

Automated analysis of the mitotic phases of human cells in 3D fluorescence microscopy image sequences

Natalie Harder¹, Felipe Mora-Bermudez², William J. Gondinez¹, Jan Ellenberg², Roland Eils¹, and Karl Rohr¹

¹ German Cancer Research Center (DKFZ), Dept. Theoretical Bioinformatics, and University of Heidelberg, IPMB, Dept. Bioinformatics and Functional Genomics, Im Neuenheimer Feld 364, D-69210 Heidelberg, Germany

²European Molecular Biology Laboratory (EMBL), Gene Expression and Cell Biology/Biophysics Programmes, Meyerhofstrasse 1, D-69117 Heidelberg, Germany

Abstract—The evaluation of fluorescence microscopy images acquired in high-throughput cell phenotype screens constitutes a substantial bottleneck and motivates the development of automated analysis methods. Here we introduce a computational scheme to process 3D multi-cell time-lapse images as they are produced in large-scale RNAi experiments. We describe an approach to automatically segment, track, and classify cell nuclei into different mitotic phases. This enables automated analysis of the duration of single phases of the cell life cycle and thus the identification of cell cultures that show an abnormal mitotic behavior. Our scheme provides a high accuracy, suggesting a promising future for automating the evaluation of high-throughput experiments.

NOTE

Please refer to the proceedings of the main conference. Since this paper was accepted for publication at MICCAI 2006 it was not included in the workshop proceedings.