MEDVIZ FROM VISION TO DECISION

SEMINAR FRIDAY 24.01.2014

PLACE: "Laboratoriebygget" Meetingroom 9.1, 9th floor
**TIME : ** 12:00-13:00

SPEAKERS/TITLES

Professor **Arvid Lundervold**, Department of Biomedicine, UiB / Department of Radiology, HUH:
"My sabbatical year 2013 - image analysis in time and space"

Postdoctor **Erlend Hodneland**, Department of Biomedicine, UiB:
"CellSegm - a MATLAB (open source) toolbox for high-throughput 3D cell segmentation"

PhD candidate **Erik Hanson**, Department of Mathematics / Department of Biomedicine, UiB:
"A PCA-based thresholding strategy for group studies of brain connectivity with application to resting state fMRI"

ABSTRACT

Lundervold:

I will give a rather personal report and reflection from my sabbatical year 2013, where image data analysis in time and space has been the common theme. The title of the talk refers both to the geographical locations and time periods in which my sabbatical work took place, and also the spatio-temporal image analysis research topics themselves. The aim is to convey the common ground and generic nature of this kind of research - across different biomedical applications and research environments. In brief:

* Bergen (Neuroinformatics and Image Analysis Laboratory) January - June 2013: Longitudinal data analysis of brain white matter integrity in cognitive aging.

* Dubrovnik (2013 IEEE SPS Summer School on Biomedical Image Processing and Analysis, Centre for Advanced Academic Studies), June 2013: Texture analysis in medical imaging; Brain and neuron connectivity.

* Rochester, Minnesota (The Mayo Clinic, Radiological Informatics Laboratory), October 2013: Dynamic contrast enhanced (DCE) and multi-parametric MRI of the moving kidney and from endometrial carcinoma [data from Bergen / MedViz research cluster]

* Berkeley, California (UC Berkeley, Helen Wills Neuroscience Institute), July - December 2013: Structural and functional brain connectivity from multimodal MRI; Graph representations and Network analysis.

The talk will conclude with current research perspectives for our lab, and can also be regarded as an invitation to further discussions on biomedical imaging and data analysis challenges of mutual interest. More details about our research can be found at: www.neuroinformatics-imageanalysis.org

Hodneland:

CellSegm, developed at Department of Biomedicine/MIC, is a MATLAB based command line software toolbox providing an automated whole cell segmentation of images showing surface stained cells, acquired by fluorescence microscopy. It has options for both fully automated and semi-automated cell segmentation, and has the ability to detect various types of surface stained cells in 3D.
Major algorithmic steps are: (i) smoothing; (ii) Hessian-based ridge enhancement; (iii) marker-controlled watershed segmentation; (iv) feature-based classfication of cell candidates. After detection and outlining of individual cells, the cell candidates can be subject to further analysis, specified and programmed by the end-user, or they can be analyzed by other software tools. Segmentation of tissue samples having appropriate characteristics can also be performed in CellSegm. The command-line interface of CellSegm facilitates scripting of the separate tools, all implemented in MATLAB, offering a high degree of flexibility and tailored workflows for the end-user. The modularity and scripting capabilities of CellSegm enable automated workflows and quantitative analysis of microscopic data, suited for high-throughput image based screening.

For further details and code examples, see: Hodneland E, Kögel T, Frei DM, Gerdes HH, Lundervold A. Source Code Biol. Med. 2013 Aug 9;8(1):16.
(Paper: http://www.scfbm.org/content/8/1/16 Code: https://github.com/ehodneland/cellsegm/)

Hanson:

Functional brain connectivity can be measured from BOLD fMRI recordings using graph representations incorporating inter-regional similarity of time courses.
The resulting binary graphs are commonly constructed using thresholding of correlation values between pairwise time series anchored at their corresponding brain locations, representing the nodes in the graph. In this work we propose a new data driven approach to the challenge of selecting correlation threshold levels in group studies. Our approach addresses a collection of subject-specific graphs, thresholded at different levels. It combines information such that variability is preserved, and detection of sub-groups in the sample, having specific properties, is facilitated. The method is illustrated on simple synthetic graphs, and also tested on data from a resting state fMRI study of healthy elderly people with varying genetic risk of Alzheimer's disease.