lumen, provide important information about pulmonary diseases. Therefore reliable segmentation of an airway tree from volumetric computer CT data sets is the most important step in clinical applications for measuring and characterizing airway data [4]. Still segmentation of an airway tree from CT chest scans is very challenging. Problems are caused by inhomogenity of a bronchial lumen, adjacency of the blood vessels, and changes of intensities along airway walls. Moreover, in case of airway tree segmentation region growing is prone to leakages into lungs.

Different algorithms for airway tree segmentation from CT chest scans have been proposed in the literature. Mostly they act on 3D volumetric datasets and are region growing based approaches utilizing different techniques in order to diminish leakage probability. The most popular algorithms can be classified into one of the following groups:

- **Rule-based techniques** which utilize anatomical knowledge about airways and blood vessels [5] [6] [7].
- **Morphological techniques** using grayscale morphological reconstruction to identify local extremes in the image [8] [9] [10].
- **Wave front propagation techniques** which propagate waves to detect walls of the bronchi [8] [11] [12].
- **Template matching techniques** that search consecutive slices for oval dark rings surrounding brighter areas (airways) or dark solid oval areas (adjacent blood vessels) [13] [14].
- **Fuzzy techniques** which utilize fuzzy rules to avoid leakages and diminish number of falsely detected bronchi [15] [16].

In this paper a new approach for airway tree segmentation is presented. The method uses modified 3D region growing algorithm where the growth of an airway tree is guided and constrained by morphological gradient. In consequence leaks into the lungs are avoided.

The outline of this paper is as follows. In Section 2 a description of datasets used in this work is given. Description of the authors' two-pass region growing algorithm (TPRGA) for airway tree segmentation is given in detail in Section 3. In Section 4 results of the proposed algorithm are demonstrated using datasets from EXACT (Extraction of Airways from CT) [20] database. Finally obtained results are analysed discussed in Section 5. Section 6 concludes the paper.

2 Input Data

3D volumetric CT chest scans of forty patients provided by EXACT organizers were examined. They were acquired at different sites using several different scanners, scanning protocols, and reconstruction parameters. The dataset ranged from clinical dose to ultra low dose scans, from healthy volunteers to patients with severe lung disease, and from full inspiration to full expiration. Two datasets were provided: the training set (CASES 1-20) and the testing set (CASES 21-40).

The slices were provided with 16-bit resolution and stored as signed 16-bit monochromatic images of the resolution 512x512 pixels. Individual slices were stacked into a 3D space representing volumetric data set. Exemplary CT slices (displayed using the same window and level settings) are presented in Figure 1.

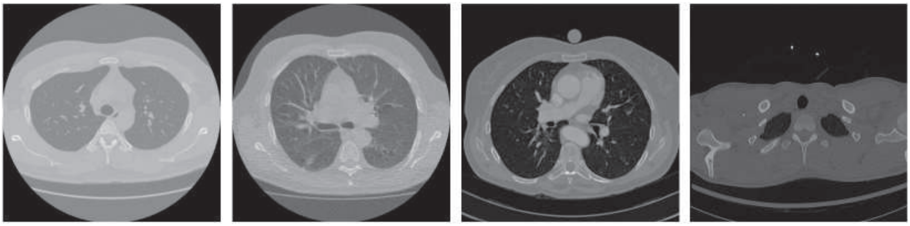

Fig. 1. Exemplary CT slices from examined datasets.

Single CT chest scan consists of about 450-600 planar transverse slices. Consecutive slices combined into a stack compose volumetric data set in three dimensional (3D) space.

3 Problems with Region Growing

An airway tree, which conducts air into the lungs, is build from an airway lumen surrounded by high density vascular wall. Both an airway lumen and lungs are filled with air.

Due to differences in their densities on CT slices an airway wall appears significantly brighter than the area of airways and lungs. Therefore in the ideal case using 3D seeded region growing with a seed point located at the first slice in the centre of the trachea it should be possible to segment complete airway tree from a volumetric CT data set. This idea is presented in Figure 2.

In practice airway walls often appear broken. In consequence region growing leaks from an airway lumen into the lungs which are of similar intensity. Region growing algorithm leaking into the lungs is presented in Figure 3.

4 The Proposed Approach

The proposed airway tree segmentation algorithm, as most approaches to the considered problem, is based on seeded 3D region growing. However during airway lumen segmentation region growing is applied twice. Moreover, leak prevention mechanism is applied in order to avoid the algorithm to consider voxels that are part of the lung parenchyma. Successive steps of the algorithm are as follows:

1. Contrast Enhancement.
2. Detection of the Seed Point.
3. First Pass of Region Growing.

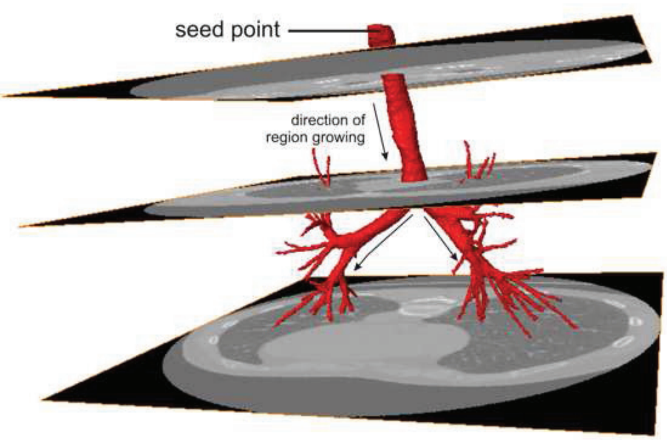

Fig. 2. The idea of an airway tree segmentaion by 3D region growing.

4. Computation of Morphological Gradient.
5. Thresholding of Morphological Gradient.
6. Second Pass of Region Growing.

Step 1: *Contrast Enhancement.* Before region growing is applied contrast of the input dataset is improved. In this stage histogram of the whole volume is normalized [17]. After normalization there are 0.5% of saturated voxels in the CT dataset.

Step 2: *Detection of the Seed Point.* A seed point for the region growing is determined automatically. It is defined as a voxel located inside the trachea.

Trachea is easy to find. Its cross sections are imaged as large oval areas and are present in the central part of the first slices of the CT chest scan. They are also significantly darker than their surrounding. Therefore in case of the presented method location of the trachea is defined using template matching method [17] searching for a dark oval area. The search starts from the first slice and is continued in consecutive ones until the oval of tracheal tube is found. Seed point is defined as its center of gravity [17].

Step 3: *First Pass of Region Growing.* When seed point is determined first pass of 3D region growing is performed on the normalized CT dataset. In order to avoid leakages into the lungs very strict criteria are used in this stage while joining consecutive voxels. The algorithm classifies the current voxel as voxel belonging to the airway lumen if its intensity and intensity of its all closest (connected) neighbours differ from the average intensity of voxels already classified to airway lumen not more than T%. Value of T is determined automatically on the first run. It equals to the lowest value for which region growing starts up. The value of T is then decreased by half after trachea is segmented. This allows

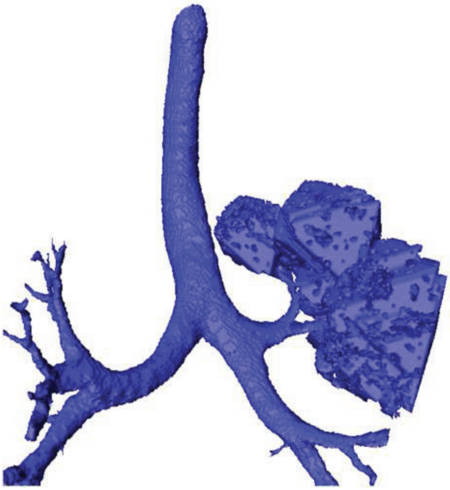

Fig. 3. Region growing leaking into the lungs.

to avoid leakages into the lungs as fluctuations of voxel intensities in case of distal bronchi are smaller than in the area of the trachea.

Step 4: *Computation of Morphological Gradient.* The following step of the algorithm aims at highlighting information connected with airway walls. In order to do so 3D morphological gradient [17] is calculated based on original (i.e. not normalized) data set.

Morphological gradient (which is a difference between results of grayscale dilatation and grayscale erosion) emphasizes sharp gray level transitions, which are also connected with airway walls. Those areas of the highest gradient which are connected with airway tree built in the third step of the algorithm define possible locations of the distal bronchi.

It is important to perform this step on the unnormalized CT dataset. Otherwise noise highlighted by histogram stretching can seriously hamper accurate segmentation of complete airway tree.

Step 5: *Thresholding of Morphological Gradient.* In order to determine areas of the highest gradient its image is thresholded with global threshold. For threshold selection ISODATA method [18] [19] is applied. Airways are supposed to be located in those binary areas which are connected with airway tree built in the second step of the algorithm.

Step 6: *Second Pass of Region Growing.* The second pass of region growing is performed again on normalized data set but not everywhere. Places of interest are determined by morphological gradient.

Region growing starts from previously segmented airway tree. It is guided and constrained by those areas of the highest gradient (determined by thresholding in previous step) which are connected to airway tree built in the third step of the algorithm. Successive voxels are joined to airway tree if both of the following constraints are fulfilled:

- current voxel is situated in the area of the highest gradient determined in the previous step;
- intensity of the current voxel differs from the average intensity of voxels classified to airway lumen not more than $2T\%$. Where value T is remembered from the third step of the algorithm (the lowest value for which region growing starts up) and changes during algorithm performance in the way as during the first pass of region growing.

Note: All algorithm parameters were determined only using the training data. Value of T selected as described above in case of all tested 40 datasets allowed to avoid the leakages into lungs. However, in some cases it was possible to tune the algorithm performance and obtain better accuracy of the results by increasing value of T manually. Therefore the presented algorithm was classified as *semi-automatic*.

5 Results and Discussion

Results obtained by the proposed airway tree segmentation algorithm are presented in Table 1 and in Figure 4.

Table 1 presents outcomes of evaluation of airway tree segmentations obtained by the proposed algorithm from the test datased. The evaluation was performed manually by EXACT organisers. Obtained segmentations were compared with the ground truth build in the way as explained on EXACT website [20] in *Information* section.

The following evaluation measures were used for results evaluation:

- **Branch count** - the number of branches that were detected correctly (i.e. branches with centerlines longer than 1 mm).
- **Branch detected** - the fraction of branches that were detected, with respect to the branches present in the ground truth.
- **Tree length** - the sum of the length of the centerlines of all correctly detected branches.
- **Tree length detected** - the fraction of tree length in the ground truth that was detected correctly.
- **Leakage count** - the number of unconnected groups of ”correct” regions that are neighboring with a ”wrong” region.
- **Leakage volume** - the volume of regions that are wrongly detected.
- **False positive rate** - the fraction of the volume of regions that are detected wrongly over the volume of all detected regions.

Trachea was excluded from the branch length and branch count related measurements. For the lekage based measures, both trachea and main bronchi were excluded.

Table 1. Evaluation measures for the twenty cases in the test set.

	Branch count	Branch detected (%)	Tree length (cm)	Tree length detected (%)	Leakage count	Leakage volume (mm^3)	False positive rate (%)
CASE21	115	57.8	61.3	55.5	6	307.2	2.61
CASE22	84	21.7	59.4	18.0	13	510.9	2.82
CASE23	84	29.6	59.9	23.0	1	0.4	<0.01
CASE24	53	28.5	44.2	27.1	0	0.0	0.00
CASE25	61	26.1	48.1	19.1	0	0.0	0.00
CASE26	44	55.0	29.1	44.3	3	196.2	2.68
CASE27	26	25.7	20.4	25.2	0	0.0	0.00
CASE28	80	65.0	56.4	51.5	0	0.0	0.00
CASE29	104	56.5	66.7	48.3	1	1.4	0.01
CASE30	118	60.5	82.9	54.3	3	84.2	0.56
CASE31	92	43.0	60.7	34.6	3	277.1	1.53
CASE32	65	27.9	45.3	20.8	0	0.0	0.00
CASE33	77	45.8	51.8	35.2	5	193.7	1.96
CASE34	173	37.8	119.0	33.3	1	6.3	0.02
CASE35	43	12.5	30.8	10.0	0	0.0	0.00
CASE36	33	9.1	24.9	6.0	0	0.0	0.00
CASE37	74	40.0	54.7	30.8	0	0.0	0.00
CASE38	49	50.0	36.3	54.6	1	0.4	<0.01
CASE39	60	11.5	45.0	11.0	5	622.0	5.77
CASE40	116	29.8	90.6	23.4	3	125.6	0.48
Mean	77.5	36.7	54.4	31.3	2.3	116.3	0.92
Std. dev.	35.4	17.1	23.5	15.7	3.2	184.6	1.54
Min	26	9.1	20.4	6.0	0	0.0	0.00
1st quartile	49	25.7	36.3	19.1	0	0.0	0.00
Median	76	33.8	53.3	29.0	1	0.9	0.01
3rd quartile	115	56.5	66.7	51.5	5	277.1	2.61
Max	173	65.0	119.0	55.5	13	622.0	5.77

In Figure 4 3D views for twelve CT datasets selected randomly from EXACT database are shown. Cases from both train and test datasets are considered in the figure. Blue colour is assigned to airway tree extracted by the first pass of the region growing. Airways segmented during the second pass of the algorithm are marked with red colour. CASE ID is indicated under each subimage.

Presented results prove that the proposed airway tree segmentation method succeeded in all 40 cases. An airway tree was segmented without significant leaks into the lungs.

The outcomes of results evaluation show that the method extract airway trees with the average accuracy of branch detection equal to 37% and average fraction of tree length equal to 36%. The average rate of falsely detected branches is less than 1% with the average leakage count equal to 2.3.

The accuracy of the proposed airway tree segmentation algorithm can be considered satisfying but also convinces to further improvements of the method.

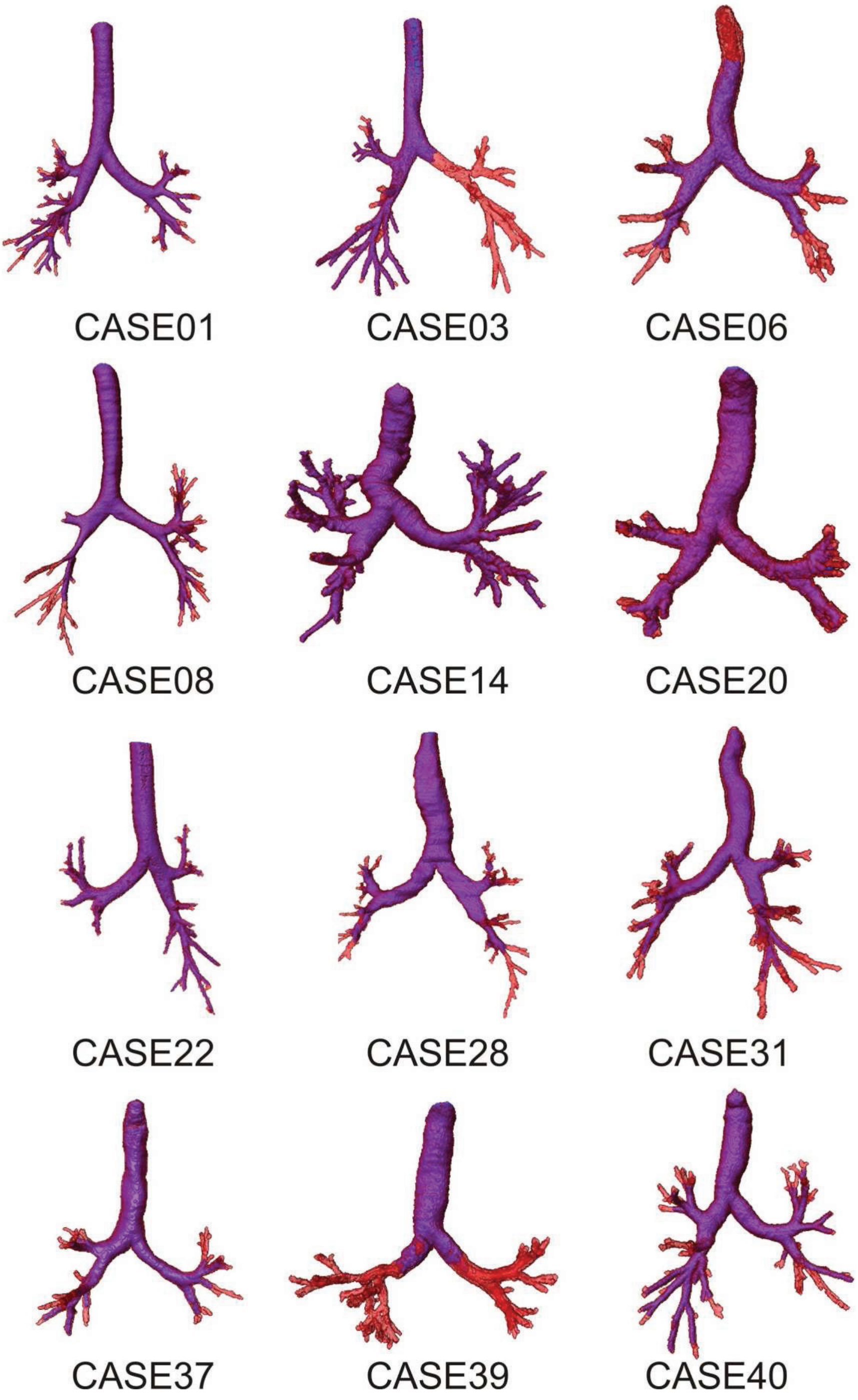

Fig. 4. Results of airway tree segmentation using the proposed method. Blue colour is assigned to airway tree extracted by the first pass of the region growing. Airways segmented during the second pass of the algorithm are marked with red colour. CASE ID is indicated under each image.

The runtime of the proposed algorithm for data set consisting of about 500 16-bit slices of the resolution 512x512 pixels measured on 1.66 GHz Intel single CPU system is not more than 10 minutes. However the method is fully parallelizable and can be adapted to multiprocessor systems (for example using OpenMP API [21]) which are supposed to cut down the runtime of the algorithm.

6 Conclusions

In this paper the problem of an airway tree segmentation from CT chest scans was considered. Especially the new method for airway tree segmentation was introduced. The algorithm is a 3D approach which extracts airway trees from volumetric CT chest scans using 3D region growing guided and constrained by a morphological gradient. This allows to diminish probability of leakages into the lungs.

The algorithm was tested on forty CT chest scans from EXACT database. They were obtained using different protocols, from patients with different level of pathological changes due to lung diseases. Results of applying the method to selected datasets were presented and discussed.

In case of all tested datasets proposed algorithm succeeded. The accuracy of obtained results (i.e. number of extracted generations of bronchi) depends on level of pathological changes in lung area. However in case of majority of datasets up to 6 generations of bronchi was extracted by the algorithm. This accuracy is sufficient for clinical applications [22] [23].

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