AMIR ASIF
York University

Application of Time Reversal Signal Processing in Radiotherapy

Medical applications of time reversal (TR) such as eradication of cancerous cells, magnetic resonance imaging (MRI) for breast cancer detection, and real time tracking of renal stones will be presented. A time reversal device has the ability of recording a signal; time reversing the recorded signal; and retransmitting the signal in the reverse direction from where the original signal was received. We derive maximum likelihood (ML) detectors to locate breast tumours based on a TR setup consisting of a P- element transmitting array and an N-element receiving array. A second medical application of TR considered in the presentation is the eradication of tumour cells using radiotherapy. Though the exact location of the infected cells is known but the propagation of the ultrasound within the human body has random fluctuations due to reflection, refraction and multipath effects. In such circumstances, it is often not possible to target the infected cells accurately, resulting in undesired destruction of the neighboring healthy cells. TR techniques are derived to achieve super resolution focusing at the tumour cells in such radiotherapy applications. We derive analytical results that provide insight into the phenomena of super resolution focusing associated with time reversal. Experimental simulations illustrate the superiority of our TR tumour detection and radiotherapy eradication techniques over the current approaches practiced by medical physicians.

BERNHARD BODMANN
University of Houston

Machine learning for automated classification in cell microscopy

This talk presents two applications of machine learning to classification problems in cell microscopy. The main purpose is to demonstrate the high degree of flexibility and reliability of this technology. The first part of the talk concerns the detection of leukemia in blood smears. This is done by classifying nucleus, nucleoli and cytoplasm, followed by higher-level morphological analysis. The second part of the talk is dedicated to classification in live-cell bright field microscopy, which complements information obtained with fluorescence microscopy for the purpose of tracking the cell cycle and for phenotyping.

JEFF COLLINS
The Medipattern Corporation

B-CAD Toward Consistent Detection and Diagnosis in Breast Cancer Sonography

Breast cancer is the most frequently diagnosed malignancy after lung cancer among women in the United States and Canada. It is estimated that approximately one in eight women will be diagnosed with breast cancer in her lifetime. Annual screening mammography has been recommended by the American Cancer Society for all women over the age of 40. Ultrasound imaging is an adjunct modality for breast cancer detection/diagnosis and provides reliable targeted screening of solid breast masses. Statistical studies indicate a 14To address and improve the identification and close observation of women who are at high risk of developing breast cancer the Medipattern Corporation has developed computer-aided detection and diagnosis technologies. B-CAD is a software package developed and designed to assist the radiologists in the process of detection and diagnosis of breast ultrasound lesions. B-CAD processes ultrasound scans, extracts the edges of the breast lesions, classifies them and generates reports according to BI-RADS (Breast Imaging-Reporting and Data System). B-CAD offers both options to semi-automatically or automatically segment breast lesions. The segmentation and delineation of lesions in ultrasound images by computer-based techniques is a very challenging task due to the low contrast and specular nature of the sonograms. Additional challenges in an automatic mass segmentation algorithm arise from the presence of tumor-like structures such as cooper ligaments, glandular tissue or subcutaneous fat and tissue related textures. Highly innovative and customized pixel classification techniques have been developed to overcome the inherent difficulties of the lesion segmentation in ultrasound images. Among others, B-CAD algorithms are capable of dealing with ambiguities and uncertainties resulting from anatomical complexities and modality-induced obstacles. B-CAD processes breast ultrasound images and generates several lesion candidates and automatically highlights the one with highest relevance. However, the radiologist has the option of selecting another lesion candidate, edit it using available functionalities and save it. Consequently, B-CAD calculates relevant morphological features such as margin, shape, orientation, echo pattern etc. in order to facilitate BI-RADS categorization of the lesion to determine further actions such as additional imaging studies or biopsy.

XIN GAO
York University

Model Selection and Network Construction For High-Throughout Biological Data

Gene-Gene dependency plays a very important role in system biology as it pertains to the crucial understanding of dierent biological mechanisms. High-throughput data provides a new platform useful to reveal the dynamic mechanism of gene-gene dependencies. In this talk, we will discuss three dierent approaches to construct a gene network. First we will review the model selection strategies in the construction of Bayesian network. Secondly we will discuss the constrained optimization problem in the modelling of Gaussain Graphical model. Third, we will discuss the choice of appropriate measure for gene-gene interaction for time series data. Various biological data set are analyzed to demonstrate the application of those methods and their implications in understanding the inherent biological mechanisms in cancer cell lines.

DAVID JAFFRAY
Princess Margaret Hospital

tba

EVA LEE
Georgia Tech

Robust Optimization to Accommodate Effects of Systematic Treatment Uncertainties in Intensity-Modulated Radiation Therapy

Efficient and reliable IMRT treatment planning is challenging even when using only a single frozen-in-time CT scan of anatomic structures. The challenge is intensified in 4-D treatment planning, which is based on highly expanded imaging datasets that provide views of structure shape and position shifts over time. Incorporating these expanded datasets into the treatment planning process has the potential to yield better treatment plans, but at the same time results in models and optimization problems that are several magnitudes larger than those associated with traditional single-time-period planning. And along with the increase in problem size, there are additional sources of uncertainty and error (e.g., uncertainties in breathing trajectories, errors in organ contour outlining related to the increased number of images). Treatment planning methods must therefore be developed that can accommodate the increased problem size, and at the same time compensate for the errors and uncertainties. In this talk, we describe various mathematical models for such robust and adaptive large-scale planning methods. Their mathematical

complexity will be analyzed, and theoretical results will be described. We will demonstrate that our methods allow a significant reduction in mean dose to normal tissue, and in some cases, higher dose to tumor volume.

HENGGUANG LI
Penn State

Preliminary Results in MRE: a Finite Element Approach

abstract tba

RODERICK MELNIK
Wilfrid Laurier

Studying Properties of RNA Nanostructures and Their Potential Applications

abstract tba

ROSS MITCHELL
Calgary

Virtual Biopsies: Non-invasive Molecular Diagnosis of Cancer

Our expanding knowledge of the genetic basis and molecular mechanisms of cancer is beginning to revolutionize the practice of clinical oncology. Increasingly, molecular biomarkers of prognosis and treatment response are being used to classify tumors and direct treatment decisions. Advanced medical imaging platforms such as MRI, PET, and CT provide incredibly detailed images of tumors that reflect their structure, biochemistry, physiology and perhaps genetics. Studies by the Imaging Informatics Lab at the University of Calgary, and others, show that information about a tumors molecular phenotype can be obtained by using novel algorithms and computational tools to more fully analyze tumor images. Such virtual biopsies, performed by applying these image-processing and machine learning techniques to routine diagnostic images (e.g. MRI, PET or CT), could be a rapid and powerful means of assaying important cancer biomarkers. If successfully validated, and proven to have suitable sensitivity and specificity, the use of non-invasive imaging-based molecular diagnostic tests would offer significant advantages over conventional surgical biopsies. For example, this could be important in the context of large heterogeneous tumors, multiple metastases, surgically inaccessible tumors, and settings where disease progression needs to be monitored frequently over time. Virtual biopsy research lies at the intersection of molecular imaging, medical imaging physics, and biocomputation, and is highly complementary to these areas. This presentation will cover

key enabling technologies behind virtual biopsies, and discuss some recent progress in this research.

ALESSANDRO OLIARO
University of Torino

Time-Frequency Representations and Applications to Signal Analysis

We are concerned with the problem of analyzing a signal, looking for the frequencies that it contains, and at which times they appear. Various types of time-frequency representations are studied, in the frame of the Cohen class; in particular, the classical and generalized spectrogram are considered, as well as Wigner type transforms. We then analyze the problem of filtering a signal, studying various kind of operators in the frame of the pseudo-differential calculus.

NATALIYA PORTMAN
University of Waterloo

Estimation of growth parameters of the Drosophila's wing disc development from a sequence of micrographs using the Growth as Random Diffeomorphisms Model

An optical imaging technique called confocal microscopy has been gaining popularity in the biological science community for its capability to visualize genes in action in embryos. Gene expression patterns seen in micrographs reveal the positions and shapes of structures long before they actually form. Having acquired such images for larval growth of Drosophila wing disc, the question arises how they can be used to infer the properties of growth. This is a challenging image understanding problem, and in my talk I will address it using a pattern theoretic model for biological growth called GRID (Growth as Random Iterated Diffeomorphisms). One of the GRID parameters, the growth magnitude,characterizes the local expansion(or contraction)rate throughout the wing disc cellular field. I will propose its estimation directly from the image data based on an appropriate optimization problem formulation and further application of Polak-Ribiere minimization algorithm. The estimate of this parameter will automatically allow estimation of the diffeomorphic transformation underlying the dynamics of gene expression patterns seen in given micrographs."

The results that I will demonstrate (including a movie of evolving in time optimal transformation applied to the initial curvilinear coordinate system of the wing disc!) are preliminary but promising. It is possible that the distribution of the growth magnitude that I have obtained is biologically meaningful. That is, we can see the locations of dividing cells that push the extant ones thus causing local contractions of the cellular

field. I am still waiting to hear an opinion from Sean Carroll, a distinguished biologist, who wrote a book "Endless forms most beautiful".

ABBAS SAMANI
University of Western Ontario

Fast Finite Element Technique for Real-time Biomedical Applications

Medical simulation tools have a potential of revolutionizing the practice of medicine by assisting clinicians in carrying out difficult medical procedures. For example, Simulation tools capable of predicting tissue mechanical response can provide clinical therapy learning environment via virtual reality. While such tools improve training proficiency, they enhance patient safety and cost less compared to conventional training on real patients. Intraoperative image based clinical procedures where images are updated to account for tissue deformation during medical procedures is another area where such simulation tools play a very significant role. Brachytherpay of the prostate, breast or lung are examples where these tools can be used effectively to update preoperative high quality images for the purpose of accurate placing brachytherapy seeds. While Finite Element (FE) Analysis is known as an accurate method in finding soft tissue deformation, it is not fast enough in applications where real-time simulation of tissue mechanical response is needed. In this presentation, a novel technique based on FE analysis will be introduced for estimating soft tissue deformation. This technique has proven to be not only accurate, but also very fast. The technique can be applied for real-time or near real-time soft tissue deformation calculation irrespective of the complexities arising from the tissue constitutive law or loading. To calculate the deformed shape of an organ, the technique involves a preprocessing step in which FE analysis is performed on a model class of corresponding organ obtained from a large number of subjects, followed by statistical analysis. Given the high degree of similarity between the shapes of each specific organ in different subjects or between shapes of a patient's organ over time, this technique is ideal for applications where real-time or near real-time estimation of a specific organ deformation is desired. To validate this technique and demonstrate its capabilities in clinical procedures, a number of biomedical applications will be shown including prostate elastography.

COLIN STUDHOLME
UC San Francisco

In utero mapping of brain tissue growth patterns from clinical MRI of developing human fetuses: An emerging field of image analysis research

Understanding normal and abnormal patterns of large scale tissue growth in developing humans is a key area of research, with many applications in clinical and basic sciences. This talk will describe the recent development of techniques that allow the formation and analysis of high resolution 3D MRI data of the developing human fetal brain in utero. The talk will describe the basic challenges to imaging tissue structure in the human fetus and current clinical diagnostic imaging techniques being used. A review of algorithms to form true 3D MR images from clinically acquired imaging data will be presented. These approaches are aimed at estimating and correcting for fetal motion occurring during MR imaging, allowing the creation of a set of motion corrected data points from which we can form 3D images of the brain tissue. Approaches to automated tissue segmentation of developing brain tissue types from reconstructed 3D images will be described. These are aimed at delineating both developed and transient tissue structures present in fetal brain anatomy. Finally, methodology to analyse the tissue volume, cortical thickness and surface folding will be described, with preliminary results on fetal and neonatal brain anatomy.

ELI VAN HOUTEN
University of Canterbury

Model Based Reconstructive Elasticity Imaging: Finding a Best Fit Between Imaging Goals and Computational Methods

Elastography, the imaging of soft-tissue elasticity, is a rapidly expanding field with a number of viable methods currently being developed in parallel. These methods are distinguishable based on the source of their raw data (most commonly ultrasound or MRI), on the manner in which the data is collected (either quasi-static, transient dynamic, or time-harmonic), and the manner in which the motion data is converted into an elasticity image (ranging from direct processing of the measured data to large scale optimisation based inverse problems). This talk explores the relation between some of these choices and the overall goal for the resulting image, i.e. is Elastography part of the screening process, the diagnostic process, or some mixture of both. The talk will look into how the computational problem changes as the quantity and quality of the data changes, and also some of the computational modelling techniques available for processing the available motion information. Specific topics include: digital image based elastographic methods; boundary element methods; shape function geometric discretization; MR Elastography,

finite element methods; more sophisticated material models; imaging results in phantom and in vivo experiments.

YURIY ZINCHENKO
University of Calgary

Multiple gEUD-type constraints for radiotherapy optimization

Radiation therapy is a well established modality for treating various cancers. Planning for radiotherapy typically involves solving an inverse problem to find a clinically suitable plan. Optimization models and methods are used to address this task. During the planing, one of the most clinically relevant treatment planning objectives is to find a treatment plan that satisfies the so-called partial volume constraints on the resulting dose distribution. A conventional mixed-integer formulation of these partial volume constraints leads to a computationally intractable model which in practice becomes extremely difficult to solve. We analyze the effects of multiple gEUD-type constraints on the resulting dose-volume distribution – a convex and tractable alternative to partial volume constraints. The analysis relies on interpreting the dose distribution as a cumulative probability distribution of the underlying random variable that represents the dose to the treatment volume. Consequently, the above problem is rephrased in terms of a well studied problem of moments. We illustrate our approach on one organ at risk for prostate cancer.