NEW SOFTWARE TOOL FOR WEGENER'S GRANULOMATOSIS CT IMAGE ANALYSIS

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1   Introduction to Wegener's granulomatosis

Biomedical image processing and analysis of its components is a common and discussed problem recently. It is closely related to early diagnostics of serious diseases.

Wegener's granulomatosis is one of them [2]. It is a multisystemic necrotizing vasculitis described by German pathologist Friedrich Wegener in 1936. Wegener's granulomatosis most commonly occurs in whites and affects men and women equally. The mean age at diagnosis is 40 years, but the disease can develop at any age. The upper respiratory tract is affected in almost all patients, and the lungs and kidneys are involved in 90% and 80% of patients, respectively. Other organs less commonly affected include the central and peripheral nervous system, spleen, and large joints [3].

2   Software description

New software [1] provides CT image visualization and semi-automatic analysis (cooperation to radiologist is needed). In addition it provides 3D reconstruction of CT images.

2.1   Main program

Main program provides image uploading, visualization, simple comparison and registration and 3D reconstruction. It can be divided into five parts, see Figure 1.
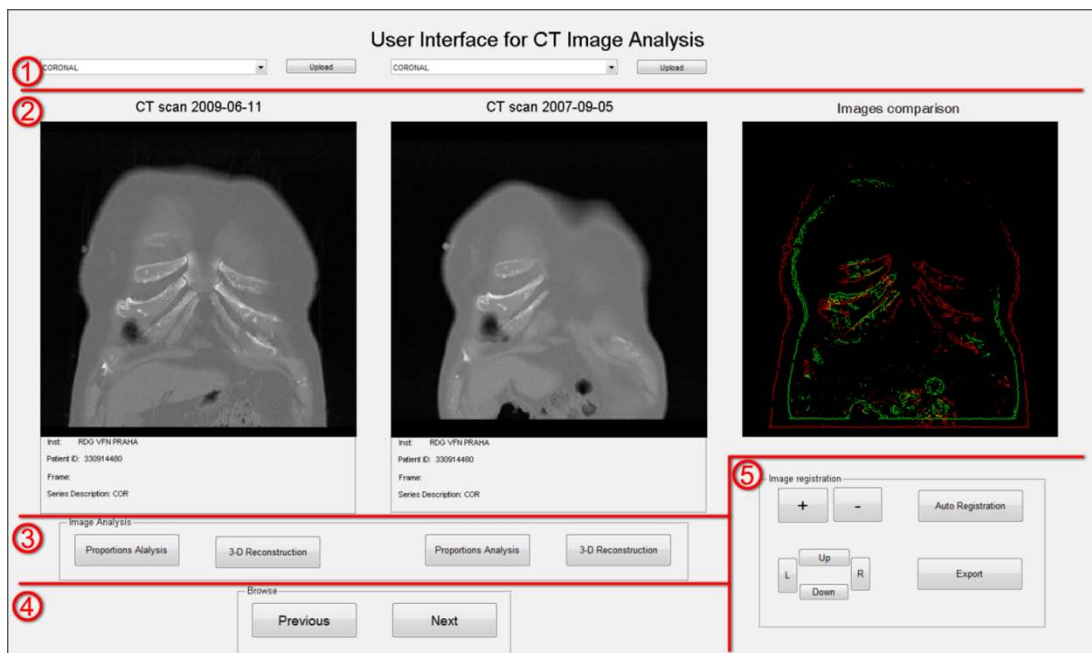

Figure 1. User interface for the main program

- **1st part -** The first part provides uploading selected image series (coronal, transverse or sagittal). It is possible to upload two different series for two different visualization (in the second part). It is important for different screening visualization and analysis.
- **2nd part -** The second part provides visualization of selected images in two windows and image comparison based on edge detection in the third window (which is used for CT finding comparison).
- **3rd part -** The third part provides proportion analysis and 3D reconstruction. This part will be described in chapter 2.3 and 2.4
- **4th part -** The fourth part includes two buttons for browsing to the next and previous image of selected series.
- **5th part -** The fifth part is a tool for the third image comparison window and it provides manual or automatic image registration, which is necessary for the comparison of selected parts with the finding(s). Automatic registration is represented by the fiction *Auto Registration,* more in chapter 2.2.

2.2 Auto Registration

The software enables automatic 2D registration based on the set of the control point pairs selected by the user (see Figure 2). The result of registration can be displayed as the overlap images or image subtraction.

First, the user has to select the control points (minimum of four pairs). To reach the desired result, the point pairs have to be selected evenly in all parts o the images and the quality of obtained parameters strongly depend on the number of selected point pairs.
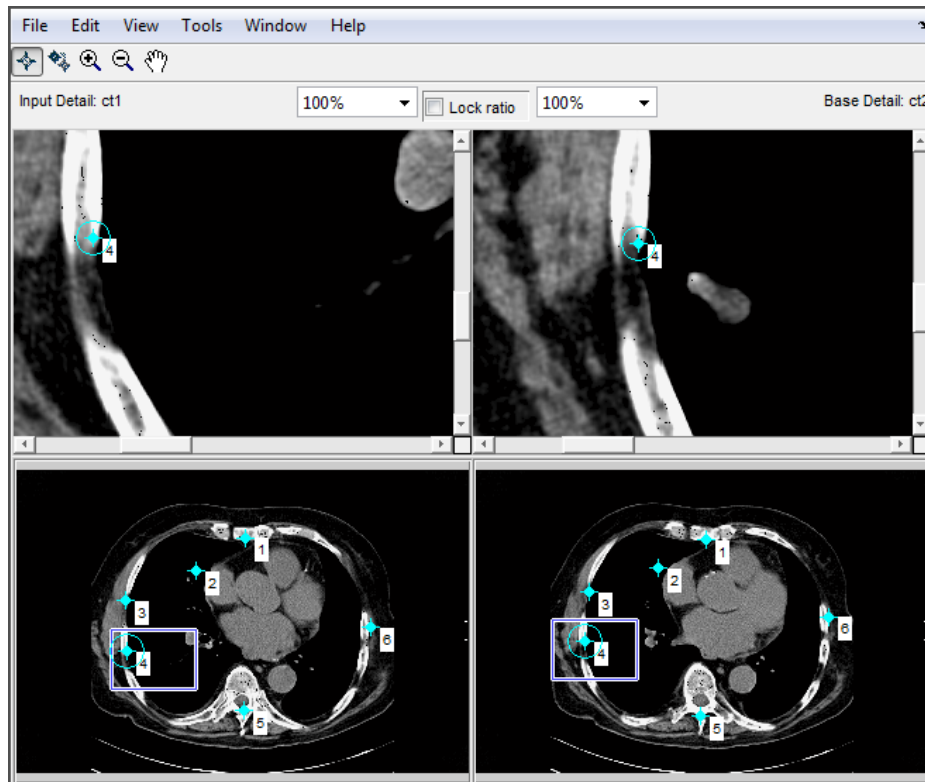

Figure 2. The window for the control point pairs selection

The registration window (see Figure 3) is displayed when the selection of all the control point pairs is done. The first part of the registration window shows the original images (the reference image and the image given for registration), the second part of the registration windows displays the result of registration.
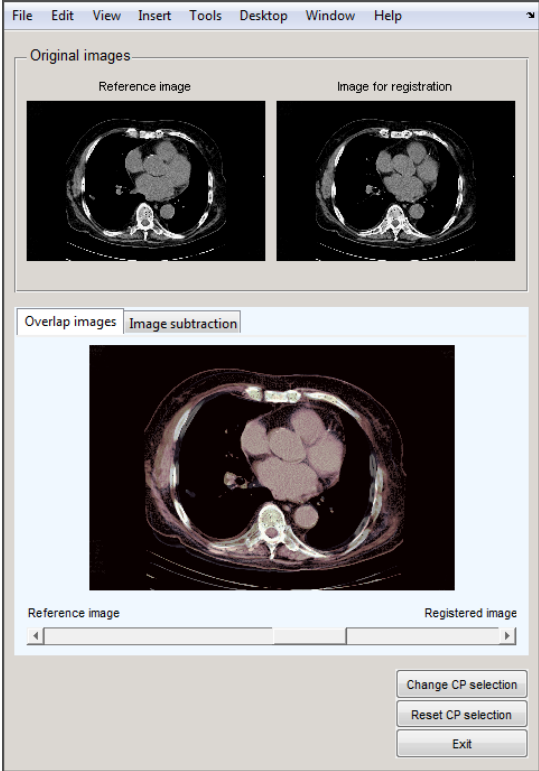

Figure 3. The registration window

The user, by switching between the tabs *Overlap images* and *Image substraction* (see Figure 3), can choose the way, how the result will be displayed; either as Overlap images or as Image subtraction. The Overlap images corresponds to the overlapping of the reference image by the registered image. The user can change the transparency of the registered image by the slider below the overlap images (see Figure 4).

Figure 4. The registration result displayed as overlapped images

The Image subtraction corresponds to subtraction of the registered image (after histogram matching with the reference image) from the reference image followed by the addition of the 128 grayscale levels, see Figure 5.
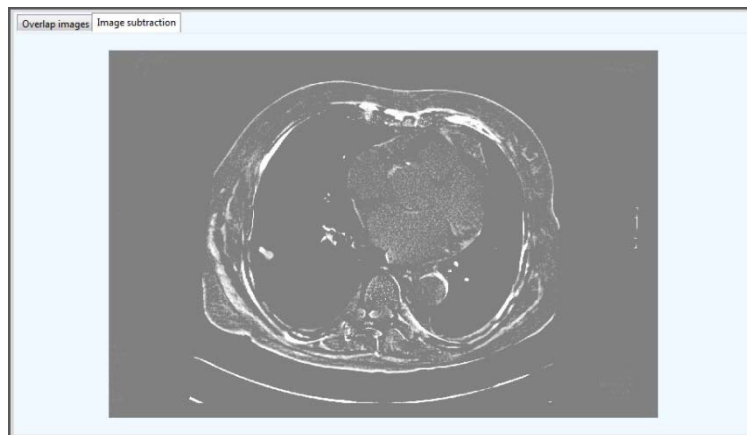

Figure 5. The registration result displayed as the image substraction

2.3 Proportion Analysis

The software enables 2D analysis of the selected image involving detection of the pathological finding, visualization of the image and detected pathological finding in different modes, determination of the characteristics of the detected pathological finding and calculation of horizontal and vertical dimensions and the shape of the detected pathological finding.

Firstly, the user has to select the region of interest in the image that one wants to analyze (see Figure 6).
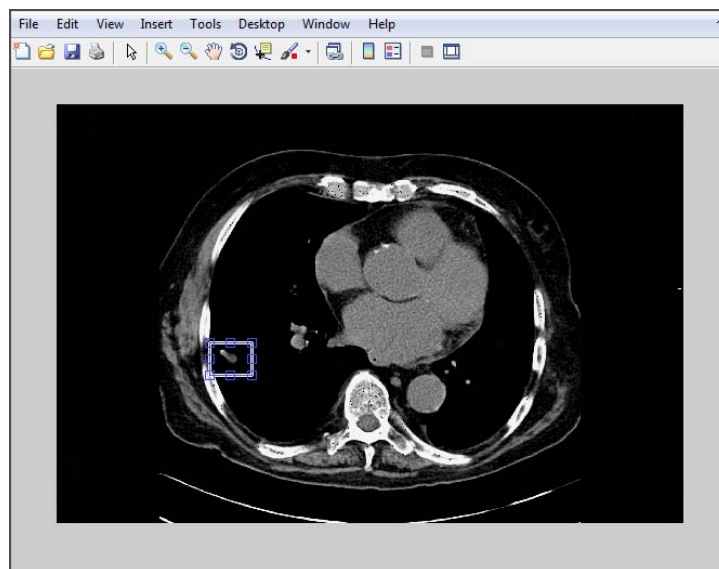

Figure 6. The selection of the region of interest

After the successful selection of the region of interest analysis window is displayed (see Figure 7).
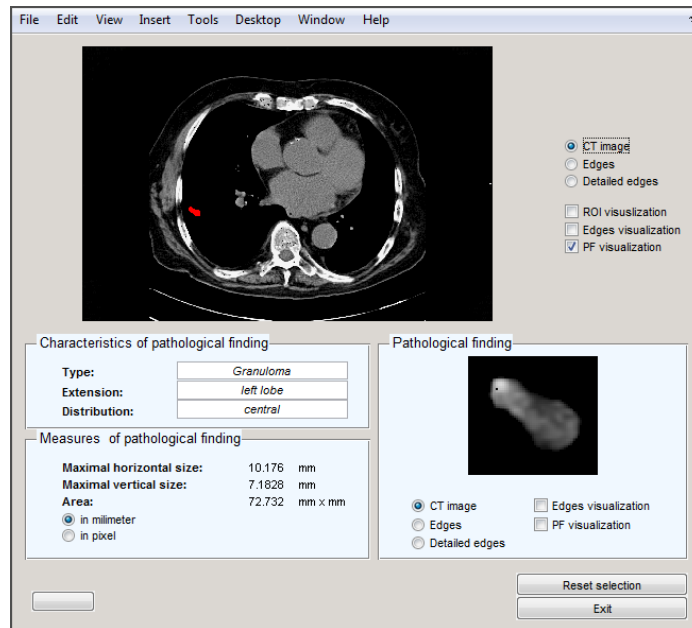
Figure 7. The analysis window for 2D analysis

The first part of the window enables visualization of the original image in different ways; grayscale image, edges and detailed edges visualization (see Figure 8a). It is also possible to highlight the selected region of interest or the edges of image or the pathological finding (see Figure 8b). The visualization and highlight options may be combined in different ways (see figure 8c).
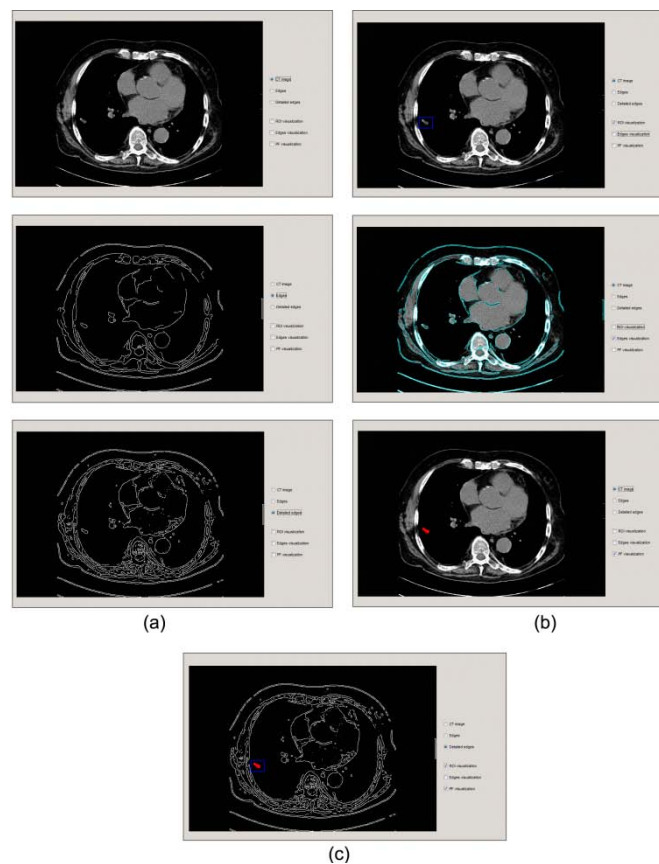

(a)

(b)

(c)

Figure 8. The visualization (a) and highlighting (b) capabilities of the analysis window for the original image. This options may be combined (c)

The *Characteristics of pathological finding* panel displays the information about the type, extension and distribution of the selected pathological finding. These data can be edited by the user, when it is necessary.

The next part of the analysis window, the *Measures of pathological finding* panel, displays the maximal horizontal and the maximal vertical extension and the area of the pathological finding. There are two choices of units; millimeter and pixel.

The *Pathological finding* panel offers similar possibilities of visualization and highlighting for the pathological finding as the first part of the analysis window offers for the original image.

The last part of the analysis window contains the button to reset the selection of the region of interest and the button to exit the 2D image analysis procedure.

2.4 3D analysis

The 3D Reconstruction button serves for visualization of the selected pathological finding. After clicking on the button, two independent figures are displayed. The first one shows the contours of layers belonging to the pathological finding (see Figure 9a). The second figure displays 3D visualization of the pathological finding (see Figure 9b). This figure is interactive, it is allowed to rotate the model or change position of scene light.
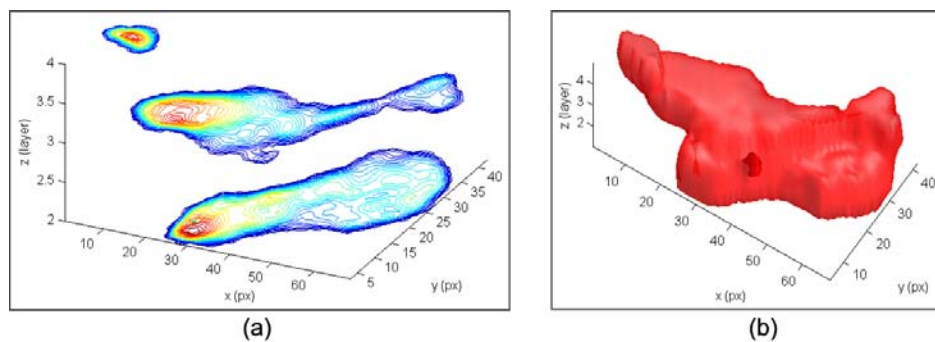

(a) (b)

Figure 9. The 3D visualization of the selected pathological finding presented (a) as a contour plot for separate layers and (b) as the 3D reconstructed model

The software is capable to create a complete 3D scene from a set of the processed CT images and highlight the pathological finding (see Figure 10).
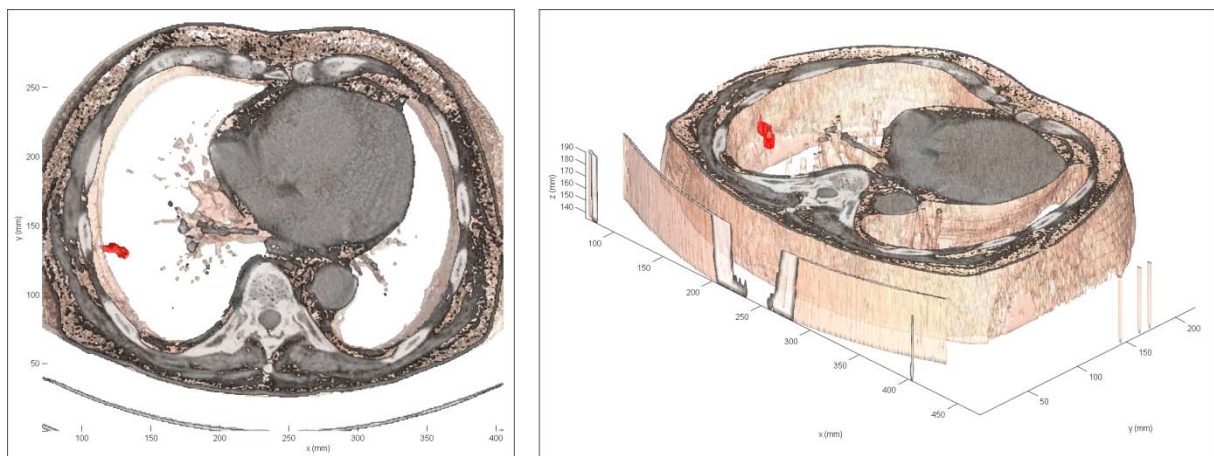

Figure 10. 3D model of the pathological finding in patient's lungs provided by presented software

3 Acknowledgements

References

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