Analysis of Microscopy and Reconstructive Images for applications in Medicine and Biology

Organisers:
Prof. Laure Blanc-Feraud (CNRS, I3S Sophia Antipolis, France)
Prof. Dave Burton (Liverpool John Moores University, UK),
Dr Aymeric Histace (University of Cergy-Pontoise, France),
Dr Bogdan Matuszewski[1] (University of Central Lancashire, UK),
Prof. Chris Moore (The Christie Hospital NHS Foundation Trust, UK),
Dr Frederic Precioso (Pierre and Marie Currie & Sorbonne University, France)

The aim of the proposed special session is to provide forum for dissemination of the most recent results and ideas in the field of automated analysis of biological microscope and medical reconstructive images. The principal focus of the session will be on image based analysis of 3D cytoskeletal structures. It is also hoped that the session would provide a platform for identifying similarities in analysis of highly complex, seemingly disordered, data acquired both on micro and macro imaging levels. It is expected that the session will attract researchers working in the emerging interface of mathematics, physics, engineering and biological sciences.

In the recent years the field of biological microscopy and reconstructive imaging and analysis has undergone a step change due to a number of significant advances, both in imaging technology and software analysis tools. For example with the reconstructive imaging and virtual microscopy being more and more prevalent, a use of fully automatic analysis methods, such as: detection, segmentation and classification; handling effectively vast data sets (in access of 3 billion pixels/voxels for single clinical investigation) are now often unavoidable. Such vast amount of quantitative information enables also statistical analysis of inherent variability of biological and anatomical structures of interest, requiring effective tools for registration, motion analysis and tracking in time-lapse image data. Additionally combination of different in-vivo and in-vitro imaging techniques has enabled measurement of different micro structural parameters providing multimodal information for construction of more accurate models at intra-, inter- and cellular levels. Deformable anatomical modelling from reconstructive imaging is now leading to adaptive medical procedures. In combination with other advances in biology, medicine, engineering and mathematical modelling this also gives a promise of a better understanding of a joint macro and micro manifestation of clinical conditions.

Although the session would touch on a number of general issues related to biological microscopy and reconstructive imaging introducing these exciting fields to the general image processing community, not the least through a number of invited talks from leading experts in the filed, the main focus will be on imaging, detection, segmentation, analysis, modelling and visualisation of cytoskeleton. The cytoskeleton is a fabulously complex, dynamic three-dimensional structure that has number of diverse functions in cell biomechanics. It has been shown that it has an important role, for example, in supporting cell structural integrity, cellular division and intra- and inter- cellular transport. Analysis of its properties can be instrumental in more comprehensive understanding of a number of clinical conditions; for example it has been widely recognised that cancer is associated with changes in cytoskeletal structures. Till recently however, the cytoskeleton was evaluated and judged in a purely qualitative way. Recent advances in cytoskeletal imaging promise availability of its more robust, accurate and quantitative image based descriptors.
Although the main theme of the session will be on imaging and analysis of complex cytoskeletal structures the high quality papers addressing other topics in molecular, intracellular, cellular, multi-cellular and tissue level microscopy imaging and analysis would also be considered.
Indicative list of the topics of interest:

- Current advances in microscopy imaging techniques and data acquisition, including: imaging techniques for acquisition of high resolution cytoskeleton images; confocal, fluorescence, optical, atomic force, electron, scanning, infrared, virtual, molecular reconstructive imaging, morphological reconstructive imaging and modelling.
- Detection, segmentation and classification of cells, cytoskeletal microtubules, actin and intermediate filaments.
- Estimation/extraction of cellular parameters.
- Motion and deformation analysis and tracking.
- Registration of microscopy and reconstructive images.
- 2D and 3D Shape and morphology analysis.
- Multi-spectral, and multimodal analysis.
- Efficient GPU implementations.
- Descriptors for highly complex data, and machine learning.
- Visualisation of large-scale multimodal microscopy and reconstructive images.
- Modelling on intra-, inter- and cellular levels through to organs.
- Micro and macro data interaction modelling.
- Applications in: diagnosis, histopathology, mass screening, cell biology, tumour identification and normal organ response modelling etc.

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1. Title of the special session

Analysis of Microscopy and Reconstructive Images for applications in Medicine and Biology

2. A description of the session

The aim of the proposed special session is to provide forum for dissemination of the most recent results and ideas in the field of cell, micro- and nano- scale imaging, automated analysis of biological microscope and medical reconstructive images. The principal focus of the session will be on image based analysis of 3D cytoskeletal structures. It is also hoped that the session would provide a platform for identifying similarities in analysis of highly complex, seemingly disordered, data acquired both on micro and macro imaging levels. It is expected that the session will attract researchers working in the emerging interface of mathematics, physics, engineering and biological sciences.

So far the session organising committee has secured ten high quality contributions to the proposed session. The contribution span topics from complex tissues network description and quantification, objective and perceived image quality, micro- and nano- imaging, through analysis of atomic force microscopy imaging data (relatively novel modality for the image processing community) to quantifying disorder in microscopy images and last but not the least estimating structure behind seemingly unstructured data. It is hoped that the session would provide a platform for identifying similarities in analysis of highly complex, data acquired at nano- micro- and macro imaging levels. From an informal discussion within imaging community it can be concluded that many more papers could be potentially submitted to this session.
It is planned that the session will focus on the above mentioned topics. It is proposed that the session should be concluded with an open “round-table” discussion forum tackling some of the topics addressed during the session. It is envisaged that such discussion will be moderated towards identifying essential problems which are still unsolved, as well as the current state-of-the-art in processing, analysis and visualisation of complex micro- and nono-structures.

It is proposed that if the number of accepted papers exceeds the limit suitable for an oral session, an associated poster session should be considered as a possibility of accommodating such submissions.

3. Invited papers tentative titles and abstracts

Paper 1

Micro-Tomography Volumes

Xavier Descombes
CNRS I3S laboratory, INRIA ARIANA group, Sophia Antipolis, France

In this study we consider 3D volumes representing brain micro-vascular network. The data consists of X-ray micro-tomography at 1 micrometer resolution. We segment the vessel network into tumor and normal tissue. The segmentation is performed by a 3 steps approach. The first step consists in binarizing the data. Some cutting in the network may appear due to noise in the data. We thus re-connect the network using a tensor voting based on approach. The segment step consists in defining region corresponding to local vascular territories. To this purpose, we first compute a distance map where the distance to the nearest vessel voxel is computed on each point. This distance map is then segmented using a watershed algorithm. The different obtained regions are finally labeled as tumor or normal. The labeling is obtained by a conditional random field modeling the graph associated to the watershed segmentation.
We have segmented different volumes corresponding to different delays after radiotherapy treatments. Based on the region graphs in the tumor and in normal tissues, we first show statistics characterizing normal versus tumor tissues. We then study the evolution of these statistics after the treatment.

Paper 2

Compressed-sensing applications in biological imaging

Marcio Marim, Yoann Le Montagner, Michael Atlan,
Elsa Angelini, Jean-Christophe Olivo-Marin

Institut Pasteur Unité d'Analyse d'Images Quantitative CNRS URA 2582

This paper will provide a review of Compressed Sensing (CS) for image quality enhancement and acquisition in biological microscopy developed in recent years. The paper will address four specific topics: (i) Algorithmic design optimization of a CS-based denoising framework exploiting a Total Variation sparsity prior and very limited number of fluorescence measurements in the Fourier domain, (ii) denoising experiments on fluorescence image data demonstrating that CS can be used as a processing tool to improve image quality while reducing the photobleaching effects, (iii) CS-based reconstructions combining Fourier magnitude measurements and Fourier phase estimation for sequential microscopy image acquisitions, (iv) a microscopy image acquisition setup successfully exploiting CS on a random-access CCD camera for digital holography. CS applications in biological imaging are actively pursued in different laboratories and are indeed a very active field of research both in the instrumentation and in the signal processing communities. The presented methods are expected to greatly improve many microscopy applications, allowing the acquisition of high-dimensional data with reduced acquisition times and opening the door to new acquisition protocols.

Paper 3

3D Microscopic imaging by Synchrotron Radiation Nano-CT

Françoise Peyrin

CREATIS, CNRS 5220, INSERM U630, INSA Lyon, Université de Lyon and ESRF, Grenoble

Biological microscopic imaging is receiving increasing interest with a bunch of new emerging modalities. In this domain Synchrotron Radiation (SR) Nano-CT opens new opportunities to image biological tissue at sub-micrometric scale and in 3D.
We shall first recall the principle of SR μCT and its advantages over standard X-ray micro-CT in terms of accuracy and signal to noise ratio to image biological samples at the micrometer scale. Then we shall briefly present two approaches that are currently developed at the ESRF (European Synchrotron Radiation facility) to reach nanometric spatial resolution, one based on parallel 3D CT and the second one on divergent CT with a Kirkpatrick-Baez optic. While in the first case image reconstruction is simply based on the standard filtered back projection algorithm, in the later case it involves a preliminary step of phase retrieval that will be described.
Applications of this technique in bone research associated to specific image analysis developments will be shown. At the micrometer scale, we shall present data on the analysis of trabecular and cortical bone in human and mice. At the nanometer scale, we shall present recent data on the osteocyte system that has so far never been investigated in 3D. Open problems for the segmentation and quantification of the complex canaliculi network will be highlighted.
In conclusion, SR nano-CT associated to dedicated image analysis is expected to yield new and unique volumetric data on biological systems at the cellular scale.

Paper 4

The Formulation Of A Non-Linear Hertzian Model In Order To Assess The Mechanical Strength Of Human Cells Based On Data From An Atomic Force Microscope

D.R.Burton, M.F.Murphy, F.Lilley and M.A.Gdeisat

General Engineering Research Institute, Liverpool John Moores University, Liverpool, UK.

There has recently been a significant growth in interest in determining the mechanical properties of living human cells. Much of this work has centred around the application of the Hertz Contact Stress model to force/displacement curves that are obtained from atomic force microscopy. However, it is widely recognised that the conventional Hertzian approach, based upon a linear elastic model for the stress strain relationship of the material, is inadequate for accurately modelling and describing the behaviour of living cells under load. This paper presents a new non-linear extension of the Hertzian model and shows results that provide excellent agreement with experimentally obtained force/displacement data from a range of different cell types. Furthermore the paper goes on to show the way in which the model can be used as a tool to distinguish between different populations of cells of different types, morphologies, or pathological status.

Paper 5

A Novel Technique For The Restoration Of Atomic Force Microscope Images Enabling An Approximation Of AFM Impulse Response

A. Ahtaiba, M.A.Gdeisat, D.R.Burton, F.Lilley and M.F.Murphy

General Engineering Research Institute, Liverpool John Moores University, Liverpool, UK.

All atomic force microscopy (AFM) images suffer from distortion, which is principally produced by the interaction between the measured sample and the AFM tip. If the three-dimensional shape of the tip is known, the distorted image can be processed and the original surface form 'restored', typically by deconvolution approaches. This restored image gives a better representation of the measured sample than the original distorted image. In this paper, we propose a method for estimating the three-dimensional shape of the AFM tip by measuring a micro-cylinder with a-priori known dimensions. The estimated tip shape is then used to restore AFM images, when measured with the same tip, under similar measurement conditions. Significantly, the impulse response of the AFM can be deduced using this method. The suitability of this new approach for restoring AFM images has been confirmed using both computer simulation and real AFM images. The proposed method is compared with standard restoration techniques and is shown to provide superior performance.

Paper 6

The Use Of Image Processing Techniques To Investigate Orientation Properties Of *Ex Situ* Polymerised Actin Filaments

G. Johnston[1], D.R.Burton[1], F.Lilley[1], A. Doyle[1], M.F.Murphy[1], G. Madden[1], M.A.Gdeisat[1], C. J. Moore[2], T. Marchant[2] and B. Matuszewski[3]

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This paper describes an investigation into whether orientation preferences are shown by *ex situ* polymerised actin fibres. The approach contrasts the use of the Hough transformation against morphological thinning, when processing images of *in vitro* actin, which were produced by Atomic Force Microscopy (AFM). Actin is a primary component of the cytoskeleton and is believed to play a vital role in cell structure. Images of actin structure produced by AFM were analysed using automated pre-processing stages. These steps were identical for the production of an initial binary image, and the image was then processed by both Hough transformation and by morphological thinning approaches. The results obtained question the validity of the Hough transform method, as the introduction of bias appeared to be systemic, and this bias could not be eliminated. As a result the Hough transform approach proved to be unsuitable for this investigation and the thinning technique was therefore used to successfully identify and locate actin orientation. Actin appears to display a bimodal distribution with a 90 degree separation, with a significant coefficient of bimodality of 0.656.

Paper 7

Quantifying structure regularity in fluorescence microscopy cell images using a novel multi-dimensional approximate entropy metric

TE Marchant[1], MF Murphy[2], GP Madden[2], CJ Moore[1]

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[2]General Engineering Research Institute, Liverpool John Moores University, Liverpool, UK.

Techniques such as fluorescence microscopy reveal in three dimensions the complex mechanical structure of the cell cytoskeleton, made up of actin filaments, microtubules and intermediate filaments. Methods to quantify the degree of order in this structure could prove useful in classifying cells and may be related to structural integrity of the cell. Approximate Entropy (ApEn) is a regularity statistic that has previously been used to quantify randomness in 1D time series data. We have extended the ApEn concept to define a multi-dimensional parameter suitable for application to three dimensional image data. This 3D ApEn parameter was applied to fluorescence microscopy images showing actin filaments in normal and cancerous human prostate cells. Differences between the ApEn calculated from the different images were observed, with cancer cells tending to have higher values indicating a lower degree of order.

Paper 8

Seeing and Quantifying Structure: Convergence of Biomedical and Perceptual Image Descriptors

Christopher John Moore

North Western Medical Physics, The Christie NHS Foundation Trust, Manchester,UK

What we see and how we see structure in biomedical images can now be reconciled with our quantification of structure using advanced descriptors. A deeper understanding of the information bounds set by optical transfer functions coupled with that of phase and phase congruency has leveraged advances in feature detection and can explain the reluctance of bio-medical professionals to discard even the least significant bits of some pictures. However, the methods adopted by skilled and professional image interrogators are rarely observed or recorded. Nor have they been linked to the latest advances in our understanding of both image processing and the spatio-temporal performance of the human visual system, including internal noise and stochastic resonance. This paper addresses that deficiency and introduces a novel extension of regularity statistic approximate entropy to higher dimensions, so that threshold structure in bio-medical images can be quantified in a self calibrating manner.

Paper 9

Histogram based segmentation using active contours: α-divergence as a distance function for medical image segmentation

L. Meziou[1], A. Histace[1], F. Precioso[1,2], B. Matuszewski[3]

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Image segmentation of biomedical and medical data is a challenging problem due to the large variety of acquisition devices (MRI, TEP, X-RAY, CT-Scan, Cone-beam CT, 3D confocal microscopy) and above all because of the associated acquisition noises (Gaussian, Poisonian, Ricien, Rayleigh, Speckle…). In the framework of region based active contours segmentation, some recent studies have shown that it was possible to define, in a variational framework, a functional that takes into account the distances between probability density functions (pdf) of the inner and outer regions of the moving curve as a criterion of evolution with respect to given pdf references. Common distances used to compare pdf are Chi-2 distance, the Kullback-Leibler divergence, the Hellinger/ Bhattacharya distance and more recently the Wasserstein distance. In this article, we propose to introduce the α-divergence measure. This choice is mainly motivated by the fact that this particular distance embeds the aforementioned classical ones (except Wasserstein distance) with respect to the value of α, and can provide a more important variety of configurations. The work presented here is focused, first, on defining the Partial Differential Equation (PDE) associated to α-divergence criterion that will lead the iterative deformation of the active contour and second, on the estimation of the performances of this criterion (precision, speed of convergence, robustness to both level and type of noise) compared to classical distances. Some practical experiments are also presented on different types of biomedical and medical data.

Paper 10

Reconstruction of 3D cellular structures from actin tagged fluorescence confocal microscopy images

B.J. Matuszewski[1], H. Gao[1], M.F. Murphy[2], D.R Burton[2],
T.E. Marchant[3], C.J. Moore[3], A. Histace[4], F. Precisoso[4,5]

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Actin is a principal component of the cytoskeleton playing an important role in cell biomechanics. Studies of its properties can be enhanced by providing information about its distribution within cells population. To address this, the propose paper will describe a method for recovery of cellular shapes (nucleus and cell membrane) from actin tagged fluorescence confocal microscopy images, and thereby providing spatial context for subsequent quantitative analysis of actin properties.

This task is very demanding due to a highly complex actin appearance, high level of noise and strong non homogeneity of the intensity and gradient information of such images. The problem is

further compounded by the missing, in places, indicators of cellular structures as well as presence of spurious indications of the cell membrane due to actin forming bundle like shapes in the intercellular space.
We propose to reconstruct 3D cellular shapes, in such data, using a novel multiphase level set segmentation framework where prior topological information and learned statistics of actin appearance and shape are applied to steer evolving contours to achieve robust results. In this framework, multiple contours representing each cell structure and intercellular space advance using different evolution rules designed to match the learned properties of the structures these contours represent. Contour evolutions are then carried out simultaneously in such a way that contours interact with each other, using a newly proposed framework, in order to keep the topological relationships and prior information about actin appearance consistent. The proposed method is fully automatic which include the multiphase level set initialisation.

5. List of authors who have agreed to present a paper

Françoise Peyrin
Jean-Christophe Olivo-Marin
Xavier Descombes
Dave Burton
Gary Johnston
Mark Murphy
Tome Marchant
Christopher Moore
Aymeric Histace
Frédéric Precioso
Bogdan Matuszewski

5. Brief biographies of the invited speakers

Professor Françoise Peyrin
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Françoise Peyrin received her PhD in Computer Sciences in 1982, and her " Docteur ès Sciences " degree, both from the University of Lyon and the National Institute of Applied Sciences (INSA-Lyon), France, respectively in 1982, and 1990. Since 1981, she has been a research scientist in the CREATIS Laboratory (CNRS #5220, INSERM U630) at INSA-Lyon and University of Lyon specialized in medical imaging and gathering about 180 staff. Since 1994, she has been a scientific collaborator at the ESRF (European Synchrotron Radiation Facility), Grenoble, France. She is leading a team on "Tomographic Imaging and Therapy with radiations" at the CREATIS Lab. Since 2007, she has been serving in the French GDR "Stic Santé" that she will lead in 2011.
Her research interest is in 3D biomedical imaging particularly in X-ray tomography, tomographic image reconstruction, image analysis and wavelet based methods. She is particularly developing new image analysis methods for the characterization of bone tissue at different scales. She has published more than 110 papers in peer reviewed journals, 15 book chapters and more than 300 papers in international conferences.
Since 1984, she has been a member of IEEE (# 03704517) and EURASIP and she has served in the IEEE BISP (Biomedical Image and Signal Processing) technical committee since 2004.

Professor Jean-Christophe Olivo-Marin
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J.-C. Olivo-Marin is the head of the Quantitative Image Analysis Unit, and the current Chair of the Cell Biology and Infection department, at the Institut Pasteur. He holds a Ph.D. and an H.D.R. in Optics and Signal Processing from the Institut d'Optique Théorique et Appliquée, University of Paris-Orsay, France. He was a co-founder of the Institut Pasteur Korea, Seoul, where he held a joint appointment as Chief Technology Officer from 2004 to 2005. Previous to that, he was a staff scientist from 1990 to 1998 at the European Molecular Biology Laboratory, Heidelberg. His research interests are in image analysis of multidimensional microscopy images, computer vision and motion analysis for cellular dynamics, and in multi-disciplinary approaches to biological imaging. He is a Senior Member of IEEE, a member of SPS and EMBS, Chair of the Bio Imaging and Signal Processing Technical Committee (BISP-TC), member of the Pattern Recognition Society and of the Editorial Board of the journal Medical Image Analysis. He has organized several special sessions dedicated to biological imaging at international biomedical conferences (ELMI'02, ELSO'03, ISBI'04, ICASSP'06, SPIE Wavelets'09) and was General Chair of the IEEE International Symposium on Biomedical Imaging (ISBI) in 2008.

Professor Xavier Descombes
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Xavier Descombes received the bachelor's degree in telecommunications from the Ecole Nationale Superieure des Telecommunications (ENST) Paris, France, in 1989, the master of science in mathematics from the University of Paris VI in 1990, the PhD degree in signal and image processing from the ENST in 1993 and the ``habilitation'' in 2004 from the University of Nice Sophia-Antipolis. He has been a postdoctoral researcher at ENST in 1994, at the Katolieke Universitat Leuven in 1995, at the Institut National de Recherche en Informatique et en Automatique (INRIA) in 1996 and a visiting scientist in the Max Planck Institute of Leipzig in 1997. He has obtained the price of "La recherche" in the human health category in 2008 and is author or co-author of more than 100 papers. He is currently at INRIA as director of research. His research interests include Markov Random Fields, stochastic geometry and stochastic modeling in image processing.

Dr Thomas Marchant,
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Thomas Marchant is a medical physicist at Christie Hospital, Manchester, UK, where he holds a research post for development of software and facilities for image guided radiotherapy. He also holds honorary positions at the Universities of Manchester and Bath in recognition of his contribution to research and academic work. His current research interests include image guidance in radiotherapy using cone-beam CT, methods for image reconstruction and artefact reduction, analysis of image quality from clinical images, and effects of motion in radiotherapy. He is author of over 40 peer reviewed journal papers and conference presentations and is currently co-investigator on two research grants from the UK National Institute for Health Research and the Engineering and Physical Sciences Research Council. His work on “cone-beam CT correction software for adaptive radiotherapy” was shortlisted for a North West NHS Innovations award in 2009.

Biographies of the remaining invited speakers can be found in the next section

6. Contact information and biography of the session organizers

Professor Laure Blanc-Feraud

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Laure Blanc-Feraud got the PhD degree in image restoration in 1989 and the "Habilitation a Diriger des Recherches" on inverse problems in image processing in 2000, both from the University of Nice-Sophia Antipolis, France. She is currently director of research at CNRS in Sophia Antipolis in south part of France and work since 1998 in a joint research group with INRIA (Ariana). Her research interests are inverse problems in image processing by deterministic approaches using calculus of variation and PDEs. She is also interested in stochastic interpretation of these models for parameter estimation. Application domains are currently Earth observation by satellite 2D imagery and biological 3D microscopy imagery. She has got several collaborations with French industries (SAGEM, CNES, THALES ALENIA SPACE) and has been PI of one national French ANR (National Agency for Research in France) project on fine structures detection in images.
She has published around 50 papers in referred international journals or chapters of books and is a regular reviewer for journal and conferences in the field of image processing. She is currently member of the IEEE Technical Committee BISP (associate 2007-2009).
She has responsibilities at French national level including vice director of the national French group gathering together researchers in the area of Signal and Image processing (GDR ISIS). This group includes a hundred of French laboratories in electrical engineering, signal and image processing informatics. She was member of a steering committee of the National Research Agency ANR (07-09), vice-director of the I3S laboratory (04-08) including more than 100 permanent professors and researchers).

Professor David. R. Burton

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David. Burton is the Director of the General Engineering Research Institute of Liverpool John Moores University, located in the Northwest UK. A Chartered Engineer and renowned scientist, he gained his Ph.D. in 1987 and was given his chair in Engineering Science in 1996. He was Director of the School Of Engineering at LJMU for five years before founding the General Engineering Research Institute in 2002. He has led the School and Institute to three consecutive outstandingly successful results in the UK Government's Research Assessment Exercises. In the 1996 and 2001 RAE's he presided over submissions that were ranked at the highest Grade 5,

indicating research of an international standard of excellence. In the latest RAE2008 the Institute received a quality profile with a weighted average score of 2.7 in the General Engineering Unit of Assessment. This rated 20% of all GERI's research as being world-leading, whilst another 40% was viewed as being internationally excellent, with a further 30% ranked as being of international standard and the remaining 10% of a national standard. Hence under Prof. Burton's leadership 60% of all GERI's research is deemed to be of internationally excellent, or higher, quality.
His research interests are centred around 3D Machine vision, non-contact measurement, digital image processing and cellular biomechanics. Prof. Burton has published over one hundred papers on measurement/modelling and has supervised over 30 PhD's. He has extensive project management experience and has collaborated with leading laboratories in Europe including the Grand Ecole Superior de Lyon, the Federal German Research Institute for Materials, the University of Leuven and the University of Uppsala. He has been an invited adviser to the Irish Department Of Education and is a regular international expert reviewer for the Annual Grant Scheme of the Finnish Academy of Sciences. He has active research links with a number of other universities in Europe, the USA and Far-East. In recent years GERI has been active in cross-disciplinary research with life-scientists in the School of Biomolecular Sciences at LJMU. This research centres around investigating the mechanical properties of living human cells. Under Prof. Burton's leadership, this cell mechanics group has developed many techniques for 3D nano-metrology on living human cells, using AFM and confocal/fluorescence microscopy. As part of this work Prof. Burton has personally developed a novel non-linear constitutive mathematical model for individual cells, linking force applied by AFM and cellular deformation.

Dr Aymeric Histace

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Aymeric Histace holds position of an Associate Professor at the University of Cergy-Pontoise, since September 2006. He is a member of the ETIS Lab (UMR CNRS 8051) in the Imagery, Communication, and Information (ICI) team. He has a PhD in image and signal processing from the University of Angers. His main research interest is in image and signal processing for computer aided medical diagnosis. He is currently leading the image processing for computer-aided diagnosis activities at the ETIS lab.
He has published 30 research papers in image processing (conferences and journal papers) focused mainly on medical application. Recently, he has participated in the "Engineering and Computational Sciences for Oncology Network (ECSON)" (www.ecson.org) project which involved 10 partners from 5 European countries and was funded by the British research funding council EPSRC. In that framework, he is in charge of the coordination of the collaborative research developed between the ADSIP Research Center of the University of Central Lancashire (Preston, UK) and ICI team.
He is also a reviewer for international journals (*Pattern Recognition Letters, Journal of Electronic Imaging*) and for several international conferences including ICIP, MICCAI and VISAPP. He was a member of the organizing committee of the special session on Engineering and Computational Sciences for Medical Imaging in Oncology (ECSMIO) at the VISAPP 2010 conference (Angers, France).

Dr Bogdan Matuszewski

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Bogdan Matuszewski obtained an MSc in electronic instrumentation in 1990 and gained a PhD in 1996 for the work on signal deconvolution, both from Wroclaw University of Technology (Poland). He holds position of a Reader in computer vision and heads the Robotics and Vision Laboratory at UCLan. He has published over 80 research papers in different areas of computer vision and image processing and successfully supervised 10 PhD students. His recent research interest is focused on a use of Bayesian methodology in combination with PDE-based data processing for modelling, classification and tracking with applications to deformable data segmentation, registration and reconstruction. Currently, he is leading a major research project "Technology in Radiotherapy Feasibility Studies (TeRaFS)" (www.uclan.ac.uk/terafs), funded by the UK's Engineering and Physical Sciences Research Council (EPSRC), where he works on analysis of complex 3D cytoskeleton structures from fluorescence confocal microscopy images, as well as on predictive analysis of facial dysfunctions for head & neck cancer patients. He was a principal investigator for other two recently completed EPSRC projects, the "Metrology Guided Radiation Therapy (MeGuRaTh)" (www.uclan.ac.uk/megurath) and "Engineering and Computational Sciences for Oncology Network (ECSON)" (www.ecson.org), were he collaborated with 10 partners from 5 European countries. More recently he has started to work with NASA on the "High Resolution Coronal Imager (Hi-C)" project. In the past he participated/led research in another eleven EU, UK Research Councils and industrial funded projects. These among others included: "Platform for analysis of multispectral and hyperspectral images from acquisition to interpretation for environmental monitoring and decision making (PIMHAI)" and "Integration of Non-destructive Testing (INDeT)" funded under the FP6 programme. He has been sessions' chair and member of program & reviewing committees for IEEE MediViz, GAMI, VISAPP conferences and the technical chair for the AECRIS conference. He has served as a reviewer for the IEEE and the EPSRC. He has numerous active collaborative links with industry and various universities across Europe.

Professor Christopher Moore

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Chris Moore Graduated with a 1st class Hons BSc in Physics from The University of Manchester in 1976 and joined the Diagnostic Radiology and Radiation Protection group in North West Medical Physics (NWMP) at the Christie Hospital. He gained an MSc in Computational Physics from The University of Salford in 1982, then completed his PhD in CT image encoding at The University of Manchester in 1988 after joining the Radiotherapy Physics group.
As a Senior Physicist (1982-87) he worked on digital image processing for diagnostic radiology and developing CT image assisted intra-cavitary dosimetric planning. As a Principal Physicist he

worked in radiotherapy physics until 1995, developing image-assisted 3D treatment planning for conformal radiotherapy delivery systems using configurable multi-leaf X-ray collimation. From 1995-2009 he was a Consultant Clinical Scientist, leading the Developing Technologies Radiotherapy Physics Section focusing on 'in-treatment' dynamic patient optical body sensing, X-ray image guided radiotherapy, structural and shape analysis in reconstructive imaging, quantification of speech and endocrine disruption post-treatment. He now leads the Developing Technologies Group, helping to grow research and development across NWMP.
He has led eight EU and EPSRC grants in the last decade and is currently engaged in collaborative projects aimed at developing dynamic sensors and image guidance for use by clinicians and patients during radiotherapy. These include the EPSRC funded Metrology Guided Radiation Therapy project and the associated Engineering and Computer Science in Oncology Network. His first NIHR NEAT project K021 'A Real-time Visual Feedback Device for Reducing Patient Movement During Radiotherapy' began in October 2008. In 2009 he began speculative research on medical image structural metrics funded through an EPSRC Feasibility Account award.
Professor Moore is an EU Framework expert assessor and a member of the EPSRC Peer Review college. He is a member of the NCRI Clinical and Translational Radiotherapy (CTRad) Basic Science Work-stream-1. He has over 100 peer reviewed publications and has secured in excess of £1M of grant funding for NWMP investigators in the last 5 years.

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After a PhD in Signal and Image Processing, obtained from Univeristy of Nice-Sophia Antipolis (France), in 2004, for his work on parametric active contours for video and image segmentation, Frédéric PRECIOSO spent a year as Marie-Curie post-doctorat Fellow at CERTH-Informatics and Telematics Institute, in Thessaloniki (Greece), where he worked on semantic evolutionary methods for object extraction and information retrieval. He is associate professor at ENSEA since 2005, member of the ETIS Lab (UMR CNRS 8051) and got the "Habilitation a Diriger des Recherches" on machine learning for multimedia data classification and content-based retrieval in 2010. His current main topics of interest concern video object detection and classification, content-based video indexing and retrieval systems, scalability of such systems. He is coordinator of several French research projects and involved in international research programs. He has participated in the "Engineering and Computational Sciences for Oncology Network (ECSON)" (www.ecson.org) project which involved 10 partners from 5 European countries and funded by the UK's Engineering and Physical Sciences Research Council (EPSRC) and he is currently external partner in "Technology in Radiotherapy Feasibility Studies (TeRaFS)" (www.uclan.ac.uk/terafs), funded by EPSRC, where he works on analysis of complex 3D cytoskeleton structures from fluorescence confocal microscopy images. He is a reviewer for several international journals (*Elsevier Pattern Recognition, IEEE trans. On Image Processing...*) and for several international conferences including ICIP, ISBI, ICPR. He is also associate member of IEEE Technical Committee BISP (2011-2013).