Minisymposium *Multivariate and/or Multidimensional Image Processing in Biomedical Applications*

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Nowadays many different modalities are available in medical imaging, including computed tomography (CT) scans, functional or dynamic contrast-enhanced magnetic resonance imaging (fMRI) or (DCE-MRI), positron emission tomography (PET). The 2D/3D + time images produced by these advanced devices are useful for cancer diagnosis, radiotherapy or surgery planning, active study of human brain, tumour angiogenesis quantification, etc. In addition, the most recent microscope systems in biomedical laboratories are based on multi/hyper-spectral imaging for brightfield or fluorescence microscopy.

High throughput exploitation of these multivariate and/or multidimensional images requires advanced image processing methods and algorithms. To take into account jointly the spatial and the temporal/spectral information as well as the way to combine or to reduce the different temporal/spectral dimensions need adapted mathematical models. Moreover, extension of standard image processing approaches to 4D images leads to inefficient algorithms in terms of computational requirements (memory overload, time of computation, etc.).

In this framework, the aim of this minisymposium was to draw an overview of some recent developments in the field by French and German teams. We focus in particular on techniques which lie in mathematical morphology, multivariate data analysis, statistical classification, graph-based representations and algorithms, stochastic modelling, optic fow estimation, etc.

G. Noyel, J. Angulo, and D. Jeulin, from Mines ParisTech (France), consider automatic segmentation of DCE-MRI series in angiogenesis imaging. The approach is based on stochastic watershed segmentation for hyperspectral images and more specifically, the paper focuses on new methods to generate random germs regionalized by a previous classification in order to use probabilistic watershed on hyperspectral images. These germs are much more efficient than the standard uniform random germs. The algorithms are illustrated

A.D. Fitt et al. (eds.), *Progress in Industrial Mathematics at ECMI 2008*,
Mathematics in Industry 15, DOI 10.1007/978-3-642-12110-4_28,

to compare the obtained segmentation which is then needed for detecting the eventual tumours.

J. Angulo, from Mines ParisTech (France), discusses individual nucleus modelling and segmentation, from fluorescence labelled images, of cell populations growing in complex clusters. The proposed approach is based on models and operators from mathematical morphology. Cells are individually marked by the ultimate opening and then are segmented by the watershed transformation. A cell counting algorithm based on classical results of Boolean model theory is heuristically used to detect errors in segmented clustered nuclei.

J. Stawiaski, E. Decencière, and F. Bidault, from Mines ParisTech (France) and Institut Gustave Roussy (France), present a segmentation method of 3D time-series images for radiotherapy planning. The aim of this study is to propose some techniques for the segmentation of tumors surrounding or contained in the lungs. The 4D images are produced using a respiration gating procedure and computed tomography. It uses a 4D watershed algorithm, combined with graph-based techniques to delineate the tumors in the time-series.

K. Rohr, W.J. Godinez, N. Harder, S. Yang, I.-H. Kim, S. Wörz, and R. Eils, from University of Heidelberg (Germany) and German Cancer Research Center (DKFZ), summarise in their paper tracking and registration approaches developed for automatic analysis of multidimensional biomedical images. The tracking approach allows computing the trajectories of cells in fluorescence microscopy image sequences. The registration approach enables to geometrically align cell microscopy images by using elastic transformations.