ISCO Amsterdam, 2008;30(2):121.

Development of Densitometric and Texture Algorithms within the Aperio Algorithm Framework (AAF) for Virtual Slide Analysis. Cellular Oncology

David McCleary[1], Dr. Jim Diamond[1], Prof. Danny Crookes[2], Dr Heike Grabsch[3] and Prof. P W Hamilton[1].

1. Bioimaging and Informatics Research Group. Centre for Cancer Research and Cell Biology, Queen's University Belfast
2. School of Electronics, Electrical Engineering and Computer Science. Queen's University Belfast
3. Section of Pathology and Tumour Biology. Leeds Institute of Molecular Medicine, University of Leeds

Digitisation of an entire glass slide at high power produces a high resolution, diagnostic quality, digital image known as a virtual slide. Virtual microscopy is an exciting, emerging technology that is revolutionising pathology, opening up new opportunities for e-learning, image analysis and machine vision. Despite the rapid advantages in scanning technology, progression in the area of algorithm development for virtual microscopy has been relatively slow, mainly due to image size and the propriety image formats used by many of the scanning manufactures.

This study set out to produce a suite of low-level quantitative features (including densitometric, morphological and Markovian texture features) which can be combined to produce high-level algorithms to run on Virtual slide images. The features were implemented inside the AAF which is a Software Development Kit (SDK) that allows users to run C-code from within Aperio ImageScope (a standalone application for viewing and annotating virtual slides). The code can be run directly on the entire image or by defining a region of interest.

The algorithms produced consistent results on a variety of virtual slides and their pathological relevance was demonstrated in three main applications: (1) the assessment of tumour differentiation in tissue microarrays (TMAs) using texture computation, (2) the densitometric evaluation and scoring of TMA immunohistochemistry and (3) the analysis of disorganised nuclear chromatin signatures in cancer using texture analysis.

Virtual microscopy and whole slide image analysis has enormous potential but the application of complex algorithms applied to entire slides is computationally intensive. This will require novel high performance computing (HPC) approaches to deliver accuracy and speed in the quantitative evaluation of tissue histology and this group have been working in tandem to deliver an HPC framework for virtual slide imaging. High performance computing together with advanced algorithm development on virtual slides could potentially revolutionise the tools available to diagnostic pathologists, support emerging fields such as automated tissue microarray analysis and establish digital pathology as a relevant discipline over the next few years.