A Flexible Suite of Software Tools for Medical Image Analysis

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Abstract— **A new methodology of an intelligent software development for medical image analysis is proposed. The kernel of this software is a script interpreter that may be supported by an intellectual script generator. Commands of the interpreter are basic functions of image processing. The script generator forms new image processing scripts after analysis of image properties. This allows to change a processing sequence and the software interface. Software of such type may be self-transformed for different classes of medical images and various tasks in real time**

Keywords-medical image processing; intelligent software; script generator

I. INTRODUCTION

Computer engineering includes many different parts that influence to properties of software, for example, organization of functional support in the software affects the presentation of the user interface, and so on. Medical software has specifically requirements to software organizations. Such requirements depend of condition of solving tasks, knowledge of software user, and environment of user's work place. Therefore, the modern requirements to medical software is dynamic organization of functional, user interface and data managing for medical radiological methods, optical microscopy, endoscopy and ophthalmology, etc.

Any software may be divided into compiled programs and interpreters. Sometimes, software is represented as mixture of these variants. Such software for science has a compiled kernel that includes GUI (graphical user interface), basic functions and calculations, and different types of data representation. An interpreter usually is used as saved history of operations applied to a new image processing. In this case, the interpreter allows to create additional simple functions on base kernel possibilities but can not change the software [1]. We propose to use an interpreter as a kernel for our software. In this case the interpreter is used as a manager of action. It supports by performance of the functions, calculations, and GUI events. So, we can change the software design and organization by correction of interpreter scripts without a compilation stage. In other side, complex function and calculation are realized in external public compiled modules. This will keep the speed of calculation such as the compilation software. Today, similar software organization is used for web and game development. It is named an "open software architecture".

Our software is based on a mixture of a compiled library and an interpreter with many image processing functions. In result the software may be divided into two parts: for the professional software developers and the software designers or users. The interpreter has possibilities for including additional functions from a compiled dynamical library. It allows to change software properties and software applications without a compiling stage. On other side users can change the graphical interface for improvement comfort conditions for development and easy evolution of software. We apply such a technique for developing histology image analysis software [3].

Modern computer support and facilities in microscopy bring new perspectives in studying of cell structures. At the same time, the most commonly used method for a tissue analysis is still the well known morphological method, which allows to get reasonable biological conclusions after an image analysis. Group of morphological features, which are used for detection of similar types of cells and for organ and tissue fragment analysis, is noticeably extended. Usually, there is no any relation between different types of features. Therefore, types of histological tissue fragments are separated from each other by their morphological features. Systematization of histological objects is very important in order to provide a morphological analysis and oncologist diagnosis.

There are different approaches to segmentation of biomedical images. One of the most popular of them is based on mathematical morphology. Many morphology algorithms for cell segmentation have been proposed through the last years [3]. The initial image segmentation is determined by classifying the image local variation information obtained with dilation and erosion operations. A median filter may be used to smooth the segmented image. It removes small regions of misclassified pixels while avoiding significant changes to the cell profiles. The erosion operation is finally used to restore the cell areas. An edge-based segmentation may be divided into two independent stages: edge detection and edge linking. The obtained edges are used to determine the cell locations and contour model is further used to select the set of edges involved in the cell locations. Nedzved, et al. [4] have proposed an edge-based potential aimed at the elimination of local minima due to undesired edges. This

approach integrates knowledge about features of the desired boundaries apart from gradient strength and eliminates local minima, which make the segmentation results less sensitive to initial contours. Color is an important feature in the histological image segmentation. There are several effective algorithms for automatic detection of cells and other histological objects [5]. However, these algorithms work under certain conditions to solve particular problems.

In addition, the new workplace is changing the software requirements. It is necessary to estimate functionality and compatibility of existed tools and data of software development to define a dynamical system of medical software developing. It has to be revised tasks, initial data, diagnostic features and characteristics.

The rest of the paper is organized as follows. In Section II we review properties of two different classes of medical images: histological and radiological ones. In Section III we describe a variant of software development which may be self-transformed after preliminary image analysis. In Section IV we describe testing of the presented software generation for various medical images.

II. FEATURES OF MEDICAL IMAGE ANALYSIS

In this section, basic features of image for determination of a way of processing are described.

A. Common processing sequence for image analysis of histological samples

Usually processing of histological images may be divided into several steps:
1) Input and image enhancement;
2) Segmentation;
3) Object detection (identification);
4) Measuring;
5) Analysis.

Every step consists of execution of a set of functions. Application of functions depends on properties or image estimations. It is possible to define such estimations in many cases, for example, for contrast, noise or blurring. We can construct table of image processing functions and image estimations.

For example, for histological images application of segmentation methods depends on many image conditions. Usually, an image is decomposed to separate regions to analyze the histological sample. Therefore, the segmentation process (i.e., extraction of homogeneous regions in image) is considered as a basic step for a formal scene description. It is necessary to define a correct set of features and feature characteristics for a suitable choice of segmentation methods.

Histological objects may be defined according to tasks of image analysis. Automated histological specimen analysis is based on topological features of images. It allows to define the whole procedure of study for object extraction. However, automatic analysis of histological specimen depends on the optical magnification of the image. In each magnification there is a certain group of topological features of tissue and its components. This fact has prompted to consider histological objects over magnification of histological specimens.

Fig. 1 presents a general scheme of hierarchical analysis of objects in histological images.

Different tissue fragments, which are composed of group of homogeneous cells and fibers, form an entire image of histological sample. Usually these fragments or objects are represented by a certain texture. Therefore, a region growing can be used for extraction.

From initial image conditions it is possible to define function for quality image processing and analysis (Fig. 2).

As a result, a table of connection function and image estimation are constructed.

In each step, functions are indicated by priorities. For example, for the image improving step the higher priority is defined for noise removal, next priority level contain a contrast enhancement and correction of the borders. Priorities determine the order of the functions and the need for re-analysis using neural network.
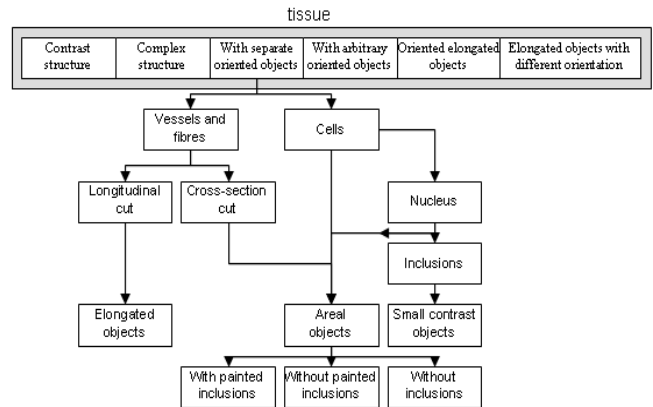

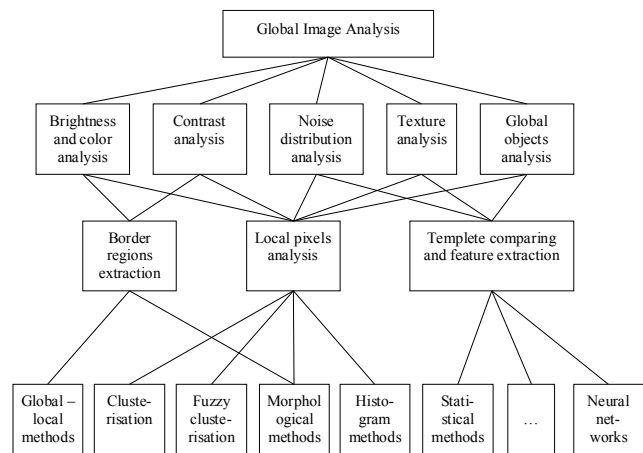Figure 1. Hierarchical scheme of histological objects.

Figure 2. Scheme of segmentation methods definition from image conditions.

Image processing functions relate to basic computer vision topics. This is corresponding to its application for image changing. Every function changes properties of image and is applying for specific processing cases. Every function introduces in an interpreter table and can be supported by additional information.

B. Requirements for a radiological investigation software

Requirements for software are defined by a team of the basic users which will use achievements of this work. This team consists of physicians and medical workers of following specialists: the attending physician the oncologist, the physician of radiodiagnostics, workers of registry. They define the basic requirements to software They define the basic requirements of users to a complex.

Input, loading and presentation of images it should be carried out by means of following possibilities:

- Possibilities of operations with raster, vector formats (including DICOM);
- Possibilities of generation and presentation of synthesized 3D images on the basis of contours, which are prepared by processing 2D layers.
- Possibilities of generation of graphic reports documents.
- Presentation through system for visualization 2D and 3D images on the monitor screen, and also for reports.

The analysis and processing of medical images of tumors includes:

- Image improving;
- Interactive function for objects selection;
- Automated function for objects detection;
- Measurements and calculation characteristics from images.

The analysis and processing of angiography images and data are expansion of the previous requirements by specificity of objects - vessels and their network. In this case it is necessary to take into consideration morphological and textural features of vascular system.

The monitoring first of all require to the ease of general interface of a complex:

- Possibilities of synchronous work with different investigations of patients,
- The organization of storage of the information focused on many cases of patient,
- Possibility of preservation of data for the further statistical analysis.

The above described requirements of users form functional requirements. Functional requirements define functionality software. developers should construct it for users tasks. Functionality defines efficiency of working out. The efficiency increase is reached by:

1) The developing of modular system of interaction program modules with loading different functionally,
2) Using of ready software packages of the simple level of initial functions,
3) The software complex should include following modules:

- The global module of synchronisation including universal principles, structures and the data for providing interaction with other modules.
- Loadings of the digital information and management of processing and analysis of medical images technology;
- The automated allocation and the analysis of slice images (for example CT);
- Volume restoration of formation and definition of volume characteristics;
- Definitions of topological features of vessels for angiographic investigation;
- Statistical comparison of results of analysis of images for different time;
- Generation of graphic documents;
- Measuring and analytical functions.

In result, the software for the radiological methods of investigation should be accompanied by additional display capabilities, and presentation and image, not only preparing the general scheme of image analysis in histological methods.

III. DEVELOPMENT OF MEDICAL IMAGE ANALYSIS SOFTWARE

This section shows foundations of a flexible suite of software tools for medical image analysis that was developed. For elaboration of structural scheme of software basis interface an estimation of functionality and compatibility of existed software development tools were done. Tasks which may be solved with software to be developed, initial data, diagnostic features and characteristics have been observed. For software developing we use C-language from Microsoft Visual Studio.

Based on material posted by Guillaume Marceau [1], who in his study used parameters of 72 implementations of programming languages, and compared them to 19 special tests, prepared by the project "The Computer Language Benchmarks Game" as a kernel chosen interpreter LUA [6].

In the first case data are processed using temporary file, which allow to analyze records (images). In another case a transfer by calling a run-time library is performed (Fig. 3).

Our software is based on the interpreter of Lua language. It was elaborated as the main module based on an interaction of complex modules. It includes a graphical interface, global variables and image storage structure. Architecture of the graphical interface was carried out by linking the Highgui library [7] from the OpenCV package [7]. The image processing and function analysis are supported by OpenCV library but connection Lua with OpenCV are realized by Lua-binding interface for a connection function of OpenCV with Lua.

An image structure is determined by a module of graphical interface into OpenCV library which is responsible for visualization and representation of images. Headers of image structures are global variables-pointer of interpreter

Lua. They have special type - userdata. Userdata corresponds to a pointer in the computer address space. This module also includes image read/write functions, basic functions of image processing and interactive contouring. All interactive functions return values in the event block, which changes global variables of the interpreter. A simultaneous usage of several modules is required for tasks of monitoring space-occupying lesion. In this case an interaction has been performing by using global variables of the Lua interpreter and properties of the userdata type of Lua interpreter.
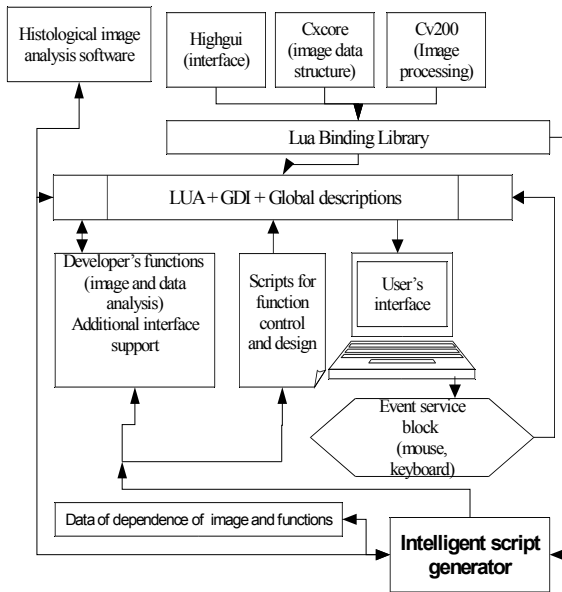

Figure 3.   Scheme of flexible suite of software tools for medical image analysis.

Short sequences of functions are called in nodes for solving basic problems. During image processing a node of Lua can provide image exchange through Lua-outlets. First it sends images to the highest Lua-outlet identificator. After that the processing is done if the state of Lua-outlet was changed. The node changes the sequence of the processing functions and their parameters in accordance with his notifications. Loop notifications are sent eventually from a slow thread at the end of the scripts processing.   The observer notification is required during the path through the each of the nodes. It is called the notify event-slot. This slot calls node's state method to get a dictionary with the node's attributes. Also it sends these attributes to the observers.

Communication between nodes in the same script is done through a direct function. This function is called by event-slots, either using a virtual method bang for the first inlet or a function pointer for other inlets. Images are processed by reference.

Adding new complex functions of processing and analysis is carrying out by group of developer's function. As an input new functions may get any global variable or text and numerical constants from the LUA interpreter.

All internal controlling of software is carrying out by text scripts of LUA, which are divided into two categories:
1.   scripts for image sequences analysis;
2.   scripts for operative functionality and setting up of software at workplace of medics.

All scripts are stored in a text form and easily accessible. However they are not for changing by user and may be edited for by developers only.

Scripts manage to software organization and create new additional function for image analysis and processing. Preprocessing analysis of images sets of image allow to define processing functions. Module of scripts generation defines such sets. It includes intelligent components for connections results of image functions processing and image characteristics. Of course such task can be solved only for particular task in our case for histology image analysis.

Every interpreter defines function through a specific table. We use it for definition connection images characteristics with a function in our software. It includes a set of feature vectors and variable of priority. The set of feature vectors defines the utility function. The variable of priority determines the position of function in the generated script. In result such software has intelligent self-programming possibilities.

In the analysis the first step is determining of global characteristics of images and defining the type of image. Single-channel grayscale image often correspond to the radiological methods of investigation in medicine. If the depth of the pixel brightness over the eight-bit image is defined as CT scans. The color image is composed of three or more channels. It is defined as histological. It remains uncertain class for eight-bit grayscale images, which can be classified as partially processed images of histology and radiological medicine. The difference halftone radiological images from histology most often lies in the way of formation of objects in images. Color histological image is formed on the basis of color in the preparation of amino acids. As a result, objects in an image composed of small specks, which form additional local boundaries. The boundaries correspond to local extremes of the brightness intensity. Therefore, a Sobel filter is performed to determine such characteristics (Fig. 4). The result is a gradient image. The distribution of brightness in this image is similar to a Gaussian distribution.

Based on the characteristics of the asymmetry and the eccentricity of histogram is determined type of images, that is belonging to the histological or radiological class.

The image type defines processing scripts and user interface. System generate separate user interface on base type definition for histological images (Fig. 5) and radiological images (Fig. 6).

A script generation module consists of two parts: image analysis and script construction. The fist part started from global image analysis that include histogram analysis and basic statistical analysis for pixels distributions, fractal and texture analysis. On the base such analysis as estimation of noise, blurring, image characteristics are calculated. From the interpreter function table image preprocessing script are generated for image improving by such estimation.
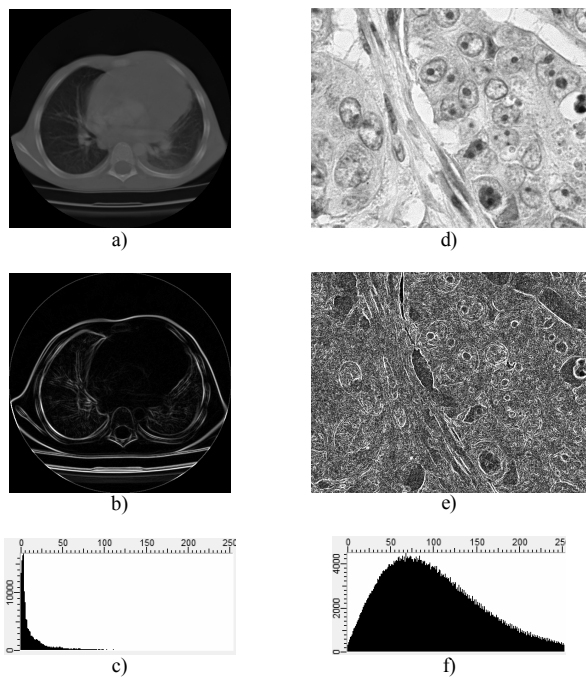
Figure 4. Examples of the results of image classification stages: a) radiological image, b) gradient of radiological image, c) histogram of radiological image gradient, d) histological image, b) gradient of histological image, c) histogram of histological image gradient.
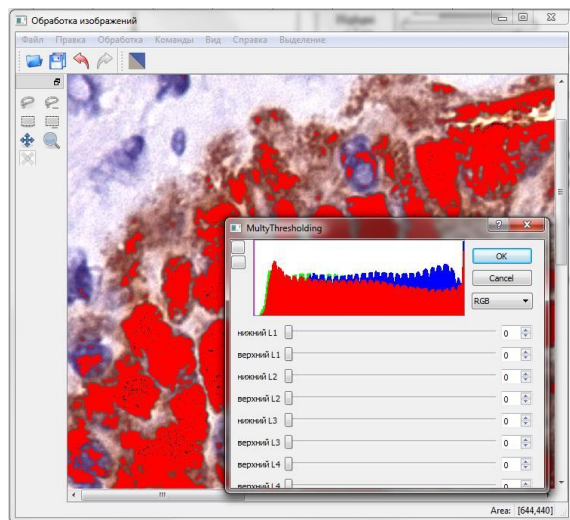

Figure 5. Screenshot of user interface generated for histological image analysis.
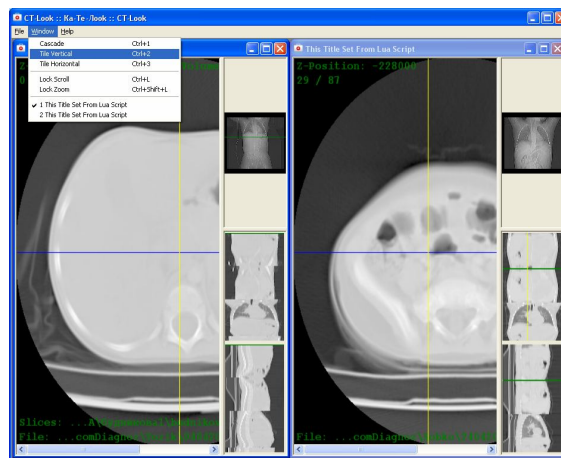

Figure 6. Screenshot of user interface generated for radiological image analysis.

Than local image analysis is going by convolution and statistical analysis of line-profile characteristics. This analysis allows to estimate characteristic of cells borders and contrast. Such estimation defines functions for image contrasting and border emphasis. After generation result image is tested for quality of processing. If the image quality is low stage of image analysis and function definition should be repeated. Such procedure generates image improving scripts that can be change by a user or developer. This script is only proposition and need to user control. The same mechanism of image analysis and function definition works for stages of segmentation and postprocessing.

As result our software constructs common script for every generation stages. Such script corresponds to function sequence for object extraction. It can be used for extraction of histological objects on the image. We use it for extraction of nuclei from histological images. Then characteristics of objects are calculated. It is necessary to detect type of objects that present at the image. We divide objects for five basic types: blobs, front, needles, dendrites and nets. Such procedure of object detection is spending by functions through script generation. Using global fractal, texture characteristics software detect geometrical type of objects and formed characteristics sets for object description.

For definition image processing function in scripts we try to use Kohonen neural network (self-organizing map, SOM) [8, 9]. It is a class of neural networks, the main element of which is a layer of Kohonen. The Kohonen layer consists of adaptive linear combiners. Estimations of global conditions on the image are used as weights in neural network. Adjusting of the input weights and vector signals quantization is closely related to a simple basic algorithm for cluster analysis (method of dynamic cores, K-means).

System is supported by script generator module. This module uses LUA-metatable of function for image processing and corresponding table with estimations of image. Thorough such table, definition of function sets going by Kohonen neural network. As a result, the module

proposed scripts for image processing as text file. Users can spend analysis of this script and change some in it.

The software is supported by uses control and changing. There are a few version of user interface for managing of image processing and choosing of analysis type. Also the software has sets of interactive function for image processing. On the basis of these tests in the fifth section draws conclusions about the effectiveness of the proposed scheme, software analysis of medical images

IV. TESTING

Now, the software has stage of developing. But we spend a few tests for determination of basic possibilities.

This software was tested on different types of histological and radiological images. We are used three types of histological images and two type of radiological image (Tab. 1). Histological images were divided by cells density: high density - more than 70% image area for cells, middle density - between 40% and 70% image area for cells, low density - less than 40% image area for cells. Tested radiological images are divided into CT and MRI images. We spend tests for image improving stage. After testing was constructed table with probability values of success image processing by generated scripts..

A rate of success probability was defined by empirically way. The software was testes by 248 medical images.

TABLE I.   TABLE OF SOFTWARE TESTING

Image type	probability of type definition	probability values of success image processing
Histological images with high density of cells	98%	83%
Histological images with middle density of cells	99%	90%
Histological images with low density of cells	87%	90%
CT images	100%	93%
MRI images	100%	95%

We take good marks for radiological images. For histological images marks are insufficient.

V. CONCLUSION

In this paper, we proposed a scheme of automatic generation of image processing function sets for analysis of histological tissue and described software for it. This software based on principles of open architecture and allows to change design and possibilities of it in real time on physician work place without compilation stage. In other side the speed of the program remains the same as in the compiled version. Developed software architecture simplifies the development of model programs for image analysis of histological images (Fig. 5) and radiological images (Fig. 6).

Marks that we take are unsatisfactory for histological images. It depends on a high complexity of images. We consider that it is necessary to change intelligent agent for script generator.

But in this paper we describe nice path for developing software for image processing. Basic possibilities of such software are possibilities of dynamical changing of interface and sequences of processing functions.

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