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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. That meeting was organised by the British Machine Vision Association 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 brightfield 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 brightfield 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 *Arabidopsis 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 in order to characterise their morphological state. They use AdaBoost to classify each cell instance into one of eight classes based spread, polariza-

tion, 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 track 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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