Bimodal System for Interactive Indexing and Retrieval of Pathology Images

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Abstract

We demonstrate the prototype of an image understanding based system [2] to support decision making in clinical pathology. The system employs all four major low level vision queues (shape, texture, color, metric measures) in content-based retrieval of visual information. The reliability of the central module of the system, the fast color segmenter, makes possible on-line analysis of the query image. The user interface is bimodal (speech and mouse input), allowing a natural communication with the system.

1 Introduction

A database of 261 color 640 x 480 images is used containing cells which belong to 3 classes of lymphoproliferative disorders (98 Chronic Lymphocytic Leukemia - CLL, 38 Follicular Center Cell Lymphoma - FCC, 66 Mantle Cell Lymphoma - MCL) and a class of healthy leukocytes (59 NORMAL). The ground truth of the cell classification was obtained through immunophenotyping by flow cytometry. The screening among leukemias and malignant lymphomas was considered for the prototype since MCL, a recently described disorder, is often misdiagnosed.
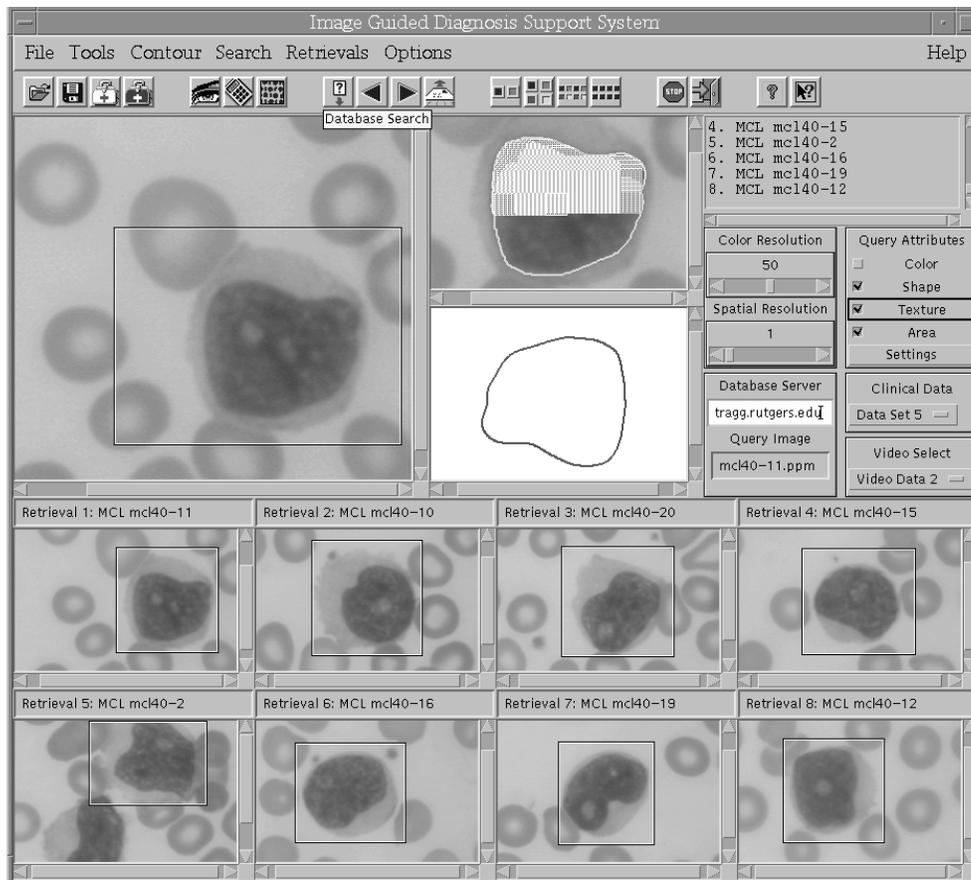

Figure 1. The user interface of the system.

2 Core System Description

A typical retrieval session is started by loading the query image and selecting a rectangular region which contains the cell of interest. The region is then automatically color segmented using an algorithm based on nonparametric cluster analysis [1]. The area of the selected nucleus is taken proportional to the number of pixels inside the nucleus region (the images in the database have all the same scale).

The nucleus shape is characterized through similarity invariant Fourier descriptors [3]. The number of harmonics which reliably represent the shape was obtained by analyzing the stability of the segmentation algorithm. The results showed that the segmentation is sufficiently stable for the use of the first 10 harmonics (40 Fourier coefficients) for the computation of the Euclidean distance between two nucleus shapes.

The texture analysis module employs the multiresolution simultaneous autoregressive model (MRSAR) [4]. A 15-dimensional feature vector of the nucleus texture is obtained in accordance to this model. The covariance matrix of the local feature vectors within each cell nucleus is also computed, and the distance between two nuclei in terms of their texture is given by the Mahalanobis distance of their MRSAR feature vectors.

By default, the system retrieves the closest eight matches by computing a *similarity metric* between the query image and each of the images in the database. The suggested classification of the query image is based on majority voting among the retrievals. Note that in addition to the four original classes this strategy may also produce a NO DECISION class.

At present, three query attributes are used: the area, shape and texture of the selected nucleus. The similarity metric is defined as a linear combination of the normalized distances corresponding to each attribute. The downhill simplex procedure [5, p. 408] was employed to obtain the weights of the linear combination. The objective function was chosen the sum of probabilities of correct decision.

System performance was assessed by implementing tenfold cross-validated classification. The cross-validated probabilities of correct decision were 0.8389, 0.9, 0.8333, and 0.73 for CLL, FCC, MCL, and NORMAL, respectively. These results are very promising if we take into account the difficult task of differentiating among lymphoproliferative disorders based solely on morphologic criteria.

3 Bimodal User Interface and Architecture

Figure 1 shows the user interface of the system during the texture analysis of the delineated nucleus. The query image *mcl40-11* is top-left, the delineated nucleus of the cell and the normalized shape of the nucleus are top-middle, and the eight retrieved images are at the bottom.

Natural communication with the search engine is provided. Queries can be formulated or refined by speech or mouse input. A fusion agent interprets the commands, calls the appropriate method, and gives voice feedback to the user. Currently the system employs a speech recognizer engine with finite-state grammar and a restricted task-specific vocabulary. The recognition is speaker-independent. Typical voice commands are:

- *Open image ##*, *Save image ##*,
- *Segment the image*,
- *Search the database*,
- *Show 2 (4, 8) retrievals*,
- *Show first (next, previous) retrievals*,
- *Show scaled retrievals*,
- *Show clinical data #*,
- *Set color (spatial) resolution #*.

Examples of voice feedback are:

- *Image ## opened*,
- *Segmentation completed*,
- *Analyzing texture*,
- *Database search completed*,
- *Suggested class: CLL(FCC, MCL, NORMAL)*.

Note that the user can modify the color and spatial resolution of the segmentation. Access to the resolution parameters is only for experiments and maintenance, in normal operations of the system they are set by default.

Clinical data related to the retrieved images can also be displayed. A video player is included showing videos which describe the current lymphoproliferative disorder.

The system was build following a client-server architecture. The client contains the user interface, segmentation module, the module for the computation of the Fourier coefficients, and the texture analyzer. The server receives the feature vectors, performs the search in the database, and sends the first eight retrievals back to the client. Client-server communication is multithreaded, Internet based, and employs Java sockets.

References

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