MICROOBJECT IMAGE ANALYSIS SOFTWARE COMPLEX

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Abstract: *This research paper presents the results of software package development using different methods of medical-biological image processing based on a comprehensive and critical analysis of trends in each stage of medical-biological image processing.*

Keywords: *Medical biological image, menu, filter, software, cell, segmentation.*

In recent years, advances in microcopy and improvement of image processing algorithms have made it possible to develop a computer analysis approach to the identification of medical-biological objects. In this area, it is possible to cite programs designed to identify cell phenotypes, diagnose and treat diseases, detect the presence of viruses in cells, and classify them. Apps like these can be used to supplement medical professionals' opinions and aid in diagnostic decision-making. Although many studies have been conducted in the analysis of medical-biological images, they have mainly focused on tissues and organs. In this case, none of the studies conducted on medical-biological images have analyzed segmentation, feature extraction, and classification, which are typical image processing steps. This study aims to develop a software package using different methods of medical-biological image processing based on a comprehensive and critical analysis of trends in each stage of medical-biological image processing.

Popular algorithms for medical-biological image analysis were programmed using the Python programming language. The software package developed for processing and analyzing their images has a modular architecture (Fig. 1).

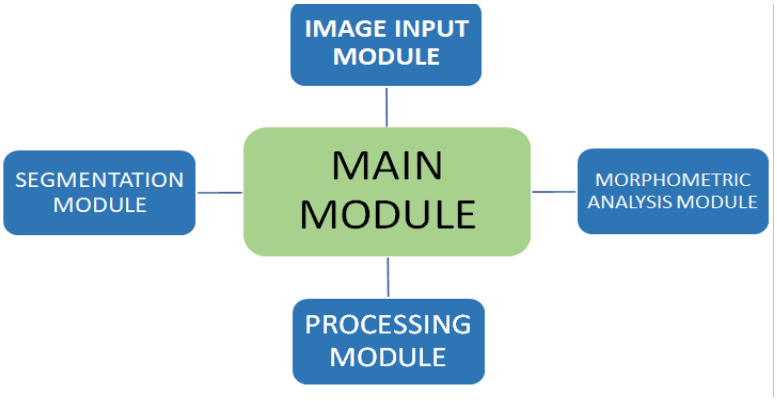

Figure 1. Software architecture

The program can load program modules suitable for the problem to be solved, and it allows to save RAM. In addition, without changing the code of the developed modules, it is possible to expand its scope and add functionality, which creates many conveniences for the user. All modules have a standardized set of input and output parameters and are implemented as libraries. It also allows you to use any modern software development tools to develop additional modules.

The software suite consists of a main menu called File, Transform, Preprocessing, Image Conversion, Multiplication, Compression, Filtering, Resize, Size, Analyze, and About, each menu has its sub-menu. A separate window for the processed image is organized so that the user can see the difference between each processing process and the original image (Fig. 2).

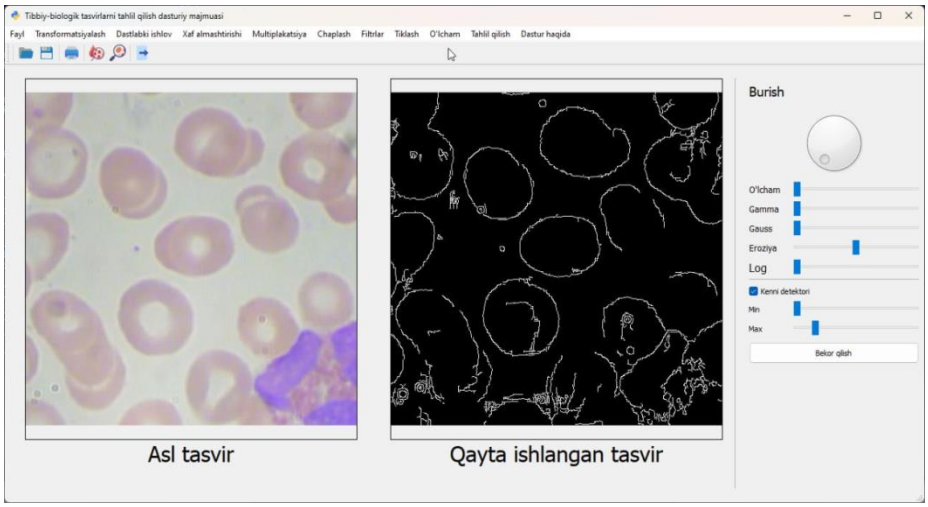

Figure 2. The main window of the software package

The "Open" button in the "File" menu, this functional button is used to open the desired image file through the program, the "Save" button is used to save the processed files, "Settings" button is to enter the program settings, the "Getimfge" button is to take an image through the microscope, to exit the program "Exit" button is used.

The "Smoothing" button in the "Preprocessing" menu is used to perform mirror smoothing of the speech file, and the "Filtering" function button is used to reduce interference by applying various filters to the image (Fig. 3).

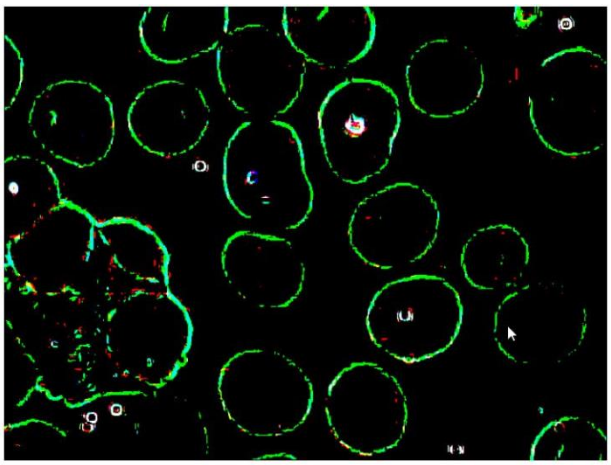

Figure 3. The result of applying filters to a given image

On the one hand, this software package can be considered as a hardware-software package with the possibility of direct communication with devices that transport and transfer image files, and on the other hand, as a software tool that provides experimental testing and image processing by loading image files from external memory.

The software package can directly read the image from the digital microscope, which is done through the file menu. The following figure shows the segmentation result.

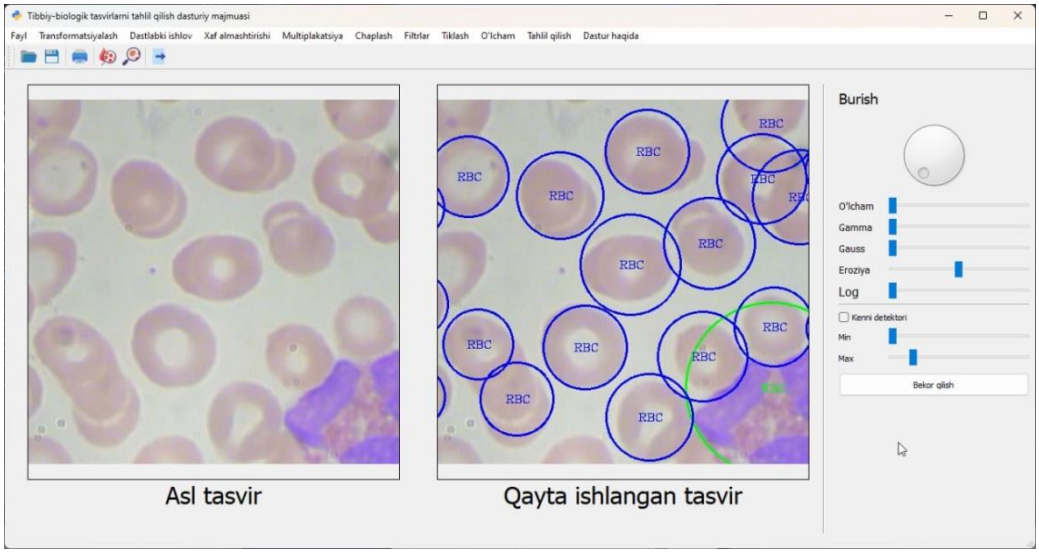

Figure 4. The main window of the software package

The software package can be used for processing, segmentation, analysis and recognition of images in fields such as medicine, biology, geology, automated diagnosis and recognition, and other image processing fields such as object detection.

The software created on the basis of the existing and popular models, methods and algorithms for the analysis of images of medical-biological microobjects has been implemented in the practical activities of several medical associations. As a result of the use of this software tool, it was possible to reduce the time spent on the diagnostic process by an average of 10%. In addition, the proposed input method made it possible to increase the refresh rate of the "live" image by an average of 2 times. Also, the segmentation accuracy was evaluated for the HV or HS color field selection technique for different micro-object images, resulting in a total average error of 0.065. It has been shown that the construction of contours and vats based on the finite area filling algorithm is on average 2.5 times faster.

The obtained results were positively received by industry experts. The conclusions are that in further studies, it is considered appropriate to conduct image analysis based on modern architectures of neural networks in the development of systems that take into account the features of micro-objects in images that meet the requirements of real-time mode.

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