Special issue on microscopy image analysis for biomedical applications

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Demand for tools that extract quantitative information from microscopy images of biological samples continues to grow. This is providing interesting challenges for computer vision researchers. Typical tasks are detection, segmentation, classification, motion analysis, and tracking of cells and subcellular compartments. Image data are acquired using various imaging technologies, each with its own characteristics. In the six papers presented in this special issue these include brightfield [1], phase contrast [7], electron [5], and fluorescence [2,3,6] microscopy. There is also considerable variation in the biological samples to be analysed. Here these include plant roots, cervical cancer cells and neuronal dendrites, for example.

These papers were selected and revised from submissions received in response to an open call for papers. Three of them [1,5,6] were developed from presentations at the symposium on microscopy image analysis for biomedical applications that we chaired in April 2010. The meeting was organised by the British Machine Vision Association (BMVA) and held at the British Computer Society in London. A further paper based on a talk given at that meeting, on nuclei detection using support vector machines, has also been published recently in this journal [4].

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Automatic analysis of adherent mammalian cells in bright-field images is a challenging task, not least because of their low contrast. It is a problem that has arguably received relatively little attention in the literature. Ali et al. [1] present methods for detection and segmentation of adherent cells in brightfield images using phase and texture features. As a side benefit, their framework allows registration of cells in bright-field and fluorescence images. They evaluate their methods by comparison to manual and fluorescence-based segmentation. Their software *sephaCe* is open-source and has been made freely available.

Esteves et al. [3] also address detection and segmentation but in a rather different setting: analysis of cell nuclei in confocal fluorescence images of *Arabidopsis thaliana* root tips. They demonstrate that an improved gradient convergence filter method allows shape priors to be imposed on this largely bottom-up process. This improves nucleus detection in scenarios where cells appear overlapping or in close proximity.

Sethuraman et al. [6] also analyse confocal fluorescence images of *A. thaliana* but are concerned with tracking cell membranes rather than segmenting nuclei. These membranes appear in a given two-dimensional slice as a network structure. Their contribution is to propose a Markov chain Monte Carlo sampling scheme for tracking this structure using network snakes.

Theriault et al. [7] segment, classify and track mouse fibroblast cells imaged using phase-contrast microscopy. They employ a battery of standard shape and appearance-based features to characterise their morphological state. They use AdaBoost to classify each cell instance into one of eight classes based on spread, polarization and orientedness attributes. They also show that the performance of their simple tracking algorithm increases as they use the classification algorithm to filter out substrate clutter. Expert-labeled datasets for time-lapse phase-contrast microscopy images of cells are scarce,

and so it is a welcome development that the authors have promised to make their data available to the wider image analysis research community interested in developing and validating algorithms for detection, classification and tracking of live cells. Such algorithms will be important for studying the biological properties of cells in migration under different conditions.

Delpiano et al. [2] adopt a different approach to motion analysis. Rather than tracking cells, they employ optical flow techniques to analyse the movement of fluorescent point sources. They perform evaluation using both synthetic data and images of hippocampal neuronal dendrites.

Finally, Hermann et al. [5] describe a fully automated system for high-throughput screening of two-dimensional crystallization experiments using transmission electron microscopy. Their software automatically explores and analyses samples deposited on carbon-coated grids at several magnifications. Image analysis is used to identify interesting regions that are then acquired and analysed at higher magnifications.

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Author Biographies

Stephen J. McKenna is Chair of Computer Vision in the School of Computing, University of Dundee. After graduating in computer science from the University of Edinburgh (1990) and obtaining Ph.D from the University of Dundee (1994), he held postdoctoral research positions at Queen Mary, University of London and Tecnopolis Csata, Italy. He has also been a visiting researcher at BT Labs and George Mason University. His research interests include the

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Dr Derek Magee is a lecturer in the School of Computing at the University of Leeds, UK, where previously he held a 5-year University Research Fellowship. He completed his Ph.D on visual livestock gait analysis at Leeds under Roger Boyle in 2000, winning the Industry prize at the British Machine Vision Conference for this work that year. His subsequent research has mainly been in the field of medical image analysis and medical simulation, although he maintains interests

in machine learning (winning the 2004 BCS Machine Intelligence prize) and sports analysis (developing commercial software that has been used for the analysis of English Premiership football).

Nasir M. Rajpoot graduated with a Ph.D in digital image coding from the University of Warwick in 2001. During 1998–2000, he was a visiting post-graduate research fellow at the Applied Mathematics programme of Yale University. Prior to that, he completed his M.Sc in systems engineering and M.Sc in computer science from Quaid-e-Azam University and Bahauddin Zakariya University in Pakistan in 1996 and 1994, respectively.

Dr Rajpoot currently holds the

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