
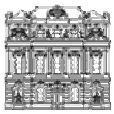

International Workshop on Image Analysis in the Life Sciences Theory and Applications

Johannes Kepler University,
Linz (Austria)

February 28 – March 2, 2007

Land
Oberösterreich

IEEE

Wednesday, February 28

13:30 – 13:45		***Opening session***
13:45 – 14:45	E. Meijering	Advances in Cellular and Molecular Bioimage Analysis
14:45 – 15:15	B. Arminger	Comparison of Various Algorithms for Phase Unwrapping in Optical Phase Microscopy
15:15 – 15:45		***Coffee break***
15:45 – 16:45	M. Loog	Medical Image Analysis and Processing under Supervision
16:45 – 17:15	F. Fruehauf	A method for ultrasound image processing
17:15 – 17:45	A. Obereder	Curve Recognition in Doppler Ultraschall Measurements
18:00		***Banquet***

Thursday, March 1

09:00 – 10:00	M. de Bruijne	Quantitative Image Analysis using Statistical Models
10:00 – 11:00	G. Schütz	Single molecule fluorescence microscopy - applications to bioscience
11:00 – 11:30		***Coffee break***
11:30 – 12:30	W. Backfrieder	Selected methods in computerized tomography
12:30 – 13:30		***Joint lunch break***
13:30 – 14:30	M. Welk	Diffusion Filters and Wavelet Methods for Image Denoising: Models and Algorithms
14:30 – 15:30	R. Ramlau	New regularization approaches for tomography
15:30 – 17:00		***Coffee break and poster presentation***
18:00 – 19:00		***Lentos Tour***
19:30		***Dinner***

Friday, March 2

09:00 – 10:00	J. Polzehl	Propagation-Separation procedures for image processing
10:00 – 11:00	S. Kannengiesser	Parallel MR Imaging Reconstruction - GRAPPA, SENSE, SMASH
11:00 – 11:30		***Coffee break***
11:30 – 12:30	K. Tabelow	Structural adaptive signal detection in fMRI and structure enhancement in DTI
12:30 – 12:35		***Closing session***
12:35		***Joint lunch break***

Talks

Advances in Cellular and Molecular Bioimage Analysis

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Advances in fluorescent probing and microscopic imaging technology have revolutionized biology in the past decade and have opened the door to studying the structure and function of cells and even single molecules. Typically such studies generate vast amounts of spatiotemporal image data containing much more biologically relevant information than can be analyzed by human observers. Hence there is a rapidly growing need for automated quantitative biological image analysis, not only to cope with the rising rate at which images are acquired, but also to reach a higher level of sensitivity, accuracy, objectivity, and reproducibility. The purpose of this lecture is to survey recent efforts in this area with specific emphasis on neuron tracing and particle tracking.

Comparison of Various Algorithms for Phase Unwrapping in Optical Phase Microscopy

(Joint work with Bernhard G. Zagar and Bettina Heise)

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Interferometric techniques belong to the standard repertoire in the field of optical metrology to give reliable quantitative results for investigating transparent objects or measuring surface displacements. Meanwhile holographic interferometric methods have also found their applications in the field of microbiology, where their quantitative nature gives an advantage over phase contrast or DIC microscopy, which yield high spatial resolution but can give only qualitative results. There exists a variety of temporal and spatial phase based interferogram analysis methods. In this paper we concentrate on phase shifting and phase demodulation techniques. Our interferometer enables us to perform both tasks in one setup simultaneously. In both applications we have the problem of unwrapping phase images for the analysis of the recorded fringe patterns. We present an FFT based 2D unwrapping algorithm that allows a simple and fast reconstruction of the phase distribution of the objects. We apply our methods for technical and biological objects.

By combining both interferometric methods the accuracy of a phase map can be improved over any single method presented. According to the application a trade-off between recording of fast dynamic processes (Hilbert phase microscopy) and accuracy (phase shifting) must be found. We demonstrated the applicability of a simple but effective phase unwrapping algorithm to determine the true phase map of microscopically imaged phase objects like living cells that can't or shouldn't be stained. This allows the recording of highly dynamic processes in living cells. The two dimensional unwrapping algorithm works fine also for highly disturbed phase images. The proposed algorithm is simple and fast allowing real-time imaging.

Medical Image Analysis and Processing under Supervision

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Like so many real-world problems, solving actual image analysis and processing problems is a difficult task. In recent years, researchers have become more and more aware of the potential of supervised techniques, or learning methods, to perform data analysis, mining, and processing. The same holds for the field of image analysis.

The first part of the talk provides a crash course on pattern recognition and tries to explain the possible benefits of these approaches. The second half subsequently demonstrates how these supervised techniques can be applied in several medical, pixel-based image analysis problems. More specifically, a segmentation, a filtering, and, possibly, a detection task are considered.

A method for ultrasound image processing

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Ultra sound is common medical diagnosis. Image processing methods can be used to upgrade this technique. In this talk such a processing tool is presented which smoothes the ultra sound image and enhance certain features in the image simultaneously. Moreover a method to speed up the calculation time is discussed.

Curve Recognition in Doppler Ultraschall Measurements

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The medical Doppler measurement is a noninvasive test that can be used to evaluate blood flow velocities in certain regions of the human body. The results of such measurements are velocity distributions which can be used for diagnostic purposes. To simplify the diagnostics for a physician the bounds for the flow velocities can be drawn in automated. The resulting bounds for each measurement are combined in a curve over time. Subsequent we detect special points of interest for the blood flow like systoles and diastoles. In this talk the arising difficulties are discussed and parts of the solution are presented.

Quantitative Image Analysis using Statistical Models

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This talk addresses the use of statistical shape and appearance models in medical image analysis. Main topics are image segmentation by joint optimization of tissue classification and shape, and the modeling of relations between shapes for use in quantification of abnormalities. Examples are included of quantitative analysis of spine deformities and atherosclerosis from CT and X-ray images.

Single molecule fluorescence microscopy - applications to bioscience

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Beyond doubt, nanobioscience represents one of the most innovative concepts in current basic and applied research. Technological advances provided the essentials for this ongoing scientific revolution, by making possible the observation, investigation and manipulation of biomaterials down to single molecules. Researchers are fascinated by the perspective to watch proteins, lipids, and DNA-molecules in their native context - the living cell - as they perform their endogenous function. Mobility measurements yield information about cellular structures down to length scales of a few nanometers. Time-resolved single molecule detection has become the method of choice to characterize structural transitions between different functional states of isolated proteins or ribozymes; the community is awaiting the first live cell investigation. It is the interplay between thousands of molecules, however, which enables the multiple tasks of signaling units, organelles and the whole cellular biosystem. A comprehensive list of molecular interactions cannot be expected for the near future; yet, single molecule detection schemes may provide a route towards the characterization of molecular complexes, which are in general too fragile to endure state of the art extraction procedures. In this seminar, I will show examples how to obtain insights into the organization of the cellular Nanocosm by single molecule experiments. In particular, we developed a technique to detect molecular cluster formation in the cellular plasma membrane of living cells. 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. We applied this technology for RNA expression profiling down to the single molecule level. 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 10^4 cells; the results are in good agreement with data obtained in ensemble studies on large samples.

Selected methods in computerized tomography

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Two main fields of research at the Medical Image Processing group at Campus Hagenberg are addressed in this talk, i.e. emission tomography in nuclear medicine and multi slice CT (MSCT) in radiology. As an illustrative example of data processing in single photon emission tomography (SPECT) an Alzheimer investigation is described. This type of study is characterized by extremely low counts. Development of a PCA filter allows noise suppression together with preservation of even weakly manifested structures. For proper reconstruction a fully 3D ML-EM algorithm was designed and implemented in a Grid-Environment, to exploit high processing power on a massively parallel cluster. Results were registered to high resolution MRI data.

High spatial and temporal resolution of modern 64 slice CT is utilized for accurate imaging of pathologies in liver tissue. The enormous amount if image data acquired during a liver study, implies the need of novel computer aided diagnosis and visualization techniques. The complex anatomical structure of the liver suggests the use of individual 3D models for careful planning of liver surgery. Level sets are used as powerful segmentation methods for automated selection of parenchyma and lobe segmentation based on parenchyma vascularisation. Tools for measurement and classification of lesions are provided. Transparent interactive visualization of parenchyma, vessels, and lesions supports modern computer-aided diagnosis.

Diffusion Filters and Wavelet Methods for Image Denoising: Models and Algorithms

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Nonlinear diffusion filtering has proven its value as a versatile tool for structure-preserving image denoising in a variety of applications. Wavelet shrinkage is another approach designed to achieve the same goal, which can capitalise on efficient wavelet transform algorithms.

It has been noticed since long that the two classes of methods yield similar results. Recent work has shown that these similarities are not just superficial. Focussing on discrete formulations, even equivalence of specific diffusion and wavelet shrinkage processes can be established.

Extending these results, new models and algorithms could be established. On one side, a new class of numerical algorithms for fairly general diffusion filters has been developed that combine good preservation of fine image details with favourable stability properties and are very simple to implement. On the other hand, new wavelet shrinkage strategies can be designed which use a diffusion-inspired coupling of wavelet coefficients to achieve excellent rotation invariance.

The fundamental ideas of this framework and resulting algorithms will be presented in this talk.

New regularization approaches for tomography

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The reconstruction of a function from tomographic data is usually an ill-posed problem and requires regularization methods. Tikhonov regularization has frequently been used to compute a stable approximation to the solution of linear as well as nonlinear operator equations $F(x) = y$. The solution is approximated by a global minimizer of the Tikhonov functional,

$$x_\alpha^\delta = \arg\min_x J_\alpha(x) = \arg\min_x \left\{ \|y^\delta - F(x)\|^2 + \alpha\Omega(x, \bar{x}) \right\} \ ,$$

where Ω denotes the chosen penalty term, y^δ the noisy data and $\bar{x}$ is an a priori guess to the solution. The regularization parameter α has to be chosen in dependence of the noise level such that $x^\delta_{\alpha(\delta)}$ converges to a solution of the equation as $\delta \to 0$. The penalty term has a vital influence on the features of the reconstruction. In most cases, in particular for nonlinear operators, the penalty $\Omega(x, \bar{x}) = \|x - \bar{x}\|_X^2$, with X a Hilbert space, is chosen. In the following, we will propose two different types of penalties for tomographic applications: sparsity constraints and a penalty on the perimeter of the singularity set of a function. The resulting schemes were applied to SPECT and CT data.

Propagation-Separation procedures for image processing

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The talk presents a class of structural adaptive smoothing methods developed at WIAS. This includes the pointwise adaptive approach (Spokoiny) and stagewise aggregation suggested by Belomestny and Spokoiny (2004). The main focus will be on the Propagation-Separation (PS) approach proposed by Polzehl and Spokoiny (2006). The method allows to simultaneously identify regions of homogeneity with respect to a prescribed model (structural assumption) and to use this information to improve local estimates. This is achieved by an iterative procedure. The name Propagation-Separation is a synonym for the two main properties of the algorithms. In case of homogeneity, that is if the prescribed model holds with the same parameters within a large region, the algorithm essentially delivers a series of nonadaptive estimates with decreasing variance and propagates to the best estimate from this series. Separation means that, as soon as in two design points X_i and X_j significant differences are detected between estimates, observations in X_j will not be used to estimate the parameter in X_j. Both points are separated. The power of the approach will be demonstrated using examples from imaging.

Parallel MR Imaging Reconstruction - GRAPPA, SENSE, SMASH

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Magnetic Resonance Imaging (MR Imaging, MRI) is a well-established medical imaging method capable of producing images of the inside of the human body with arbitrary slice orientation. The signal is produced by radio frequency radiation of the magnetic moments of hydrogen and other nuclei after excitation with external radio frequency signals in the presence of a strong static magnetic field. Signal reception is performed through wire loops, called rf coils, usually in the shape of a loop array with typically 8-32 elements. Due to its flexible contrast mechanisms - especially in soft tissue - MRI is the method of choice for many diagnostic questions, for example, in neurology, orthopedics, oncology, and cardiology.

MRI is a computed tomography method; the raw data consist of samples of the spatial frequency spectrum of the object. One primary drawback of this type of acquisition is the need to repeat the cycle of excitation and data acquisition many times with altered settings of additional, switchable magnetic fields - the so-called phase encoding steps. Recently it has been shown that a part of these phase encoding steps can be replaced by additional information contained in the manifold of signals simultaneously received in the rf coil array, thus speeding up the data acquisition considerably. These methods, known by colorful acronyms such as GRAPPA, SENSE and SMASH, are collectively known as parallel imaging, and consist largely of the solution to linear systems of equations; they are regarded as almost universally useful in MRI, and have found their way into clinical practice in record time.

This talk will give a short introduction of MRI as a diagnostic imaging method. Some fundamental principles of image formation will be discussed, and the basics of parallel imaging will be explained. Finally, a few special variants of parallel imaging will be introduced and presented in the context of their numerical mathematics.

Structural adaptive signal detection in fMRI and structure enhancement in DTI

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Medical Images from imaging modalities such as MRT or CT suffer from significant noise. However, commonly applied non adaptive noise reduction tends to oversmooth structures of interest and reduces the effective spatial resolution. We propose adaptive smoothing methods which overcome these drawbacks. We demonstrate how these methods can be efficiently used in functional MRI and diffusion tensor imaging.

Poster

Modeling and estimation of fluorescence video-microscopy image sequences

(Joint work with Charles Kervrann and Patrick Bouthemy)

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The development of system biology is characterized by the design of new techniques producing vast amounts of data. Only automatic approaches for analysis and interpretation will allow researchers to face this challenge. In our studies, we aim at analysing the dynamic of the Rab6 protein involved in the intra-cellular transport. This GTPase is thus tagged with GFP and image sequences of the living cell are recorded using wide field video-microscopy. The observe scene contains small bright spots corresponding to vesicles moving with a high velocity along microtubules. Most of them are coming from the Golgi apparatus, which appear as a very intense and large region, and are reaching specific locations at the periphery of the cell. We propose a model for fluorescence image sequences which distinguish fast moving component from slowly varying part of the images.

In the case of images showing fluorescently tagged particles, the global image intensity can slowly vary along time. This can be due to several physical phenomena such as photo-bleaching or diffusion of fluorescent proteins within the cell. Therefore, a stationary model for the background is too restrictive. Nevertheless, we have conducted experiments showing that the intensity variation w.r.t. time can be captured by a linear model for each pixel which provides a compact representation of the background intensity dynamics. The estimation of the two coefficients at each pixel location is achieve through a pointwise adaptive estimation procedure allowing us to take into account the correlation between them as well as their spatial correlation.

The second part of our modeling is dedicated to the analysis of the dynamic of fast moving particles. The analogy between the intra-cellular traffic and the internet traffic led to a network-based modeling. In this model, a key parameter is the flow between origin nodes and destination nodes. The problem of the estimation of these flows is called network tomography. We show that for simulations of membrane trafficking, the origine-destination flow can be estimated by adapting the methods designed for the analysis of telecommunication networks.

The simulation of the proposed model provide realistic image sequences on which image processing algorithms can be tested. Furthermore, the parameters of the simulation allow the biologist to better understand the observed phenomena. Finally, an estimation of these parameters is an indirect way to describe and summaries the content of image sequences. However, if the network tomography avoid the difficulties that traditional tracking methods encounter, the application to real images sequences has still to be improved.

Proposal for Developing Framework to Evaluate Scoliotic Spine Progression based on Image Analysis and Visualization Techniques

(Joint work with H.F. Wilkinson, T. L. R. Mengko, A.G. Veldhuizen, P.M.A. van Ooijen and G. J. Verkerke)

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Scoliosis is a three-dimensional deformity of the spinal column that is characterized by both lateral curvature and rotation of the vertebra. The scoliosis progression needs to be observed regularly to decide the best treatment. The main focus in scoliosis diagnosis is accuracy and radiation exposure problems.

In this research, we develop a framework that is able to measure the scoliosis deformity and follow the progression of the deformation process of the spine by means of an imaging evaluation system. The framework consists of a set of scoliosis assessment procedures, which are established in a period of time. During the first visit of a patient, two 2D radiographs in posterior-anterior and lateral orientation are taken. In the framework, each acquired image is enhanced separately by applying pre-processing techniques to remove the noise and to accentuate the spinal parts. Each vertebra is localized by means of a deformable model. Then, the features of a vertebra are extracted. The curvature can be determined by measuring the geometrical orientation of each spinal component. The whole spinal column can be generated by connecting the resulting localized spinal components. The three-dimensional shape of the spine is constructed by adapting a spinal template taken from a CT-image to the features of each image orientation. Additionally, an image registration method is used to rectify the geometrical defects due to different acquisition angle.

To minimise the detrimental effect of radiation exposure in X-Ray, the next visits for scoliosis evaluation are conducted by a using three-dimensional Ultrasound imaging system. In this step, a set of 3D spine images are acquired. Image pre-processing of the ultrasound images is established to detach the noise, bone, and soft tissue parts. Then, landmark points are determined on the bony parts to build the spinal column and the 3D curvature can be calculated by connecting the correlated points and calculating the geometrical orientation. The three-dimensional shape can be obtained by adapting the vertebral template to the landmark points. In this research, we also will investigate the feasibility of taking X-Ray radiographs from different angles to decrease the disturbances from ribs, lungs, heart and sternum. Moreover we will study new features in each vertebra which are able to notify about scoliosis. The proposed framework will be evaluated on simulated as well as actual X-ray and Ultrasound images. By performing this framework, it is expected that the scoliosis progression can be evaluated more accurately and frequently with lower radiation risk to patient, so that the treatment can be determined more precisely resulting in a better shape of the spine.

EEG Imaging; Subtopographic EEG Source Localization After Spatio-temporal Wavelet Decomposition

(Joint work with Tamer Demiralp, Ahmet Ademoglu)

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Localization of the cognitive activity in the brain is one of the major problems in neuroscience. Current techniques for neuro-imaging are based on Functional Magnetic Resonance Imaging (fMRI), Positron Emission Tomography (PET), and Event Related Potential (ERP) recordings. The highest temporal resolution is achieved by ERP, which is crucial for temporal localization of activities. However, the spatial resolution of scalp topography for ERP is low. To overcome the limitation of scalp topography, several current-density estimation techniques were developed whose goal is to find the locations of the threedimensional (3d) intracerebral activities by solving an inverse problem. However, scalp topologies constituted by multiple sources makes the inverse problem more complicated. There is a severe limitation for the inverse parametric solution algorithms that they can only perform well for the temporally uncorrelated sources. The parametric inverse methods typically assume that the sources can be represented by a few equivalent current dipoles of unknown location and moment to be estimated with a non-linear numerical method. In this study, a spatio-temporal decomposition method is proposed to separate the temporally correlated sources using their topographies prior to their localization by parametric inverse solutions. Temporal decomposition allows for the extraction of each temporal frequency component as subbands like alpha, theta, delta while spatial decomposition of these subband topographies yields subtopographies whose spatial frequency bands are determined by the depth and extension of individual dipole sources. The outputs of the spatiotemporal decomposition process are then localized for their dipole sources. The method is applied to several simulated ERP data mimicking the superficial, deep, focal and distributed source configurations together with temporal correlations. It also addresses to the problem of isolating the correlated sources through their superposed topographies.

Hierarchical Scale Space Pre-Segmentation based on Attraction Areas for MR-images from Atherosclerosis-plaque

(Joint work with M. Jäger, E. Nagel and O. Hellwich)

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Atherosclerosis is a severe disease affecting the arterial blood vessels. Especially the dislocation of Atherosclerosis-plaques can cause dangerous heart attacks or strokes. With modern methods of medical imaging like MRI it is possible to support the diagnosis more precisely and without precarious exposure to radiation. Unfortunately, it remains very difficult to image human plaques in-vivo.

We want to support the detection of plaque structures with modern methods of image analysis. The first step in reaching this aim should be an adequate segmentation process. On many actual measured MR-images, an unambiguous visual recognition of plaques is not possible even by a cardiologist. This lack of information encouraged us to concentrate on a hierarchical pre-segmentation of plaque images without the use of prior knowledge. An all-embracing pre-segmentation should contain all visible segments including their boundaries that a human observer would perceive without having special information about the semantics of the observable image elements. A particular focus is the detection of plaques in multi-channel MRI datasets. The pre-segmentation should also be applicable to other medical structures and should be combined with specific prior knowledge concerning the region of interest in future extensions to the work presented.

Primarily we denoised ex-vivo images of arterial profiles with anisotropic diffusion modified by a curvature term. For the subsequent hierarchical segmentation, we calculated a linear Gaussian scale space. For our 1-channel approach we simply averaged 4 channels of the imaged arterial plaque to produce the input image. At each scale in scale space, a robust detector localises critical points (maxima, minima and saddle points) and linked them across scales to form critical paths. Those trajectories describe the dislocation of critical points in scale space and contain information central to the hierarchical topology of the input image.

The concept of attraction areas assures the existence of exactly one segment for every extremal path. Regarding a certain scale plane, an attraction area exists for every extremal point which is bordered by an iso-intensity curve determined by the corresponding saddle-intensity on that scale. They are shaped by a region growing segmentation which well known problem is the formation of so-called grey-value bridges that causes an unintended enlargement of the attraction area. The calculation of some equidistant grey-values in the intensity range of a 3x3-neighbourhood supports approximating the appropriate iso-intensity border for our attraction area. Unfortunately we cannot avoid the enlargement for all segments found, and furthermore we receive attraction areas which belong to extrema with very low relevance. So we applied a weighting function that selects relevant segments and respects important characteristics of a critical path and the resulting attraction area (e.g. length of critical path or the normalized integrated gradients along the segment boundary). In combination with a threshold, we can select segments by importance and get appropriate attraction areas for our hierarchical segmentation. We construct the hierarchical structure from the nested structure of all selected segments and visualise them in a hierarchical tree.

To include all important information in every channel of a multi-channel MRI dataset, we currently work on a multi-channel approach. We also developed differential operators to construct critical pathes. Retrieving relative intensities still reveals little problems and shows some artefacts parallel to the coordinate axis.

Simulated Dataset for Verification and Validation of DT-MRI Analyzing Tools

(Joint work with M.Özkan)

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In diffusion tensor MRI (DT-MRI), each voxel is assigned a tensor that describes local water diffusion. In this study, a simulated DT dataset for analyzing the diffusion characteristics is developed to verify and validate DT images post-processed with various DT analyzing codes. This module is intended as a resource for DT-MRI analyzing tools to verify and validate the analysis results. The b factor in our study is the B matrix of size 1x7. In our sample, 6 diffusion weighted images and a null image namely the T2 image creating a set of intensity images of size 256x256x7 is generated for the analysis. The idea is to fulfill the routine DT analysis from the apparent diffusion coefficient ADC image instead of the DT images. This inverse analysis methodology is preparing the basis of the image information to be investigated as known values. According to the Stejskal Tanner equation, $D = [D_{xx}, D_{yy}, D_{zz}, D_{xy}, D_{xz}, D_{yz}]$ is calculated in the algorithm. After the validation of the algorithm with the simulated diffusion tensor dataset, real MR data of human brain and myocardium are used. The eigensystem D is calculated in every pixel, ADC is represented with respect to D. The other characteristic values of diffusivity namely fractional (FA) and relative (RA) anisotropy values are calculated. Developing a reliable and rapid tractography algorithm for the clinical use regarding to these verified results is the future study of the work in progress.

Analyzing microarrays with single molecule sensitivity

(Joint work with Jaroslaw Jacak, Fritz Aberger, Robert Schlapak, Stefan Howorka, Leila Muresan, Anna-Maria Frischauf and Gerhard J. Schütz)

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We developed a microarray platform for PCR free RNA expression profiling of minute samples. It utilizes a novel scanning system for ultra-sensitive high-resolution fluorescence imaging. Specialized biochips - optimized for low autofluorescence and weak unspecific adsorption - with cm2 size were read out with 200 nm pixel size. The resulting 16 bit images contained typically a few giga pixels. For the quantification of the signals within such images novel analysis algorithms have been implemented.

For microarray localization, the high resolution images were first software-binned (10x10) and a grid fitting process was performed on the binned image. For subsequent analysis, sub-images each containing one microarray spot were loaded at full resolution. For counting of single molecule signals, the trous wavelet filter bank method was used. For this, the sub-images were decomposed via a sequence of low-pass and band-pass filters and wavelet planes on four different scales were generated. Features that exceeded the noise within their wavelet plane by 3 times the standard deviation and which were local maxima in the original image were counted as peaks. The intensity the localized peaks was determined by a subsequent least-squares fitting procedure.

This study was supported by the GEN-AU program of the Austrian Federal Ministry of Education, Science and Culture, by the Austrian Research Fund, by the state of Upper Austria and by the Research focus "Life Sciences and Health" of the University of Salzburg.

Automatic Quantitative Analysis of MRI Brain Images with the Software SPM5

(Joint work with A.L.J van Hulzen, M.J.W. Greuter and P.E.Sijens)

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This study concerns the tool of brain image analysis to acquired MRI scans, with the aims of quantifying total brain volume in healthy volunteers, and of checking whether SPM5 can serve as the gold standard for brain image analysis. A basic review of the voxel-based morphometry method SPM5 is provided, and aspects of comparison between an alternative method available to assess brain morphometry and SPM5 are discussed. Further reviews are given for image segmentation and smoothing (as applied in the neuroimaging field), and of the statistical test appropriate for quantifying total brain volume of MR brain image data.

Early results are presented from initial work using DICOM import, tissue segmentation, total brain volume calculation, and paired t-test (statistical) to analyse the MR structural image. Some limitations of the work are discussed, and plans for future work are outlined.

MedVis

(Joint work with S. Baumgartner, J. Dirnberger, F. Fellner, J. Trenkler, C. Fellner, G. Haase, L. Muresan, R. Richter and E.P. Klement)

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A prototype of a 3D visualization tool for medical images has been developed in the UAR together with the Institute of Graphics and Parallel Processing (GUP) of the JKU in Linz [1]. This software is currently in use by our medical project partners (AKh Linz - Prim. Dr. Fellner, WJ Linz - Prim. Dr. Trenkler). The physicians there use it to classify and survey aneurysms. Based on this software package several plugins are planned.

The first plugin deals with hemodynamic simulations since aneurysms are protuberances of the blood vessels growing due to pressure caused by the pulsatile blood flow. Coevally to this growing process, the vessel wall is dilated until the aneurysm ruptures leading to severe damages up to death. Therefore it is necessary to get an early diagnosis to improve the surviving chances of the the patient. Flow patterns can support the physicians decision which therapy is adequate. The medical treatment of aneurysms can be done either by branching of the concerned region or by minimal invasive catheter surgery where the aneurysm is filled. For the simulation of the blood flow in the vessels we plan to use coupled Navier-Stokes and Navier equations (fluid structure interaction problem).

A second plugin should cover the field of fiber tracking. A number of different methods and algorithms for tracing anatomical fibers from 3D tensor fields are available. In a first step these algorithms will be evaluated. Furthermore we will try to improve the results by connecting maps of the human brain with the results obtained from the fiber tracking procedure (knowledge based system).

Scope

The field of image analysis in biology and medicine has been evolving rapidly in the recent years due to new methods and improved computational possibilities on one hand and new or improved imaging techniques and devices on the other hand. This workshop brings together industrial, clinical and academic researchers in order to discuss:

- New imaging techniques and the mathematical problems they raise
- New mathematical tools for coping with image quality issues
- New computational approaches in order to reduce significantly computation times

Due to the interdisciplinary nature of the subject, time will be reserved for discussions.

Organizers

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- Department of Knowledge-Based Mathematical Systems
  Fuzzy Logic Laboratorium Linz-Hagenberg
- Johann Radon Institute for Computational and Applied Mathematics
- Upper Austrian Technology and Research Promotion
  (Land Oberösterreich)
- IEEE Engineering in Medicine and Biology Society