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AUTOMATION OF PRELIMINARY HISTOLOGICAL DIAGNOSTICS OF ONCOLOGICAL DISEASES

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The principal scheme for automation of preliminary histological diagnostics of oncological diseases is described in the paper. A brief review of systems which are close to this scheme and based on automated and semi-automated segmentation approaches and morphometrical analysis are presented here. Processing of images with different optical magnifications is a kind of the system since making a diagnostic decision is based on data obtained from processing of several images of one histological preparation.

Keywords: preliminary diagnostics, oncology, histology, image analysis, segmentation

INTRODUCTION

Computer application improves arithmetic precision for investigation in morphology which is the most reliable approach in the diagnostic process [1]. An approach is realized in the form of the biopsy, cytological and histological investigation where histological and cell structures of different tissues of the human body are the prime object of analysis. In particular, this method is vital in diagnosing of various human diseases.

Automated systems exclude mistake of human factor and decrease expended time for process of verification diagnosis but they are amassed only in big medical centers. At the same time clinicians are trying to identify complex forms of disease and reduce to mistaken diagnostics. Therefore there are a lot of cases, when incorrect untimely treatment results to disablement or death. Therefore the task of automation for morphology diagnostics is very important in medicine. The computer system for morphological diagnostics improves accuracy of diagnostics and compensates deficit of morphologist-specialists.

The main goal of the paper is to describe a principal scheme of system for preliminary histological diagnostics of oncological diseases based on image analysis algorithms and foundations of stepwise processing of images of one preparation under different magnification.

A brief overview of automated systems for microscopic analysis of hematological, cytological, and histological biomaterials is also presented here. This theoretical and practical experience is a starting point for the co-operation between Russian and Belarusian scientists in the framework of the INTAS Project N 04-77-7067 and for their own investigations in the field of medical image processing and automation of diagnostics.

1. OVERVIEW OF SYSTEMS OF BIOMEDICAL IMAGE ANALYISIS

Automation of histological image analysis is actively developed nowadays. A round group of automated systems for optical microscopy, which are process both histological and cytological types of images, has been born. The most popular analyzers are the foreign one like Argus 20, Histometrix, CIRES [2].

We use a software system “Black Square” (Versions 1.0. and 1.1), developed in Information Research and Development Ltd. (Moscow, Russian Federation) [3,4] for automating the analysis of

cytological specimen images. The software aims at segmentation of the lymphoid cell nucleus in the cytological specimen images, selection of geometrical, statistical, granulometrical, and spectral features of the nuclei, calculation of its values and feature storing in the database. The subsequent analysis of feature descriptions of the nuclei populations of the same patient makes it possible to make a preliminary diagnosis.

In NShell software, user interaction is organized as follows: 1) segmentation cells of interest in the images of cytological specimens manually or/and automatically; 2) selection groups of features to be calculated; 3) selection a database, where the data should be recorded; 4) execution feature calculation module of the software. The scenario can be applied to other tasks by: 1) certain objects of interest should be, first, segmented from the input images; 2) some features of segmented objects should be calculated and stored in the database.

Currently, the specialization of the "Black Square" for automation of histological specimen analysis is in progress.

There are several automated computer systems developed in Republic of Belarus. "Bioscan-IW", "Contour" and "Cytron" are the most interesting of them. The first one represents a set of functions and toolkit which can create a required script by internal language for solving a particular histological tasks [5].

"Conour" is intended for analysis of color biomedical images and for differential diagnostics of diseases of thyroid glands [6]. The system carries out a morphological analysis of nuclei, aggregates, lymphoid cells of thyroid glands and differential diagnostics of main forms of thyroid diseases. Extraction of objects of interest (nuclei, cells, aggregates) can be provided in manual, semi-automated and automated modes. The system contains a toolkit for editing of extracted objects and database for its storing.

A morphological application for diagnostic of diseases of human organs "Cytron" [7] is also developed and supported by Belarusian specialists and based on morphometrical investigations of tissue, cells and cells accumulation in human organs. An idea to of stepwise processing of images of one preparation under different magnification which is described below is used in the system.

2. THE PRINCIPAL SCHEME OF PRELIMINARY HISTOLOGICAL DIAGNOSTICS OF ONCOLOGICAL DISEASES

According to degree of optical magnification of histological specimen images some objects are better seen than others, which loose their avowed definition. Each optical value marks out definite group of topological characteristics of tissue and its constituents.

The stages of image processing using segmentation and object extraction should be differentiated in the same way. On the first stage an image of tissue is analyzed on small optical magnificence, which allows to yield a pattern of tissue. This pattern is composed from different fragments. Images of cells, fibers and vessels are to be processed on the next stage. Objects on these images form cells patterns where the ration of color characteristics of background and objects are play an important role. Background is formed mostly by interstice, very small cells and fibers or participles.

Taking into account all remarks, which are important in developing of system for histological diagnostics, the principal scheme should include the following blocks (fig.1): input, segmentation, analysis and results.

Block of input includes the procedure of images inputting, entering of name of organ and tissue. It has to provide a reading from files and camera.

Block of segmentation is intended for tissue and cell patterns definition. The first image (PLAN) is used for definition of tissue pattern. The main characteristic of this image is presence of small objects which are have to be extracted. Simple methods of thresholding segmentation (fig. 2) on the base of brightness histogram analysis can be used here. The result is a binary image of cells and artifacts.

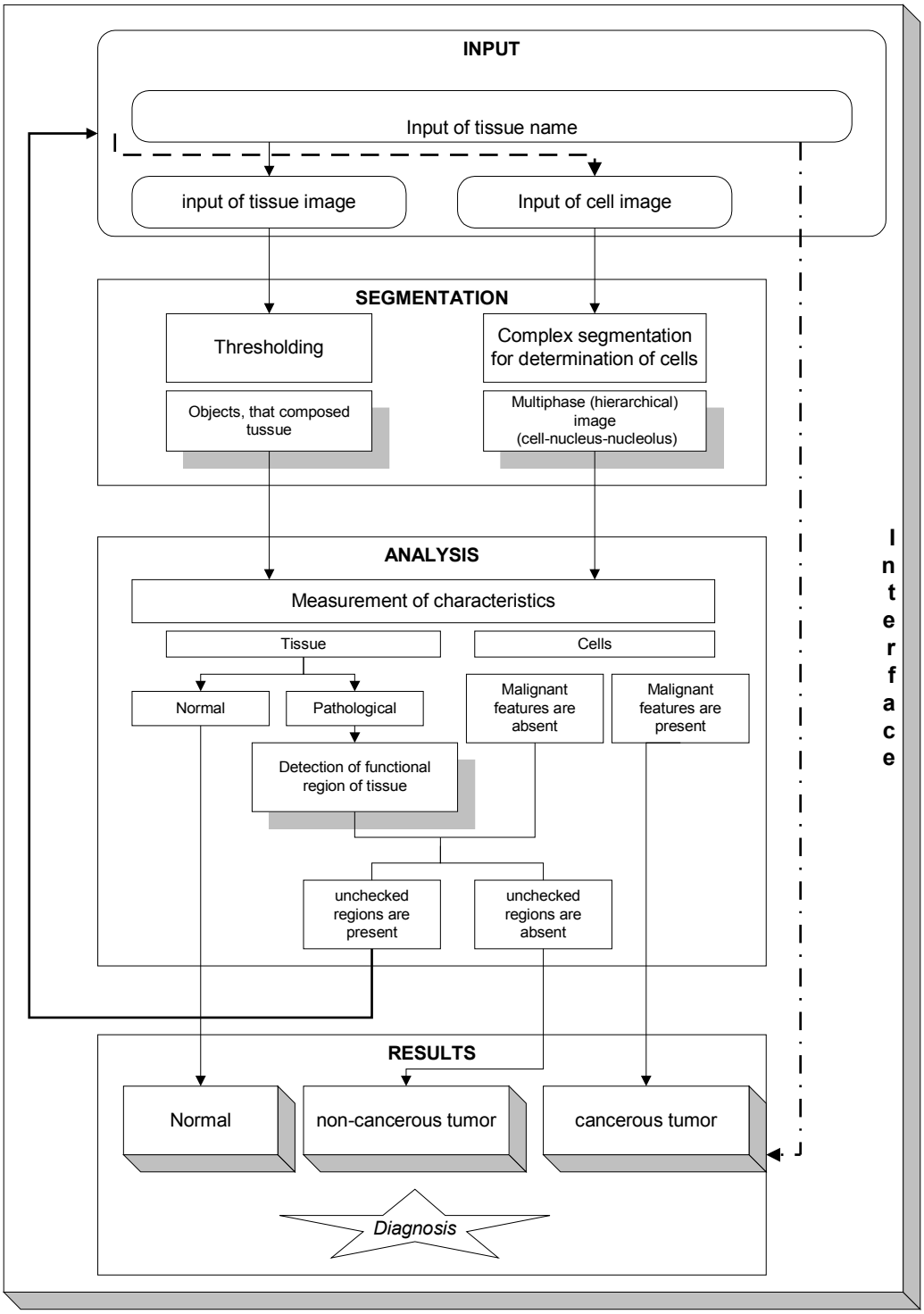


Fig. 1. Interaction of main blocks of the system

For cells pattern definition segmentation is performed according to the type of histological objects in images. Patterns obtained by segmentation can be corrected with the aid of mathematical morphology. Analysis of object topology allows to define objects which are correspond to cells and to delete others. The resulting binary image has to consist of whole objects, which are nearly similar to cell patterns. The hierarchy of internal objects (nucleus and nucleolus) should be preserved (fig.3).

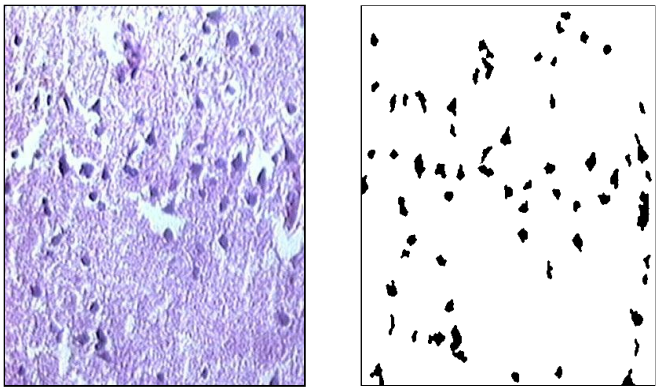


Fig.2. Image of tissue of cerebrum and the result of its segmentation

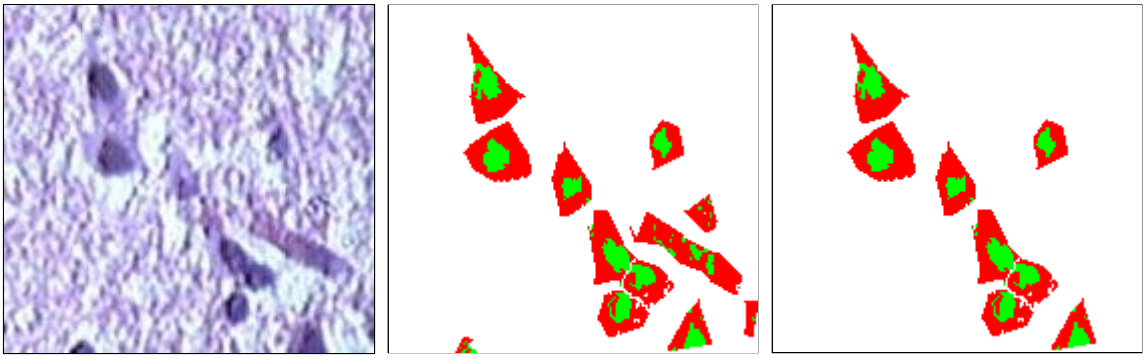
Block of analysis includes measurements and it analysis for decision-making. It consists of several stages with tissue and cells analysis.

Firstly the tissue analysis is performed and texture characteristics, mean intensity of objects, their orientation and square are calculated in the framework of analysis.

Objects of the same class are merged to form a region. Obtained regions are analyzed then. If one region is placed inside another, a decision about presence of oncological fragments is making and the recommendation about carrying out of cells analysis is giving.

More complex segmentation methods are used for cell structure extraction: edge detection, watershed, thresholding segmentation of color spaces, region growing and others.

Cell analysis is performed on the corresponded binary or hierarchical image (fig. 3). Geometrical characteristics, cells and nuclei brightness are calculated. In the presence of nucleolus the form of it is also defined.



a) b) c)

Fig.3. Image of cells with large magnification: a) initial image, b) result of binarization and morphological processing, c) images of cells after topological analysis

Conclusions are drawn by several features are: polymorphism (difference in size of cells), polychromism (difference in color), presence of mitosis (together with another features at asymmetric property in mitosis), anaplastics (strong difference between cells). In case of absence of these features, next region in the image of tissue is extracted and recommendation about cells analysis is given. In other case the decision of malignant tumor is made.

In ***the block of results*** a preliminary diagnosis is made, which is based on tumor and tissue data obtained.

CONCLUSION

The paper presented the results obtained within the investigations concerning design of automated systems for preliminary histological diagnostics of oncological diseases. It describes shortly a well known Russian and Belarusian systems which are based on image processing approaches and morphometrical study and close to a final goal: to create an information technology and supporting software for automated diagnostics based on analysis of images with different magnification of one histological preparation through modern techniques oriented to image mining.

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