Nature inspired methods for automatic detection and classification in cytogenetic systems

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Challenge

The use of automatic methods for feature extraction and data classification can be highly beneficial for diagnosis procedures based on molecular techniques. The main objective is therefore to develop automatic classification tools for molecular cytogenetics systems. These tools consist of automated image processing algorithms that include "intelligent" features, which will result from integrating natured inspired optimization methods, and can be used for diagnosis. A software package aimed at being used in the laboratory will all allow the interface of these tools with the clinical staff.

A common diagnosis procedures used in cytogenetics is the Fluorescence In Situ Hybridization (FISH), see e.g. the review paper [1]. FISH is a specialized technique used to prepare samples that are used for molecular cytogenetic analysis. Fluorescent labeled probes are used to mark specific chromosomes and the use of different colors for the probes allows the simultaneous detection of different targets. The basic procedure uses three colors (red, green and blue) and consists of four main steps: sample preparation, pre-treatment, hybridization and detection. We will focus only in this latter step, i.e. the detection of hybridizations, which is a highly labor-intensive task that is normally carried out by the laboratory technicians.

Another diagnosis procedure used in cytogenetics is the karyotyping, see e.g. the reference [2]. The karyotyping is a common procedure for the analysis and classification of chromosomes from images of a metaphase cell and results in the karyotype generation. The basic steps for automated karyotyping consist of individual chromosome localization, segmentation and classification. The classification part implies the re-orientation, straightening and measurement of individual chromosomes.

Existing laboratory technologies still demand that the samples are human manipulated, in the two cases previously described. Also the detection and classification procedures can be manually performed by human visual inspection using a microscope, although these are extremely time consuming and demand for highly qualified clinical staff. It is well accepted that automated classification systems can help the diagnosis by reducing the processing time while releasing the staff to other high-level activities [3]. Several approaches have been proposed in the literature for the use of automatic detection and classification tools in molecular techniques, see e.g. [4,5,6,7].

Toward this end we propose to use nature inspired optimization algorithms together with image processing, which allow the automatic segmentation and classification of relevant information. The majority of the current detection applications, which are normally proprietary systems from the fluorescence microscope manufacturers, are rather stiff and very expansive. Therefore we propose to develop software that integrates "smart" features for pattern recognition, using e.g. snakes techniques, neural networks, fuzzy goals or genetic algorithms, and are capable of producing quantitative results.

The target group include laboratory staff that works with diagnosis techniques centered on analysis by visual inspection, but also the scientific community working in the field of nature-inspired optimization algorithms: these activities will contribute to new developments within nature-inspired optimization, which will be necessarily triggered by the specific needs of the application. A side benefit will be the improvement of data acquisition methods from molecular tests, which result from the introduction of intelligent algorithms to support diagnostic activities in the laboratory.

KEYWORDS: Automated cytogenetic systems, Image processing, Nature-inspired optimization methods

REFERENCES

[1] Liehr, T. and Claussen, U. (2002) ``Current developments in human molecular cytogenetic techniques'', Current Molecular Medicine 2(3):283-97.

[2] ``An International System for Human Cytogenetic Nomenclature'', (1985) ISCN 1985. Report of the Standing Committee on Human Cytogenetic Nomenclature.

[3] Wang, X.; Zheng, B.; Wood, M.; Li, S.; Chen, W. and Liu, H. (2005) ``Development and evaluation of automated systems for detection and classification of banded chromosomes: current status and future perspectives'' J. Phys. D: Appl. Phys. 38:2536-2542.

[4] Moradi, M. and Kamaledin Setarehdan, S. (2006) ``New features for automatic classification of human chromosomes:A feasibility study'', Pattern Recognition Letters 27:19-28.

[5] Wu, Q.; Liu, Z.; Chen, T.; Xiong, Z.; Castleman, K.R., (2005) ``Subspace-Based Prototyping and Classification of Chromosome Images'', IEEE Trans. on Image Processing, 14(9):1277-1287.

[6] Wu, Q. and Castleman, K. R. (2000) ``Automated Chromosome Classification Using Wavelet-Based Band Pattern Descriptors'', cbms, p. 189, 13th IEEE Symposium on Computer-Based Medical Systems.

[7] Jennings, A. M. and Graham J. (1993) ``A neural network approach to automatic chromosome classification'', Phys. Med. Biol. 38:959-970.