**HemaCAM, a novel self-learning automated digitalization module, part of the HaemCell solution.**

Sylvie Thoinet¹, Céline Darnaud¹, Franck Seguy¹, Thorsten Zerfass², Yves Boucaud-Maitre¹

¹Saint Joseph Saint Luc Hospital, Lyon, France
²HORIBA Medical, Montpellier, France, ³Fraunhofer Institute for Integrated Circuits (IIS), Erlangen, Germany

**OBJECTIVES**

Tracability of patient records is nowadays a priority in order to ensure quality in laboratories. The presence of numerical data, graphic, and cytological results within the same screen, optimises and verifies the diagnosis in haematology.

This informed approach is at the core of the “Hemacell” modular solution from HORIBA Medical. This combines a platform for the haematological analysis (ABX Pentra DX120), data management (ABX Pentra ML) and a system to acquire and automatically recognize cell images (HemaCAM, by Fraunhofer IEK). We tested the HemaCAM, to evaluate its performance in normal cell identification. Furthermore, we assayed its capability to correctly discriminate between normal and abnormal cells.

**Adaptive database capable of evolutive learning**

Images validated by laboratory experts were entered into the HemaCAM database. This allowed us to define reference cells (~13000) into the cell identification mathematical model. We standardized parameters of the slide preparation (staining, counting area), and the optimal number of cells to be counted according to the reference analyser results. We created a database of seven subpopulations (enriched sub-populations) of the 18 available in the HemaCAM: polymorphonuclear neutrophils, eosinophils, and basophils, lymphocytes, monocytes, and additionally nuclear shadowed, and large platelets.

**Evaluation**

Following the establishment of the enriched sub-populations reference database, samples were selected for the evaluation (300 normal and 100 abnormal), based on the results of the reference analyser in the laboratory. They were then tested on the ABX Pentra DX120 and HemaCAM. The abnormal ones (with flags or alarms) were additionally analysed with a microscope (200 cells were counted for each smear).

**Enriched sub-populations**

We calculated the sensitivity (class recall) and the specificity (class precision) of the HemaCAM in recognizing and correctly classifying cells into the seven enriched WBC subpopulations.

**Table N°1** shows the Class Recall: TP / (TP + FN) -> True Positive Rate (TPR), corresponding to the Sensitivity; the Class Precision: TP / (TP + FP) -> True Positives Rate (TPP) corresponding to the Specificity (TP: True positive, FN: False negative, FP: False positive).

**Table 1. Class recall (sensitivity) and class precision (specificity) obtained for the seven enriched sub-populations.**

**CONCLUSIONS**

In this study, the HemaCAM system highlighted new functionalities compared to those of existing systems for automated cell image acquisition and identification and showed a satisfying performance to classify the 7 sub-populations tested. The quality of the optical components, combined with a good depth of field, creates a remarkable final image resolution. The creation of a new database is now in progress to add more sub-populations (WBC, RBC & PLT Image). Further studies will be necessary to evaluate the evolutive learning capacity of the system.

The software and the environment are very intuitive and user-friendly. This ease of use, the rapidity of the learning process, and the ability to create specific cases make HemaCAM a promising tool adapted to staff training. A complete integration of the automatic cell recognition (HemaCAM) and the data management (ABX Pentra ML) module offers a great platform for exploiting the global haematological data of patients.

HaemCell Solution is a perfect answer to the requirements of security and traceability of the laboratory workflow.