

# Software for Wegener's granulomatosis CT image analysis

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**Abstract:** Contribution introduces a new software for CT image analysis. It is a complex application which combines visualization, 2-D image analysis and 3-D reconstruction. Software serves to radiologists as a tool for CT finding analysis, detection and early diagnostics. It provides object detection, estimation of horizontal and vertical dimensions, comparison of selected CT findings, shape and volume calculation or three dimensional reconstruction of selected object.

Software was made for Wegener's granulomatosis disease diagnosis and analysis.

**Keywords:** CT image analysis, edge detection, 3-D reconstruction, Wegener's granulomatosis

## 1 Introduction

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. 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.

## 2 Software description

New software provides CT image visualization and semi-automatic analysis (cooperation to radiologist is needed).

### 2.1 Main program

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

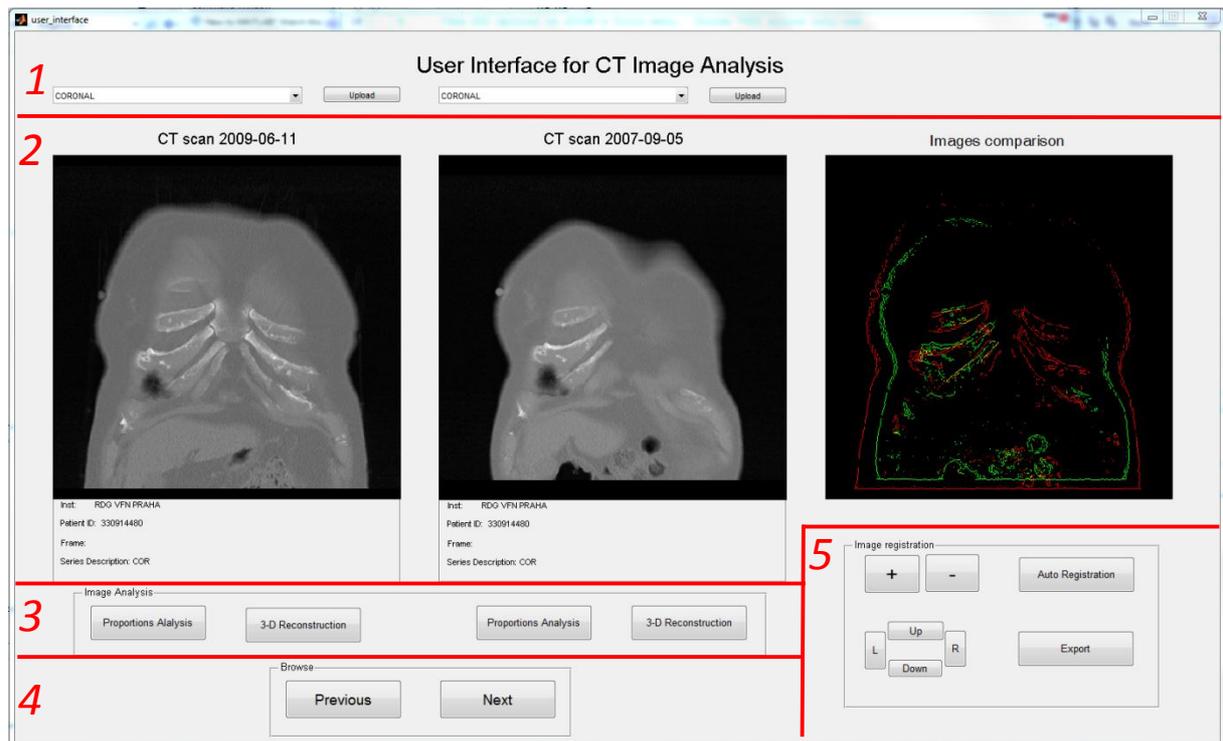


Figure 1. User interface for the main program

### 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 3-D 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 finding(s). Manual registration is represented by left set of buttons - zoom in, zoom out and move in all directions. Automatic registration is represented by the right button *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. The result of registration can be displayed as the overlap images or image subtraction (for more information see below).

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 of the images, see Figure 2.

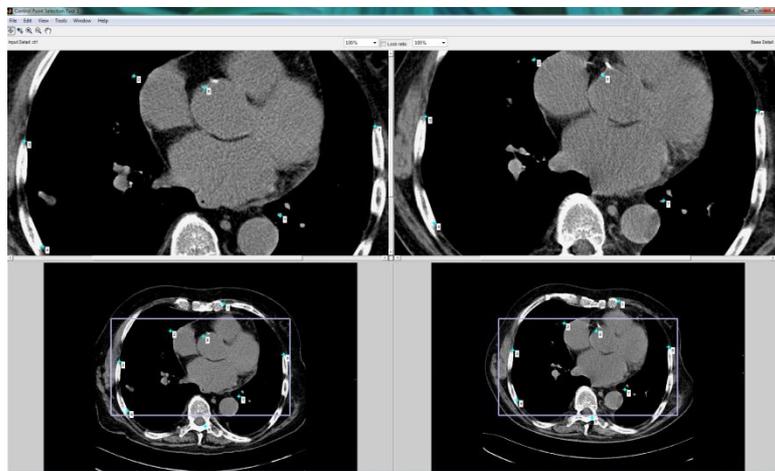


Figure 2. The selection of the control point pairs in selected images

Then the registration window is displayed (see Figure 3).



Figure 3. The registration window

The first part of the registration window shows the original images (the reference image and the image given for registration), see Figure 4.

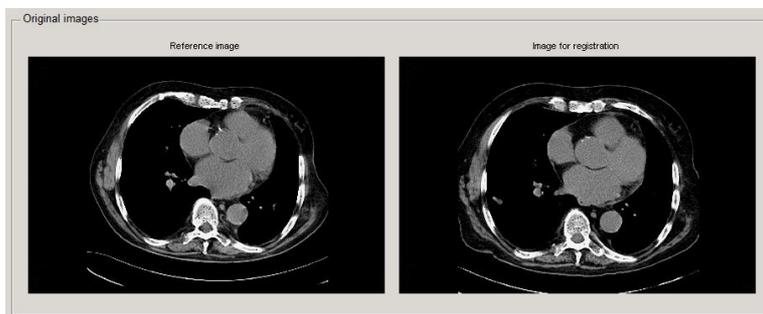


Figure 4. The first part of the registration window shows the original images

The second part of the registration windows displays the result of registration (see Figure 5).



Figure 5. The second part of the registration window displays the result of registration

The user, by switching between the tabs (see Figure 6), can choose the way, how the result will be displayed; either as Overlap images or as Image subtraction.

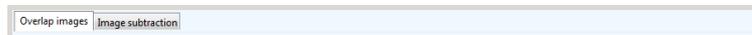


Figure 6. The tabs determine the way, how the registration result will be displayed

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 7).



Figure 7. The slider to change the transparency of the registered image

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 8.

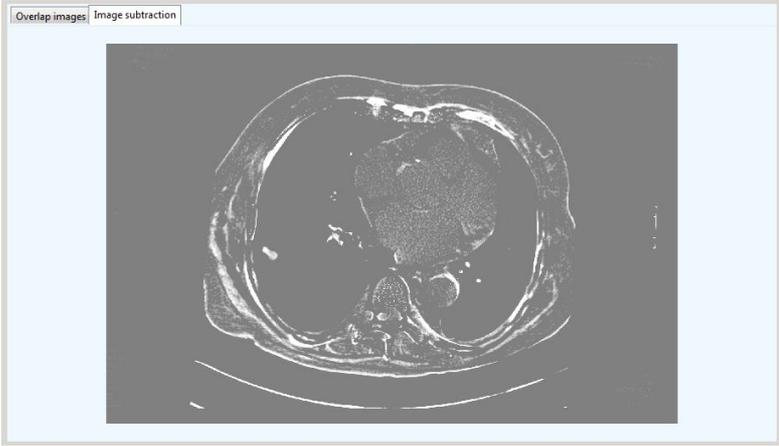


Figure 8. The registration result displayed as the image subtraction

The rest of the registration window contains the button to change the selection of the control point pairs (Change CP selection button), the button to reset the selection of the control point pairs (Reset CP selection button) and the button to exit the registration procedure (Exit button), see Figure 9.

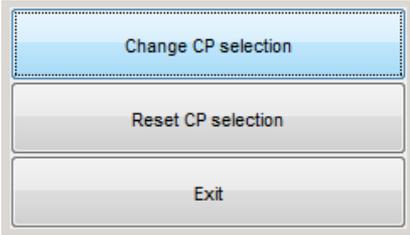


Figure 9. The buttons to change/reset the selection of the control points and the button to exit the registration procedure

## 2.3 Proportion Analysis

The software enables 2D analysis of the selected image involving detection of 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 (for more information see below).

Firstly, the user has to select the region of interest in the image that one wants to analyze (see Figure 10).

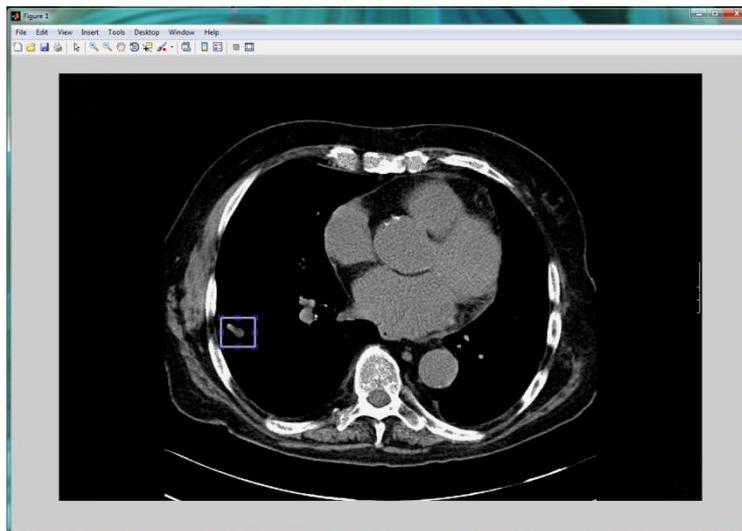


Figure 10. The selection of the region of interest

Then the analysis window is displayed (see Figure 11).

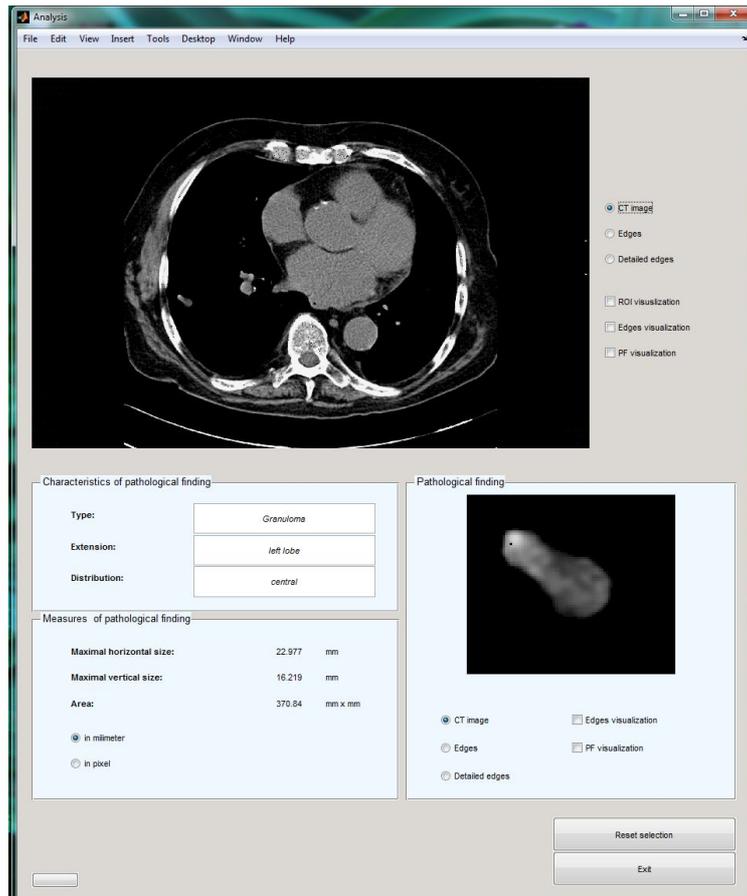


Figure 11. The analysis window for 2D analysis

The first part of the window enables visualization of the original image in different ways; grayscale image, edges and detailed edges visualization (see Figure 12).

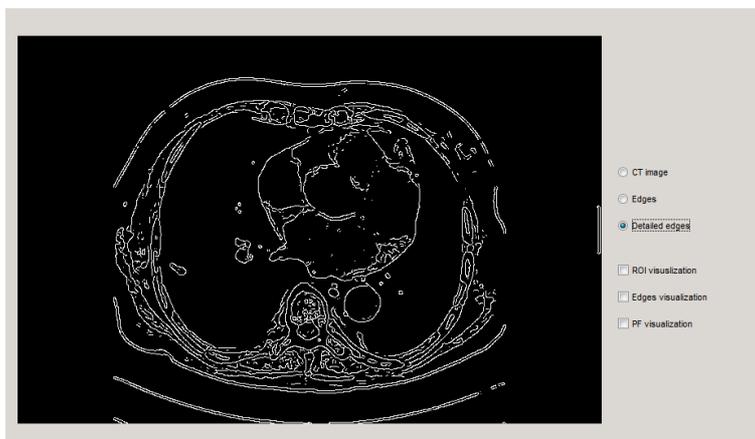
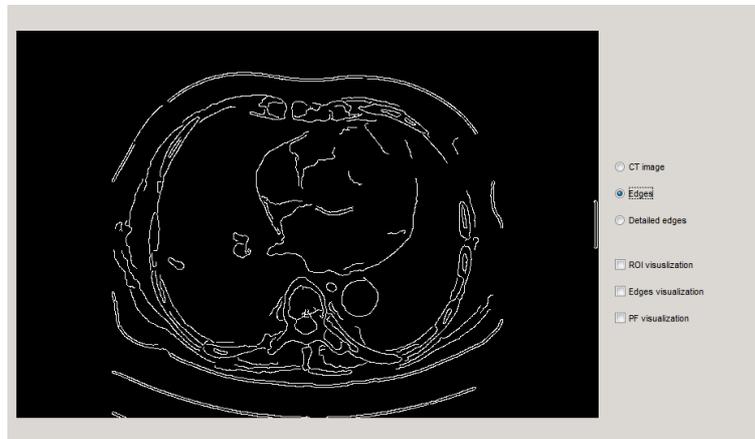
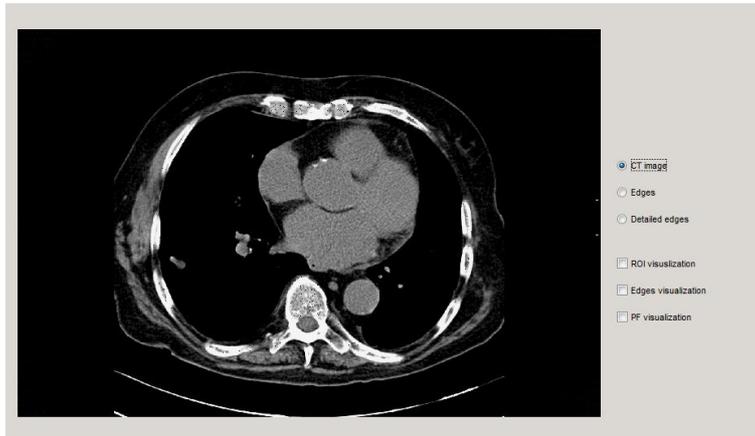


Figure 12. The visualization capabilities of the analysis window for the original image

It is also possible to highlight the selected region of interest or the edges of image or the pathological finding (see Figure 13).

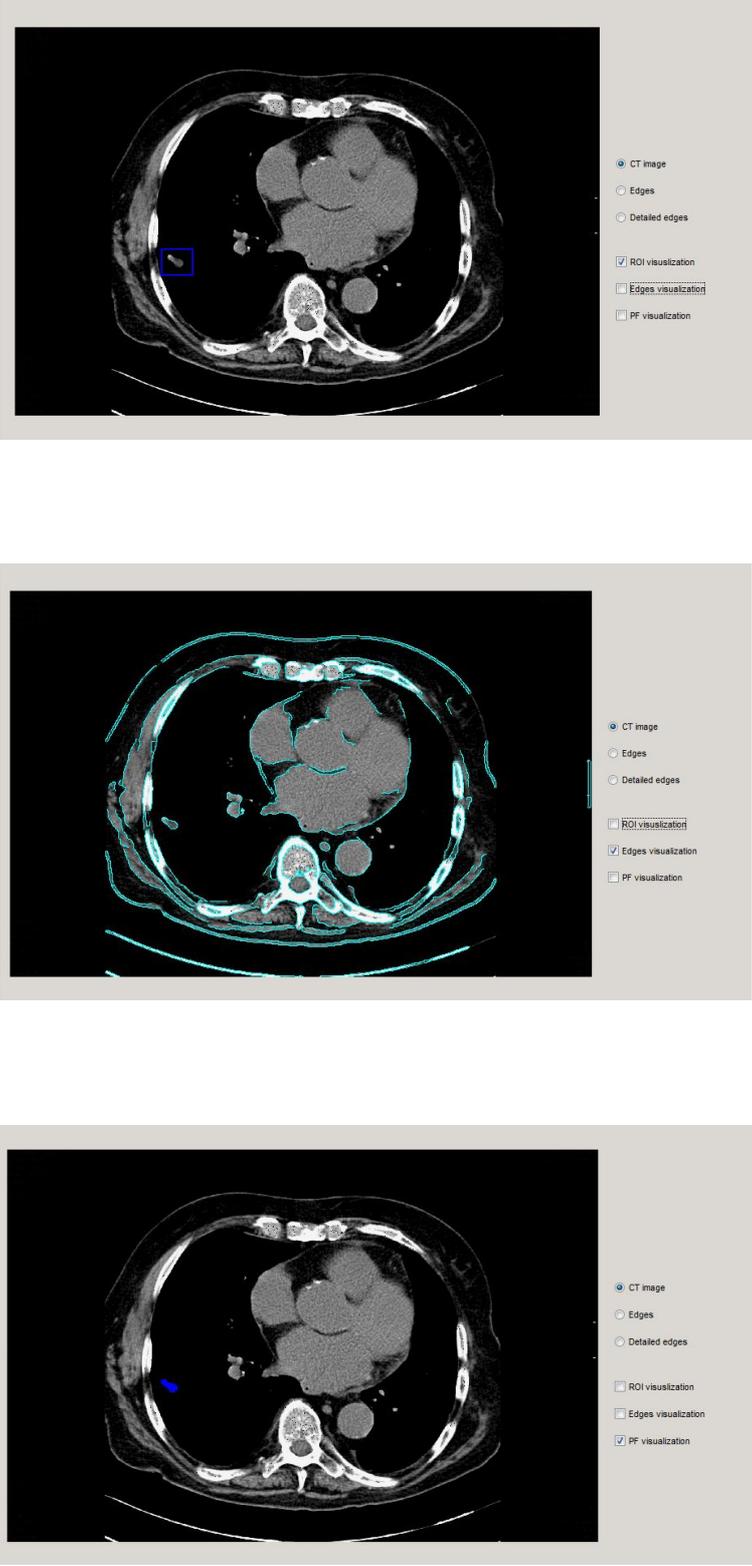


Figure 13. The highlight capabilities of the analysis window for the original image

The visualization and highlight options may be combined in different ways (see figure 14).

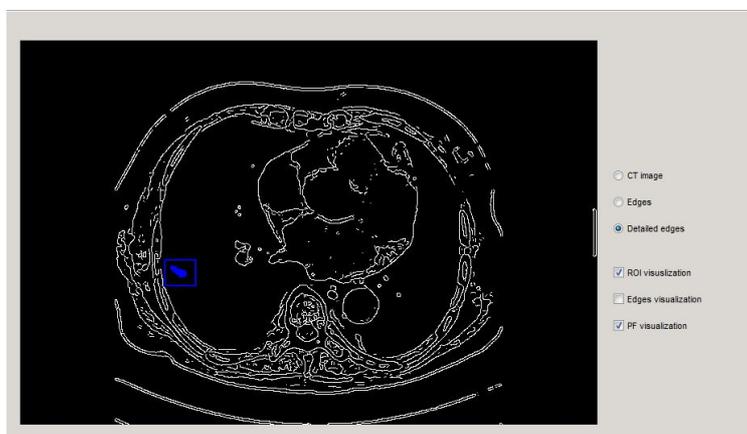


Figure 14. One of the possible visualization and highlight options combinations

The rest of window is devoted to the pathological finding, namely, its characteristics, measures and its visualization (see Figure 15).

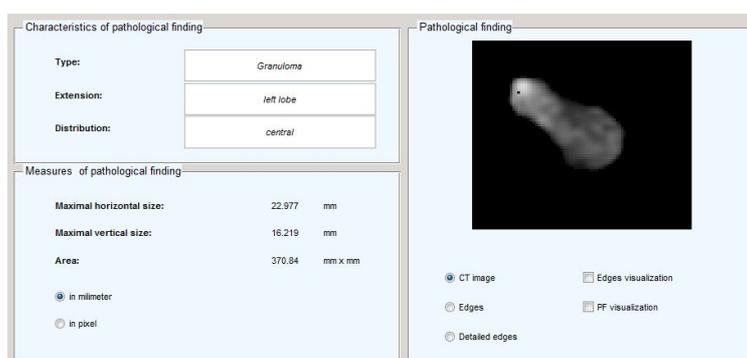


Figure 15. The part of the analysis window devoted to the pathological finding

The Characteristics of pathological finding panel contains the information about type, extension and distribution of the pathological finding. These data can be edited by the user. The default value of type is *granuloma*, the default value of extension is *left lobe* or *right lobe* (according to the localization of the pathological finding) and the default value of distribution is *central* (see Figure 16).

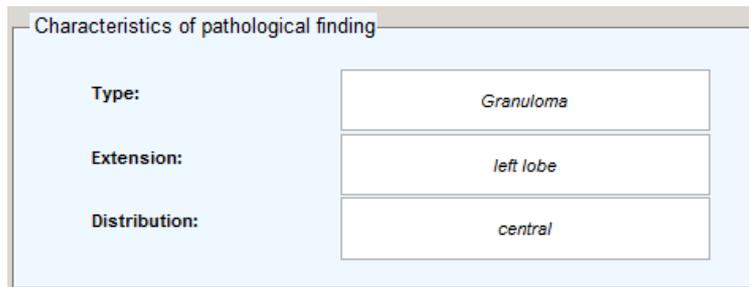


Figure 16. The Characteristics of pathological finding panel

The Measures of pathological finding panel displays the maximal horizontal size, the maximal vertical size and the area of the pathological finding. The user has two choices of units; millimeter and pixel (see Figure 17).

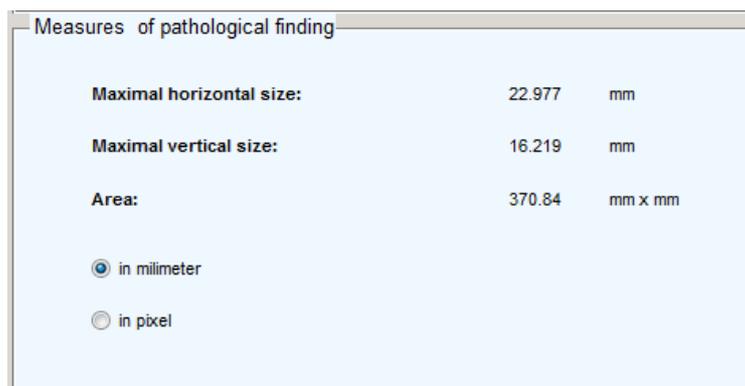


Figure 17. The Measures of pathological finding panel

The Pathological finding panel offers similar possibilities of visualization and highlighting for the pathological finding as the first part of the analysis window for the original image (see Figure 18).

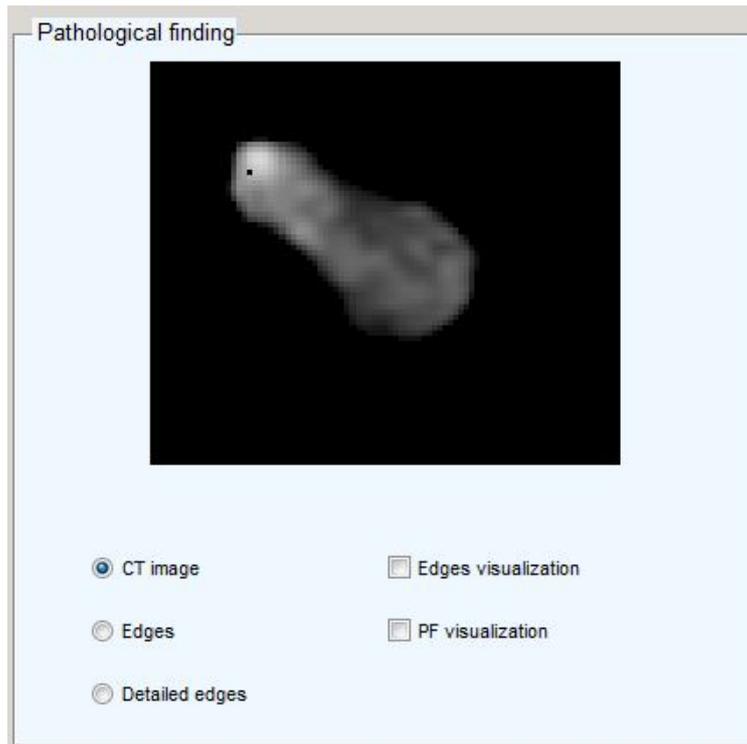


Figure 18. The Pathological finding panel

The last part of the analysis window contains buttons to reset selection of the region of interest (Reset selection button) and for termination of 2D analysis of the selected image (Exit button) as depicted in Figure 19.

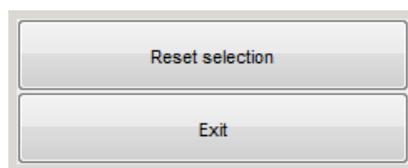


Figure 19. The Reset selection and Exit buttons

## 2.4 3-D analysis

The *3-D Reconstruction* button serves for visualization of pathological finding. After clicking on the button, two independent figures are displayed. The first one shows the contours of layers belonging to pathological finding (see Figure 20). The second figure displays 3D visualization of the pathological finding (see Figure 21). This figure is interactive, it is allowed to rotate the model or change position of scene light.

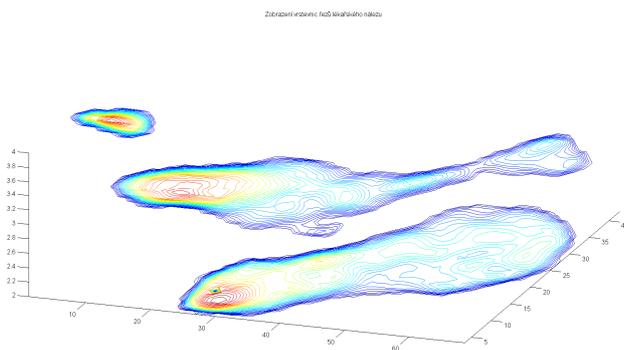


Figure 20. Contours of 3-D model

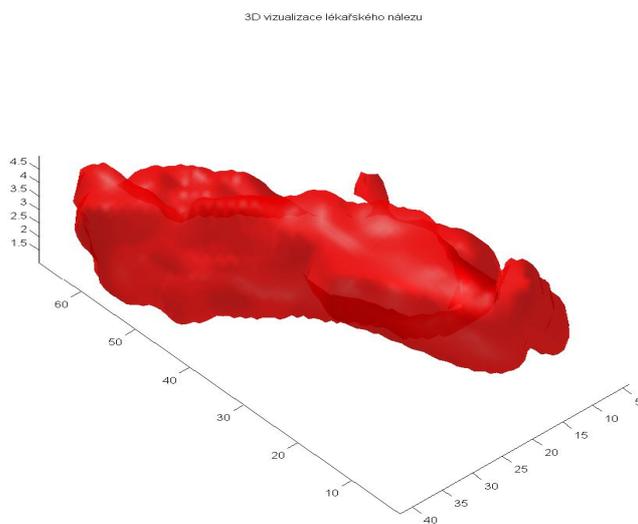


Figure 21. 3-D visualization

## 3 Acknowledgements

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