

COMPUTER VISION FOR 3D STACK CELLULAR MICROSCOPY IMAGES WITH MARKOV RANDOM FIELDS

Sean Robinson^{1,2,3,4,5}, **Jaakko Nevalainen**¹, **Ville Härmä**²,
Johannes Virtanen², **Matthias Nees**², **Laurent**
Guyon^{3,4,5}, **Itebeddine Ghorbel**^{3,4,5}, **Xavier Gidrol**^{3,4,5}

¹ University of Turku, Finland

² VTT Technical Research Centre of Finland

³ Université Grenoble-Alpes, France

⁴ CEA, iRTSV, Biologie à Grande Echelle

⁵ INSERM, France

The analysis of 3D *in vitro* cell culture is particularly relevant to the study of epithelium carcinogenesis such as prostate cancer. The study of multicellular structures in 3D as well as in time is increasingly important both for developmental biology and phenotypic screening. High-throughput cellular microscopy requires both automatic computer vision and statistical analysis techniques. Segmentation and the identification of portions of the image that are of interest is the first step in computer vision. We present initial segmentation results for 3D stack cellular microscopy images using a Markov random field. We show that a large amount of useful information is lost when considering the max projection image compared to the 3D stack.

Keywords: Computer vision, Markov random fields, 3D stack images.