

CT IMAGE STRUCTURAL ANALYSIS ALGORITHM DESIGN

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Abstract

Basic elements to design a simple method /algorithm for structural analysis of a lung CT image are presented, using Image Processing ToolBox in MatLab. The structural image analysis method search and count all image ramifications, and create a measurement tool for future image comparing and lung’s health evolution.

Key words: CT image structural analysis, lung density measurement, biometrics application design

1. Introduction

This paper presents an efficient five steps method for CT digital image analysis and processing, using MatLab’s Image Processing Toolbox [1]. This paper focuses on the essential steps for designing an efficient structural analysis method or metric, i.e. ramifications density, to compare two lung CT (Computer Tomograph) images. all the steps are tested, illustrated and documented for an effective lung CT image (fig.1).

The result is a density value that approximate the number of lung’s ramifications extracted from the 2D CT image. CT lung-density gives a good reflection of the degree of hyperinflation [2, 3]. From the 3D to 2D projection perspective, there is a lot of overlapping, so the exact ramification density value cannot be extracted from a 2D image. Although, this approximate value can be used as comparing metric because of the repetition of the projection process in all the CT lung images.



Fig. 1: Original CT lung image.
Resolution: 512x460 pixels, 256 gray levels

2. Five steps image structural analysis method presentation

For a better understanding and visualization of each step, consider a reference image smaller, cropped from the original (fig.2 and fig.3).

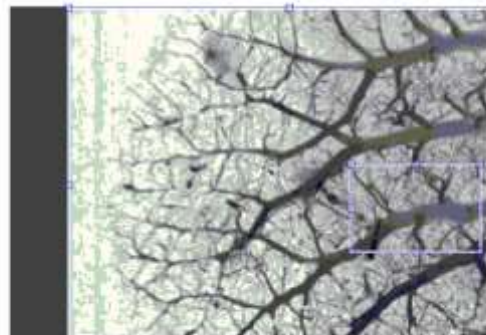


Fig. 2: Cropping a rectangular zone from the original (seen as negative). Rectangular marked zone resolution: 60x80 pixels

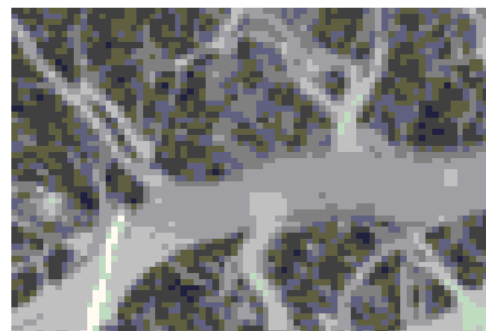


Fig. 3: Reference image *imref* to be structural analysed (zoomed in 6 times). Resolution: 60x80 pixels, 256 normalised gray levels

The initial step, numbered Step 0, is to normalize all the images that have to be later analyzed and compared. All the images will be transformed to 256 gray levels, will be cropped at the same spatial and transformed to the same color resolution, i.e. values interval [0, 1].

Step 1 Applying a threshold filter for transforming 256 gray levels images into a binary (logical) image, with only two values: 0 – black, 1 – white.

```
thresh_filter = graythresh(imref);
imrefbw = im2bw(imref, thresh_filter);
```

The threshold filter used was proposed by the Japanese N.Otsu [4]. It minimizes the variance between black and white color classes. In this case, the threshold value resulted is $thresh_filter = 125 / 255 = 0.49$, exactly on the middle of the gray interval. Fig. 4 illustrates the resulting binary image, *imrefbw*.



Fig. 4: Reference image transformed to binary image *imrefbw* presenting salt&pepper noise



Fig. 5: Reference binary image *imrefbwclean* with salt&pepper noise removed

Step 2 After binary transformation of the gray image, noise (salt&pepper) removing is

mandatory. This operation is done using one of the morphological functions, *bwareaopen(imrefbw, area)*. The morphological operation on the binary images are formalized and precisely defined in the Digital Processing Images field [5]. This efficient methods/ algorithms are also implemented in library functions [6].

```
imrefbwclean = bwareaopen(imrefbw, 16);
```

In this case, all the noise (white areas greater than 16 pixels, for example a 4 x 4 square) are removed. The resulting clean image after step 2 is shown in Fig. 5. Fig. 6 contains the same cleaning result applied on the initial image, the lung image.

The first steps, from 0 to 2, are only the image preparation part of the analysis method. They are the same for all the images to be compared, i.e. same initial spatial and color resolution, a binary threshold deduced by the same minimizing algorithm, the same area value for noise removal.

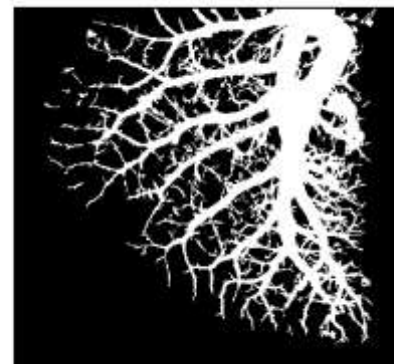


Fig. 6: Initial lung CT image after binary transformation and noise removal, *im0bwclean*. Resolution: 512x460 pixels

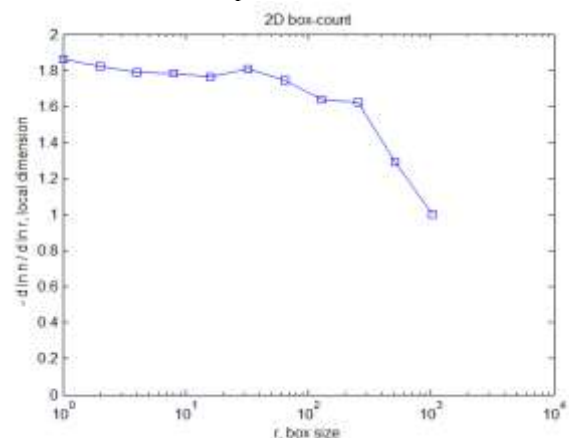


Fig. 7: Fractal dimension of the Fig. 6 image is near 1.82. The value is calculated using boxcount method, the value on the curve is on the left

A possible continuation for designing a comparing metric is to use a tool for determination the fractal dimension of the binary image. In the case of lung's images, the bronchi system is fractalised. Next function call illustrates this possibility, and the result appears in Fig. 7.

figure., boxcount(im0bwclean, 'slope');

The sensitivity of the fractal dimension metric has a poor efficiency in this case, all the lung's CT images oscillate with their fractal dimension around 1.8 value, so it cannot be used to precisely compare lung images.

Step 3 Transforming binary thick Image to a skeleton or thin binary image is needed. The morphological functions packet contains multiple choices to erode the thick surfaces or objects to one pixel width curve. The essential condition is to preserve the structural elements we are looking for, i.e. ramifications. Best result is obtained using 'thin' method, as illustrated in Fig. 8.

imrefthin = bwmorph(imrefbwclean, 'thin', Inf);



Fig. 8: Binary image *imrefthin* obtained after 'thin' transformation. All the ramifications were preserved



Fig. 9: Final image *imramifications*. Each little white square correspond to a ramification (see fig. 8).
Number of resulted ramifications is 40

Step 4 Determination of the structural elements, i.e. ramifications. This is the most important step of the method. It is a three operations step, due to the sensitivity of the 'branchpoints' morphological detection algorithm. The results of the ramifications detection have to be refined, i.e. to reduce the number of very close (spatially) results. Two extra morphological operations can be used, 'closing' and 'shrinking'. Each 'Inf' (from infinitum) parameter occurrence means that the morphological operation is repeated until nothing change between two successive steps.

*imtemp = bwmorph(imrefthin,'branchpoints');
imtemp = bwmorph(imtemp, 'close');
imramifications = bwmorph(imtemp, 'shrink', Inf);*

The result, illustrated in Fig. 9, shows the spatial position of all the ramifications. The number of the ramifications, 40 white spots in the image, can be used for creating the compare metric we are looking for.

Step 5 is the final step. Counting the spatial density of the lung ramifications can be done by counting all the white spots in the final image (step 4) with *bweuler* method and divide the value to the normalized image resolution.

*no_ramifications=bweuler(imramifications);
densit=no_ramifications/ resolution=40/(60x80)
=0.0083*

The resulted density value can be used as comparing metric between two lung images, from different patients, or from the same patient but at different moments during the time.

3. Conclusion

The structural analysis method for measuring the ramification density in along CT image can be done in five steps.

Step 0 - normalize all the images that have to be later analyzed and compared.

Step 1 - applying a threshold filter to the lung image.

Step 2 - salt&pepper noise removal in the binary image.

Step 3 - transforming thick Image to a skeleton or thin image by preserving structural elements, i.e. ramifications.

Step 4 - determination of the structural elements, i.e. ramifications.

Step 5 - counting structural elements (ramifications) and calculate its spatial density value.

The method, illustrated by Fig. 10, applied from first step to the final step (fifth) on the initial lung CT image lead to the following result.

$$\begin{aligned} \text{final_density} &= \text{final_no_ramification} / \text{resolution} \\ &= 901 / (512 \times 460) = 0.0038 \end{aligned}$$

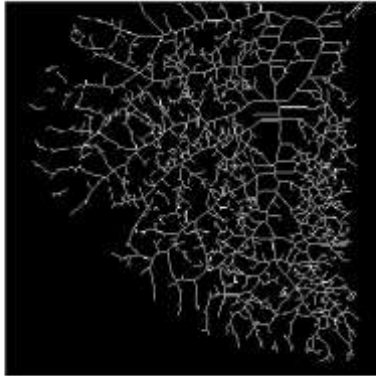


Fig. 10: The “skeleton” of the initial CT lung image. The intention is to determinate all the ramifications

The spatial density of the structural elements can be used as comparing metric between Ct images. This method, with specific adjustments can be extrapolated to other Digital Image Analysis fields, like biometrics. The source images all have in common the fractal distribution of the structural elements.

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