

## **The M<sup>5</sup> framework for exploring the Human Cytome**

**Peter Van Osta, Bart Vanherck,  
Kris Ver Donck, Luc Bols and Johan Geysen  
MAIA SCIENTIFIC  
Cipalstraat, B-2440 Geel  
Belgium  
Email: [pvosta@maia-scientific.com](mailto:pvosta@maia-scientific.com)**

**KEY WORDS:** High throughput screening, cytome, spatial, spectral, temporal, 5D, brightfield, fluorescence.

Exploring the phenomena which take place at the cellular level requires an approach which enables the management of a large multidimensional data flow. We present a framework, designed to manage the acquisition of experimental data, object detection and quantification.

The M5 framework is designed to provide a management system to explore a multidimensional space, consisting of up to 3 spatial, one spectral and one temporal axis. Each of these axes can be sampled at a varying inner and outer resolution, according to the possibilities and limitations of the instruments attached to the acquisition module and the processing capabilities of the object recognition and quantification modules. In addition the core has a module which manages the exchange of data with other systems or a GUI and the internal data storage system.

The kernel of the system as such only knows about dimensions, not about a particular device attached to the system, here only the physical layout of the space to be explored matters. The acquisition module manages the interaction with hardware components used to acquire the data and translates machine specific information back and forth. All acquired data are stored for review and validation.

For object recognition, the stored data are presented to an object detection system which at the moment uses detection principles based on human vision principles to detect objects of interest. The detected objects are then presented to a quantification module which can associate quantitative measurements to each object and its interrelation to the physical group (cell) it belongs to.

In order to be able to scale up the processing power of the system it is implemented on Unix and in ANSI C and C++. Communication with the other systems is done with open standards in order to assure multi-platform operation when required.

Examples will be given of the application of this framework to cell-based research and also about its application to tissue research.

The system design and implementation we present here is meant to manage the physical exploration and subsequent data flow of a large scale cytome exploration, such as the Human Cytome Project