

OAGM08

Program at-a-glance

26. May 2008

09:30 - 10:30 Registration
10:15 - 10:30 Greeting
10:30 - 11:30 Invited Speaker I
11:30 - 11:45 Coffee Break
11:45 - 13:00 Oral Paper Session 1 (3 talks)
13:00 - 14:15 Lunch
14:15 - 15:15 Invited Speaker II
15:15 - 15:30 Coffee Break
15:30 - 16:20 Oral Paper Session 2 (2talks)
16:20 - 16:25 Poster introduction
16:25 - 16:40 Coffee Break
16:40 - 17:30 Poster Session
17:45 - 18:45 ÖAGM meeting
19:00 Dinner

27. May 2008

09:00 - 10:00 Invited Speaker III
10:00 - 10:15 Coffee Break
10:15 - 11:30 Oral Paper Session 3 (3 talks)
11:30 - 11:45 Coffee Break
11:45 - 12:35 Oral Paper Session 4 (2 talks)
12:35 - 14:00 Lunch
14:00 - 14:30 Invited Speaker IV
14:30 - 14:55 Oral Paper Session 5 (1 talk)
14:55 - 15:10 Best Paper Award

26. May 2008

09:30 - 10:30	Registration	
10:15 - 10:30	Greeting	
10:30 - 11:30	Invited Speaker I Prof. Lucas van Vliet <i>Quantitative microscopy: The role of image processing to study cells, sub-cellular constituents and individual molecules</i>	(50 min talk + 10 min discussion)
11:30 - 11:45	Coffee Break	
11:45 - 13:00	Oral Paper Session 1 Recognition	(3 x 20 min talk + 5 min discussion)
	11:45 - 12:10 Katrin Amlacher, Lucas Paletta, Patrick Luley, Gerald Fritz and Alexander Almer <i>Geo-Indexed Object Recognition in Urban Scenarios</i>	
	12:10 - 12:35 Stefanie Peters <i>Automated Design of a Hybrid Texture Analysis System for Defect Detection</i>	
	12:35 - 13:00 Markus Storer, Martin Urschler, Horst Bischof and Josef A. Birchbauer <i>Face Image Normalization and Expression/Pose Validation for the Analysis of Machine Readable Travel Documents</i>	
13:00 - 14:15	Lunch	
14:15 - 15:15	Invited Speaker II Prof. Fred Hamprecht - <i>Exploiting Spatial Context in the Classification of Magnetic Resonance Spectroscopic Images</i>	(50 min talk + 10 min discussion)
15:15- 15:30	Coffee Break	

15:30 - 16:20	Oral Paper Session 2: Chair: Horst Bischof Medical imaging I	(2 x 20 min talk + 5 min discussion)
	15:30 - 15:55 Alfredo Lopez, Karl Fritscher, Thomas Trieb, Rainer Schubert and Julian Mattes <i>Cardiac 4D Image Sequence Registration Using Bridging Points</i>	
	15:55 - 16:20 Roland Swoboda and Josef Scharinger <i>A 3-D Statistical Shape Model of the Left Ventricle - Geometric Prior Information for Recovering Shape from Projective Bi-Planar X-Ray Images</i>	
16:20 - 16:25	Poster Introduction	1 Page per Poster by the Session Chair
16:25 - 16:40	Coffee Break	
16:40 - 17:30	Poster Session	
	Markus Diem and Robert Sablatnig <i>Border Detection of Visual Tags</i>	
	Christian Eitzinger, Manfred Gmainer and Wolfgang Heidl <i>A Framework for Adaptive Image Classification in Surface Inspection Tasks</i>	
	Adrian Ion and Walter Kropatsch <i>Mapping a Coordinate System to a Non-rigid Shape</i>	
	Stefan Lang, Enkelejda Tafaj and Peter Bastian <i>Reconstruction of Neuronal Structures from EM-Data by 3D-Segmentation Operators</i>	
	Bernhard Moser and Thomas Hoch <i>Misalignment Measure Based on Hermann Weyl's Discrepancy</i>	
	Peter Roth, Helmut Grabner, Christian Leistner, Martin Winter and Horst Bischof <i>Interactive Learning a Person Detector: Fewer Clicks - Less Frustration</i>	
	Stefan Thumfart, Richard HAH Jacobs, Frans W. Cornelissen and Christian Eitzinger <i>A Feature based Approach towards Predicting the Perceived and Aesthetic Properties of Visual Textures</i>	
	Roshan Dharshana Yapa and Koichi Harada <i>Breast Skin-Line Estimation in Mammograms Using an Enhanced Fast-Marching and Mathematical Morphological Technique</i>	
17:45 - 18:45	OAGM general meeting	
19:00	Dinner	(Mostbauer z'Linz)

27. May 2008

09:00 - 10:00	Invited Speaker III Prof. Wiro Niessen – <i>Advanced Image Analysis for developing Quantitative Imaging Biomarkers</i>	(50 min talk + 10 min discussion)
10:00 - 10:15	Coffee Break	
10:15 - 11:30	Oral Paper Session 3; Chair: Walter Kropatsch Medical imaging 2	(3 x 20 min talk + 5 min discussion)
	10:15-10:40 Julian Mattes <i>Comparing Shape and Motion of Biological and Medical Objects - Methodological Aspects and Applications</i>	
	10:40-11:05 Peter Widhalm, Georg Langs, Rene Donner, Negar Fakhrai, Philipp Peloschek and Robert Sablatnig <i>Estimation of Fit Confidence in Active Shape Model Search for the Reliable Measurement of Knee Alignment</i>	
	11:05-11:30 Gerald A. Zwettler, Roland Swoboda, Franz Pfeifer and Werner Backfrieder <i>Fast Skeletonization for Medial Axis Extraction on Tubular Large 3D Data</i>	
11:30 - 11:44	Coffee Break	
11:45 - 12:35	Oral Paper Session 4; Chair: Csaba Beleznai Tracking - reconstruction	(2 x 20 min talk + 5 min discussion)
	11:45 - 12:10 Nicole M. Artner, Salvador Buenaventura Lopez Marmol, Csaba Beleznai and Walter Kropatsch <i>Kernel-based Tracking Using Spatial Structure</i>	
	12:10 - 12:35 Markus Heber, Matthias R��ther, Horst Bischof and Stephan Pack <i>Photogrammetric 3D Reconstruction of Lightning Discharges</i>	
12:35 - 14:00	Lunch	

14:00 - 14:30	Invited speaker IV Prof. Schuetz - <i>Single Molecule Fluorescence Microscopy - Applications to Biology</i>	(25 min talk + 5 min discussion)
14:30 - 14:55	Oral Paper Session 5 Reconstruction	(20 min talk + 5 min discussion)
	14:30 - 14:55 Florian Kleber and Robert Sablatnig <i>High Resolution Imaging for Cultural Heritage Applications</i>	
14:55 - 15:10	Best Paper Award	and closing

Quantitative microscopy: The role of image processing to study cells, sub-cellular constituents and individual molecules
Lucas van Vliet

Microscopy offers a way to visualize cells, sub-cellular constituents and even molecular interactions. Different modalities span the range from individual molecules to cells in tissue. Some of them yield a single snapshot of a "frozen" scene whereas others permit time-lapse imaging to study dynamic problems. Although physics limit both the resolution and the signal-to-noise ratio of the observed images, advances in image processing has demonstrated it usefulness to extract relevant information. We will demonstrate the central role of image processing in a variety of tasks such as: nonlinear image restoration, quantification of object properties in digitized images, computational super-resolution to image single molecules, and quantification of the stiffness of macro molecules such as DNA.

Exploiting Spatial Context in the Classification of Magnetic Resonance Spectroscopic Images

Michael Kelm, Bjoern Menze, Fred Hamprecht

Magnetic resonance spectroscopic imaging yields data with three spatial and one spectral dimensions. The spectra can reveal metabolic perturbations that result, for instance, from cancer. However, SNR is poor, spatial resolution is low and the spectra are frequently plagued by artefacts.

Artefacts related to field inhomogeneities can be reduced, and more morphological detail obtained, by increasing the spatial resolution of the spectroscopic images at the expense of an even worse SNR. We develop and evaluate methods for the automated classification of spectra that work even under these conditions of extremely poor SNR, by exploiting spatial context.

Both generative and discriminative methods, namely Markov and Conditional Random Fields, are discussed and compared in terms of their classification performance. We show that both approaches outperform a mere single-voxel classification if the resolution is high and the SNR is low; and that the discriminative method is superior to the generative approach for most noise levels.

Advanced Image Analysis for developing Quantitative Imaging Biomarkers

Wiro Niessen

Biomarkers comprise anatomic, physiologic, metabolic, biochemical, biophysical, and molecular parameters which can be used to determine the presence and state of disease. Conventional biomarkers are commonly assessed by laboratory tests or physical examination. Owing to the advancement of imaging technology, and the development of contrast agents which are targeted to processes associated with specific diseases, the role of imaging biomarkers is rapidly increasing in medicine. Imaging biomarkers are expected to have a large impact in medicine, e.g. for better understanding the mechanisms of disease, for drug discovery and development, screening, improved diagnosis, and monitoring of treatment. In drug discovery, it has the potential to be used as a surrogate endpoint in clinical studies. In screening and diagnosis, it may lead to more sensitive and specific diagnosis. In treatment monitoring, it may be used to assess the response to treatment at an earlier stage, enabling individualized patient treatment.

Whereas most conventional biomarkers (laboratory tests) are quantitative, a processing step is required to extract quantitative parameters from imaging data. Therefore, there is an important role for quantitative image analysis in the development of imaging biomarkers, and in their application in medical decision making and treatment monitoring.

In this talk we will discuss advanced medical image analysis methods to develop, implement and validate quantitative imaging biomarkers. Examples of their potential will be shown in cardiovascular disease, neurodegenerative disease, and cancer.

Single Molecule Fluorescence Microscopy - Applications to Biology

Gerhard J. Schuetz

The cellular plasma membrane structure affects interactions between membrane constituents by influencing their movements at the nanometer scale. We apply single molecule fluorescence microscopy to resolve the plasma membrane structure at a nanoscopic length-scale by employing the high precision for localizing biomolecules of down to 15nm. Minimum invasive labeling via fluorescent ligands was sufficient to image the lateral diffusion of individual protein molecules on a sub-millisecond time scale. We applied this technology to study the motion of single glycosylphosphatidylinositol- (GPI-) anchored proteins in the plasma membrane of living cells 1. In contrast to results obtained by tracking gold-labeled membrane proteins, the single molecule fluorescence data reveal free Brownian motion of the proteins down to length scales of ~70nm, indicating no constitutive confinement zones. We also studied the mobility of this GPI-protein in cellular nanotubules, recently discovered cylindrical structures which interconnect different cells, yielding the tube radius (65nm) and the diffusion constant along versus perpendicular to the tube axis. We found isotropic diffusion behavior, thereby further confirming the absence of significant interaction with actin which is aligned parallel to the tube axis 2. In addition, we developed a technique to detect molecular cluster formation in the cellular plasma membrane of living cells 3. With this methodology, individual aggregates can be selectively imaged, and the load of each cluster can be determined. We applied this technique to investigate the association of a fluorescent lipid analogue in living Jurkat T cells. Aggregates containing up to 4 probe lipids were observed to diffuse freely as stable platforms in the plasma membrane, shedding new light on the current debate concerning the existence of "lipid rafts".

The development of ultra-sensitive detection schemes also has a strong impact on bioanalysis, as the sensitivity of biochemical assays could be dramatically increased. Whenever the available amount of sample is the limiting factor for unambiguous diagnosis e.g. in medical diagnostics, bioanalytics with single molecule sensitivity can be expected to become even an enabling technology. To specifically address this aspect, we developed a device for single molecule imaging on large surface areas such as biochips 4. We applied this technology for RNA expression profiling down to the single molecule level 5. The performance of the system was evaluated using oligonucleotide microarrays. For full complementary 60mer oligonucleotides a detection limit of 1.3fM target concentration - corresponding to only 39.000 molecules in the sample - and a dynamic range of 4.7 orders of magnitude have been achieved. The applicability of the system to PCR amplification-independent gene expression profiling of minute samples was demonstrated by complex hybridization of cDNA derived from the equivalent of only 104 cells; the results are in good agreement with data obtained in ensemble studies on large samples.

1. Wieser, S., Moertelmaier, M., Fuertbauer, E., Stockinger, H. & Schutz, G. J. (Un)Confined Diffusion of CD59 in the Plasma Membrane Determined by High-Resolution Single Molecule Microscopy. *Biophys J* 92, 3719-28 (2007).
2. Wieser, S., Schütz, G. J., Cooper, M. E. & Stockinger, H. Single Molecule Diffusion Analysis on Cellular Nanotubules -Implications on Plasma Membrane Structure below the Diffraction-Limit. *Appl Phys Lett* in press.
3. Moertelmaier, M., Brameshuber, M., Linimeier, M., Schütz, G. J. & Stockinger, H. Thinning out clusters while conserving stoichiometry of labeling. *Appl Phys Lett* 87, 263903 (2005).
4. Hesse, J., Sonnleitner, M., Sonnleitner, A., Freudenthaler, G., Jacak, J., Hoglinger, O., Schindler, H. & Schutz, G. J. Single-molecule reader for high-throughput bioanalysis. *Anal Chem* 76, 5960-4 (2004).
5. Hesse, J., Jacak, J., Kasper, M., Regl, G., Eichberger, T., Winklmayr, M., Aberger, F., Sonnleitner, M., Schlapak, R., Howorka, S., Muresan, L., Frischauf, A. M. & Schutz, G. J. RNA expression profiling at the single molecule level. *Genome Res* 16, 1041-5 (2006).