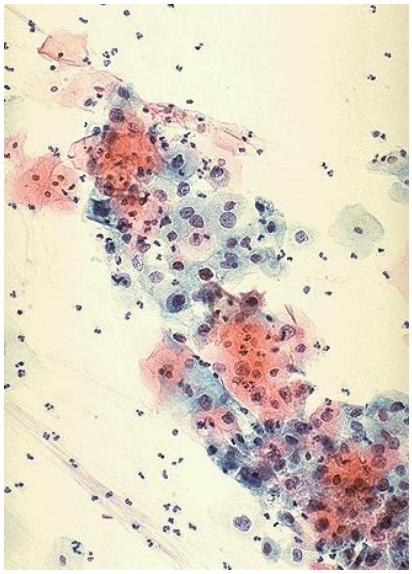
Research project proposal – Mathematical models for 3D analysis of chromatin texture in cell nuclei to improve cervical cancer diagnostics



Motivation

Cervical cancer is killing a quarter of a million women every year. Screening based on ocular inspection of so called PAP-smears by a trained cytotechnologist has proven to be very effective for reducing mortality due to cancer. Efficient systems for automated analysis of PAP-smears could reduce cost and further increase access to reliable cancer diagnostics. Unfortunately, existing analysis systems are neither cost effective nor reliable in low resource settings.

Project description

The aim of this project is to develop image analysis methods for extraction and analysis of the 3D-distribution of nuclear chromatin from stacks of 2D images of PAP-stained cells from cervical cancer screening samples acquired at different focus levels. The overall goal is to improve reliability of early detection of malignancy associated changes. The work includes evaluation and application of state-of-the-art deconvolution methods, and development of new methods for extraction of as much 3D information as possible from the available focus stacks. In addition, the work will involve development of novel 3D texture analysis tools, facilitating accurate and reliable differentiation of malignant and non-malignant cells. Mathematical models will be developed utilizing, among others, methods of discrete mathematics, numerical optimization, Fourier analysis, statistics . Computer implementations and testing of the derived methods are expected as well.

References

- Malm, Patrik. "Image Analysis in Support of Computer-Assisted Cervical Cancer Screening." Doctoral thesis, Acta Universitatis Upsaliensis, (2013).
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- Lindblad, Joakim, et al. "Optimizing optics and imaging for pattern recognition based screening tasks." Int. Conf. on Pattern Recognition (ICPR), IEEE, Stockholm, Sweden, Aug. 2014. To appear.

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