

Mathematical Methods in Medical Imaging

Time: Thursday May 19, 09.15-16

Place: Glashuset, B25, Campus Linköping

On the occasion of joint visits by professor Gabor T. Herman, New York, and professor Yair Censor, Haifa, we decided to organize a seminar day. Very graciously professor Per-Erik Danielsson, Dept. of Electrical Engineering, professor Matts Karlsson and docent Magnus Borga, Dept. of Biomedical Engineering also volunteered to present their recent research in medical imaging. We wish all interested most welcome.

Lars Eldén, Tommy Elfving, Scientific Computing Group, Dept. of Mathematics, Linköping University.

PROGRAM

- 9.15-10.00 **Yair Censor**, University of Haifa (yair@math.haifa.ac.il).
A unified approach to physical and equivalent uniform dose constraints in intensity-modulated radiation therapy (IMRT) via the split feasibility problem.
- 10.00-10.30 Coffee
- 10.30-11.15 **Magnus Borga**, Linköping University (magnus@imt.liu.se).
Canonical Correlation Analysis (CCA) and Adaptive Filtering Techniques in Functional Magnetic Resonance Imaging (fMRI)
- 11.15-11.45 **Tommy Elfving**, Linköping University (toelf@mai.liu.se).
A sparsity scaled block algebraic reconstruction technique.
- 11.45-12.30 **Per-Erik Danielsson**, Linköping University (ped@isy.liu.se).
Iterative improvement of non-exact reconstruction in cone-beam CT.
- 12.30-14.30 Lunch
- 14.30-15.15 **Matts Karlsson**, Linköping University (matka@imt.liu.se).
Biomedical modelling and simulation - towards individual models of the human cardiovascular system
- 15.15-16.00 **Gabor T. Herman**, City University of New York (gabortherman@yahoo.com). *Direct Reconstruction of Label Images from Projections*

ABSTRACTS

- **Yair Censor**, University of Haifa (yair@math.haifa.ac.il).
A unified approach to physical and equivalent uniform dose constraints in intensity-modulated radiation therapy (IMRT) via the split feasibility problem.

Abstract The multiple-sets split feasibility problem requires to find a point closest to a family of closed convex sets in one space such that its image under a linear transformation will be closest to another family of closed convex sets in the image space. We propose and study a unified model for handling physical dose constraints and equivalent uniform dose (EUD) constraints appearing in the inverse problem of intensity-modulated radiation therapy (IMRT) treatment planning in a mathematical framework based on the split feasibility problem. The model does not impose on the constraints an exogenous objective (merit) function but the optimization algorithm minimizes a weighted proximity function that measures the sum of the squares of the distances to the constraints sets. This guarantees convergence to a feasible solution if the split feasibility problem is consistent (i.e., has a solution) and convergence to a solution that minimally violates the physical dose constraints and the EUD constraints – otherwise. We present computational results that demonstrate the validity of the model and the power of the proposed algorithmic scheme.

- **Magnus Borga**, Linköping University (magnus@imt.liu.se). *Canonical Correlation Analysis (CCA) and Adaptive Filtering Techniques in Functional Magnetic Resonance Imaging (fMRI)*

Abstract The functional processes of the human brain are still poorly understood although much effort has been focused on revealing its secrets. A relatively new and promising tool for this purpose is functional magnetic resonance imaging (fMRI). The purpose of fMRI is to map sensor, motor and cognitive functions to specific areas in the brain. The physical basis of the method is that oxygenated and deoxygenated blood have different magnetic properties, a difference that can be measured in an MR-scanner. As it is essential to capture the state of the brain at each volume acquisition, a very fast imaging sequence called echo planar imaging (EPI) is used. Unfortunately the EPI images suffer from low signal to noise ratio which makes the detection of active brain regions a challenging problem. Typically, less than 5% of the brain activity. Furthermore, the shape of the temporal activity pattern that is searched for is partly unknown.

To cope with these problems, adaptive filtering methods can be employed.

We have developed an adaptive filtering method based on Canonical correlation analysis (CCA) for this purpose. In statistics, CCA is a well known analysis method, introduced by Hotelling in 1936 as a method for finding the maximum correlation between linear combinations of two sets of variables. I will present how adaptive spatial and temporal filtering can solve the detection problem in fMRI by the use of CCA.

- **Tommy Elfving**, Linköping University (toelf@mai.liu.se). *A sparsity scaled block algebraic reconstruction technique.*

Abstract Algebraic reconstruction techniques were first proposed in 70:s by professor Herman and his group. The main application is for such problems where the data is noisy and/or sampled in a non-uniform or incomplete manner. For large problems so called simultaneous algorithms have the advantage of being easy to efficiently implement in a multi-processor computer system. On the other hand they often suffer from slow convergence. The method we study here is an iterative projection method for solving linear equalities and/or inequalities. The method allows component-wise weighting while working with orthogonal projections onto the individual hyperplanes/halfspaces of the system. The weight, for each component of the reconstructed image, is inversely proportional to the number of nonzero elements in the corresponding column of the matrix. This weighting compares favourably with the classical Cimmino-type scaling used in simultaneous algorithms. The method is also extended to blocks of equations/halfspaces (ordered subsets methods).

- **Per-Erik Danielsson**, Linköping University (ped@isy.liu.se). *Iterative improvement of non-exact reconstruction in cone-beam CT.*

Abstract Contemporary reconstruction for helical cone-beam CT is mostly based on non-exact algorithms, which produce unacceptable artifacts for cone angles above a certain limit, which may differ, from one algorithm to another. We report on attempts to extend the applicability of these algorithms to higher cone angles by suppressing artifacts by means of iterative post-processing. The iterative loop includes a ramp-filtering step before back-projection which promotes fast convergence. The scheme has been applied to the original PI-method as well as to Siemens' AMPR and WFBP methods. Using ordered subsets in the iterative loop for WFRP, in one single iteration we achieved almost spotless images for cone angles as high as ± 9 degrees.

- **Matts Karlsson**, Linköping University (matka@imt.liu.se). *Biomedical modelling and simulation - towards individual models of the human cardiovascular system*

Abstract The future of computational mechanics in biomedicine deals with creating individual models of the human heart and vascular systems for enhanced diagnostics, intervention planning and follow-up. Magnetic resonance imaging has developed far enough that we are able to non-invasively obtain time-resolved three-dimensional data including individual anatomy as well as velocities of the blood, the myocardium and vessel walls. The use of these vast amounts of data (more than 1000 images for one patient) is impossible without computer support. From the obtained data, new parameters such as relative pressure in the blood pool and strain/strain-rate in the myocardium can be extracted. Combining these parameters with anatomical information and tools for computer simulation the accuracy of diagnostics in the individual patient is greatly enhanced. Furthermore, planning of necessary interventions can be performed and optimized. The outcome of such interventions can even be simulated. As a bonus, MRI enables the possibility to perform individually tailored follow-up procedures where relevant parameters are automatically extracted.

With information about the geometry we can now turn to the material properties: the heart is a chemically controlled electro-mechanical pump. The pump itself is quite easy to model in terms of a pressure-volume relationship on a global level, but for a more detailed analysis we need to take into account passive as well as active properties. The passive properties of the heart include non-linear finite elasticity and quasi-linear visco-elasticity in combination. The anisotropy of the heart is of importance since the muscle fibres can only contract along the fibre direction and since the fibres are arranged in sheets, the shear strains within the heart wall will relocate the force direction. The heart wall is also influenced by biphasic porosity due to the transportation of blood in and out of the myocardium. The inflow/outflow through the heart wall is strongly coupled to the architecture of coronary arteries and veins. The active properties of the heart are much more complex to model. The contractile properties of the muscle fibres are dependent on the sarcomere length and history which in turn is controlled by cellular calcium and available metabolic energy supply. Finally, the activation sequence through the entire heart has to be included. This includes detailed modelling of the motion of the wave front of an electrical wave that will travel through the heart and serve as trigger for each of the muscle cells. Methods for automatic characterization of flow patterns

and structures that can be applied to measured data from e.g. magnetic resonance imaging as well as data from computer simulations are of great importance for the future clinical setting to find the vital few among the trivial many". The old saying that "Messen ist Wissen" is the reality of today's biomedical modelling and simulation.

- **Gabor T. Herman**, City University of New York (gabortherman@yahoo.com).

Direct Reconstruction of Label Images from Projections

Abstract This talk is on joint work with my student Hstau Y. Liao and is based on his doctoral dissertation.

Three-dimensional reconstruction from electron-microscopic projections is a methodology used to obtain the structure (and consequently the function) of biological macromolecules; this is an essential component in our search towards the understanding of living organisms and is useful in practical areas such as drug design. The aim is to identify the spatial arrangement of various types of building blocks of the molecule (such as proteins and RNA). The current approach is to first reconstruct from the electron micrographs a three-dimensional distribution of the atomic density and then segment this distribution into the building blocks. However, as we are approaching higher and higher resolution, this approach becomes less and less satisfactory (to some extent due to the fact that the atomic density in a very small volume is not a reliable indicator of the kind of matter that occupies the volume).

We propose to eliminate the intermediate stage of estimating the atomic density distribution and suggest instead to produce directly a spatial distribution of labels (indicating the presence of things such as proteins and RNA). We achieve this by using low-level a priori knowledge regarding the possible arrangements of the various building blocks in a molecule and thus reformulating the reconstruction problem as an estimation problem. The mathematical and computational procedures that we have developed to solve this essential problem of electron microscopy are general enough to find immediate applicability in other areas of medical imaging (for example, for estimating the distribution in the body of various tissue types, as is needed for attenuation correction in single photon emission tomography or in treatment planning in radiation therapy) and in other fields such as materials science (see X. Fu, E. Knudsen, H.F. Poulsen, G.T. Herman, B.M. Carvalho, and H.Y. Liao, *Optimization of an algebraic reconstruction technique for generation of grain maps based on diffraction data* Proc. SPIE, vol. 5535, pp. 261-273, Developments in X-Ray Tomography IV; Ulrich Bonse (Ed.), 2004).