

A system designed for exploring the human cytome

P. Van Osta, B. Vanherck, K. Ver Donck, L. Bols and J. Geysen

MAIA SCIENTIFIC, Ciplastraat 3, B-2440 Geel, Belgium
A Harvard Bioscience Company

presenting author: pvosta@maia-scientific.com

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We are currently in a transition stage from genomics to proteomics, cytomics, organomics and model organisms. With the increasing availability of tools and instruments to study phenomena of increasing dimensionality and complexity at high speed and quality, quantifying and analyzing biological phenomena of a higher order of complexity will be possible at high speed. We hereby present the model of a scaleable system to manage a large scale exploration of the human cytome for an endeavor such as a Human Cytome Project [1].

Cytomics can be regarded as the study of cellular events which integrates genomics and proteomics with the dynamic evolution going on in cells and tissues. The biological phenomena in cells evolve in a multidimensional space which consists of 3 spatial (XYZ), a spectral (λ) and a temporal (t) dimension. Each of these 5 dimensions can be explored in a variety of combinations and at a varying inner and outer resolution.

The system, designed to explore this multidimensional space, consists of an instrument (MIAS™) on one side and a distributed software component on the other side (eaZYX™), see Figure 1. The interaction between an instrument and the kernel and its modules allows for the exploration of this 5 dimensional space at a certain inner and outer resolution or a subset of these 5 dimensions. Both the implemented software and the hardware allow for this exploration, but each software-hardware combination will also limit the extent of the exploration concerning the scale and the inner and outer resolution. The system uses several types of algorithms for the analysis of images, of which one set is based on the principles of human vision [2]

Examples and applications will be shown for which the framework is being used today in biomedical research, such as cell based assays, model organisms such as *C. elegans* and tissues. The system is used for both bright field as fluorescence imaging and combinations of both. In order to allow image acquisition of biological processes close to real life conditions, the system can use extremely weak fluorescent signals without the need for image integration or high intensity light sources. In addition to current applications, future developments of the system will be presented. Extensions of both the software and hardware will be discussed and their meaning for the use of the software-hardware combination for a project at a scale of the Human Cytome Project.

¹ Valet G, Tárnok A, Cytomics - New Technologies: Towards a Human Cytome Project, Cytometry (2004), in press.

² The principles of scale space applied to structure and colour in light microscopy. P. van Osta, J.M. Geusebroek, K. Ver Donck, L. Bols, J. Geysen, and B. M. ter Haar Romeny. Proceedings of the Royal Microscopical Society, Sept., 37(3), pp. 161-166, 2002.

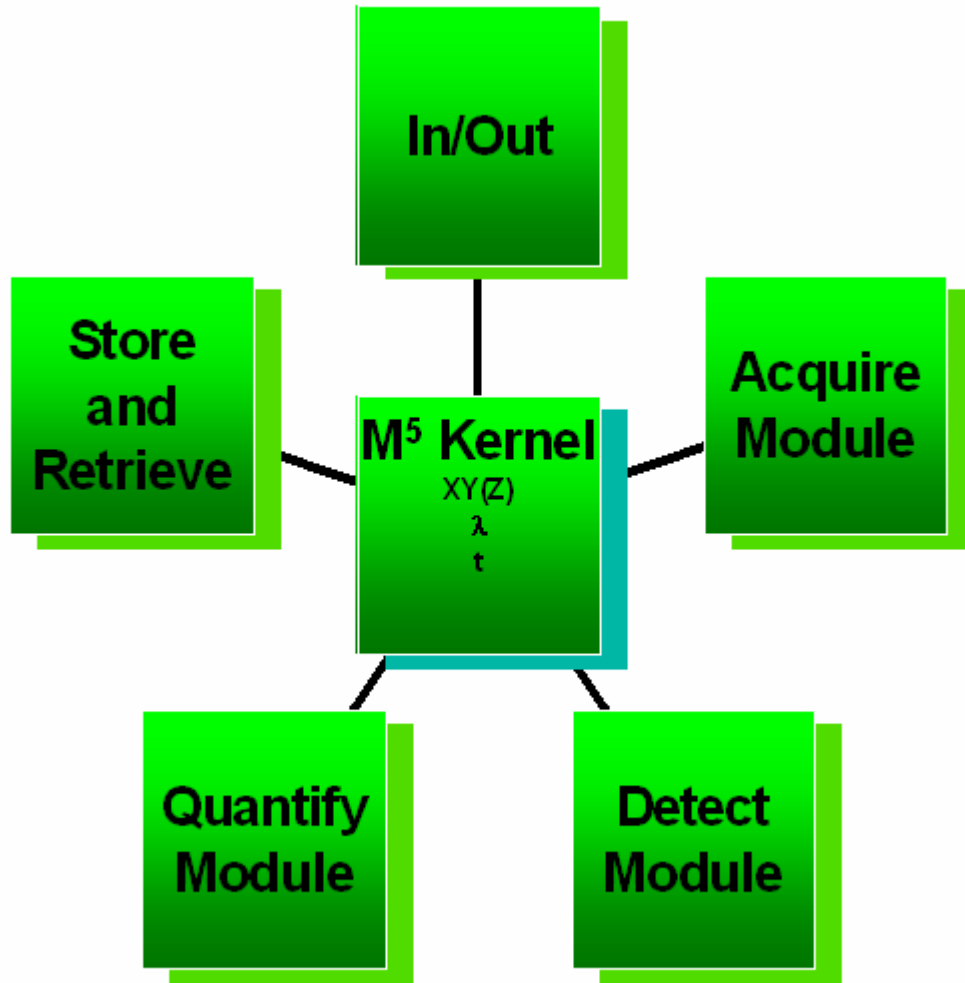


Figure 1. The central dimension management kernel and the 5 basic modules of the eaZYYX system.